International Seminar:
'Strengthening Agroforestry Programs in Higher Education for Food Security In Sub-Saharan Africa – SAPHE'

Analysis of adaptive genetic variation

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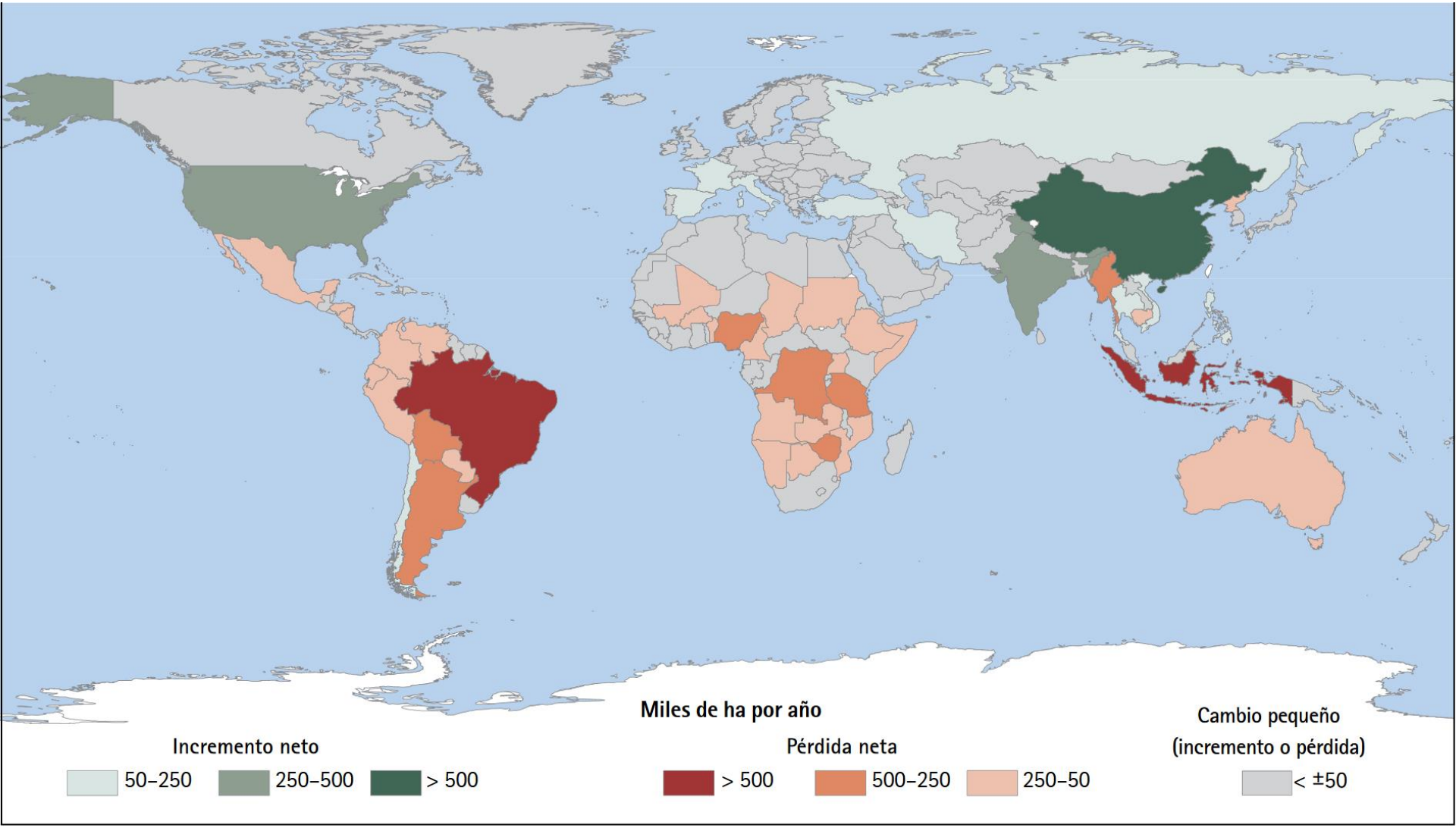
Outline

- Introduction
- What?
- How to?
- Methods and tools
- Examples
- [Practical issues/Discussion…]

Pre-Introduction

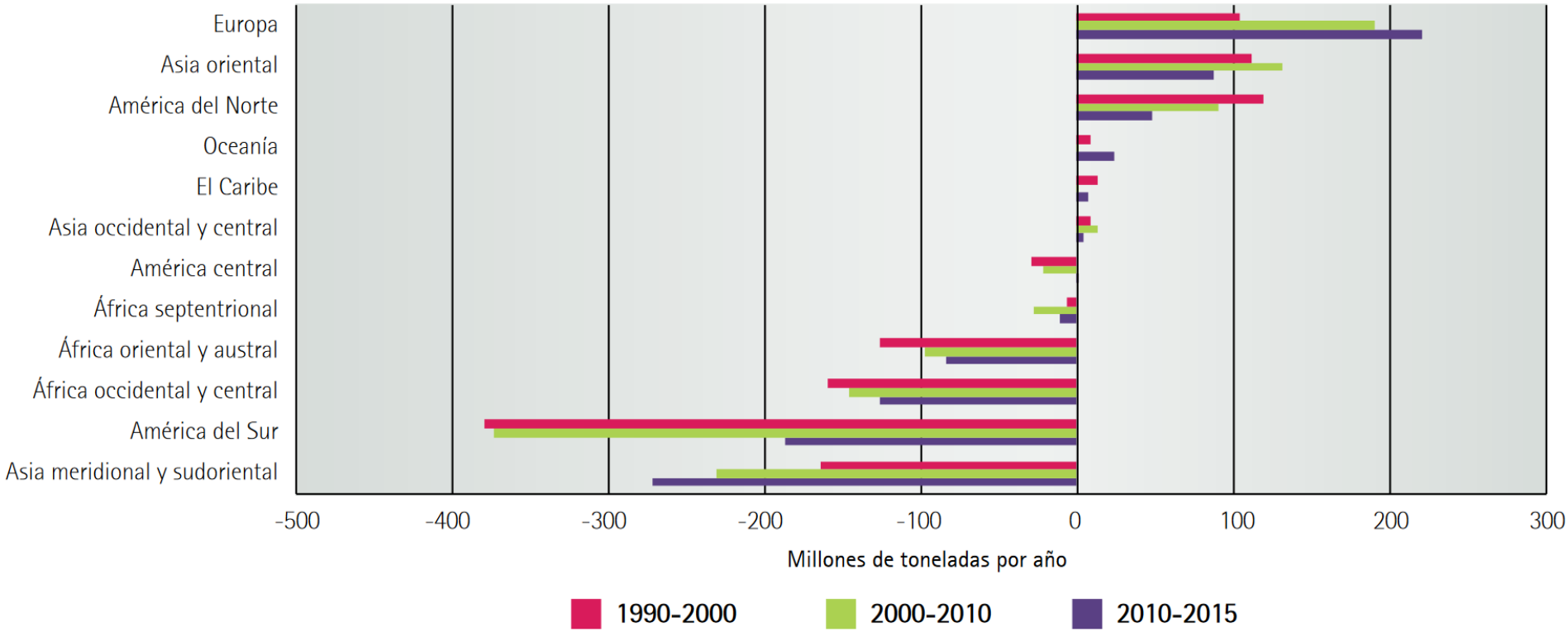
Usefulness
Exportable methodology
Practical cases

Net annual gain/lost 1990-2015



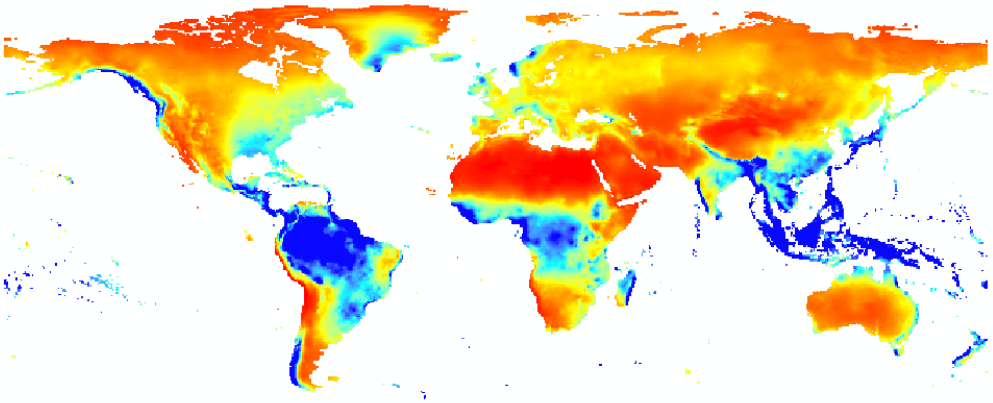
ÁFRICA (58 países y territorios)				
Variable (unidad, año)[a]	**Total**	**Dirección del cambio[b]**	**Cambio anual[b] (%)**	**Disponibilidad de datos[c] (situación/ tendencia)**
Área de bosque (millones de ha, 2015)	624	↓	-0,49	A/A
Bosque natural (millones de ha, 2015)[d]	600	↓	-0,54	A/A
Bosque plantado (millones de ha, 2015)	16	↑	1,34	A/A
Cambio neto anual del bosque (millones de ha, 2010–2015)	-2,8			A/*
Cambio neto anual del bosque natural (millones de ha, 2010–2015)[d]	-3,1			A/*
Cambio neto anual del bosque plantado (millones de ha, 2010–2015)	0,2			A/*
Existencias en formación en los bosques (miles de millones de m^3, 2015)[e]	79	↓	-0,37	A/A
Existencias en formación en los bosques (m^3 por ha, 2015)[e]	128	↑	0,13	A/A
Carbono en la biomasa por encima y por debajo del suelo (Gt, 2015)[e]	60	↓	-0,43	A/A
Carbono en la biomasa por encima y por debajo del suelo (toneladas por ha, 2015)[e]	96	↑	0,07	A/A

During the last 25 years the forest biomass Carbon stock has been reduced 11,1 Gt, It equivalents a reduction of 442 millions of tons at year

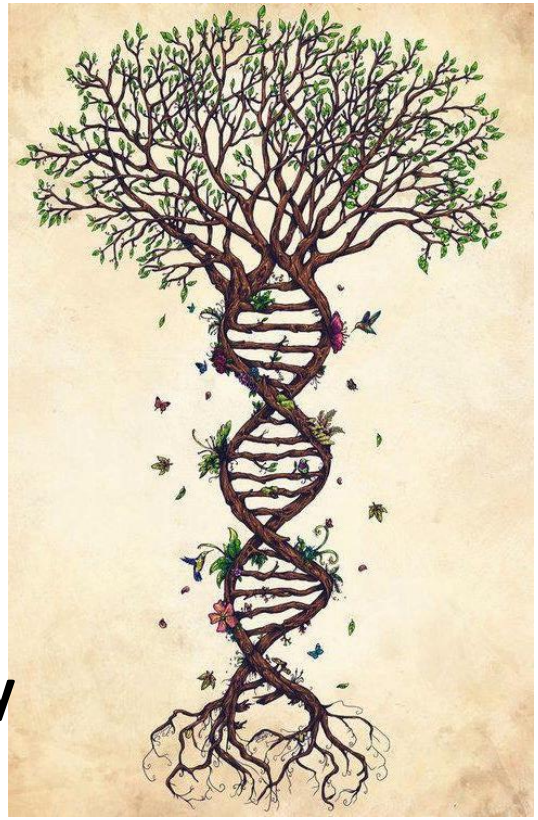


Introduction

Climate dynamics

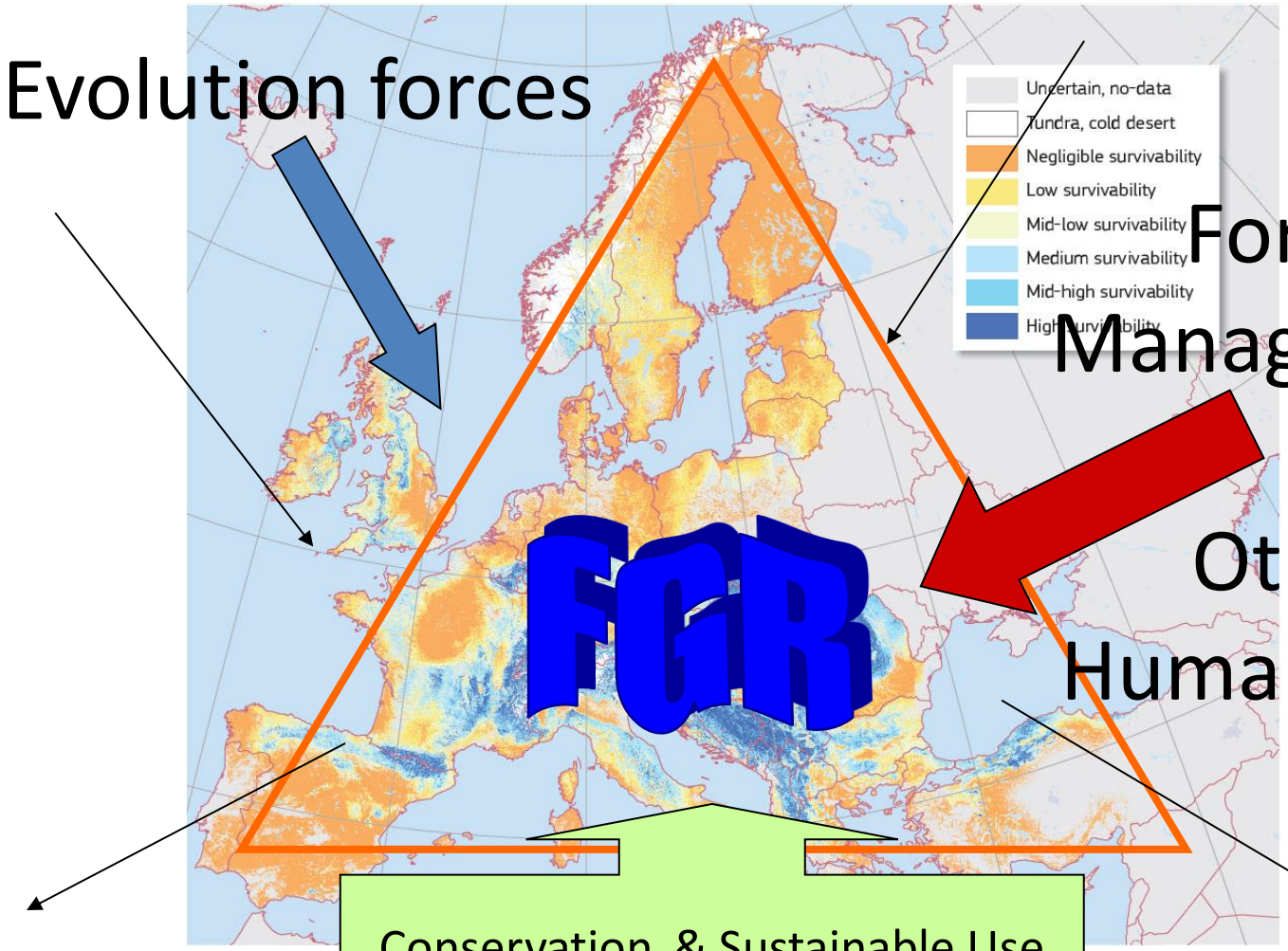


Genetics (adaptation)



Human activity

DIFFERENT TIME SPAN BUT SIMILAR EFFECTS



Genetics: Evolution Forces

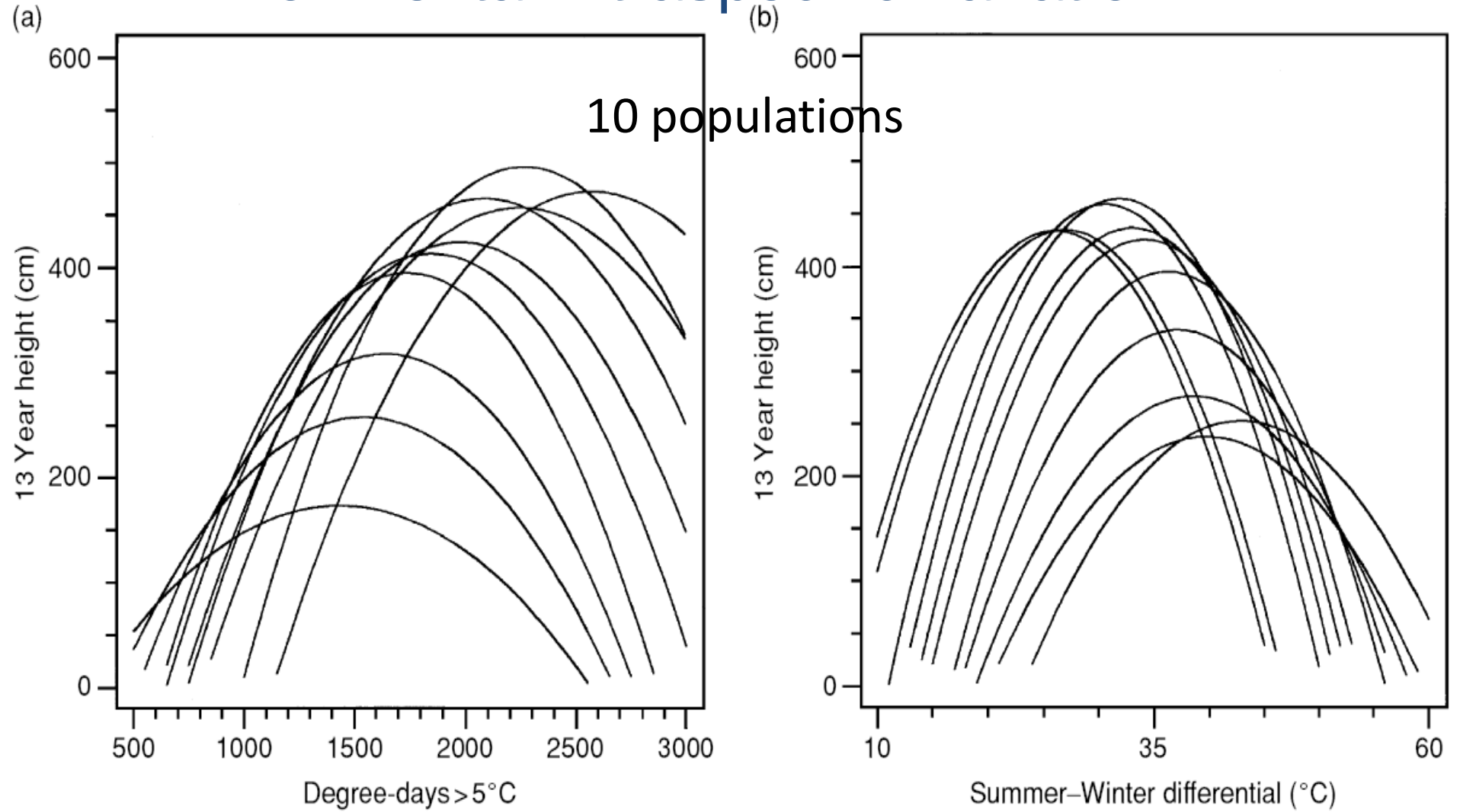
- Genetic drift: non directional / random changes in frequency between generations / small pops.
- Natural Selection: Adaptive changes (fitness, reprod. success)
- Migration: Gen exchange among populations.
- Reproductive Systems Gene recombination in successive generations
- Mutation: Gene changes at molecular level
- "Life's little mysteries" Gene flexibilty (Phen-Plas) Autorganizative , novelties, ….

Genetic diversity

- Existing variation among “populations”
- As consequence of evolution processes & …

- One of the most powerful resource for fighting against global change

Environmental intraspecific Variation



Rehfeldt, G.E., N.M. Tchebakova, Y.I. Parfenova, W.R. Wykoff, N.A. Kouzmina, and L.I. Milyutin. 2002. Intraspecific responses to climate in *Pinus sylvestris*. *Global Change Biology* 8: 1-18.

Adaptive Variation

Contrary to “neutral” variation
Environmental adaptation related traits
Survival
Growth (Low: suboptimal or drought defense)
Water use efficiency

Low economical importance but evolutive/adaptive
Reproductive potential (flowering, mating synchr. ,
seed ripening, etc)

$P=G+E$ $V_p= V_G +V_E = V_A+ V_{NA}+ V_E$

Use for Conservation FGR

"Quantification"

Structure, distribution & patterns of Adapt. variation inter/intra pop.

Variation in metapopulations

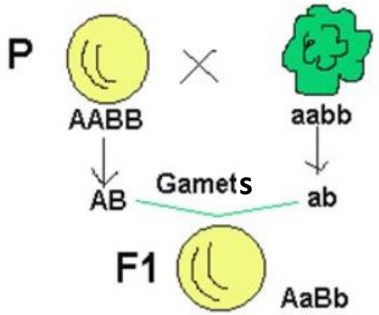
Basic information in reduced N_e populations

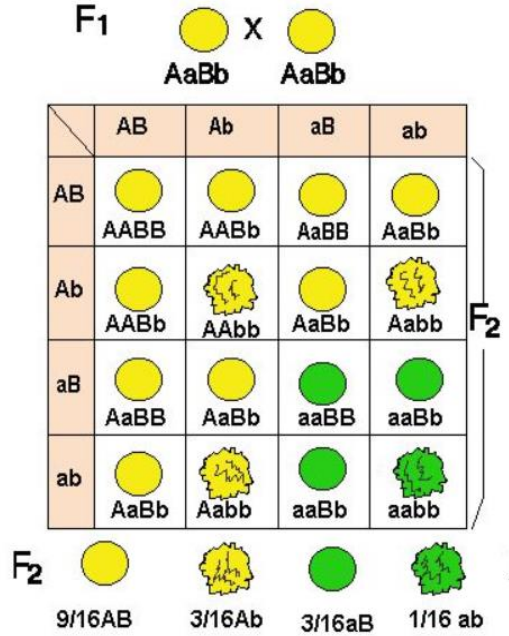
Info about threatening level

.....

Genetic diversity based on neutral markers can NOT substitute direct measurements of quantitative variation in adaptive traits and particularly for forest genetic resources conservation

What





Mendel Laws

X

AAAAAAAA aaaaaaaa

AaAaAaAa

Quantitative Genetics:

NO direct relation phenotype & genotype

Continuous distribution genotypes

What /How to

- Goal
  Tools for addressing analytical problems without fixed laws
- Variability

  - Existence
  - Dealing and understanding (adaptiveness?)
  - Modeling and controlling

experimental error

Kol R Lap R Lyo R Lnh R Val R Total R

Kol A Lap A Lyo A Lnh A Val A Total A

Qst por sitio y año

Inflection point (detail)

Population genetic (above diag) and [illegible] correlations with *n.s. indiv. heritabilities* in diagonal

Standard errors in small numbers

h^2_{indiv}	c		b		m		t10		t90		dur		budset	
c	1.0883				0.6877	0.0162	0.1968	0.0295	0.5238			0.0239	-0.593	0.0
b	-0.[illegible]33	0.0277	0.5428		-0.8924	0.0005	0.515	0.0225	-0.[illegible]		0.0007	-0.9745	0.0015	-0.9988	0.0
m	0.428	0.0250	-0.7906				-0.407		0.9639		0.0022	0.9402	0.0036	0.9854	0.0
t10	0.4238	0.0252	0.228						-0.6357		0.0183	-0.6938	0.0159	-0.5563	0.0
t90	0.2338	0.0290	-0.8971						0.7054	0.1472	0.997	0.0002	0.9951	0.0
dur	0.1535	0.0299	-0.89						0.9874	0.0008	0.8379	0.0952	0.9844	0.0
budset	0.241	0.0289	-0.8655						-0.8183	0.8142	-0.810			0.

pop repeat h2 (h2 fam) Qst pop Qst fam

c htot h m t10 t90 dur b

ara94 ara95 ara99 cur94 cur95 nav94 nav95 global

P														
rep				0154	0.9410	0.0393	0.8548	0.0879	0.					82
Qst					0.5232				0.[illegible]					5

**Fami[illegible]l (below di[illegible]s with *n.s. family*

Standa[illegible]

h^2_{fam}	c		b		m		t10		t90		dur		budset	
c	0.9182	0.0150	-0.1037	0.0303	0.1831	0.0296	0.5324						0.0727	0.0
b	-0.2723	0.0284	0.8469	0.0264	-0.778	0.0121	0.0798						-0.7072	0.0
m	0.434	0.0249	-0.5731	0.0206	0.8265	0.0295	0.299						0.6319	0.0
t10	0.[illegible]	0.0235	0.0028	0.0307	0.6048	0.0194	0.8952						-0.0783	0.0
t90	0.[illegible]	0.0290	-0.7167	0.0149	0.8601	0.0080	0.1138						0.6838	0.0
dur	0.1161	0.0302	-0.7165	0.0149	0.7157	0.0150	-0.1234						0.653	0.0
bds	0.1288		0.467		0.345	0.0270	0.0727						0.9046	0.
	0.1620		0.1369		0.1308		0.1364		0.1421		0.1471		0.1361	

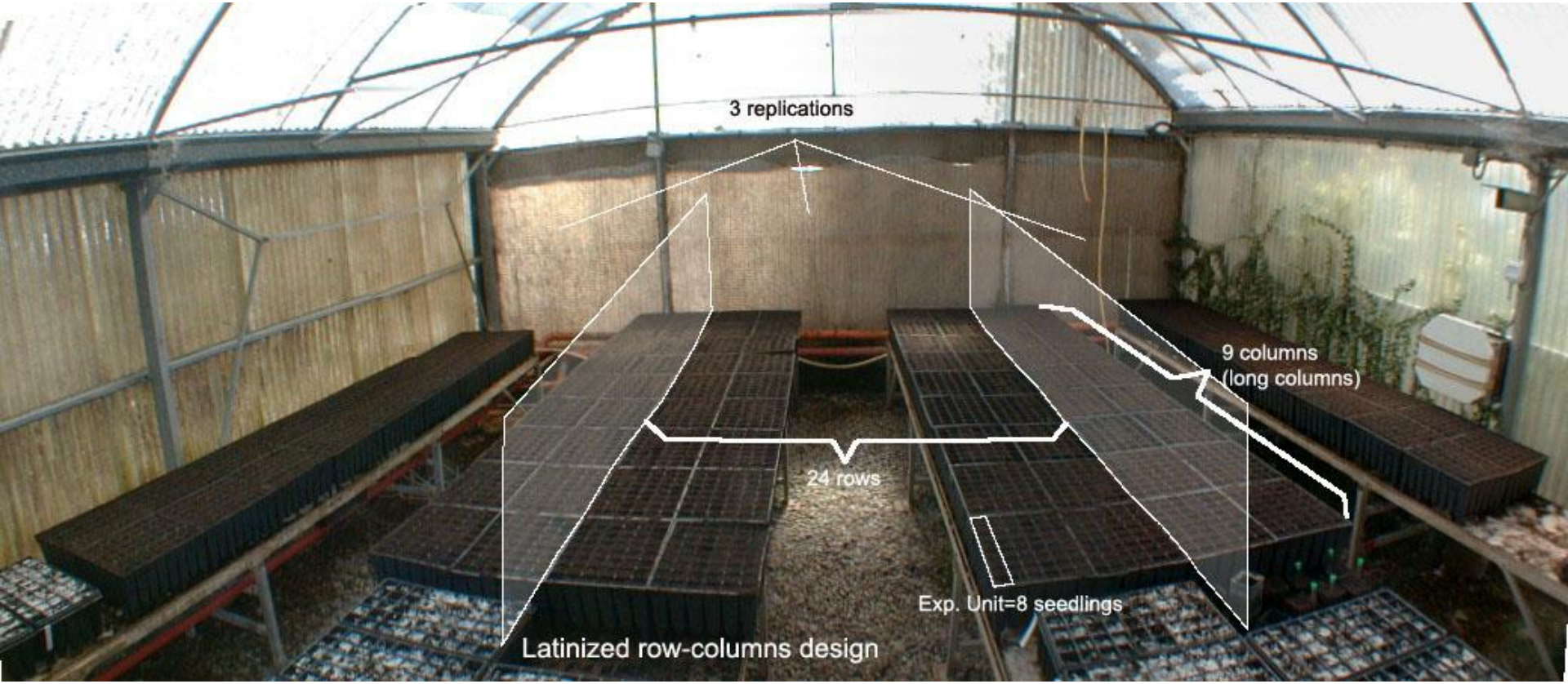
Provenance Trials

Progeny test

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

Mixed model REML BLUP & BLUE

Layout designs



Provenance Trials

$$Q_{st} = \frac{\sigma^2_{between}}{\sigma^2_{between} + 2\sigma^2_{inside}} = \frac{\sigma^2_{prov} + \sum_i \frac{\sigma^2_{provx\,\alpha_i}}{n_i}}{\left(\sigma^2_{prov} + \sum_i \frac{\sigma^2_{provx\,\alpha_i}}{n_i}\right) + 2h^2\sigma^2_{error}}$$

$$r^2_{pop} = \frac{\sigma^2_{pop}}{\sigma^2_{pop} + \frac{\sigma^2_{colum}}{b.r/f} + \frac{\sigma^2_{block}}{b/p} + \frac{\sigma^2_e}{p.n}}$$

$$h^2_{fam} = \frac{\sigma^2_{fam}}{\sigma^2_{fam} + \frac{\sigma^2_{colum}}{b.r} + \frac{\sigma^2_{block}}{c} + \frac{\sigma^2_e}{f.n}}$$

$$h^2_{indiv} = \frac{4(or\,3)x\sigma^2_{fam}}{\sigma^2_{fam} + \sigma^2_{colum} + \sigma^2_{block} + \sigma^2_e}$$

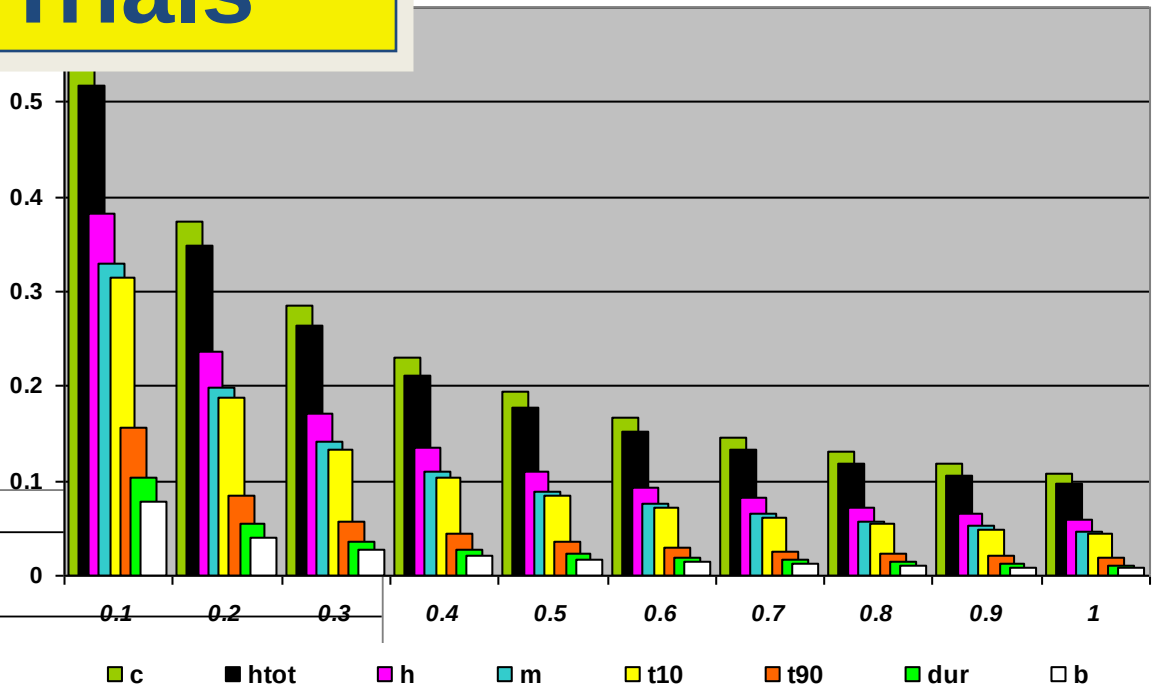
Progeny Trials

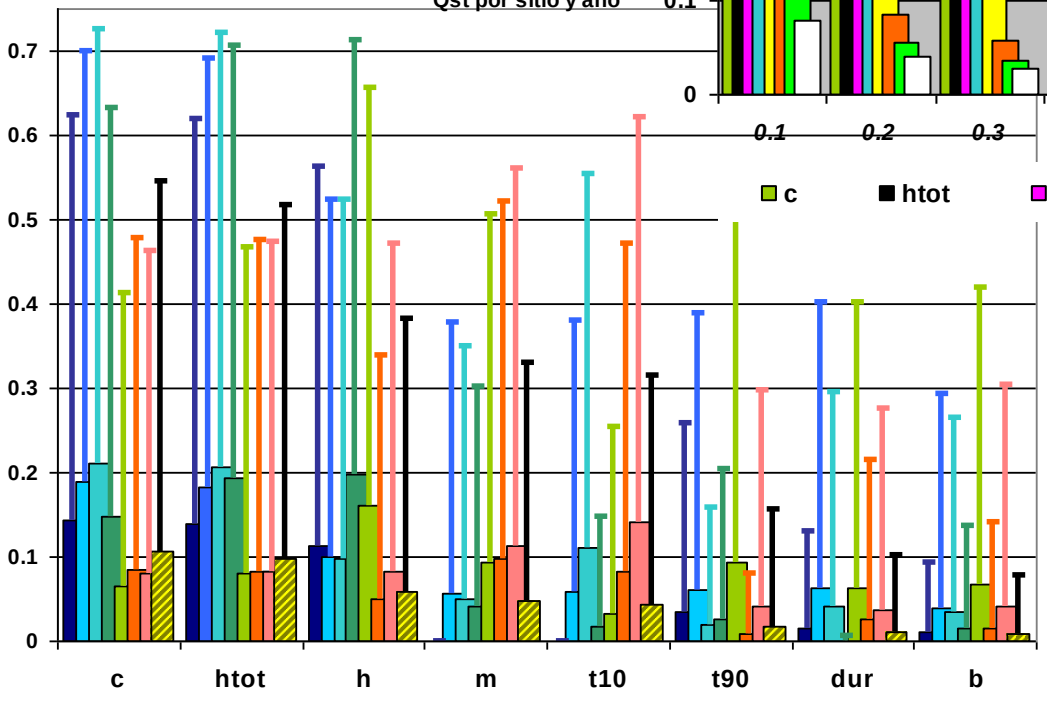
$$Q_{st}\,pop = \frac{\sigma^2_{pop}}{\sigma^2_{pop} + 2(4\sigma^2_{fam})}$$

$$Q_{st}\,fam = \frac{\sigma^2_{fam}}{\sigma^2_{fam} + 2(h^2_{indiv}.\sigma^2_e)}$$

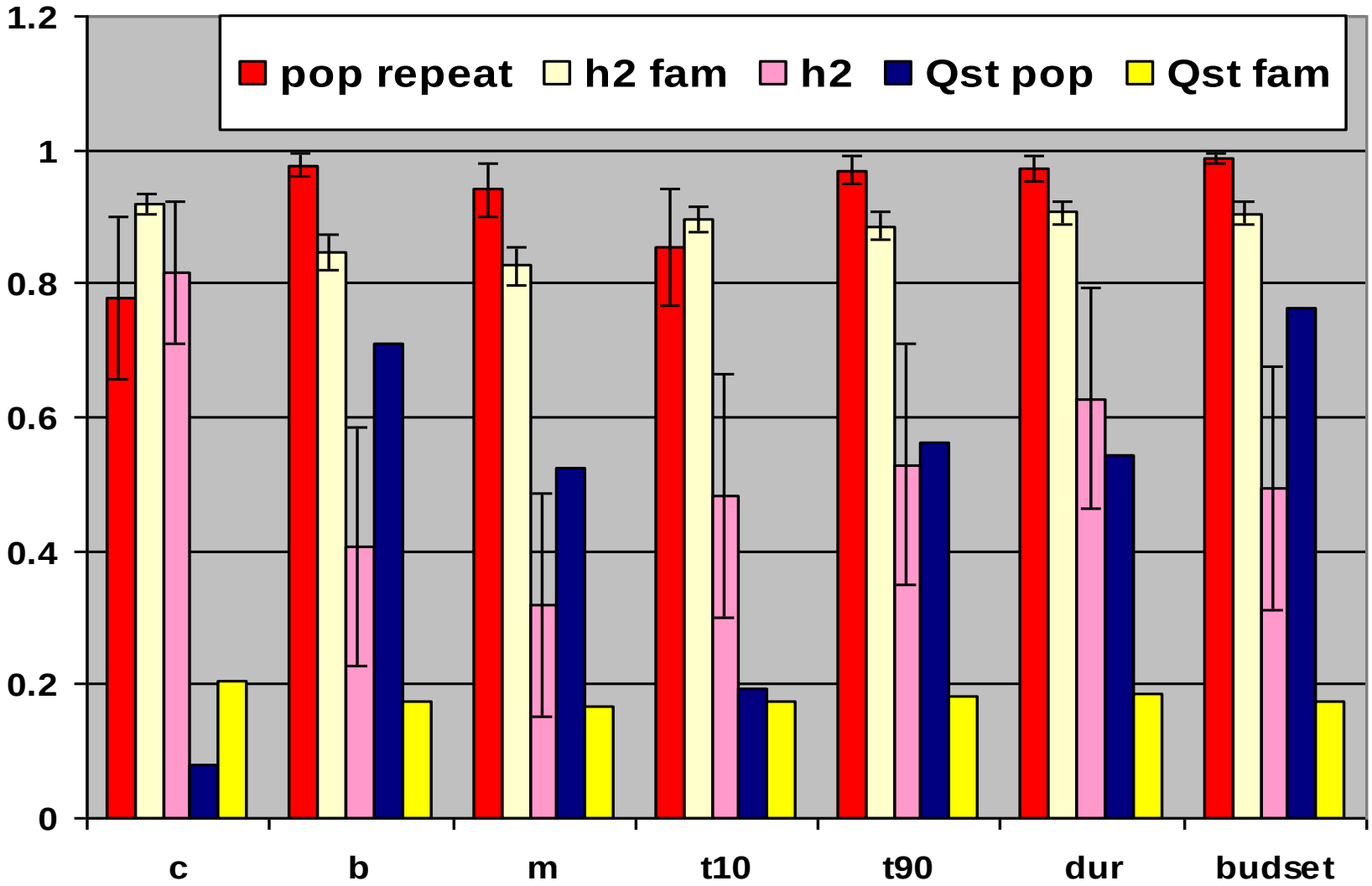
Provenance Trials

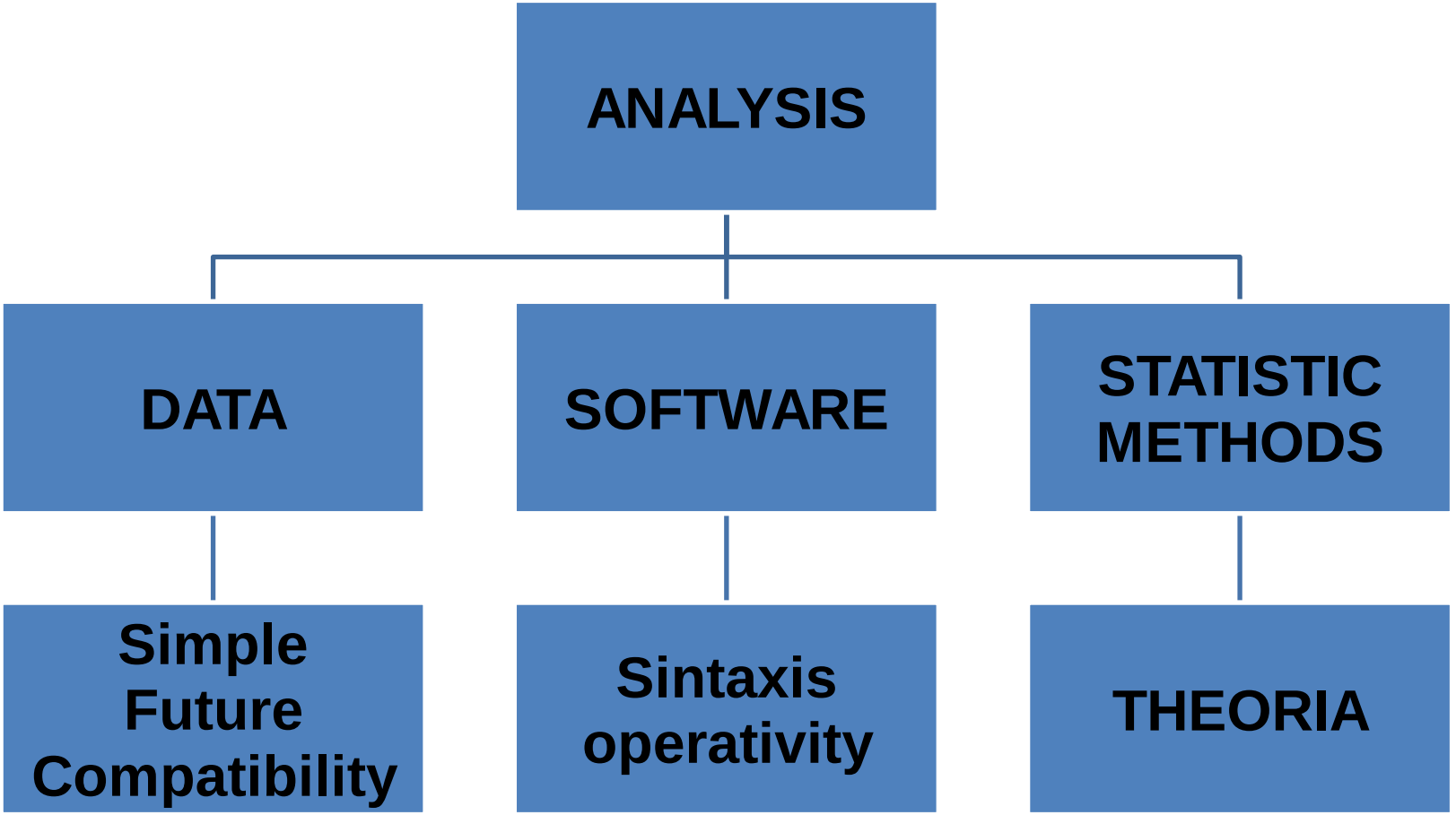
Q_{st}





Progeny Trials




ANALYSIS
DATA
SOFTWARE
STATISTIC METHODS
Simple Future Compatibility
Sintaxis operativity
THEORIA

How to

Genetic evaluation

- Design and Analysis of experiments
  - Basic Principles
  - Conventional and current (IB) designs
  - Software

How to

Genetic evaluation

- Adaptive variation
  - Trials (Spp /prov /prog /clon)
  - Conservation Utility

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. Replicatio**n**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

“typical numbers & expressions”

4 replications

25 plants per plot

randomization

4 treatments

2 border lines

latinization

3 sites

RCB

25 genotypes

5 x 5 m spacing

single tree plot

Principles (ii)

Operational Limiting factors

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

Experimental design

Initial assumptions or constraints:

Additivity
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

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

Model y = treat;

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

Model y = treat blq;

Experimental design

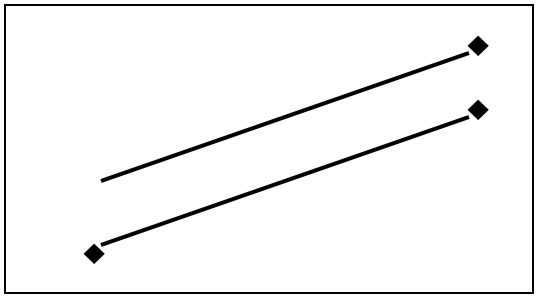
Possible structure of treatments

Factorial: total combination all x all

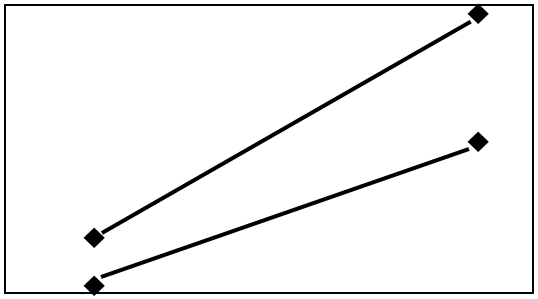
Possibility interactions study (GxE)

Reaction norms

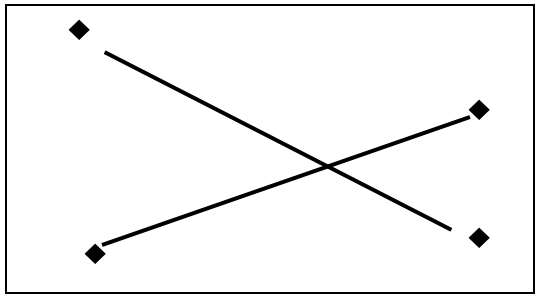
$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \varepsilon_{ijk}$$



No interaction



quantitative interaction



qualitative interaction

Experimental design

Possible structure of treatments

Hierarquical or nested: Impossible combination

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

Model: y = pop fam(pop);

Is it important the treatment structure ?

F E.M.S.

other structure + important.....

¿Fixed o Random?

F E.M.S.

1. Critical 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 possible.
Results & conclusions from anova can be extrapolated + level
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			

$\sigma^2_e + c_1 \Phi_\alpha$

$\sigma^2_e + n \sigma^2_{ab} + nb \sigma^2_a$

¿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 → Software

¿Fixed o Random?

GLM

Model y =loc blq(loc) var var*loc;
Random loc blq(loc) var*loc /test;

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

MIXED MODELS

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

Additivity: $B\text{-}C = (B\text{-}C)_3$

$= (B\text{-}A)_1 - (C\text{-}A)_2$

Experimental error independent of treatment

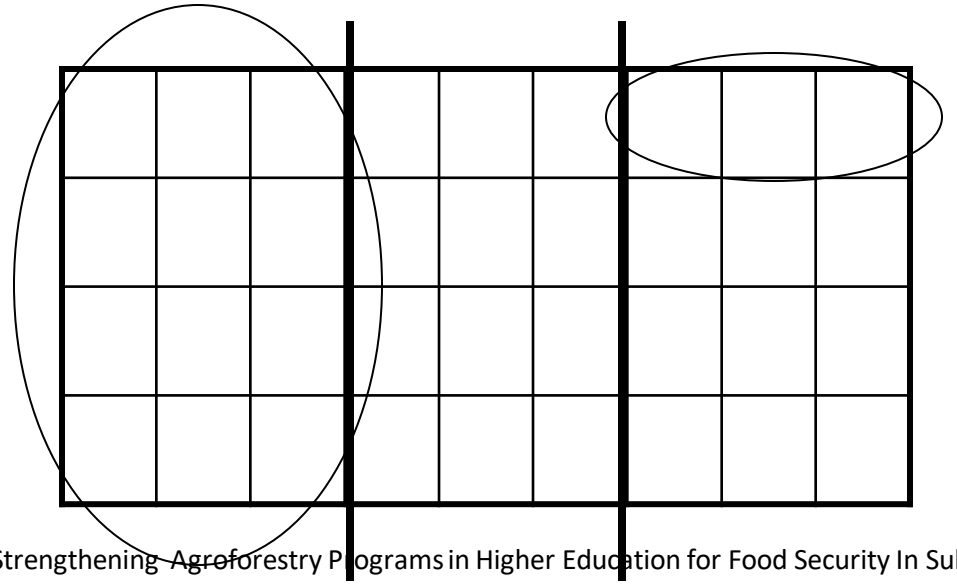
Incomplete Blocks

- 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

I.B. design Efficiency

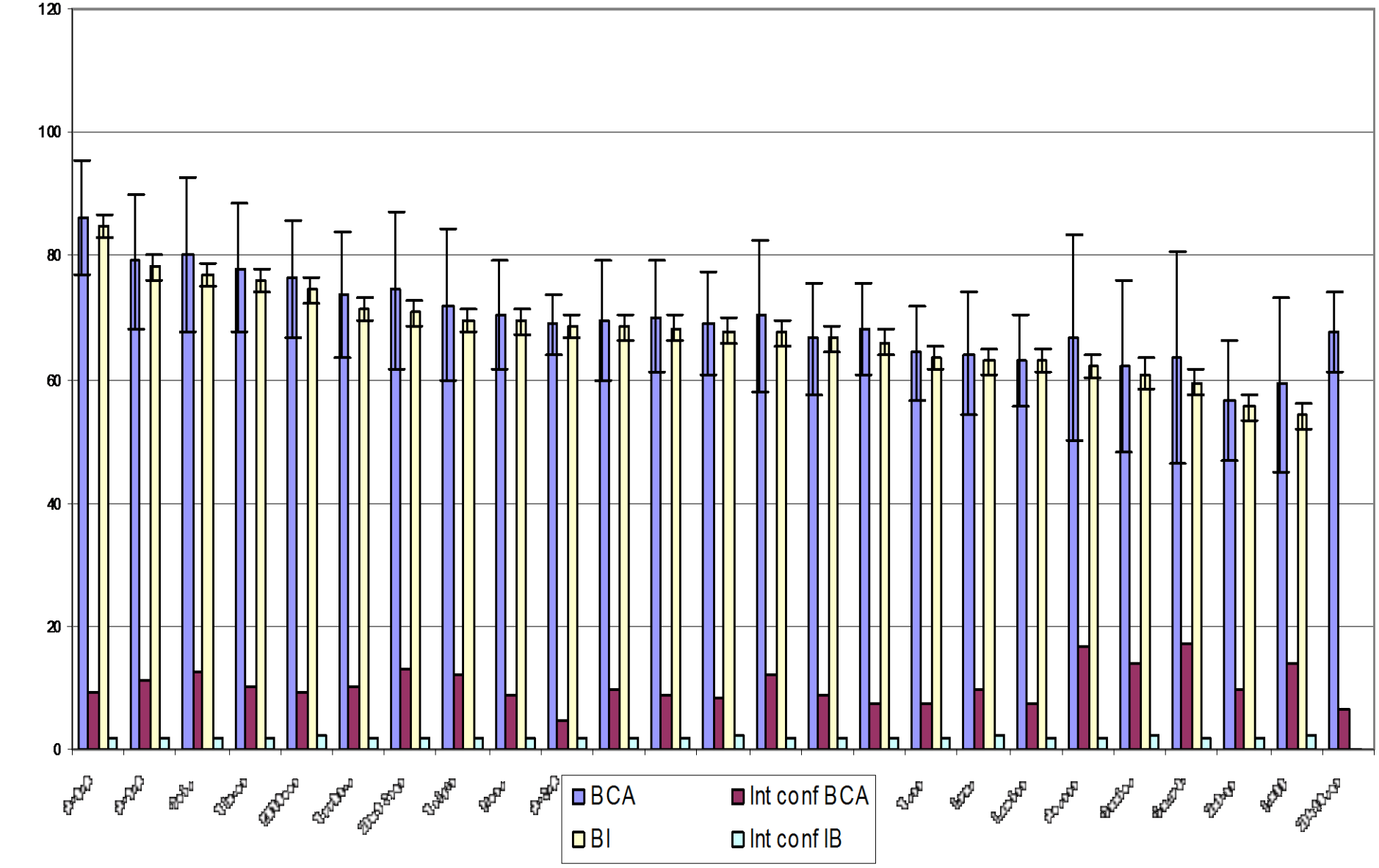
Objective: To compare genotypes highest accuracy

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

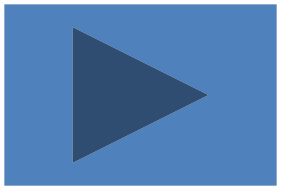
$$\frac{\sqrt{\left(\frac{2\sigma^2}{r}\right)}}{\sqrt{\left(\frac{2\sigma^2}{rxE}\right)}}^2 = E$$

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

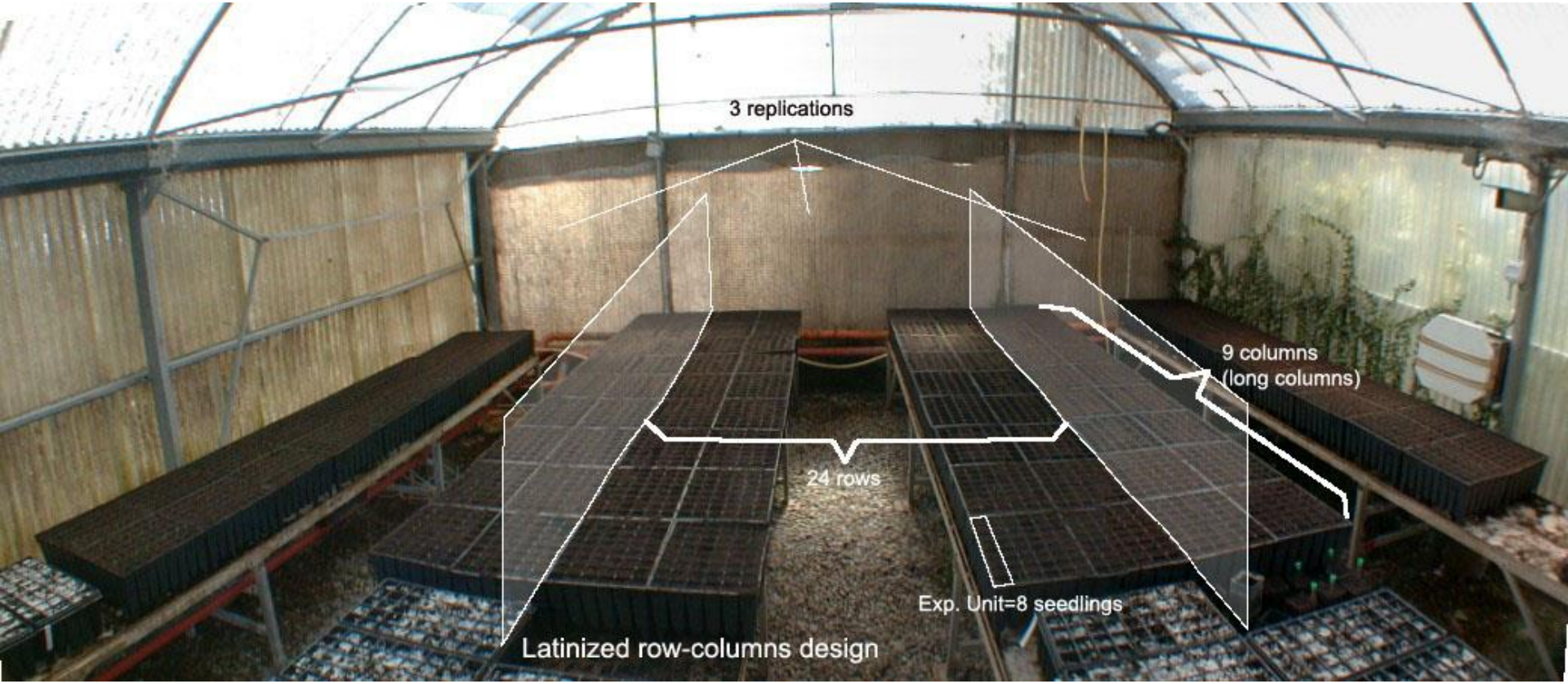
"Efficiency" ~ costs

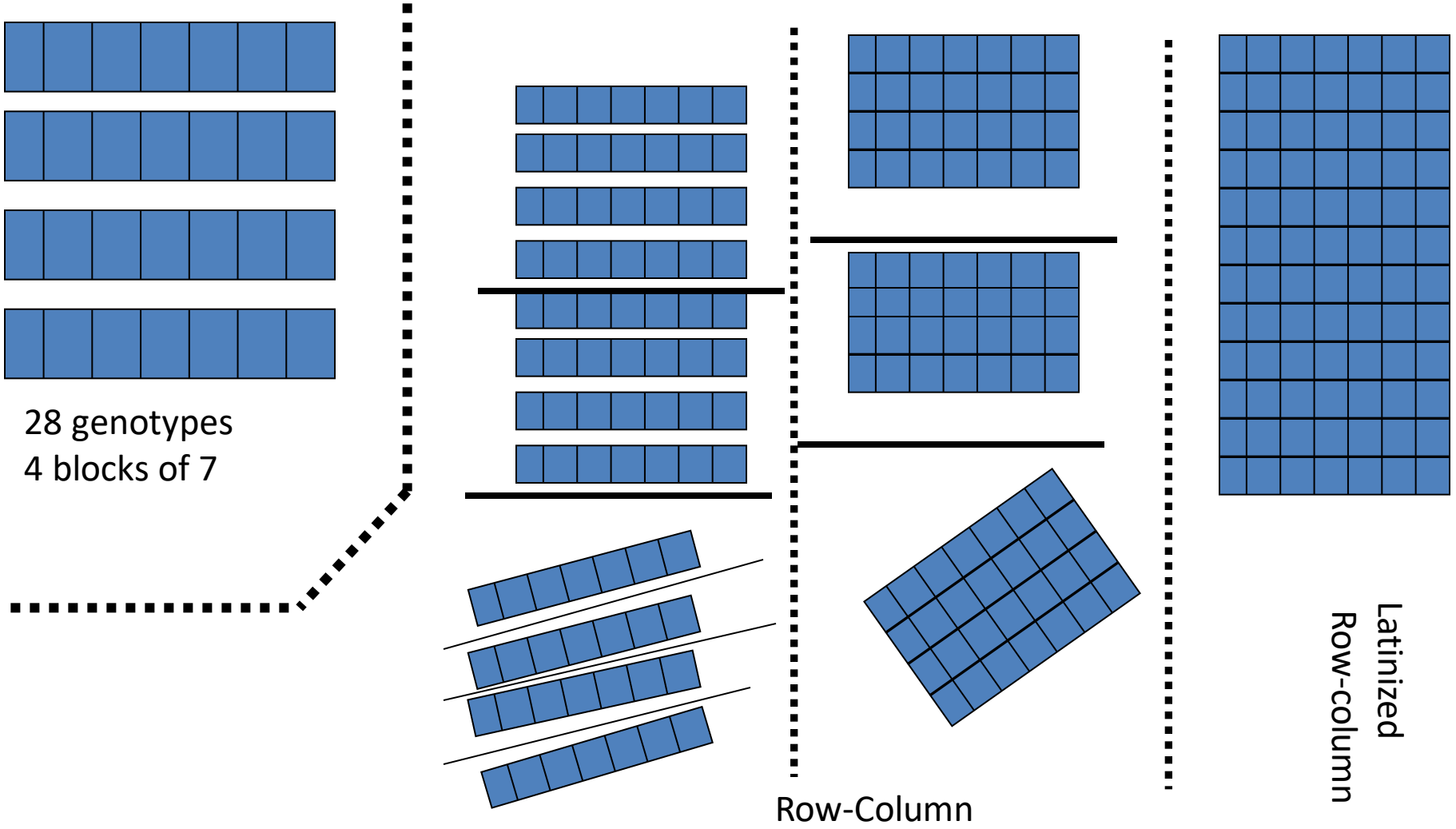

120
100
80
60
40
20
0
BCA
Int conf BCA
BI
Int conf IB

For simple and RCB AZARsXXI.exe



Layout software: CyCDesigN




28 genotypes
4 blocks of 7
3 rep α-lattice
Row-Column
Latinized
Row-column

http://www.vsni.co.uk/software/cycdesign/

VSNi

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CycDesigN

Search

CycDesigN is a computer package for the generation of optimal or near-optimal experimental designs. It comprises three modules: **CycDesigN** is a computer package fc
It provides the most comprehensive design generati
involved in field, glasshouse and laboratory trials.

The designs include cyclic, alpha and factorial desigr
designs, t-latinized and partially-latinized designs as
a result, the algorithms incorporate the most recent
CycXover is a sub-system, generates optimal or neai
crossover experiment involves the application of sec
periods.

The observations made on each subject at the end o
applied in the current period, and the carry-over effe
designs are also known as change-over or carry-ove
your output from a CycDesigN or CycXOver session i
generate either GenStat or SAS code for the analysis
CycAnalysis manual. So CycDesigN's focus is on the
treatments, as in variety trials.

In contrast, GenStat concentrates on the more tradit
and strip plots, criss-cross designs, Latin and Graeco
designs. CycDesigN is written in Visual C++ and runs

Current users can download it here.

Commercial | Academic | Not-for-profit

Windows

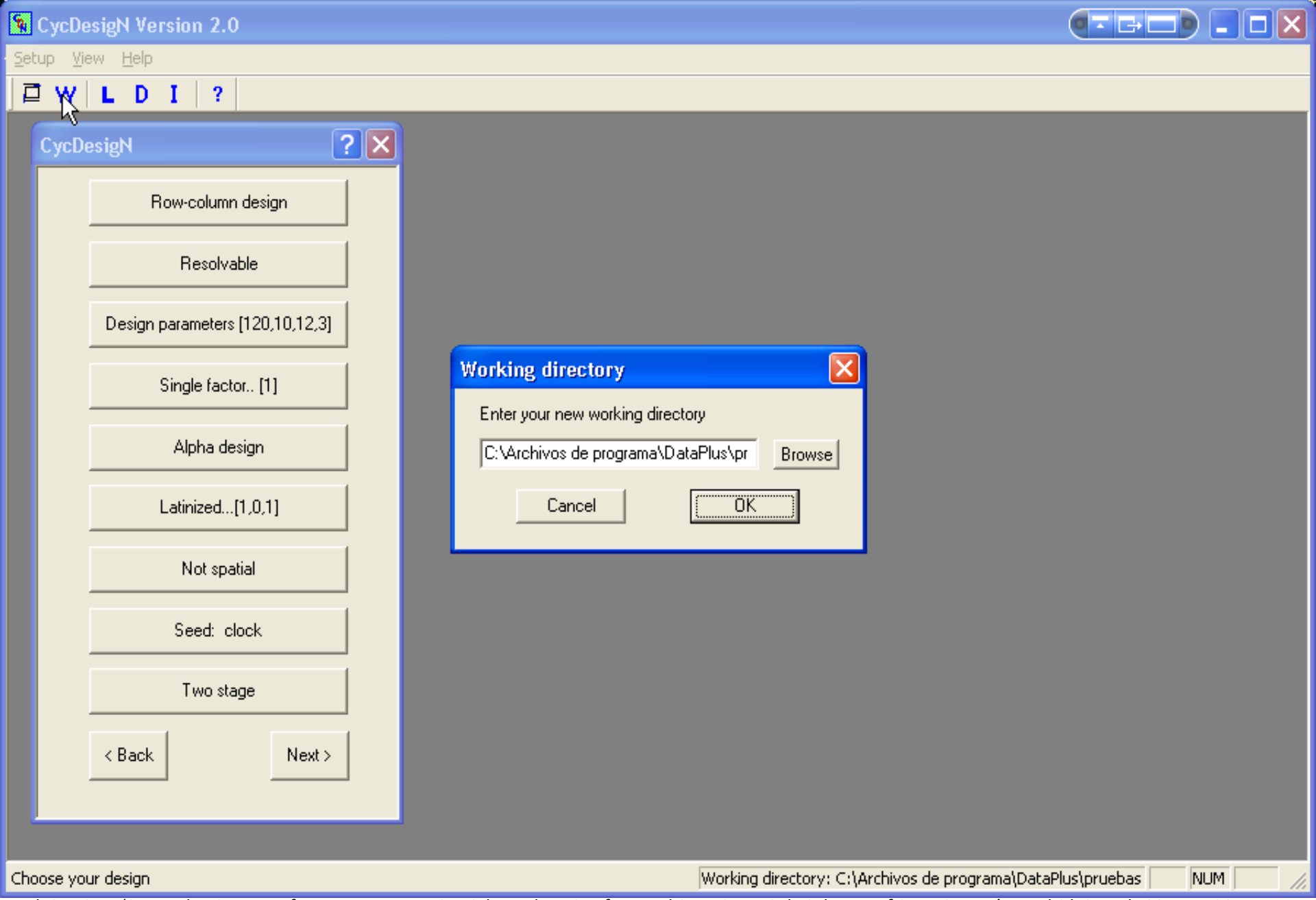
Genstat Commercial for Windows	msanova Commercial for Windows	ASReml 4 Commercial for Windows	CycDesigN Commercial for Windows	ASReml-R 3 Commercial for Windows
£1,028.00	£768.00	£780.00	£240.00	£780.00
Select	Select	Select	Select	Select

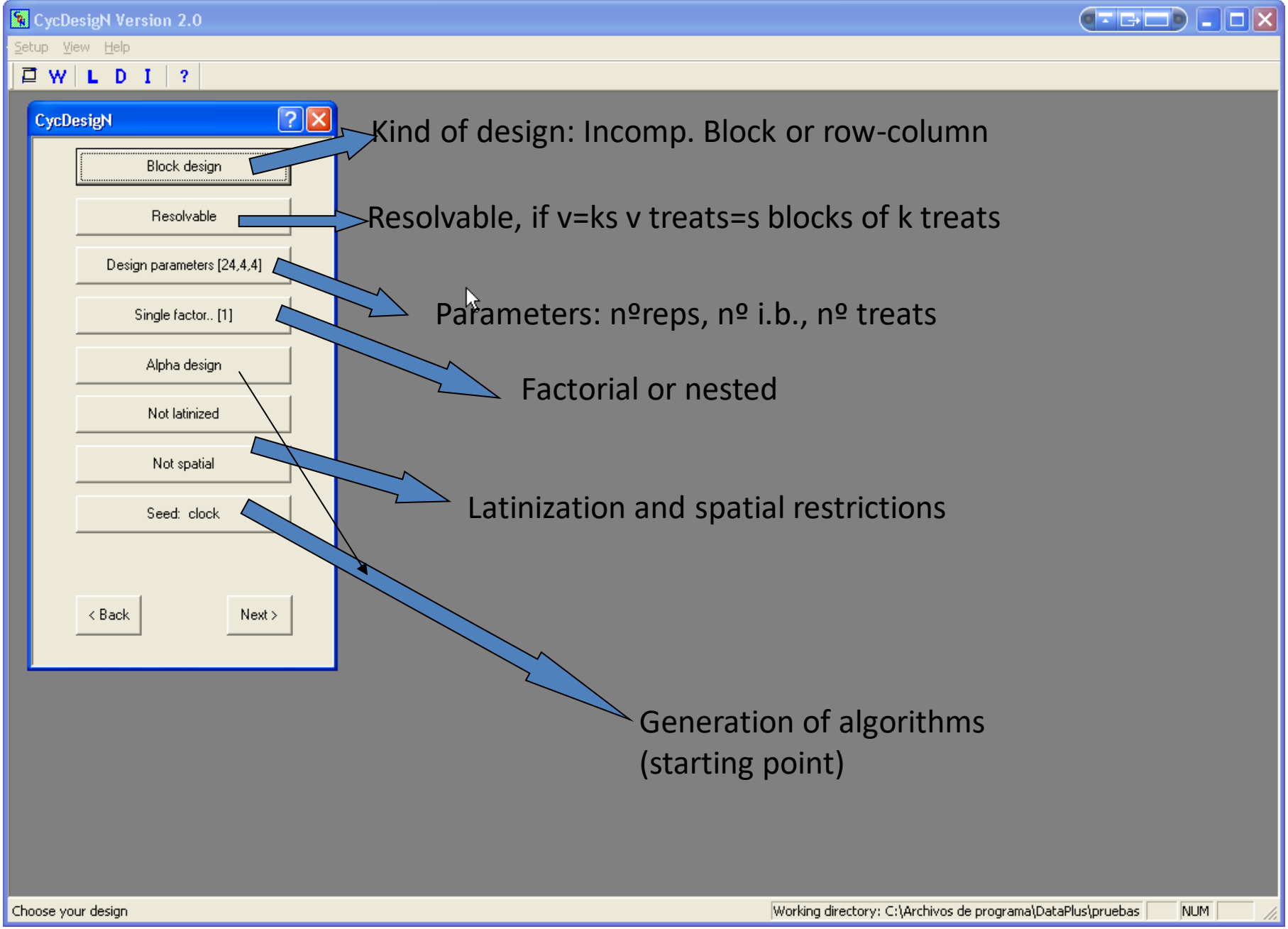
CSIRO Forestry and Forest Products
Canberra
Australia

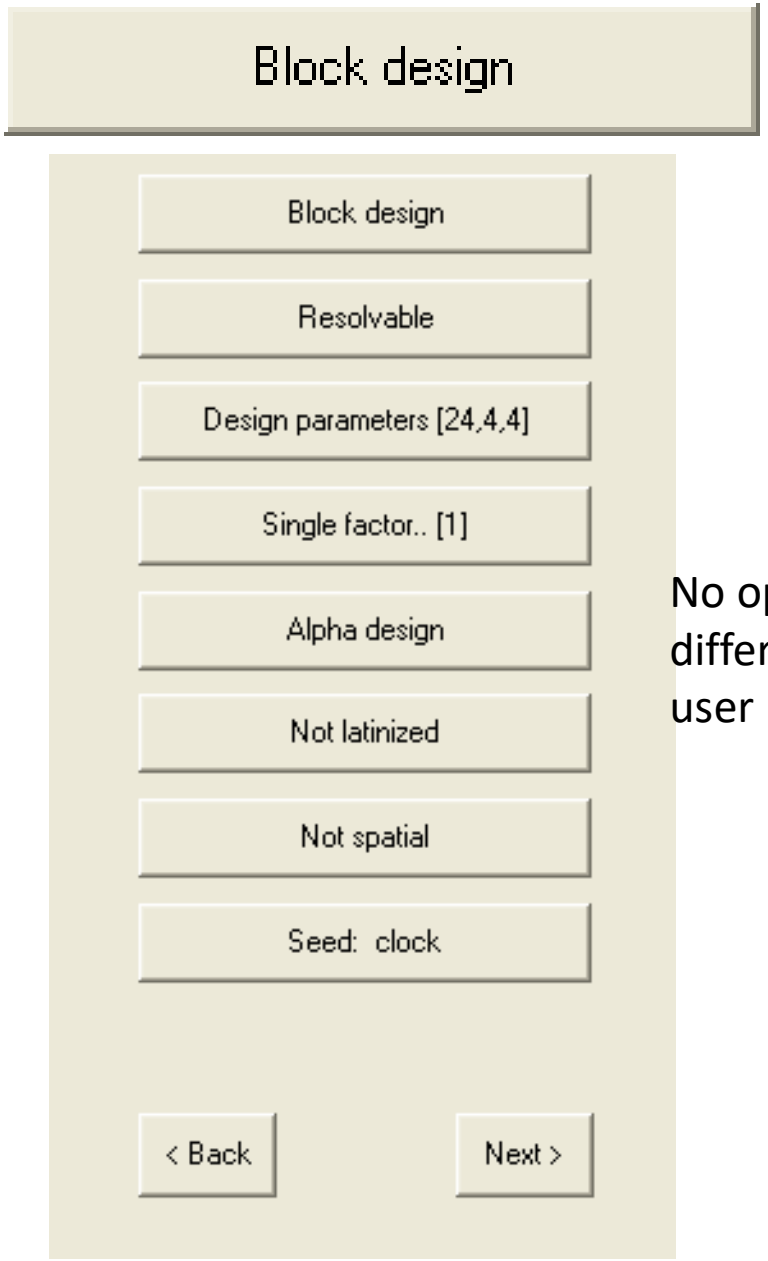
The University of Waikato
Hamilton
New Zealand

CycDesigN

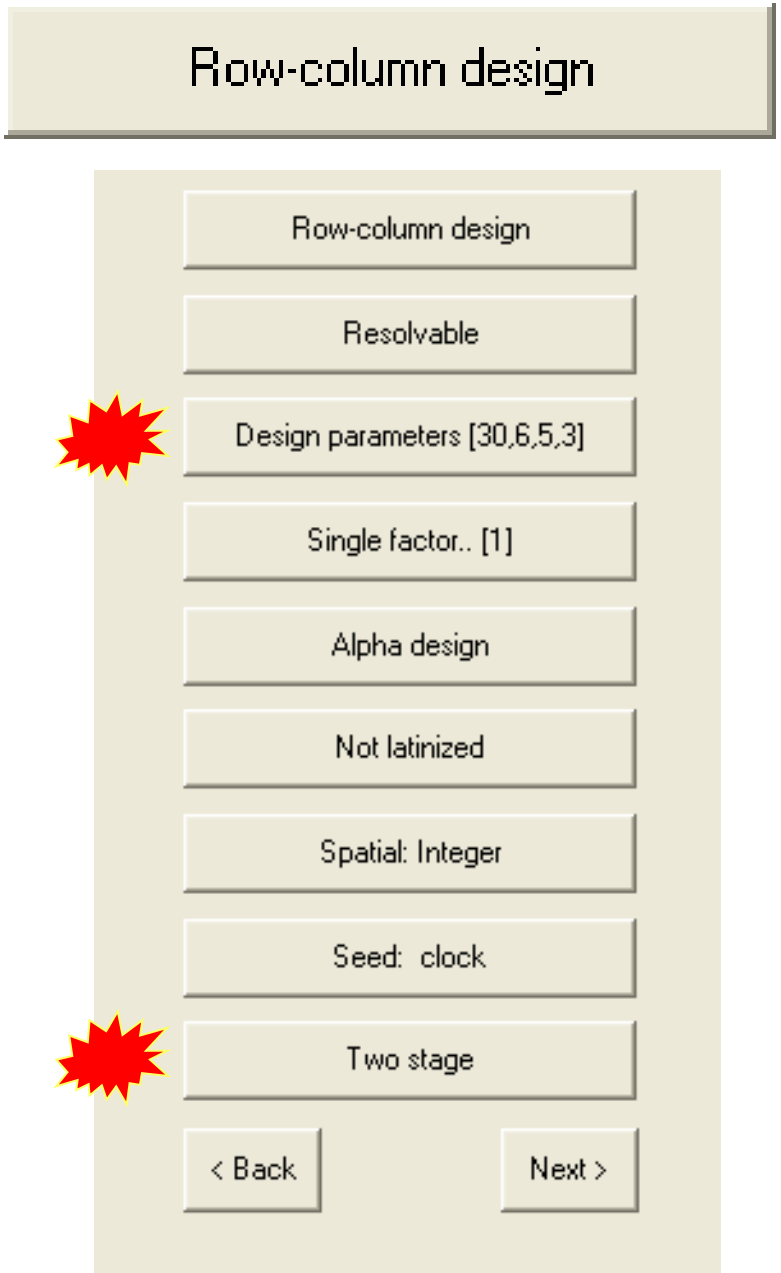
Version 2.0


CycDesigN Version 2.0
Setup View Help
W L D I ?
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
Choose your design
Working directory: C:\Archivos de programa\DataPlus\pruebas
NUM


CycDesigN Version 2.0
Setup View Help
W L D I ?
CycDesigN
Block design
Resolvable
Design parameters [24,4,4]
Single factor.. [1]
Alpha design
Not latinized
Not spatial
Seed: clock
< Back
Next >
Kind of design: Incomp. Block or row-column
Resolvable, if v=ks v treats=s blocks of k treats
Parameters: nºreps, nº i.b., nº treats
Factorial or nested
Latinization and spatial restrictions
Generation of algorithms
(starting point)
Choose your design
Working directory: C:\Archivos de programa\DataPlus\pruebas
NUM

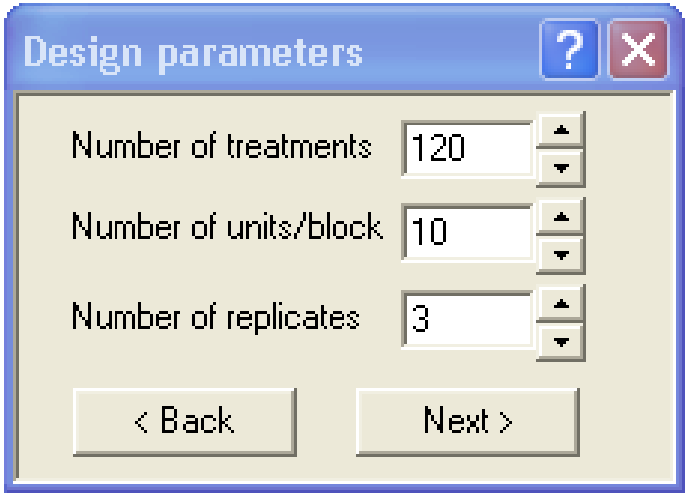


No operative differences for user

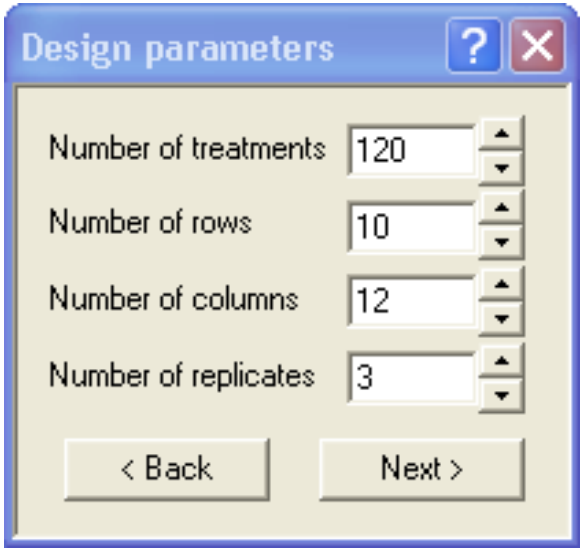


Design parameters [120,10,3]

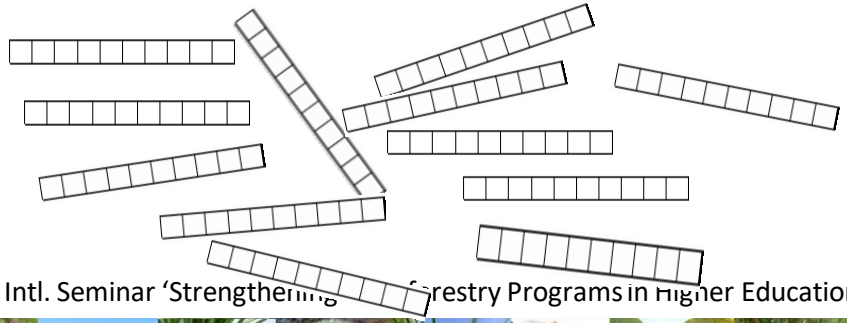
Block design



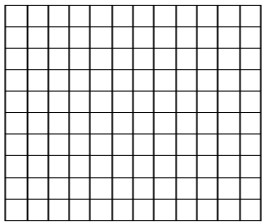
Row-column design



12 I.B. of 10 treat.

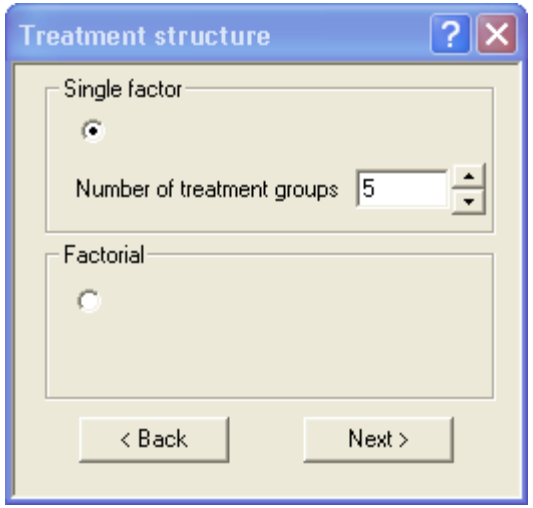


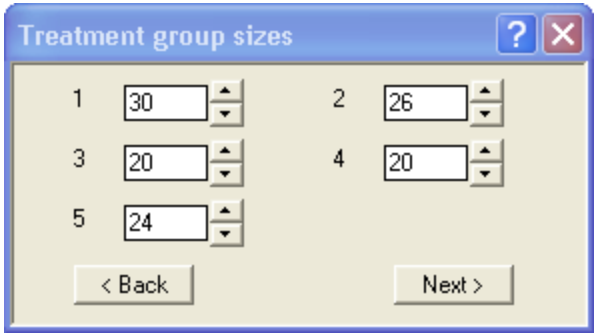
1 REP



Single factor.. [5]

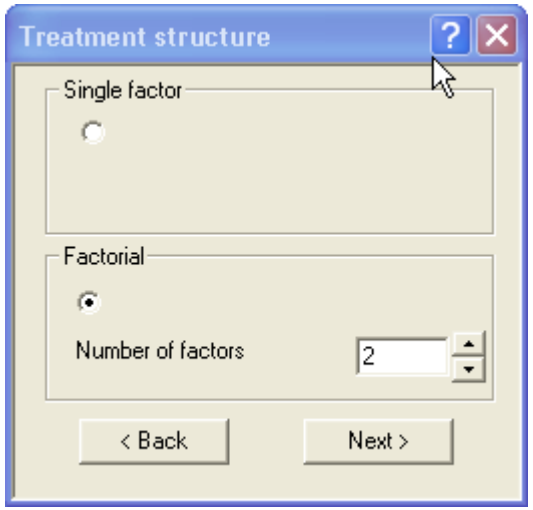
NESTED
5 POPULATIONS:
30, 20, 24, 26 y 20
Families respectiv.

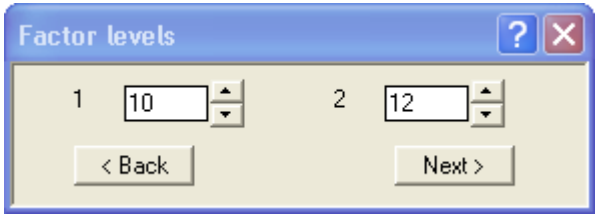


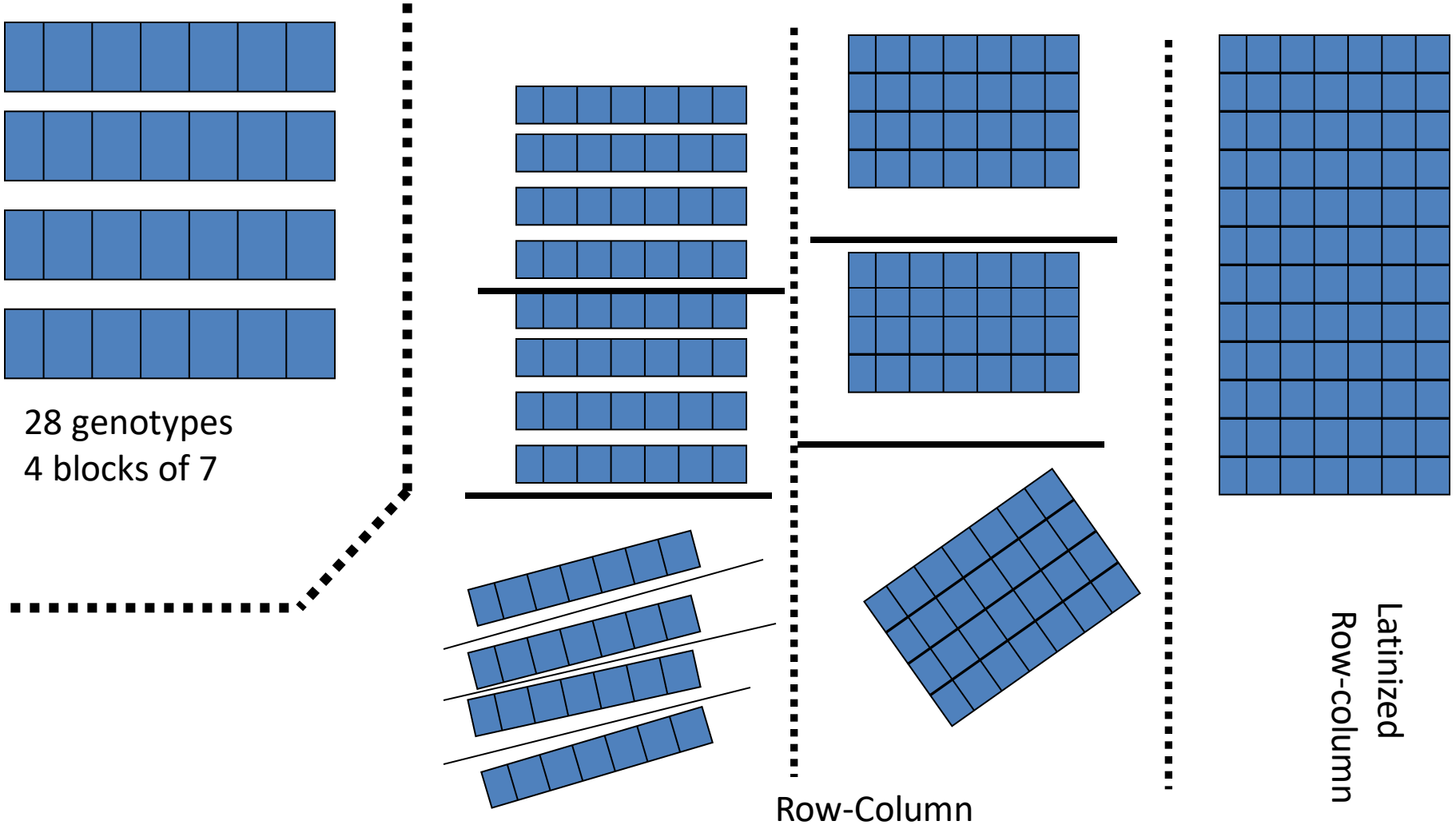


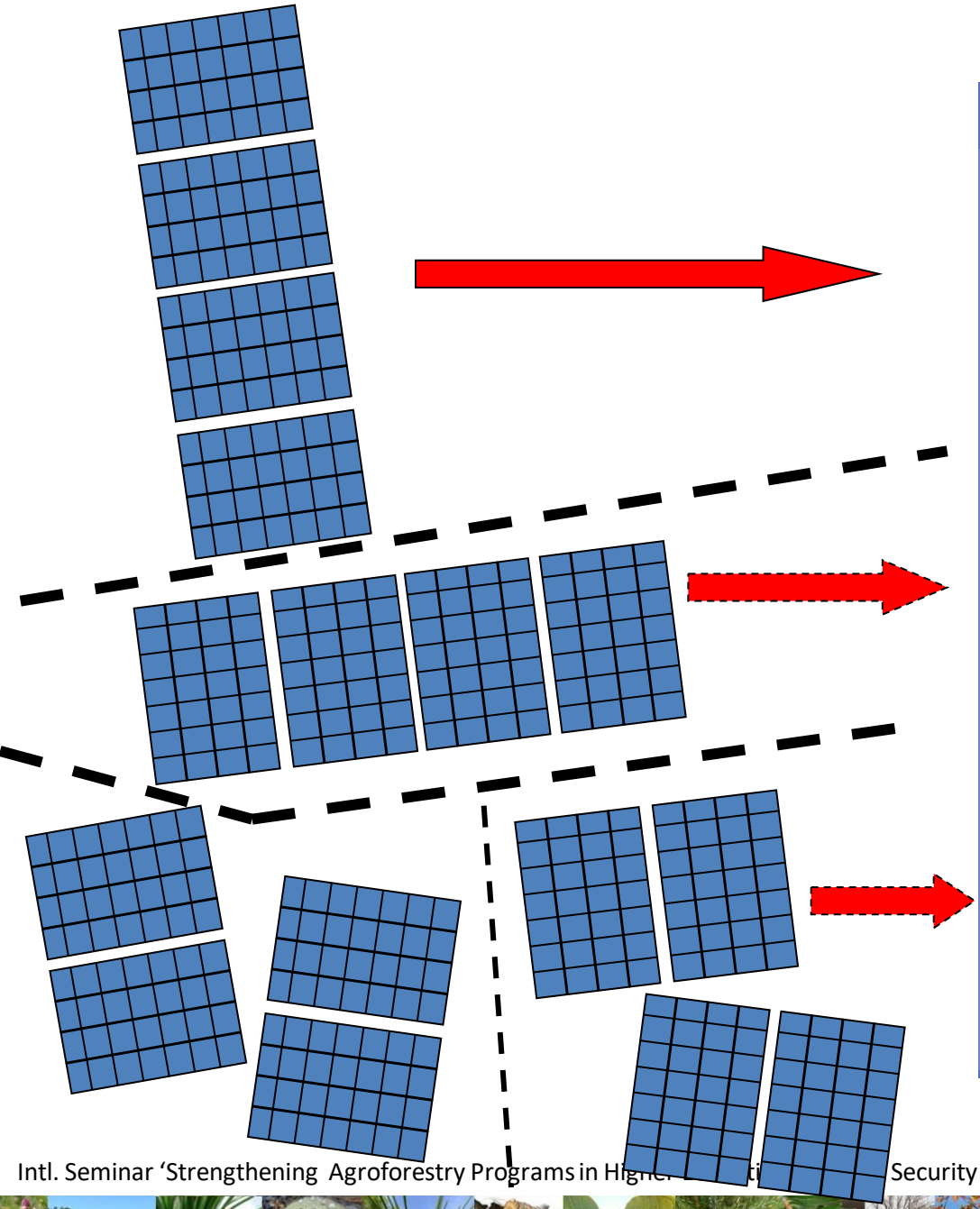
FACTORIAL:

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






28 genotypes
4 blocks of 7
3 rep α-lattice
Row-Column
Latinized
Row-column



Latinized design

Columns

Not latinized

Latinized

Number of contiguous columns 1

Rows

Not latinized

Latinized

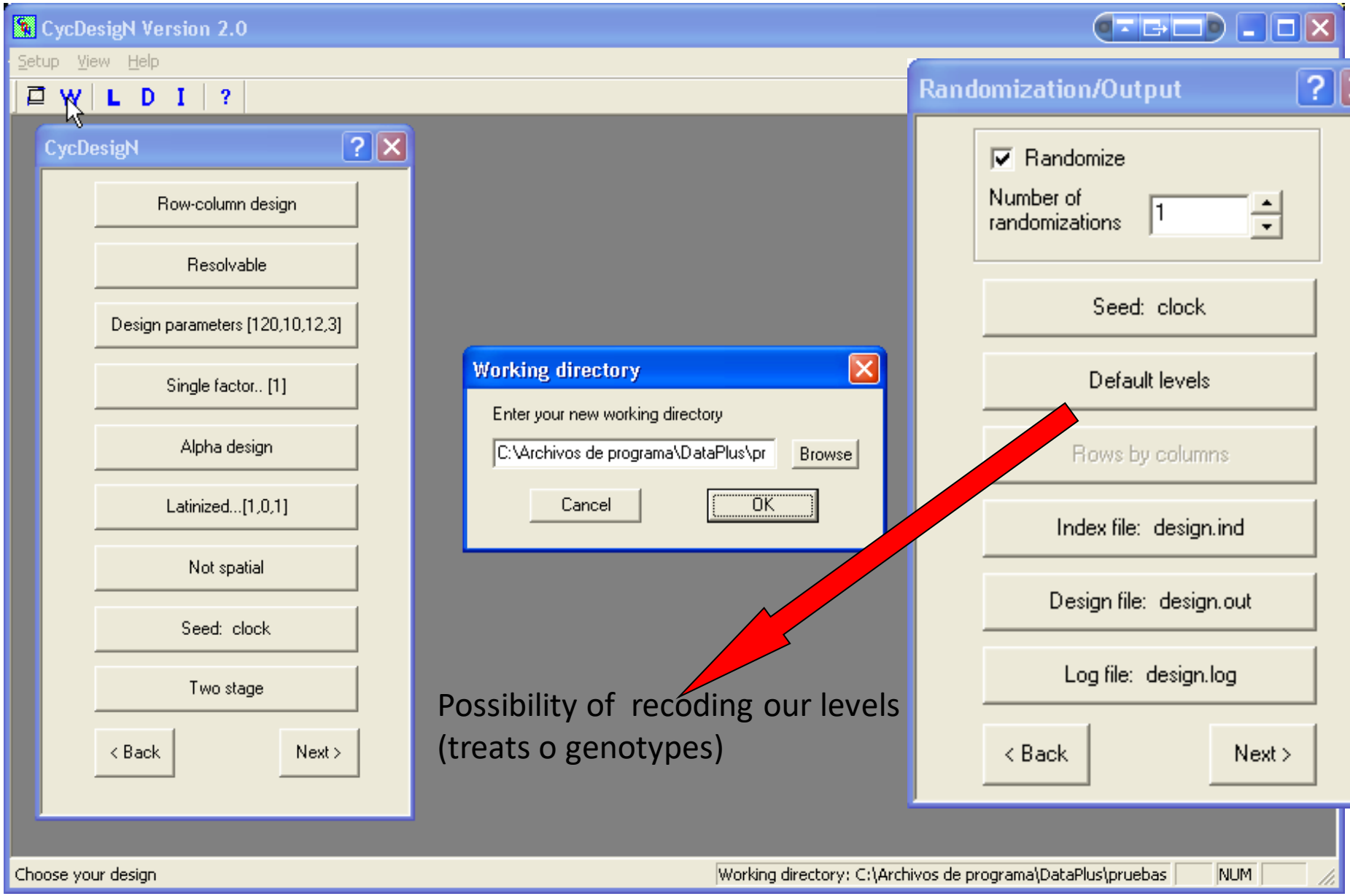
Number of contiguous rows 1

Replicate layout

Number of groups 2

< Back

Next >


CycDesigN Version 2.0
Setup View Help
W L D I ?
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
< Back
Next >
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


design.log

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.ind - Bloc d

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.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  14  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
```

Data collection

- Maps (file: “design.out”)
- Forms (file: “design.ind”)
  - Specialized software
  - Imagination
- ***Word & Excel !!!***

Templates for data recording

- From file: “design.ind”
  - Open with MS Office Word
  - Return code: ^p
  - Replace ^p by ^p ^p ^p ^p ^p….
  - ^p n-times n:number of plants per experimental unit
  - Save as .txt (unformated text)

Templates for data recording (ii)

- Attention to specifications when saving as .txt:
  - Windows default
  - Unchecked boxes
- After saving change the extension to .csv

Templates for data recording (iii)

- Open with MS Office Excel
  - Click in the first column
  - Data / text in columns
  - Delimited / tab, space & *consider consec. sep. as one*
- Save as excel file
- Use formulas & regular excel tips


Thanks for
your attention