INTRO TO TRIAL PREPARATION

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Checklist for planning an experiment

- ✓ Define the objectives
- ✓ Identify the sources of variation
- ✓ Experimental design
- ✓ Specify the measurements
- ✓ Run a pilot experiment?
- ✓ Specify the model
- ✓ Outline the analysis
- ✓ Review/revise the above decisions

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Purpose of the trial

- Why to conduct a trial?
- Objective of the trial?
- Selection/availability of resources:
  - Germplasm
  - Machinery
  - Inputs

- Design
- Management
- Analysis
- Learning

Trial Design

- When we design an experiment there are three components that should carefully be taken
  - Treatment design
  - Error-control design
  - Sampling/observation design

Treatment design

- Which treatment *factors* should be included?
- How many levels of each factor?
- Will there be combination of the factors?
- What will be the range of factor levels?

Error-control design

- What is the actual arrangement of the treatments in the experimental plan? (CRD, RCBD, IBD, etc)
- Depending on the **availability of experimental units**, the **structure** of those units, **precision** of estimation desired.

Sampling and observation design

- What kind of observations will be taken?
- Are the observational units the same as the experimental units?

The three principles of experimental design

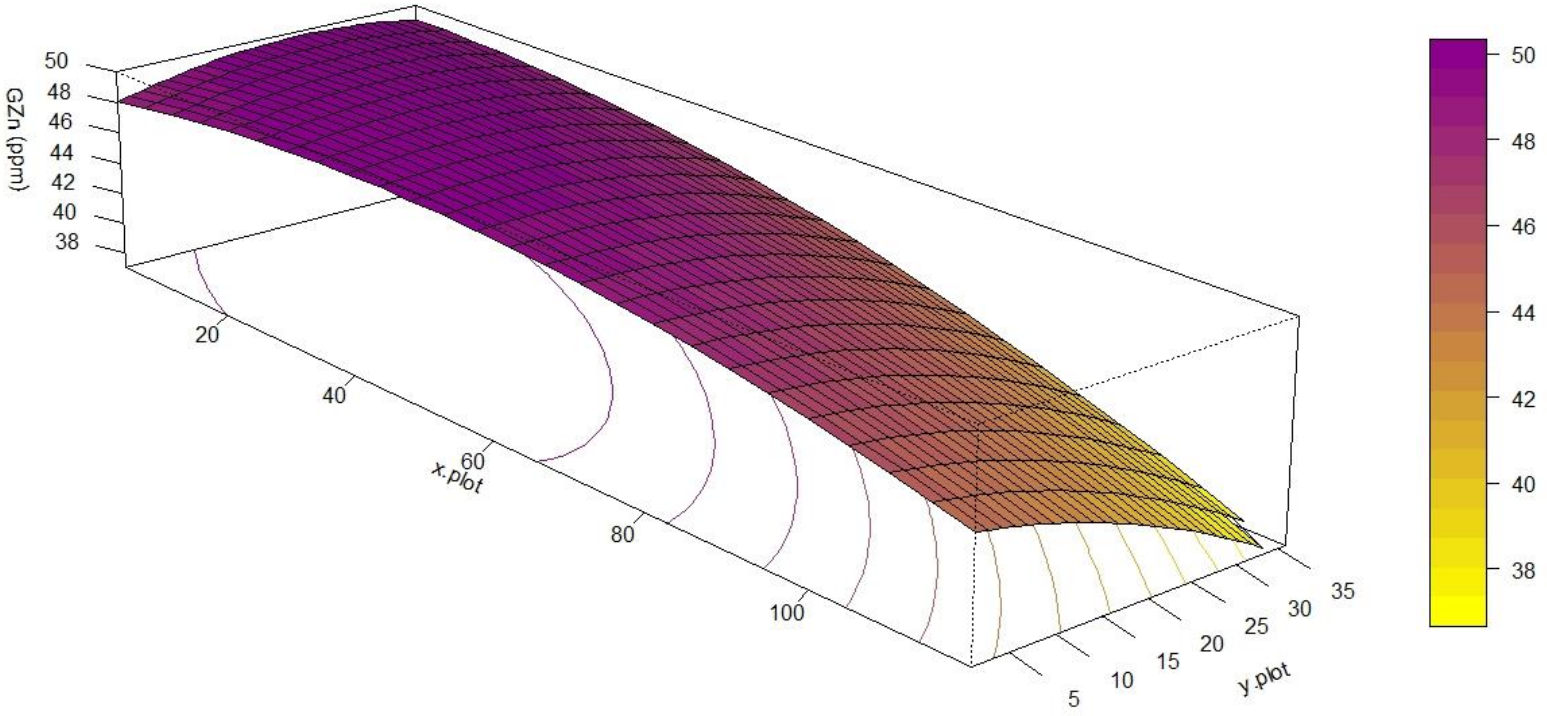
Replication → Each treatment (or some of the treatments) must be applied to several EU. Replications will allows to estimate the exeperimental error.

Randomization → This leads to an unbiased estimate of variance as well as unbiased estimate of treatment differences.

Local control (blocking) → The partition of the total set of experimental units into subsets (blocks) that are as homogeneous as possible.

Trial designs

RCBD



Perhaps the most known & used block design

Experimental units (EUs) are blocked

Each block (*b*) with *t* (treatments)

EU ∴ Each block is complete

Big variability between blocks makes it more efficient

Trial designs

α—Lattice (Incomplete block design)

Plots/Block < # genotypes (*t*)

Lattices can revert to complete blocks ∴ are never less efficient than a RCBD

t = 0, 1, …, *t*-1

t = *ks*; *k* = *b* size & *s* = number of *b* in each replicate (*r*)

α array = ***k* x *r*** with a(p,q) elements;
p = 0, 1, 2, … k-1; q = 1, 2, …, r

Develop the α* intermediate array ***k x rs*** cyclically

Trial designs

α—Lattice (Incomplete block design)

Construction

- t = 0, 1, …, t-1
- $t = ks$; $k = b$ size & s = number of b in each replicate (r)
- α array = ***k* x *r*** with a(p,q) elements in the set of residues mod s; $p = 0, 1, 2, \ldots k\text{-}1$; $q = 1, 2, \ldots, r$
- Develop the α* intermediate array ***k x rs*** cyclically
- Add s to all elements in row 2, 2s in row 3, and so on

					mod s		α array	α* = kxrs											α** (final array)												
	v	k	r	s	p (1,.. K-1)	q (1,..r)																								
1	20	5	3	4	1	1	0 0 0	0 1 2 3	0 1 2 3	0 1 2 3									0 1 2 3	0 1 2 3	0 1 2 3									
2					2	2	0 1 2	0 1 2 3	1 2 3 0	2 3 0 1									4 5 6 7	5 6 7 4	6 7 4 5									
3					3	3	0 2 3	0 1 2 3	2 3 0 1	3 0 1 2									8 9 10 11	10 11 8 9	11 8 9 10									
4					0		0 3 1	0 1 2 3	3 0 1 2	1 2 3 0									12 13 14 15	15 12 13 14	13 14 15 12									
5							0 3 2	0 1 2 3	3 0 1 2	2 3 0 1									16 17 18 19	19 16 17 18	18 19 16 17									
																			Rep 1				Rep 2				Rep 3			
																			1 2 3 4				1 2 3 4				1 2 3 4			Blocks

Hinkelman & Kempthorne, 2005

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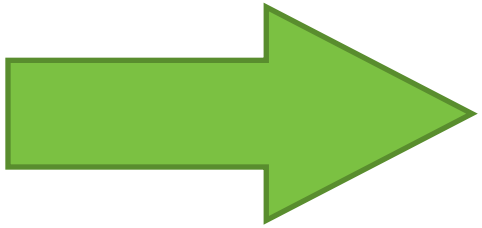
Trial designs

α—Lattice (Incomplete block design)

Construction R Example

```
library(agricolae)

trt<-1:30
t <- length(trt)
# size block k
k<-5
# Blocks s
s<-t/k
# replications r
r <- 2
outdesign<- design.alpha(trt,k,r,serie=1)
book<-outdesign$book
book
plots<-book[,1]
dim(plots)<-c(k,s,r)
for (i in 1:r) print(t(plots[,,i]))
outdesign$sketch
```



```
$rep1
     [,1] [,2] [,3] [,4] [,5]
[1,] "23" "1"  "6"  "15" "2"
[2,] "28" "25" "19" "22" "30"
[3,] "13" "11" "4"  "24" "10"
[4,] "7"  "26" "14" "3"  "5"
[5,] "18" "9"  "20" "8"  "27"
[6,] "12" "29" "21" "16" "17"

$rep2
     [,1] [,2] [,3] [,4] [,5]
[1,] "2"  "28" "29" "11" "3"
[2,] "17" "22" "9"  "4"  "23"
[3,] "14" "10" "1"  "18" "12"
[4,] "21" "26" "25" "6"  "8"
[5,] "19" "24" "16" "20" "5"
[6,] "15" "27" "30" "7"  "13"
```

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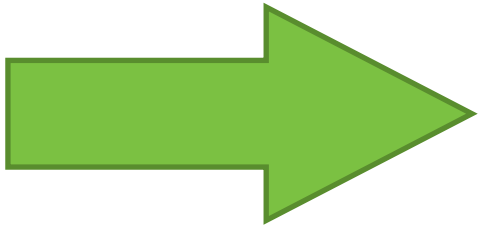
Trial designs

α—Lattice (Incomplete block design)

Construction R Example

book<-outdesign$book
book



plots	cols	block	trt	replication
11	1	1	15	1
12	2	1	29	1
13	3	1	1	1
14	4	1	2	1
15	5	1	4	1
16	1	2	17	1
17	2	2	12	1
18	3	2	30	1
19	4	2	23	1
20	5	2	8	1
21	1	3	21	1
22	2	3	3	1
23	3	3	27	1
24	4	3	16	1

Trial designs

α—Lattice (Incomplete block design): The model

$$Y_{ijk} = \mu + R_j + SB_k(R_j) + G_i + \varepsilon_{ijk}$$

μ = general mean,
G_i = effects of the genotypes,
R_j = effects of the replicates
SB_k = effects of the sub-blocks
ε_{ijk} = random residual

Trial design

α—Lattice (Incomplete block design): Analysis

Analysis in R

```r
library(lmerTest)
library(tidyr)
library(reshape2)

wd = "C:/Users/LCRESPO/Documents/CIMMYT/BPAT review/TPE response"
setwd(wd)


d = read.csv("TPEs yield data ESWYT 34-38 INDIA & MEXICO.csv")
mv = read.csv("env-covsFinal 24-38 eswytV2.csv")

locs = unique(d$Loc_no)
mv.locs = mv[mv$Loc_no %in% locs,]
rownames(mv.locs) = mv.locs$t.occ
mv.locs = mv.locs[, c(4, 17:ncol(mv.locs))]

d = d[order(d$Loc_no, d$Cycle, d$Occ),]
d$tons.ha = as.numeric(levels(d$tons.ha))[d$tons.ha]
d$Rep = as.factor(d$Rep)
d$Sub_block = as.factor(d$Sub_block)
d$GID = as.factor(d$GID)
d$Gen_no = as.factor(d$Gen_no)
d$TPE = as.factor(d$TPE)
d$Occ = as.factor(d$Occ)

```

```r
m1 = lmer(tons.ha ~ t.occ + (1|t.occ:Rep:Sub_block) + (1|GID/t.occ),
          data = d)
summary(m1)


### split of data frame into single site/trials
d.list = split(x = d, f = d$t.occ)

### Function to fit linear mixed model
trial.analysis.single = function(df = df){
    lmm.s = lmer(tons.ha ~ 1 + (1|GID) + (1|Rep) + (1|Rep:Sub_block),
                 data = df)
}

### Apply function over elements of trial list
l.s.random = lapply(d.list, trial.analysis.single)

### Apply H2 function over list of linear models for variance components
stats.list = lapply(l.s.random, function(x){
    h2.single(lm = x, df = d, varg = "GID", reps = 2)
    })

### Formatting the output of H2 function applied to the list of lm
stats.df = as.data.frame(stats.list)
stats.df = as.data.frame(matrix(unlist (stats.list),
                        nrow=length(stats.list), byrow=TRUE))
colnames(stats.df) = names(stats.list$`34eswyt.121`)
stats.df$t.occ = paste("t.occ", names(stats.list), sep = "")

```

Trial design

α—Lattice (Incomplete block design): Analysis

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Trial design

α—Lattice (Incomplete block design): Analysis

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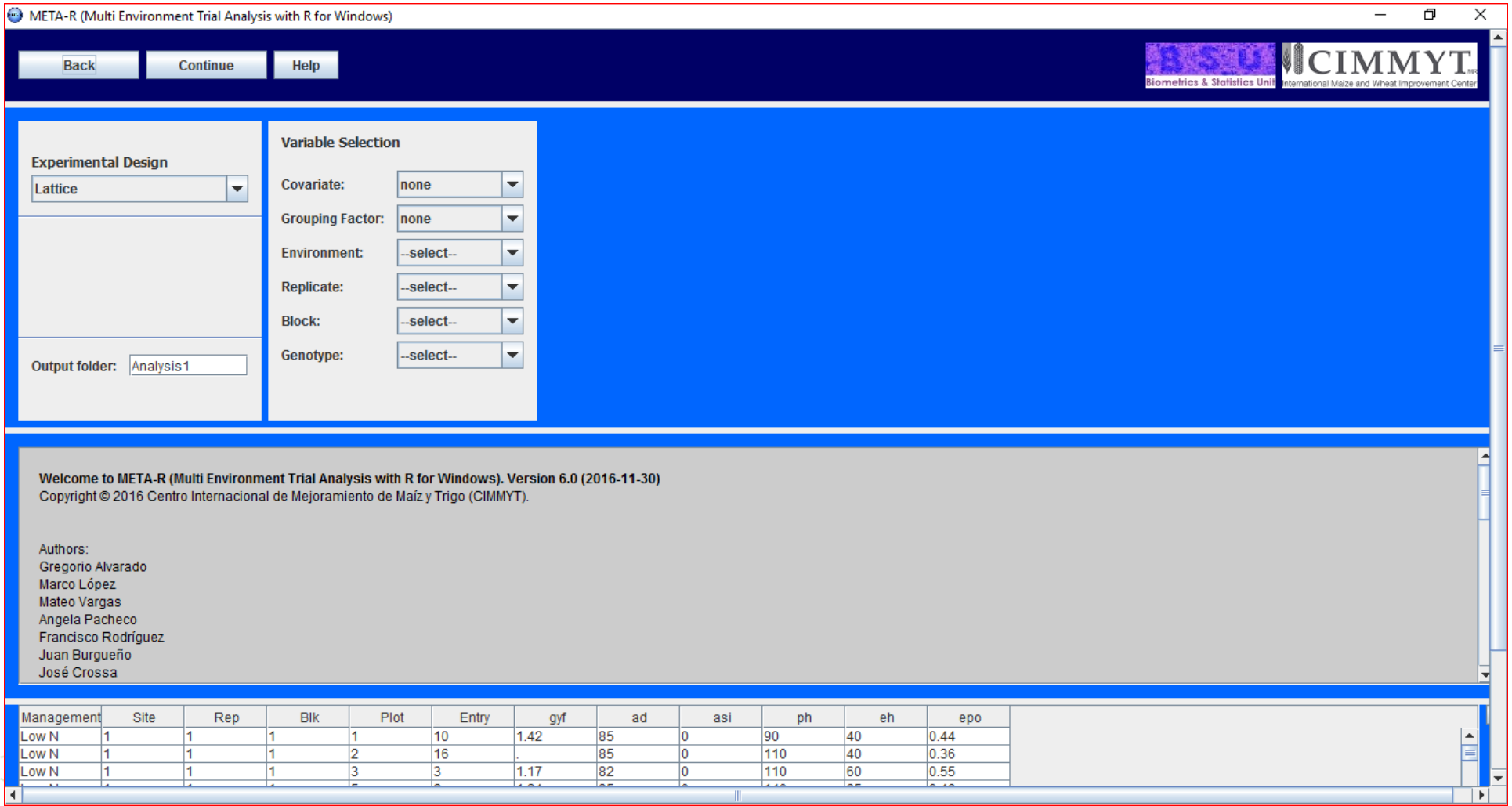
Trial design

α—Lattice (Incomplete block design): Analysis



Management	Site	Rep	Blk	Plot	Entry	gyf	ad	asi	ph	eh	epo
Low N	1	1	1	1	10	1.42	85	0	90	40	0.44
Low N	1	1	1	2	16	.	85	0	110	40	0.36
Low N	1	1	1	3	3	1.17	82	0	110	60	0.55

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Trial designs

Augmented designs

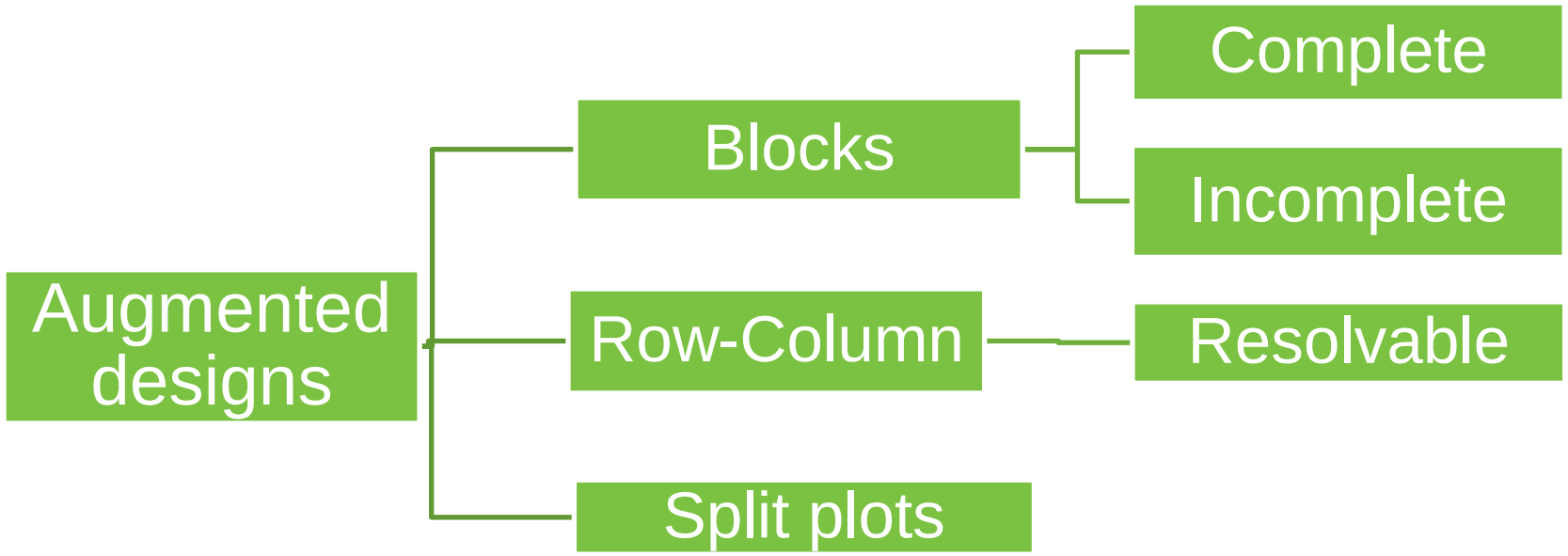
Contain *c* checks or standard treatments replicated *r* times, and *n* new treatments or genotypes included once (usually) in the experiment

1. The number of checks can be any kind and number *c*.
2. The number of new entries can be any number *n*.
3. The new treatments can be considered as random or as fixed effects.
5. Some of the designs in this class allow for screening when other factors are present, thereby revealing genotype-by-factor interactions.

Federer & Crossa, 2012

Trial designs

Augmented designs



Federer & Crossa, 2012

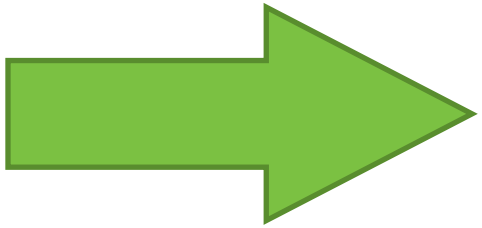
Trial designs

Augmented designs

Checks: A, B, C, D
New entries: 20-26
Blocks: 5

Construction in R:

```
# 4 treatments and 5 blocks
T1<-c("A","B","C","D")
T2<-20:26
outdesign <-design.dau(T1,T2, r=5,serie=2)
# field book
book<-outdesign$book
by(book,book[2],function(x) paste(x[,1],"-",as.character(x[,3])))
```

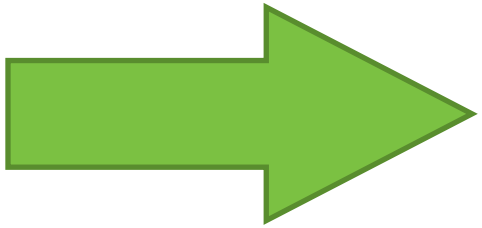


```
block: 1
[1] "101 - A"  "102 - 20" "103 - C"  "104 - 22" "105 - B"  "106 - D"
------------------------------------------------------------
block: 2
[1] "201 - 25" "202 - C"  "203 - D"  "204 - 24" "205 - A"  "206 - B"
------------------------------------------------------------
block: 3
[1] "301 - B"  "302 - 21" "303 - A"  "304 - C"  "305 - D"
------------------------------------------------------------
block: 4
[1] "401 - D"  "402 - B"  "403 - 26" "404 - A"  "405 - C"
------------------------------------------------------------
block: 5
[1] "501 - C"  "502 - B"  "503 - D"  "504 - 23" "505 - A"
```

Trial designs

Augmented designs

```
book<-outdesign$book
book
```



plots	block	trt
101	1	22
102	1	24
103	1	B
104	1	C
105	1	D
106	1	A
201	2	D
202	2	21
203	2	B
204	2	23
205	2	C
206	2	A
301	3	A
302	3	C
303	3	D
304	3	B
305	3	20
401	4	26
402	4	B
403	4	A

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Trial designs

p—Rep

In Multi-environmental (MET) testing, augmented designs can miss adjustment if checks have different error variance.

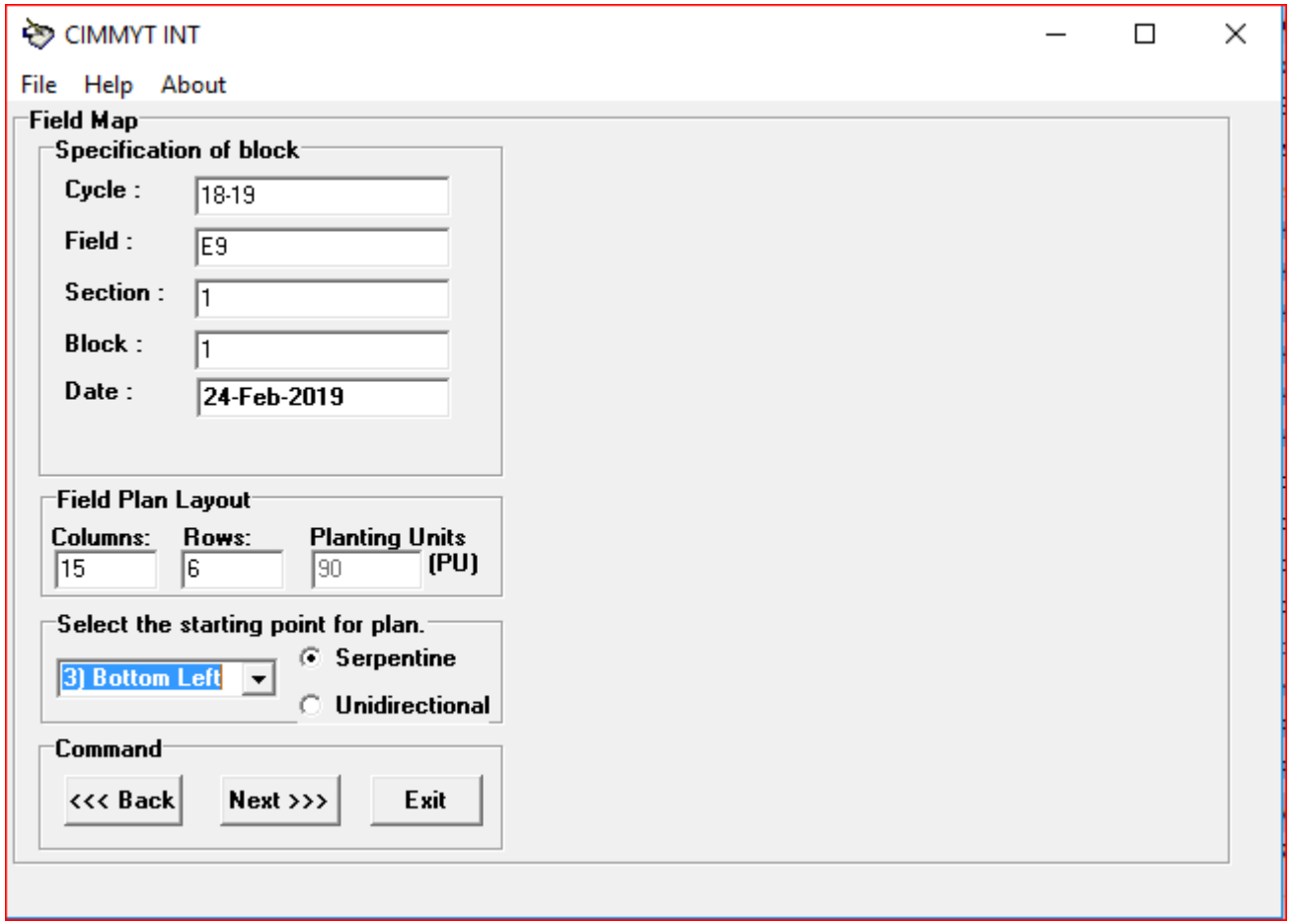
AugD allocate high number of plots to checks.

Cullist et al 2016 proposed P-rep designs: Replace replicated checks with new entries.

Williams et al 2011, applied the concept to Augmented designs in MET

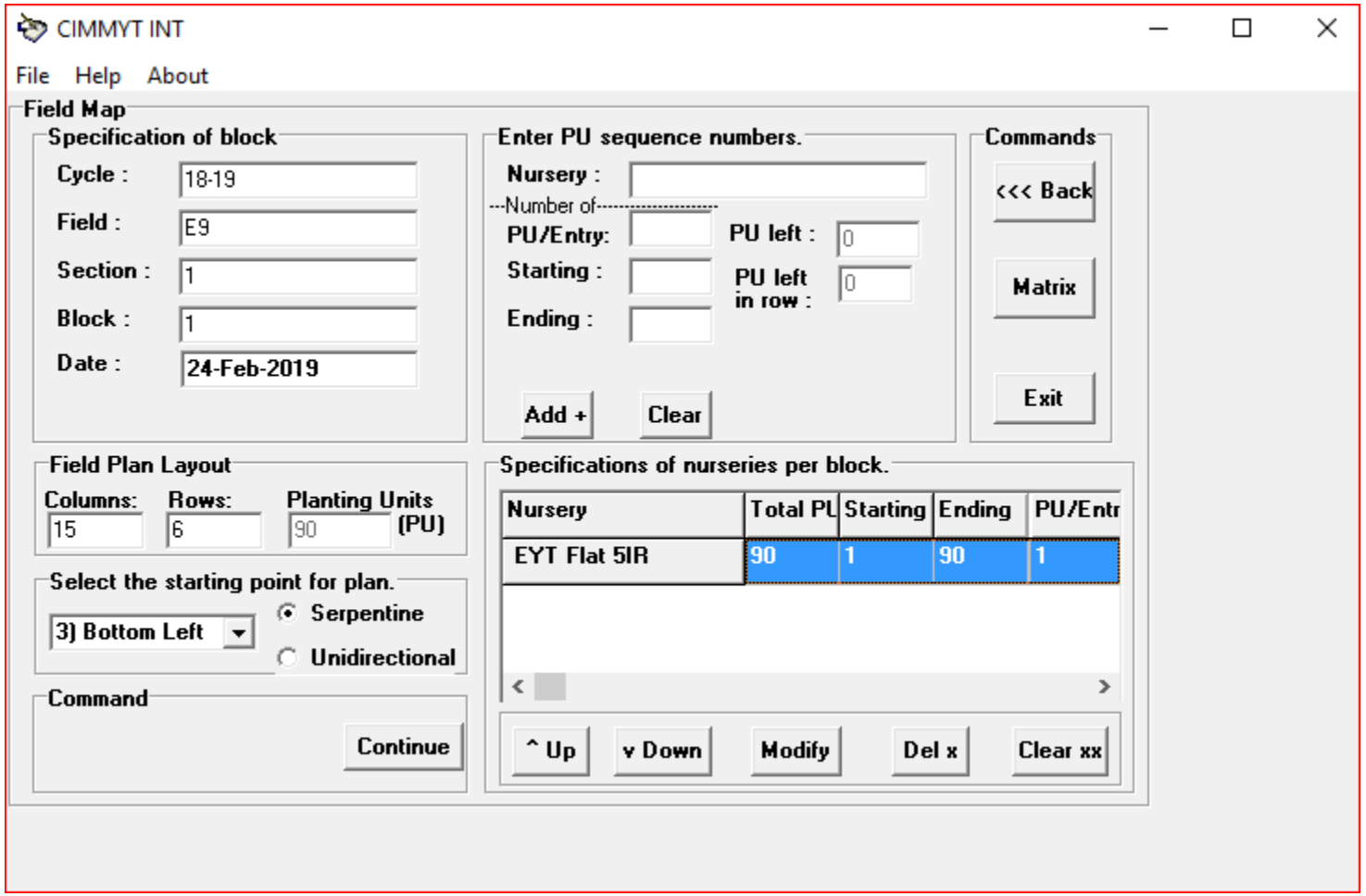
Field Maps


FieldMap


CIMMYT INT
File
Help
About
Field Map
Specification of block
Cycle :
18-19
Field :
E9
Section :
1
Block :
1
Date :
24-Feb-2019
Field Plan Layout
Columns:
Rows:
Planting Units
(PU)
15
6
90
Select the starting point for plan.
3) Bottom Left
Serpentine
Unidirectional
Command
<<< Back
Next >>>
Exit

Field Maps


FieldMap


CIMMYT INT
File
Help
About
Field Map
Specification of block
Cycle :
18-19
Field :
E9
Section :
1
Block :
1
Date :
24-Feb-2019
Enter PU sequence numbers.
Nursery :
---Number of----------
PU/Entry:
PU left :
0
Starting :
PU left in row :
0
Ending :
Add +
Clear
Commands
<<< Back
Matrix
Exit
Field Plan Layout
Columns:
Rows:
Planting Units (PU)
15
6
90
Select the starting point for plan.
3) Bottom Left
Serpentine
Unidirectional
Command
Continue
Specifications of nurseries per block.
Nursery
Total PU
Starting
Ending
PU/Entr
EYT Flat 5IR
90
1
90
1
^ Up
v Down
Modify
Del x
Clear xx

Field Maps

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16		
1		BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG 100		RELLENO
2		BORLAUG	390	389	388	387	386	385	384	383	382	381	380	379	378	377	376		EYTBW-Flat-5IR 03
3		BORLAUG	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375		EYTBW-Flat-5IR 03
4		BORLAUG	360	359	358	357	356	355	354	353	352	351	350	349	348	347	346		EYTBW-Flat-5IR 03
5		BORLAUG	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345		EYTBW-Flat-5IR 03
6		BORLAUG	330	329	328	327	326	325	324	323	322	321	320	319	318	317	316		EYTBW-Flat-5IR 03
7		BORLAUG	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315		EYTBW-Flat-5IR 03
8		BORLAUG	290	289	288	287	286	285	284	283	282	281	280	279	278	277	276		EYTBW-Flat-5IR 02
9		BORLAUG	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275		EYTBW-Flat-5IR 02
10		BORLAUG	260	259	258	257	256	255	254	253	252	251	250	249	248	247	246		EYTBW-Flat-5IR 02
11		BORLAUG	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245		EYTBW-Flat-5IR 02
12		BORLAUG	230	229	228	227	226	225	224	223	222	221	220	219	218	217	216		EYTBW-Flat-5IR 02
13		BORLAUG	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215		EYTBW-Flat-5IR 02
14		BORLAUG	190	189	188	187	186	185	184	183	182	181	180	179	178	177	176		EYTBW-Flat-5IR 01
15		BORLAUG	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175		EYTBW-Flat-5IR 01
16		BORLAUG	160	159	158	157	156	155	154	153	152	151	150	149	148	147	146		EYTBW-Flat-5IR 01
17		BORLAUG	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145		EYTBW-Flat-5IR 01
18		BORLAUG	130	129	128	127	126	125	124	123	122	121	120	119	118	117	116		EYTBW-Flat-5IR 01
19		BORLAUG	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115		EYTBW-Flat-5IR 01
20		BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG	BORLAUG 100		RELLENO

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Field trial management

Management Practices

- A key aspect in crop production
  - Sowing systems
  - Irrigation systems
  - Crop Management

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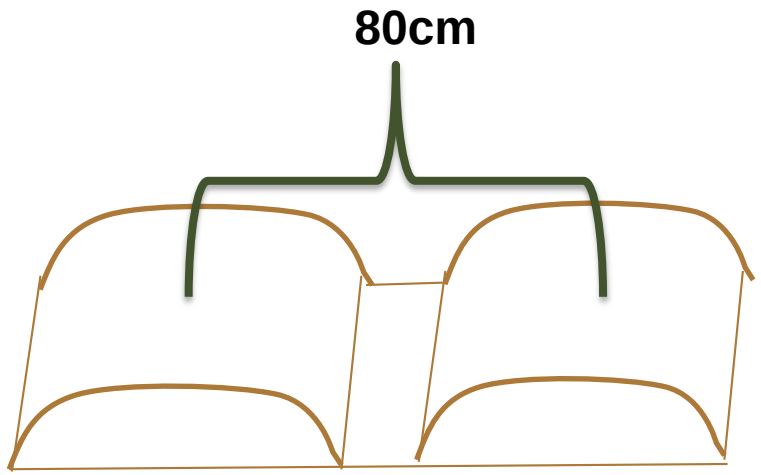
Field Preparation

Tillage

- Conventional tillage : Turning and loosening of topsoil layer using disc or plough
- Conservation tillage : Sowing on previous crop residue (30% or more) with minimum soil disruption
- Zero tillage : Direct sowing over previous crop, with no residue turnover

Sowing Systems

- Raised Bed
  - 2/3/4 rows
  - Bed size varies,
    - 80cm at Obregon station
    - 3-row spacing 18cm



- Flats
  - 6 or 8 rows
  - 6-row spacing 18cm

Sowing systems

- Hand planting : used for planting small plot 1m or less, head rows/plant to rows/disease evaluations
- Machine planting : planting plots of 2m or larger.
- Plot sizes for yield trials is 2m or larger (4m)
- Seeding rate: 120-180kg/ha for bread wheat & durum wheat

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Irrigation systems

- Flood furrow/basin irrigation : irrigated environment trials
- Drip irrigation : drought and irrigated yield trials
- Sprinkler irrigation : disease nursery (eg. Fusarium)

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Harvest Management


Hand harvest


Combine harvest


Arrangement


Barcode Tags


Barcode based weighing


Inventory app

Thank you for your interest!