

# Statistical Data Analysis for Post-Graduate Students Using R Programming Language

Facilitators

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# Introduction to Research Process

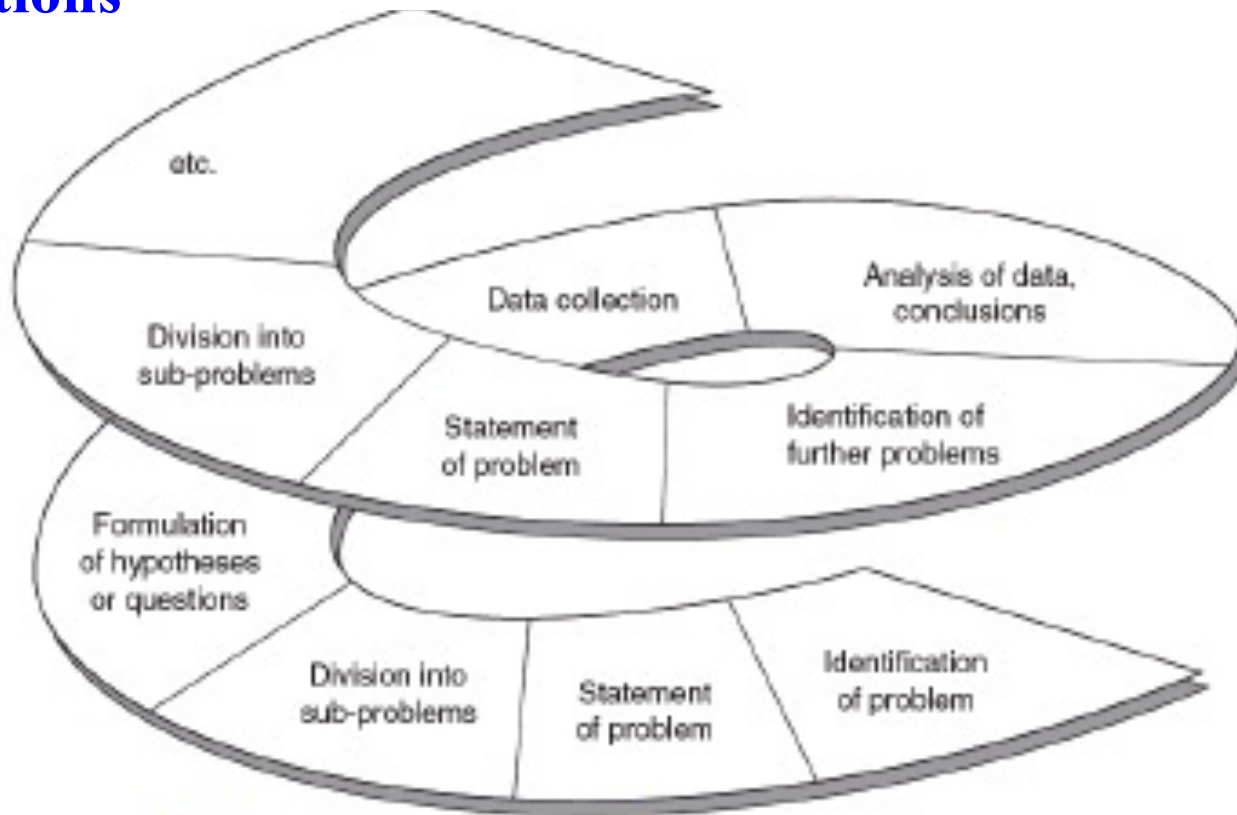
# Introduction to Research process

## Definition of Research

- Research is a process of **systematic inquiry** that entails collection of data; documentation of critical information; and analysis and interpretation of that data/information, in accordance with suitable methodologies set by specific professional fields and academic disciplines.

# Introduction to Research process

**Research cyclic – Research generate more problems – Careful observations**



# Introduction to Research process

**Process (Biological, social, etc.) generate variations**

- 1) Variation **evoked by the investigator/scientist**, e.g. different animal breeds, plant species, fertilisers, varieties, chemical doses, types of food preservative, etc.
- 2) Those **not under direct control** of the investigator, e.g. altitude, temperature, soil texture at different experimental sites, sex of animal; etc

# Introduction to Research process

## Steps in Scientific/agricultural research

- **Problem identification**
  - scientific interest      -      basic research
  - practical concern      -      applied/adaptive research
- **Literature review to identify**
  - what is known                      -      pool
  - what is unknown                      -      gap

# Introduction to Research process

## Steps in Scientific/agricultural research

- **Defining objectives** – is one of the most important stages of research
  - it is the basis for other stages of research.
  - You have to come up with specific objectives in relation to the research problem, which may be:

# Introduction to Research process

- **Hypothesis**
  - theoretical proposition or a tentative guess at the answer to a research question.
  - determine what kind of data to collect, what factors to include, etc.
- **Data collection**
  - We need data that will provide evidence for or against the hypotheses
  - A researcher usually generates his/her own data by means of an **experiment** or **survey**.
  - *Design* of survey or experiment determines the quality of results. So when we get to experimentation, we shall spend some time on **experimental design**.



# Introduction to Research process

- **Data analysis**

- Takes various forms depending on study objectives.
- Statistical -estimates, comparisons (e.g. t, F), associations (chi-square) or relationships and optimization (regression), etc.
- Economics - net benefit ratio, marginal returns, etc.
- Other (e.g. farmer's assessment/perception)

- **Interpretation**

- draw logical conclusions
- make valid inferences
- new principles or methodologies
- solution or no solution
- acknowledge limitations of the research

# Introduction to Research process

- **Dissemination of results**
  - project reports, theses
  - publications
- NB: RESEARCH - continuous, dynamic & iterative (cyclic in nature)
  - steps overlap

# Introduction to Research process

## **Roles of objectives**

- With a clearly defined objectives, the researcher can focus on the study – provide direction of the investigation
- Avoid collection of data which are not necessary and leave other necessary data
- Organize the study in a clearly defined parts or phases
- Facilitate the development of research methodology – help orient collection, analysis and interpretation of data

# Introduction to Research process

## FORMULATION OF RESEARCH HYPOTHESES

- Hypotheses are developed by asking *what, why, how, when, where, what if, ...* of different aspects of the causes of the problem. It is the hypotheses that are subjected to testing in a study.
- A clearly stated hypothesis will:
  - aid and determine the **design** of an experiment/survey
  - help identify appropriate **treatments** and **controls**
  - determine the type of **data** to collect, and
  - (probably) suggest a **method of analysis**

# Introduction to Research process

## FORMULATION OF RESEARCH HYPOTHESES

- Hypothesis is derived from a research problem which usually framed as a question
- Hypotheses are developed by asking *what, why, how, when, where, what if, ...* of different aspects of the causes of the problem. It is the hypotheses that are subjected to testing in a study – **Answers to such questions**
- Problem:
  - **Low yield (farmers' problem) and lack information on how to improve yield of Acholi white groundnut variety(Researcher's problem)**

# Introduction to Research Process

## FORMULATION OF RESEARCH HYPOTHESES

- Problem:
  - Low yield of Acholi white groundnut variety in Uganda
- “Why are farmers in Uganda getting low yield when they grow Acholi white?”
- Or “How can we increase Acholi white yield on the farmers’ fields?”

# Introduction to Research Process

## Formulation of Research Hypothesis

- In developing the hypothesis, you can be influenced by
  - An existing theory,
  - Related research,
  - Personal experience.
- “Your idea”: *Acholi white variety* has become susceptible to ground rosette virus disease

# Introduction to Research Process

## FORMULATION OF RESEARCH HYPOTHESES

- Your idea: *Acholi white variety* has become susceptible to ground rosette virus disease

Possible hypothesis

*“Resistance to groundnut rosette virus disease in Acholi white is broken down due to emergence of new virus strain.”*



# Introduction to Research process

## FORMULATION OF RESEARCH HYPOTHESES

- A clearly stated hypothesis will:
  - aid and determine the **design** of an experiment/survey
  - help identify appropriate **treatments** and **controls**
  - determine the type of **data** to collect, and
  - (probably) suggest a **method of analysis**

# Introduction to Research process

## **Some simple rules in research hypothesis formulation:**

- Hypotheses must/should be:
  - clearly relate to the problem to be addressed
  - stated in a way that suggests a solution to a problem
  - stated in such a way as to provide direction for research
  - capable of verification or rejection
  - stated as simple as possible

# Overview of Experimental Design

# Introduction

- Experiments: **Establish cause-effect relationships**
- Principles of experimental design are same irrespective of field of study: Agriculture, biological, ecological, social, economics





# Field Experiment





# Laboratory Experiment



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# Importance of experimental design

- Experimental design has two components:
  - Structure of experimental units (type & nature of exptal material) – **Variation outside the control of the researcher**
  - Structure of treatment set – **Variation under the control of researcher**



**Treatment**



**Experimental material** 23

# Experimental Unit, Treatments, Sampling Units



**Experimental Unit:** Pot

**Treatment:** Fertilizer, pesticides, varieties, etc.

**Sampling Unit:** Each plant

**Variables:** Plant height, number of combs, leaf length, number of leaves



# Importance of experimental design

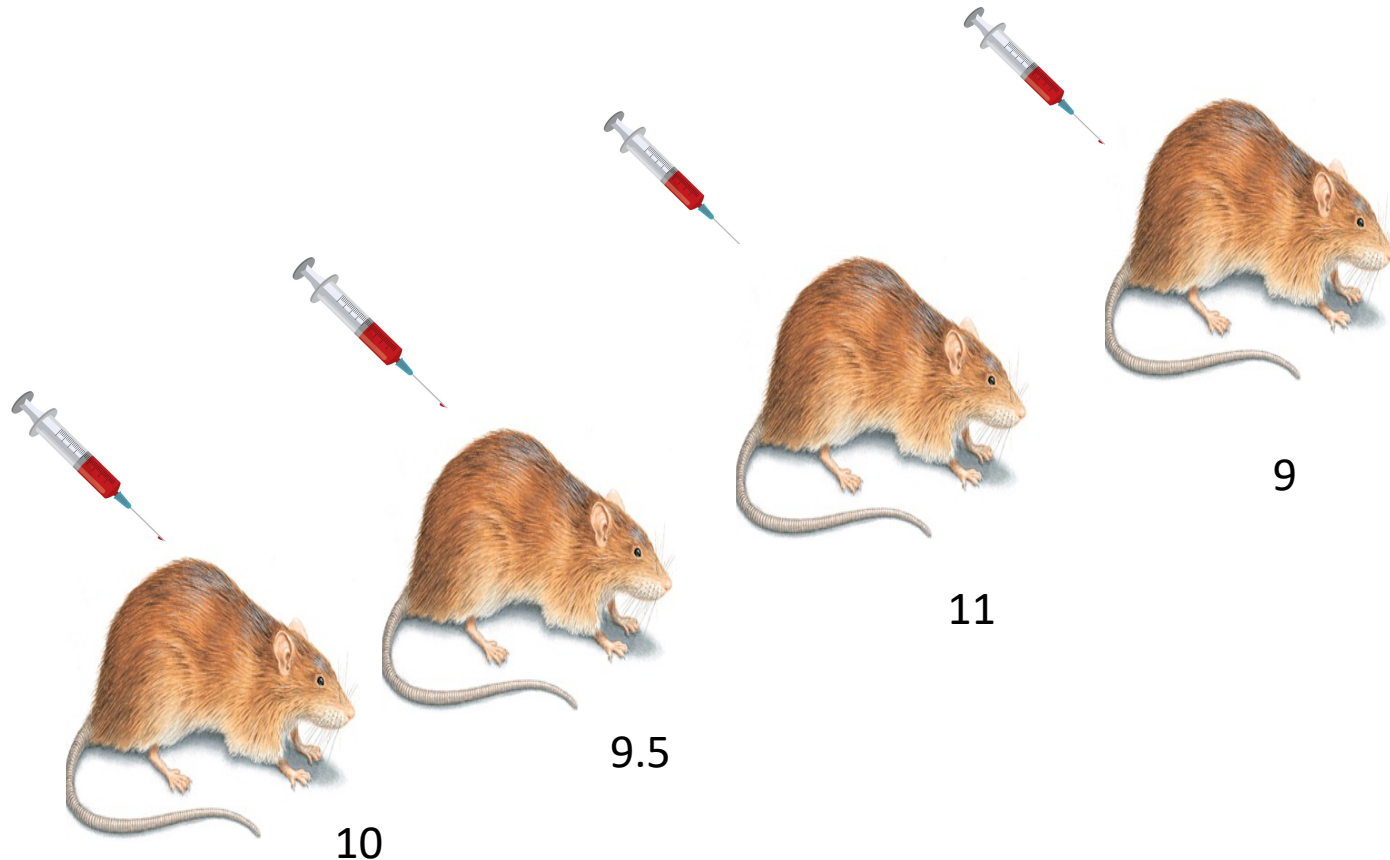
- A good experiment should provide:
  - Unbiased estimate of treatment differences



***Comparing the effect two energy drinks: Monster and Red bull***

# Importance of experimental design

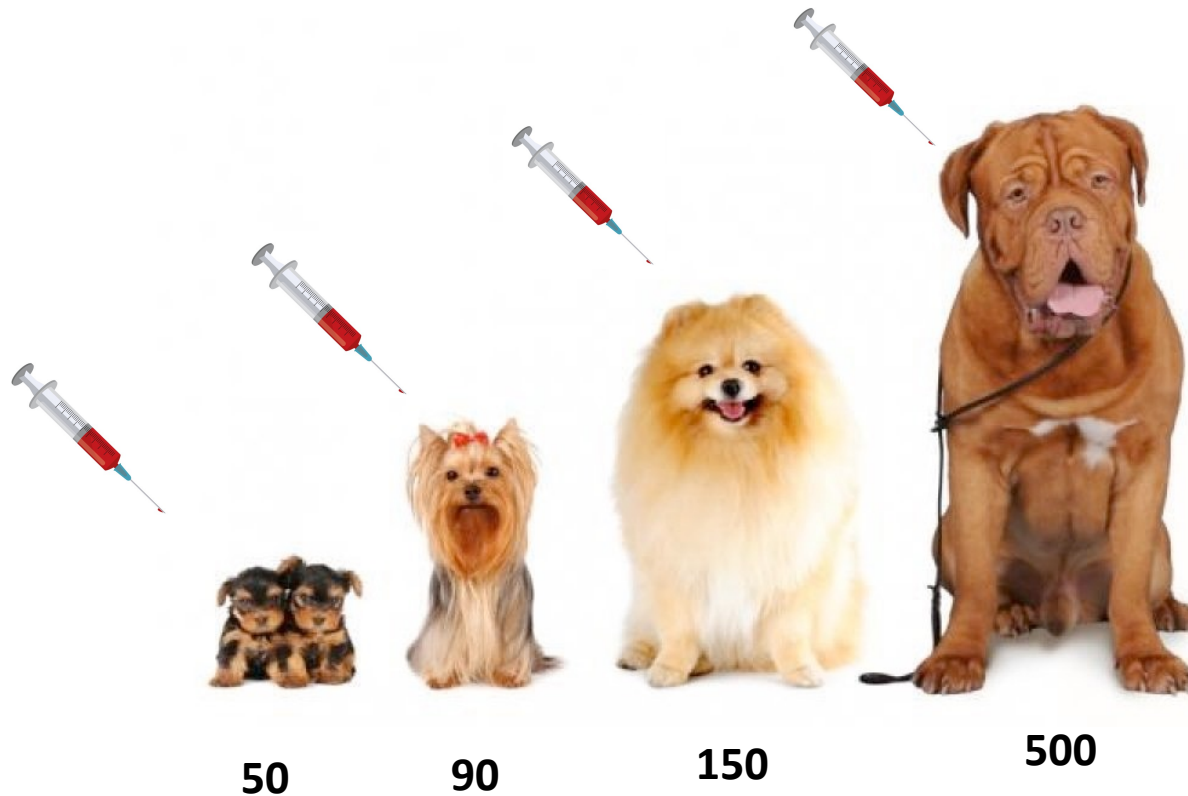
- A good experiment should provide:
  - Unbiased estimate of the experimental error



***Variation between similar experimental units receiving the same treatment***

# Importance of experimental design

- A good experiment should provide:
  - Unbiased estimate of the experimental error



*Variation between similar experimental units receiving the same treatment*

# Basic Principles of Experimental Design

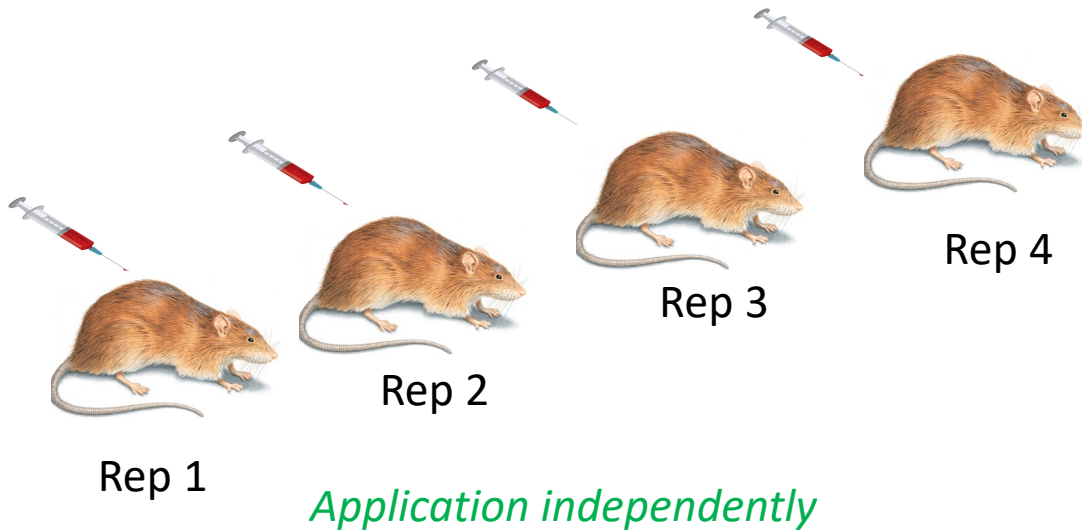
- Basic principles of experimental design are prerequisites of obtaining valid and unbiased estimates of treatment effects and experimental error
- The basic principles of experimental design area:
  - **Replication**
  - **Blocking/Local Control/Restriction**
  - **Randomization**

# Replication

What, why, how

# What is replication?

- **Replication** ( $r$ ) is the repetition of a treatment **under identical conditions** in an experiment.
- Each treatment is **applied independently** to two or more experimental units



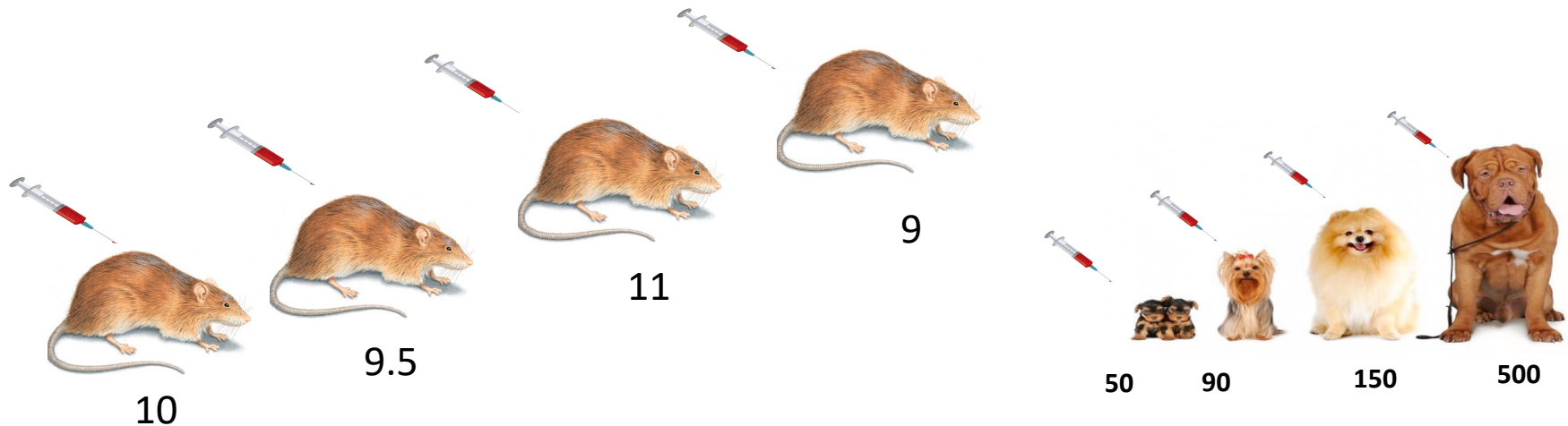
*Application not independently*

*Pseudo replication or subsampling*

# Why replicate?

## Roles of replication

- Permits estimation of experimental error variance



### Reaction times for rats

```
> reaction<-c(10, 9.5, 11, 9)
```

```
> var(reaction)
```

```
[1] 0.7291667
```

### Reaction time for dogs

```
> reaction2<-c(50,90, 150, 500)
```

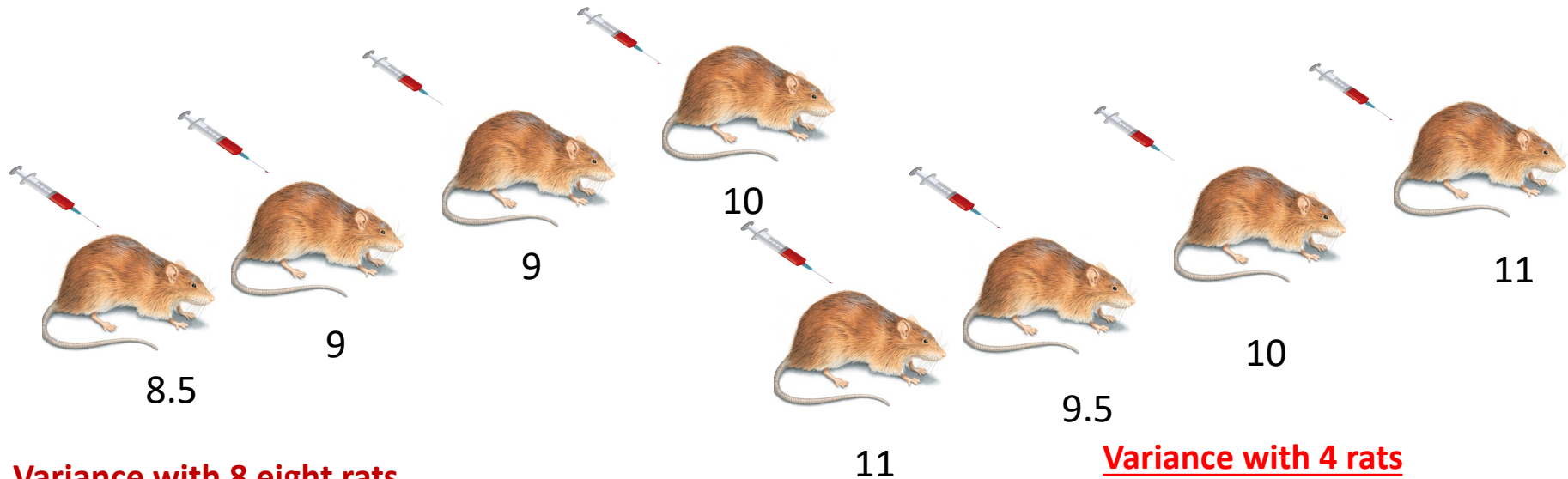
```
> var(reaction2)
```

```
[1] 42358.33
```

# Why replicate?

## Roles of replication

- Increase of replication increases precision of parameter estimate.
  - Variance of treatment mean =  $\left(\frac{\sigma^2}{r}\right)$  hence reduce standard error for treatment



### Variance with 8 eight rats

```
> reaction3<-c(10, 9.5, 11, 9, 10, 9.5, 11, 8.5)
> var(reaction3)
[1] 0.78125
> var(reaction)/8
[1] 0.09765625
```

### Variance with 4 rats

```
> reaction<-c(10, 9.5, 11, 9)
> var(reaction)
[1] 0.7291667
> var(reaction)/4
[1] 0.1822917
```



# Why replicate?

Replication is a form of insurance

- Avoid losing whole trial

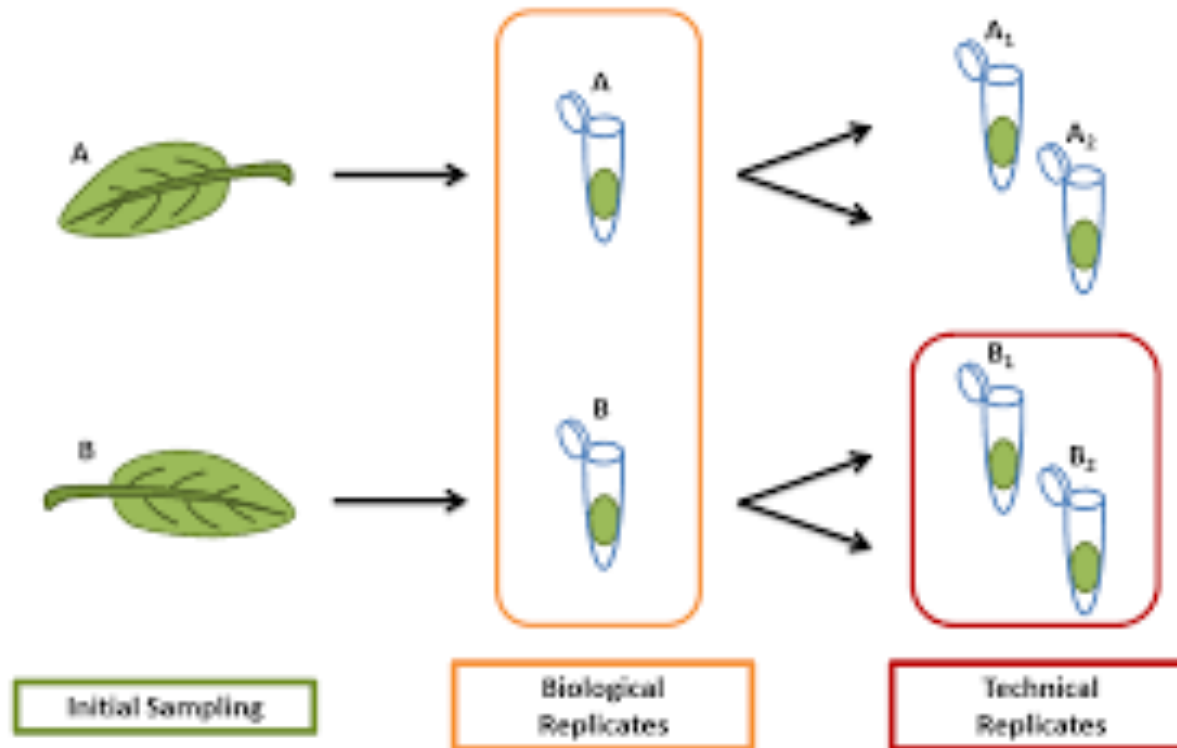
Increase range of validity

- Observe results over a larger sample of farms, soils,...
- Look at context
- How widely do **you** need to test something to be convinced of the results?



# How should it be done?

- **Avoid pseudo replications**
- **Beware of Biological versus Technical Replications**



# How many replications

## *Factors that determine the number of replications*

- Pattern and magnitude of variability in among the study subject



**Which set of potatoes is easy to represent or can be represented by few pieces?**

# How many replications

## *Factors that determine the number of replications*

- Size of the difference to be detected; the smaller the difference between treatments to be detected, the higher the number of replications



Vs



Vs



# How many replications

## *Factors that determine the number of replications*

- Required significance/confidence level
- *Available resources for the experiment*

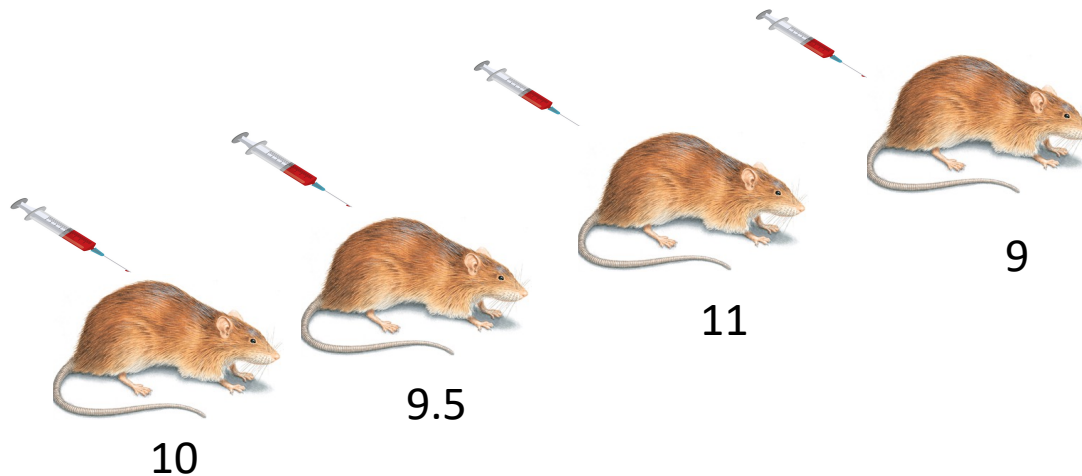


# Blocking/Restriction/LC

allowing for variation

# Blocking

- Blocking controls/minimizes non-treatment in an experiment
- Non-treatment variation confound effects of treatment
- Increases noise in an experiment and makes it difficult to detect treatment differences or effects

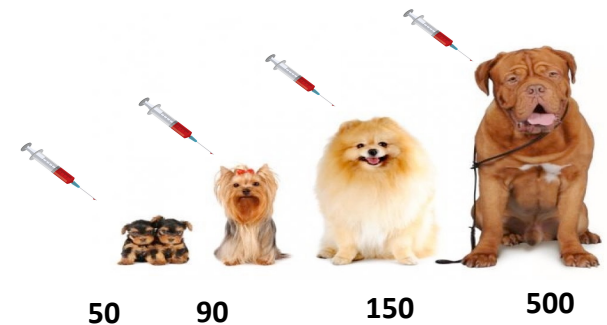


## Reaction times for rats

```
> reaction<-c(10, 9.5, 11, 9)
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```
> var(reaction)
```

```
[1] 0.7291667
```



## Reaction time for dogs

```
> reaction2<-c(50,90, 150, 500)
```

```
> var(reaction2)
```

```
[1] 42358.33
```



# Blocking





# Blocking

- These non-treatment variation needs to be controlled
  - homogeneous material
  - homogeneous management
  - careful measurement
- Blocking can allow us to remove/control the effects of variations in experimental material (*non-treatment variations*)

# Blocking

**Blocks are - groups of experimental units expected to be similar**

Examples: plots with similar soils, same animal breed, etc.



**Block 1**



**Block 2**



**Block 3**



**Block 4**

# Blocking

**Blocks are - groups of experimental units expected to be similar**

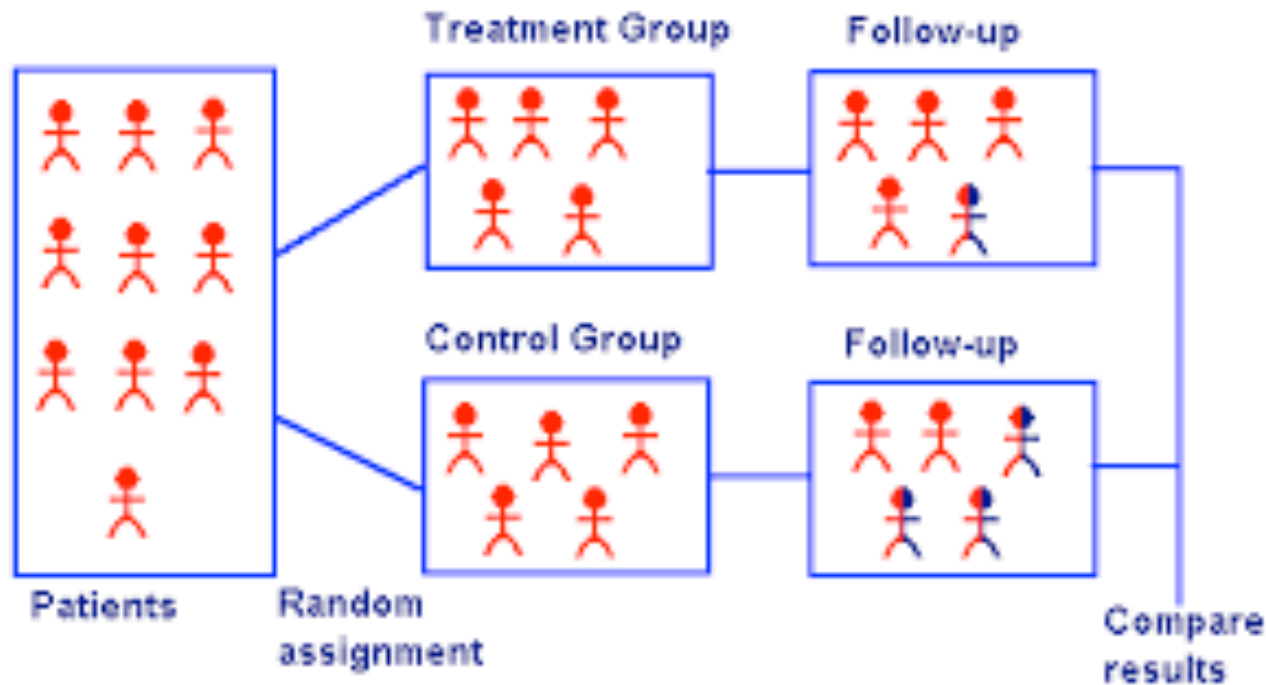
Examples: plots with similar soils, same animal breed, etc.



# Randomization

# Randomization

- Process of assigning “treatments” to the different experimental units (using probability/chance)
- Each treatment has an equal chance to end up in a given subject
- Use explicit process, not just ‘mixed up’



# Randomization

- Which plot should receive which treatment?

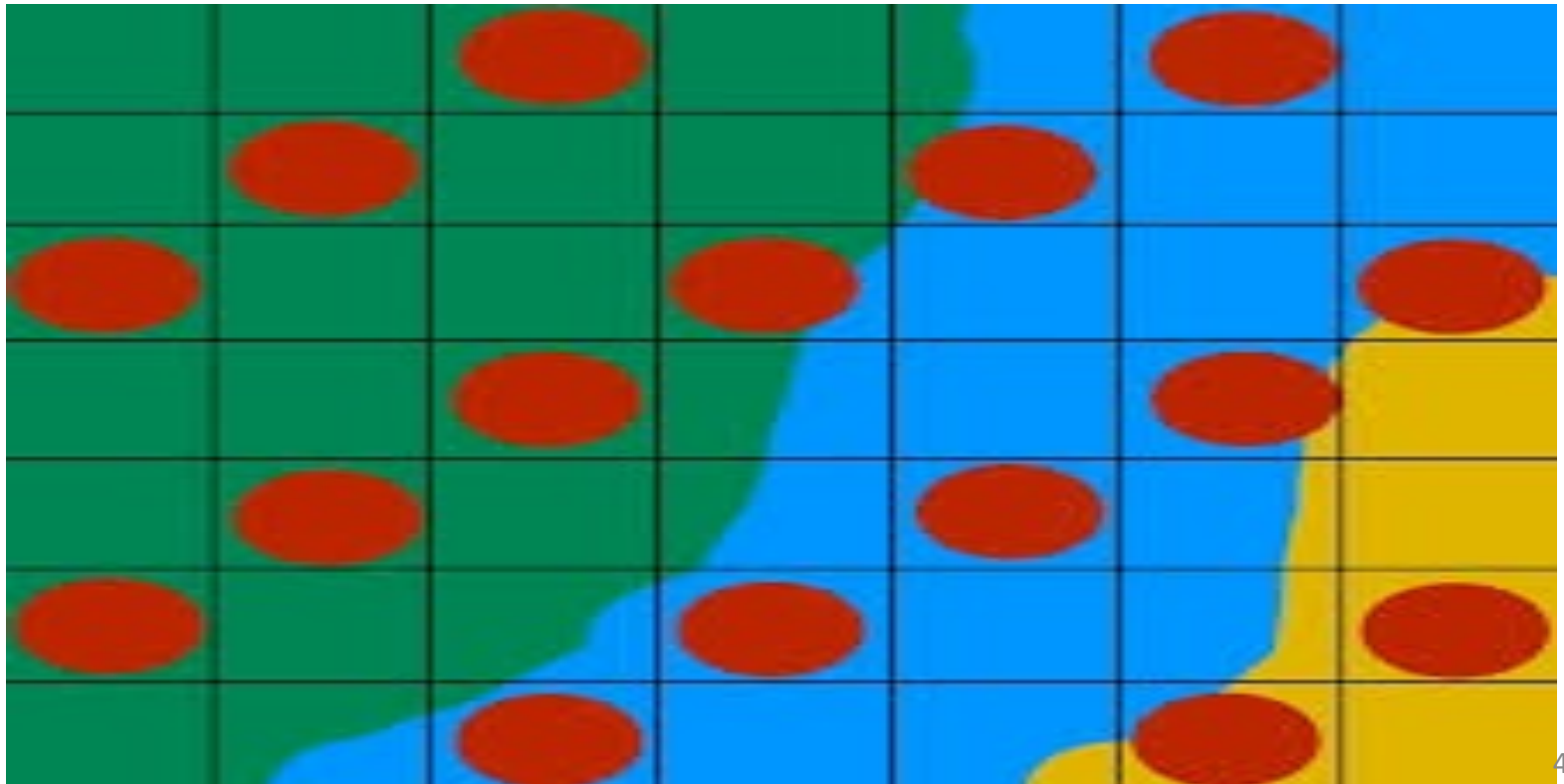
	BLOCKS		
Plots	1	2	3
1	B	C	A
2	D	A	B
3	A	C	D
4	C	B	D

# Why do Randomization?

- Avoid favouring some treatments
  - conscious
    - Plots easy to reach
  - Unconscious
    - People tend to take sub-samples close to the centre of a plot of maize
  - avoiding unknown **systematic variation**
  - “blindness” = medical researcher doesn’t know which treatment he applies to the patient
- **Unbiased estimate of residual variance**

# Why do Randomization?

- Avoiding unknown **systematic variation**
- **Unbiased estimate of residual variance**

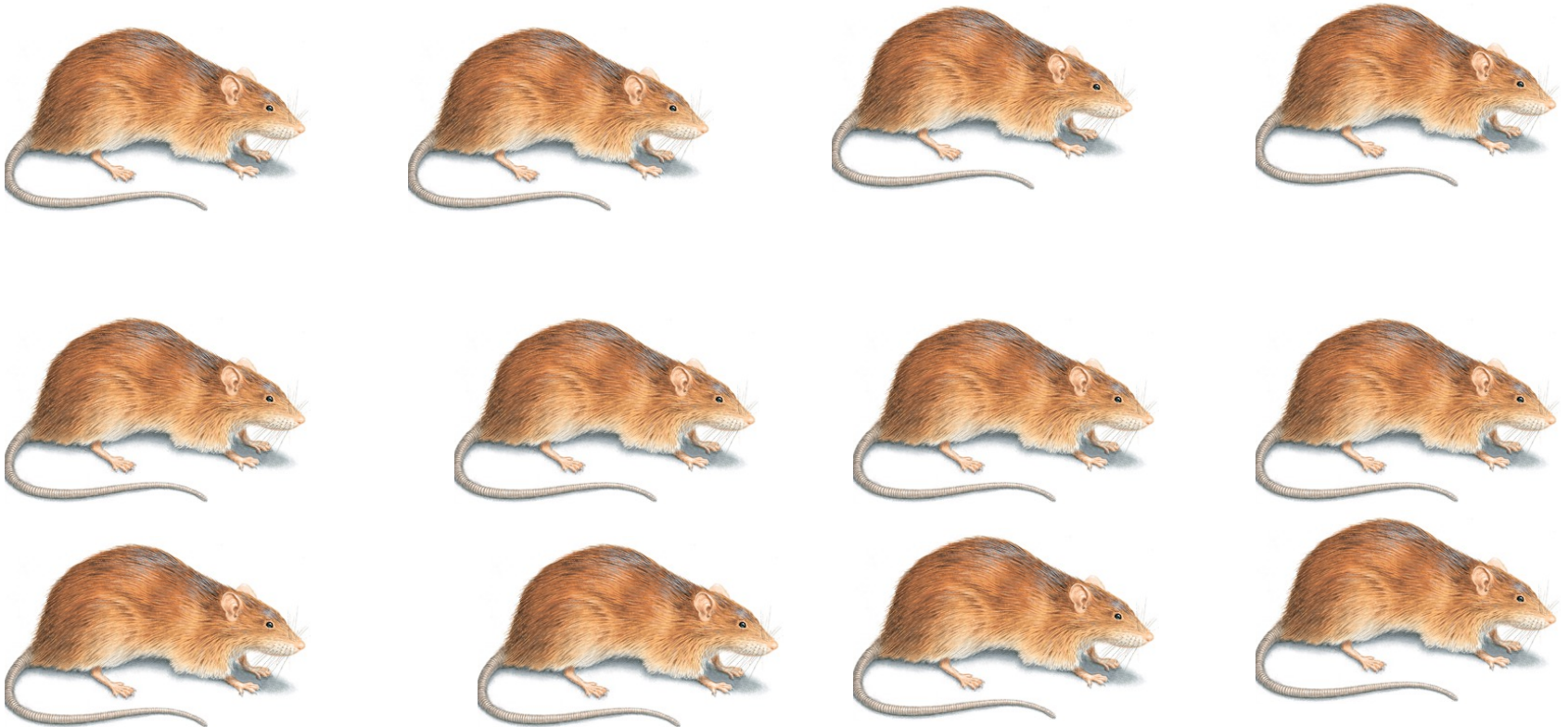




# Standard Designs

# Completely Randomized Design (CRD)

- Main Assumption: **Experimental Units are homogenous**



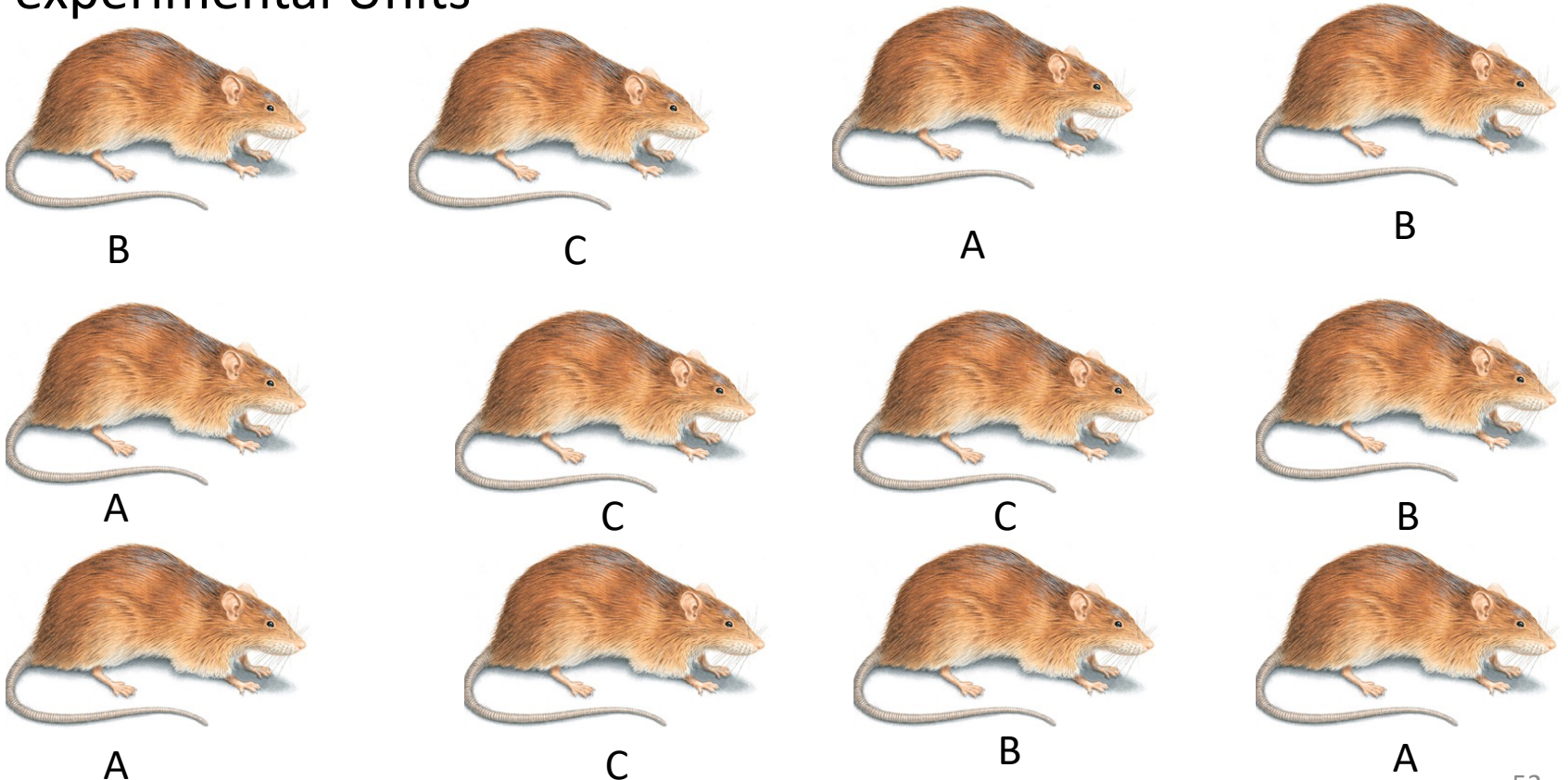
# Completely Randomized Design

```
> #randomization for CRD using R
> set.seed(500) #allow for get same randomization
> f <- factor( rep( c("A", "B", "C" ), each = 4)) #creating a vector of factor levels
(treatments)
> fac <- sample( f, 12 ) #Randomizes the order of the levels (sample 12 without
replacement)
> expt_unit <- 1:12 #
> plan <- data.frame( Rat=expt_unit, Treatment=fac )
> plan
```

	<b>Rat</b>	<b>Treatment</b>		<b>Rat</b>	<b>Treatment</b>
1	1	B	6	6	C
2	2	C	7	7	C
3	3	A	8	8	B
4	4	B	9	9	A
5	5	A	10	10	C
			11	11	B
			12	12	A

# Completely Randomized Design (CRD)

- As a result treatments are assigned completely at random to the experimental Units

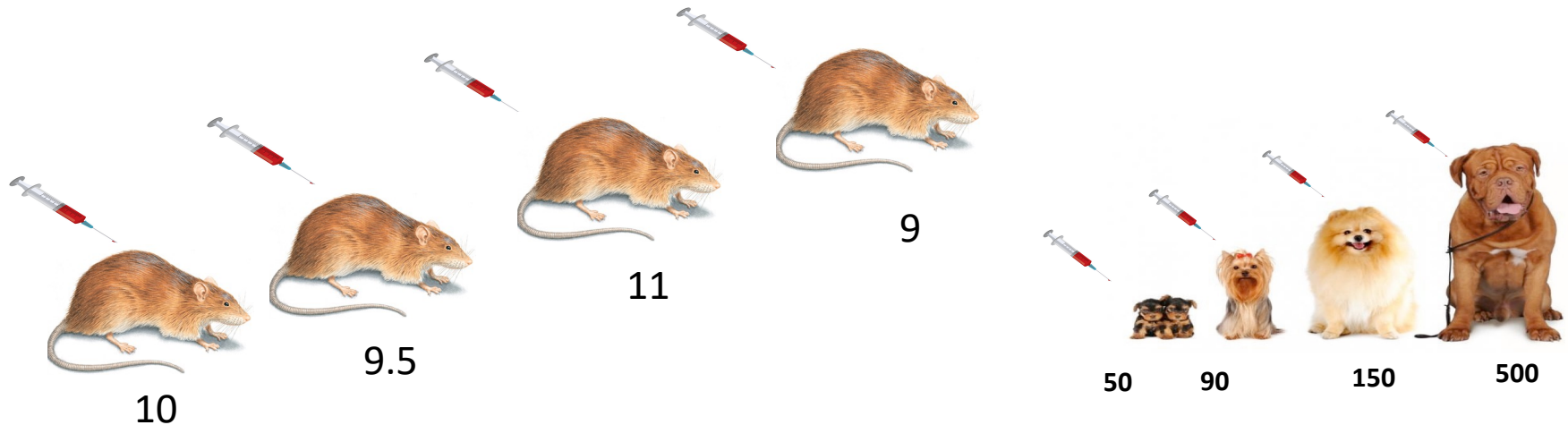


# Completely Randomized Design (CRD)

- All experimental units are assumed to be similar **with respect to characteristic that is likely to affect response to treatment**
- Commonly used in laboratory or Screen house experiments
- Application in field experiments is **very rare**

# Completely Randomized Design (CRD)

- The main objection to the CRD is that it is often inefficient.
  - Since randomisation is unrestricted, experimental error includes the entire variation among experimental units except that due to treatments.



## Reaction times for rats

```
> reaction<-c(10, 9.5, 11, 9)  
> var(reaction)  
[1] 0.7291667
```

## Reaction time for dogs

```
> reaction2<-c(50,90, 150, 500)  
> var(reaction2)  
[1] 42358.33
```



# Randomized Complete Block Design (RCBD)

- **Experimental material is not always homogenous**



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# Randomized Complete Block Design (RCBD)

- Experimental material is not homogenous
- There is a predictable trend in variability in the experimental material e.g. fertility gradient
- Experimental units can be grouped into block with homogeneity within block
- Knowledge of your experimental material is paramount



**Block 1**



**Block 2**



**Block 3**



**Block 4**

# Randomized Complete Block Design (RCBD)

**Block 1**

**Block 2**

**Block 3**

**Block 4**

**Block 5**

**Block 6**


# Randomized Complete Block Design

```
> #Randomise complete Block Design - plan
> treat <- c("A","B","C","D", "E", "F")
> b1t <- sample(treat,6) #randomization for block 1
> b2t <- sample(treat,6) #randomization for block 2
> b3t <- sample(treat,6) #randomization for block 3
> b4t <- sample(treat,6) #randomization for block 3
> b5t <- sample(treat,6) #randomization for block 3
> b6t <- sample(treat,6) #randomization for block 3
> treatment<-c(b1t, b2t, b3t) # create a combined vector for treatments in
the different blocks
> block <- factor( rep(c("Block 1", "Block2", "Block3","Block4", "Block5",
"Block6"),6))
> plot <- rep(1:4,3) #generating labels from plot in each block/category
> plan<-data.frame(Block = block, Plot.Number = plot,treatment=treat)
> plan
```

# Randomized Complete Block Design (RCBD)

- **Treatments are randomized within each block separately**
- All treatments appear in each block and every block
- Each block serve as a replicate (number of blocks = number of replications)

Block 1	C	A	D	B	E	F
Block 2						
Block 3						
Block 4						
Block 5						
Block 6						

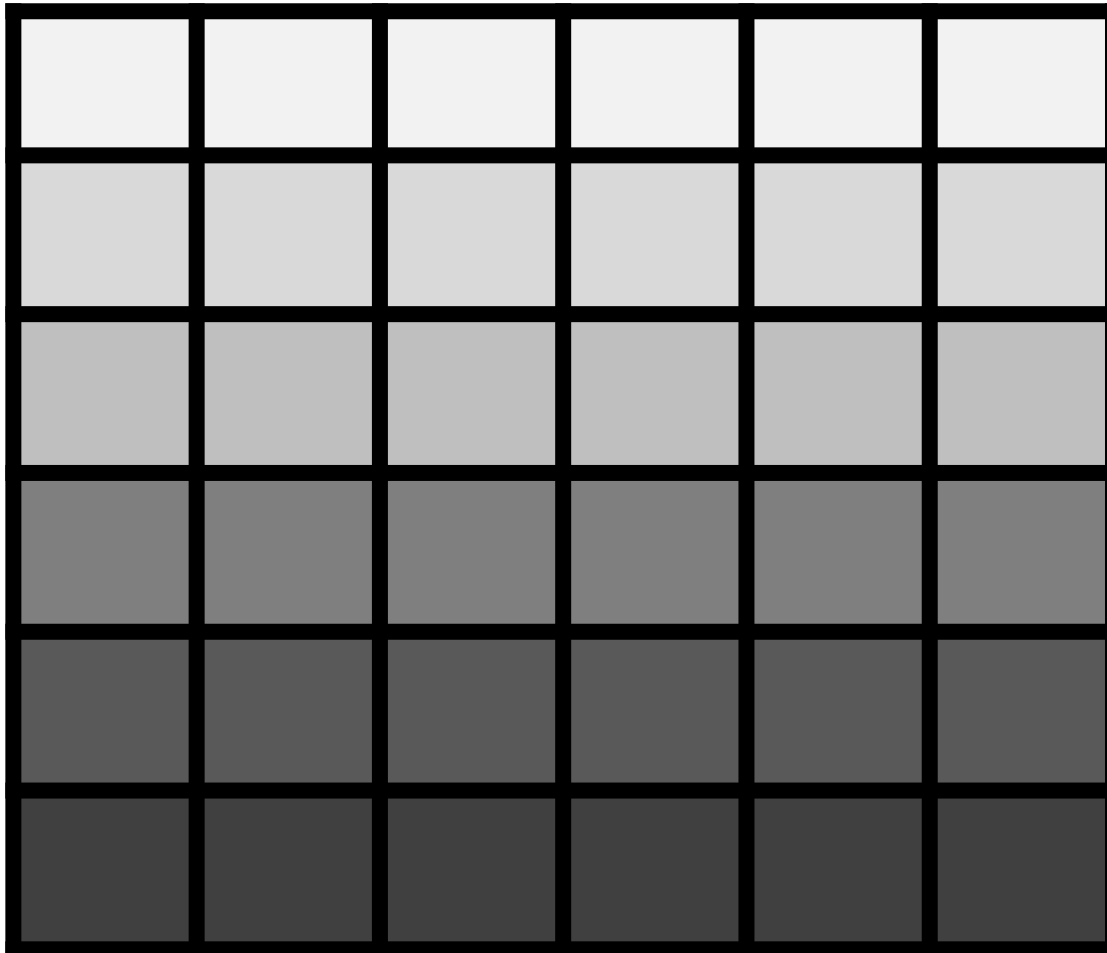
# Randomized Complete Block Design (RCBD)

```
> library(agricolae)
> treat<-c(1,2,3,4, 5, 6)
> outdesign <- design.rcbd(treat, 6, seed = 11)
> rcb <- outdesign$book
> levels(rcb$block) <- c("Block 1", "Block 2", "Block 3","Block 4","Block 5","Block 6")
> levels(rcb$treat) <- c("A", "B", "C", "D", "E", "F")
> rcb
```

	plots	block	treat
1	101	Block 1	D
2	102	Block 1	F
3	103	Block 1	B
4	104	Block 1	C
5	105	Block 1	E
6	106	Block 1	A

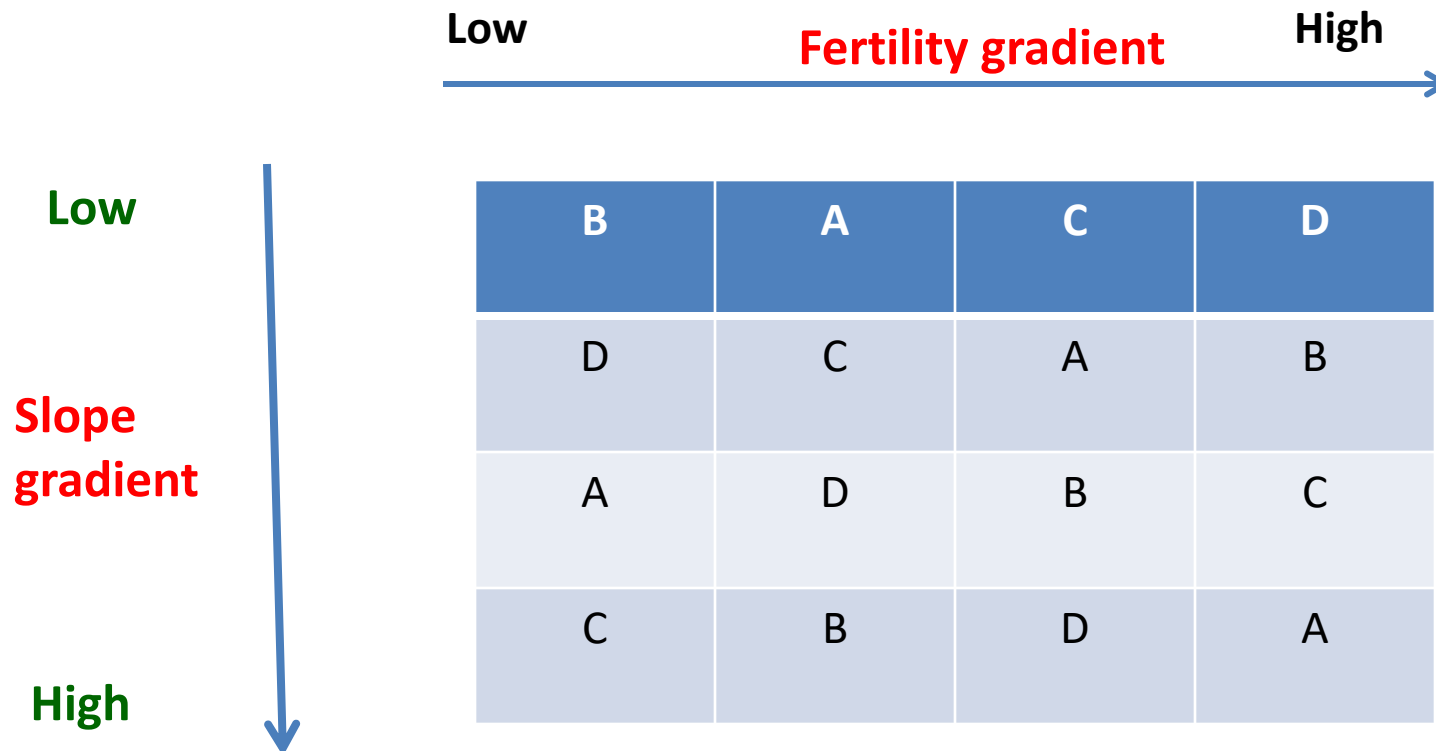
# Latin Square Design

- Only control variation in one direction—**Latin Square (2 direction)**



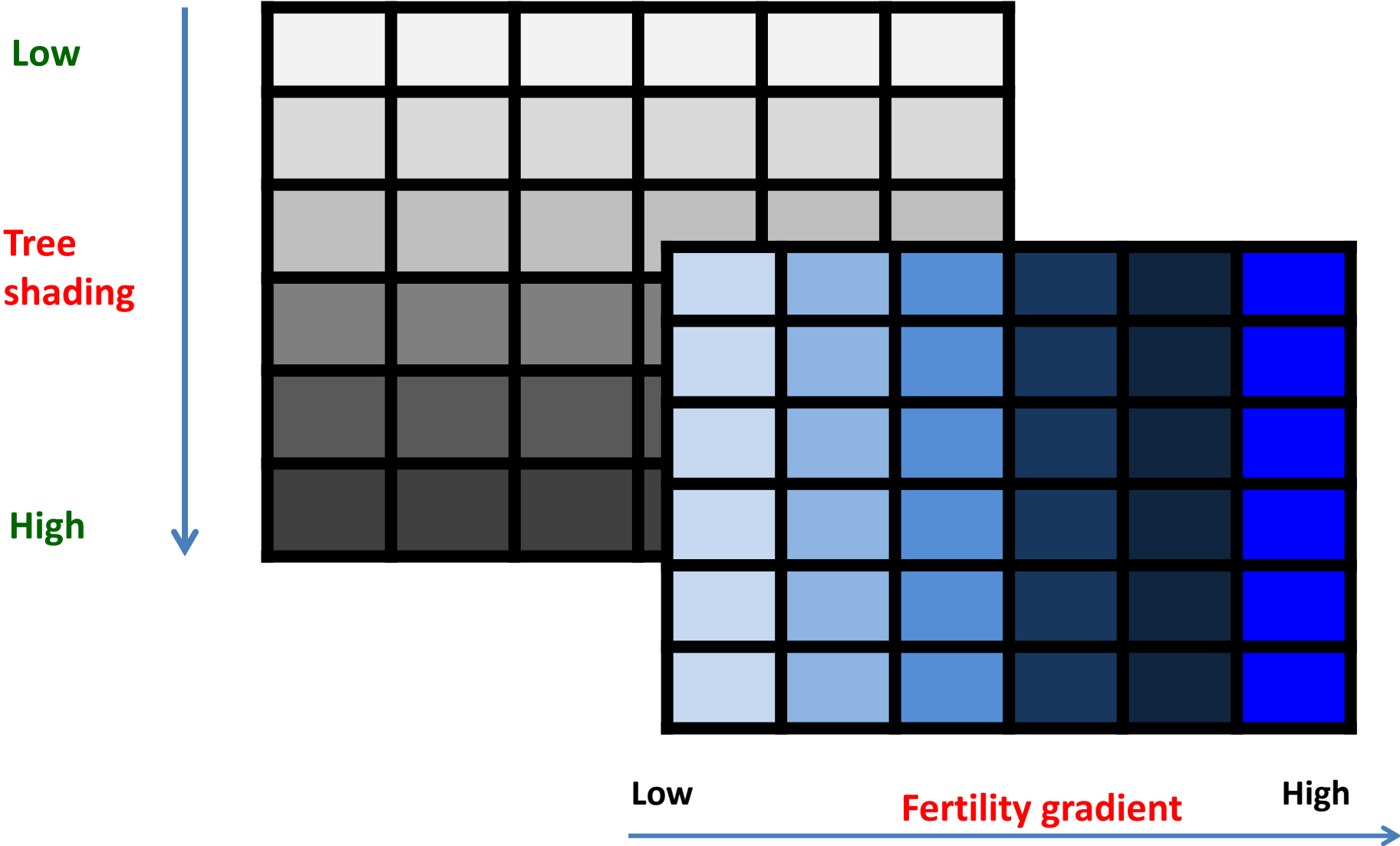
# Latin Square design

- In Latin Square, the experimenter is interested controlling two extraneous sources of variability (allows for blocking in two directions).
- Two blocking factors can be look at independently (Two RCBD)





# Latin Square Design



# Latin Square Design

	<i>Machine 1</i>	<i>Machine 2</i>	<i>Machine 3</i>	<i>Machine 4</i>
Operator 1	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>
Operator 2	<i>C</i>	<i>A</i>	<i>D</i>	<i>B</i>
Operator 3	<i>B</i>	<i>D</i>	<i>A</i>	<i>C</i>
Operator 4	<i>D</i>	<i>C</i>	<i>B</i>	<i>A</i>

# Latin Square Design



WEEK 1	WEEK 2	WEEK 3	WEEK 4
Control	Low dose	Medium dose	High dose
Low dose	Medium dose	High dose	Control
Medium dose	High dose	Control	Low dose
High dose	Control	Low dose	Medium dose

# Latin Square design

- Laid out in Rows and Columns in this way is called a LATIN SQUARE: .i.e., each treatment occurs once and only once in each row block and column block. Thus:
- **Number of Replications = Number of Rows = Number of columns = Number of treatments**
  - The total number of plots is the square of the number of treatments
  - If you can block on two (perpendicular) sources of variation (rows x columns) you can reduce experimental error when compared to the RCBD

# Latin Square Design

- Square requirement: Limitation for large experiments
- Inefficient for small experiments: Few error degrees of freedom
- Several incomplete Latin Square designs exist (Youden Design)

# Latin Square Design

## Generating Latin Square in R

```
> Nutrition <- c("Nutrition 1", "Nutrition 2", "Nutrition 3", "Nutrition 4", "Nutrition 5")  
> outdesign <- design.lsd( Nutrition, seed = 23)  
> lsd <- outdesign$book  
> levels(lsd$row) <- c("Week 1", "Week 2", "Week 3", "Week 4", "Week 5")  
> levels(lsd$col) <- c("Animal 1", "Animal 2", "Animal 3", "Animal 4", "Animal 5")  
> head(lsd)
```

# Latin Square Design

```
> head(lsd)
```

	plots	row	col	Nutrition
1	101	Week 1	Animal 1	Nutrition 1
2	102	Week 1	Animal 2	Nutrition 4
3	103	Week 1	Animal 3	Nutrition 2
4	104	Week 1	Animal 4	Nutrition 3
5	105	Week 1	Animal 5	Nutrition 5
6	201	Week 2	Animal 1	Nutrition 4



# Split-Plot “Design”

- Split- plot is used with **a factorial treatment structure**
- One factor require larger area for application – used mainly for logistics reasons
- Can be used with CRD, RCBD or Latin Square – it is more of treatment arrangement than design
- Involves split a larger experimental unit onto which the first factor is applied into the smaller units onto which the second factor is applied

# Split-Plot “Design”

- One factor require larger area for application – used mainly for logistics reasons



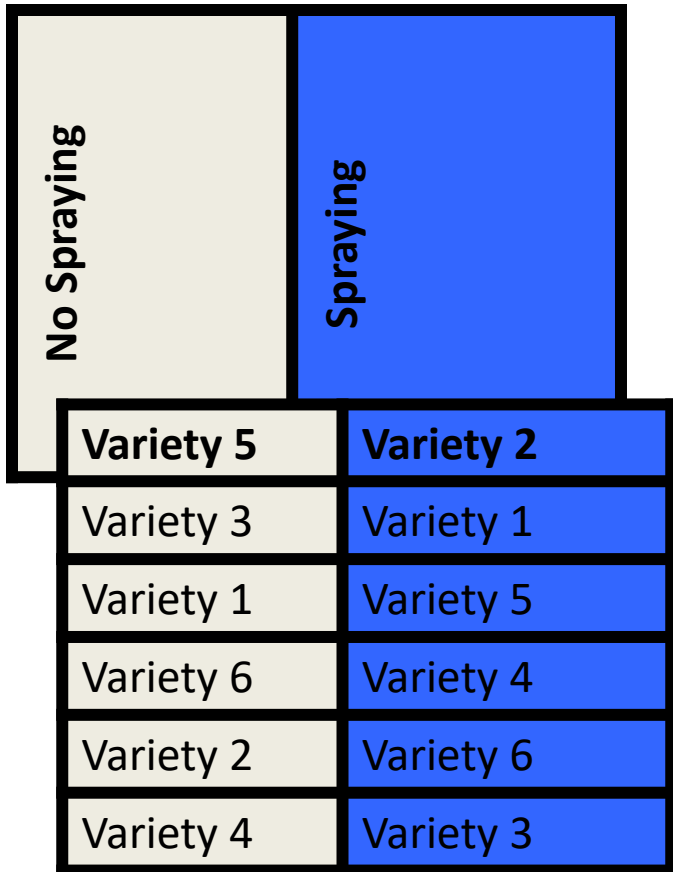
**Tray A**



**Tray B**

# Split-Plot “Design”

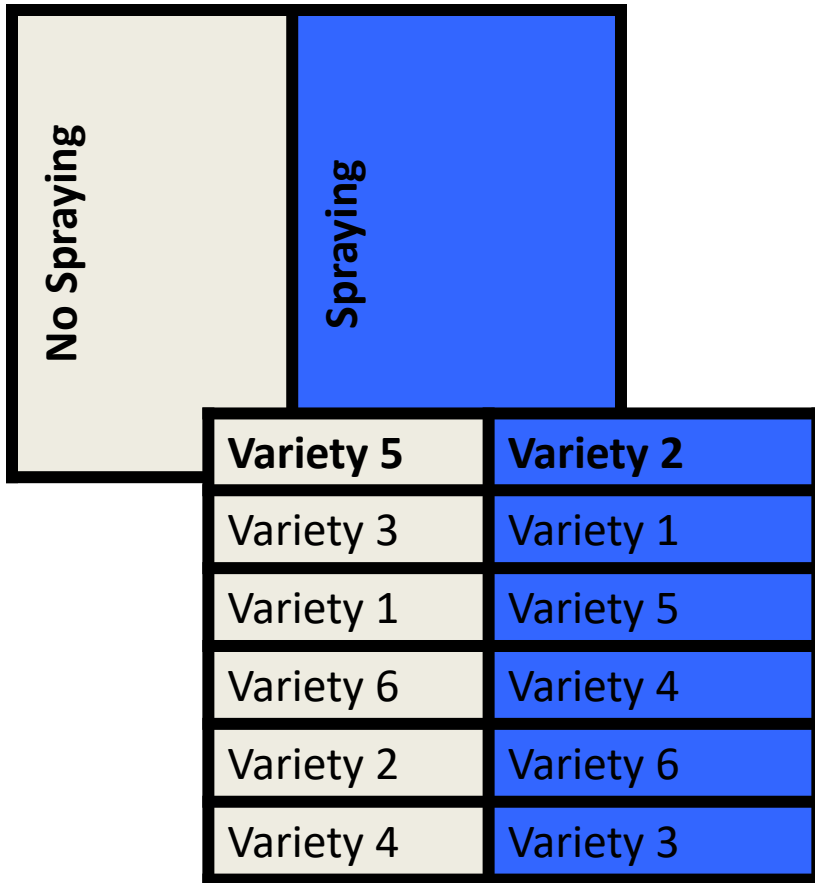
Block 1



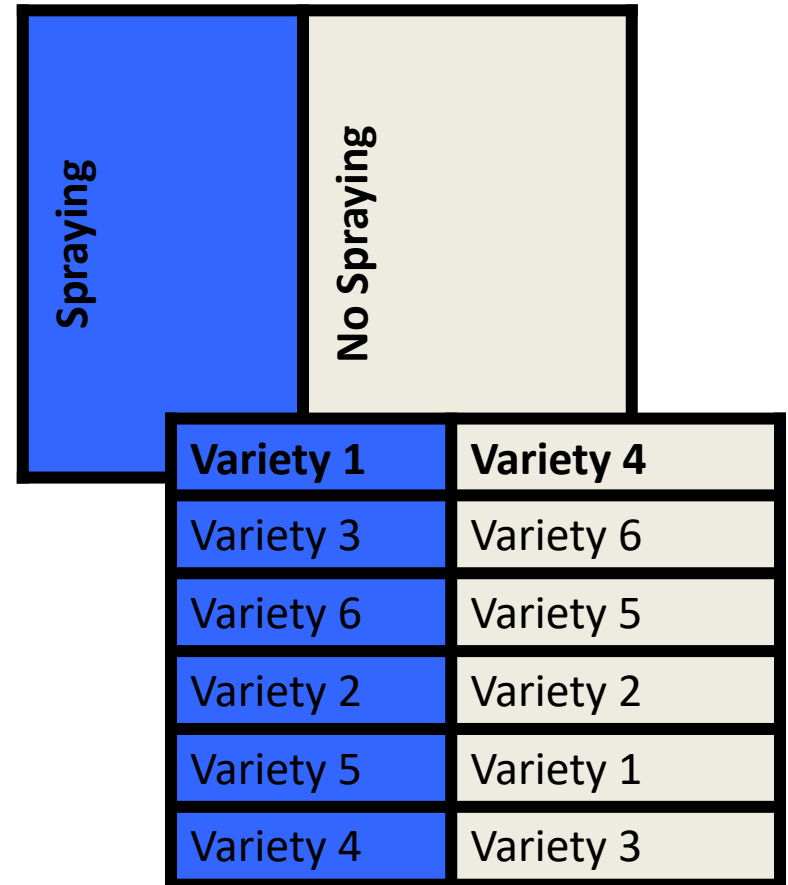
- Used with ***factorial*** treatment structure
- One factor require larger area for application – used mainly for logistics reasons
- Can be used with CRD, RCBD or Latin Square – it is more of treatment arrangement than design
- Involves split a larger experimental unit onto which the first factor is applied into the smaller units onto which the second factor is applied

# Split-Plot “Design”

Block 1



Block 2



# Split-Plot “Design”

Block 1

No Spraying		Spraying	
Variety 5	Variety 2	Variety 5	Variety 2
Variety 3	Variety 1	Variety 3	Variety 1
Variety 1	Variety 5	Variety 1	Variety 5
Variety 6	Variety 4	Variety 6	Variety 4
Variety 2	Variety 6	Variety 2	Variety 6
Variety 4	Variety 3	Variety 4	Variety 3

- The split can proceed as long as it is required or feasible
- Randomization for the levels of different factors are done separately
- First randomly assign **spraying** to the main plot and then assign varieties to the sub-plots
- – *implication is that different experimental errors are used for testing different factors*

# Split-Plot Design

```
library(agricolae)
```

```
treatment1<-c("Spray", "No Spray")
```

```
treatment2<-c("Variety 1","Variety 2", "Variety 3","Variety 4","Variety 5","Variety 6")
```

```
design.split(treatment1, treatment2,r=3, design="rcbd",serie = 2,
```

```
  seed = 10, kinds = "Super-Duper", first=TRUE,randomization=TRUE)
```

```
  #treatment1 = treatment in the plot
```

```
  #treatment2 = treatment in the subplot
```

```
  #r = replications or block (3)
```

```
  #seed = randomization seed for repeat
```

# Incomplete Block Designs



# Introduction to IBD

- **Importance of blocking**

- ❖ Decrease experimental error and provide more precise comparison of treatments - increase precision
- ❖ Be able to make comparisons under more uniform conditions (within blocks)

# Introduction to IBD

- **Challenges faced in blocking**
  - ❖ Large number of treatments require larger blocks
  - ❖ As blocks get larger, the conditions become more heterogeneous
    - precision decreases



**If We have 9 treatments we may need to borrow the neighbour puppies**

# Introduction to IBD

- **Challenges faced in blocking**
  - ❖ Blocks based on natural grouping of experimental units may have fewer experimental units compare the number of treatments



# Introduction to IBD

- **Challenges faced in blocking**

- ❖ Sometimes it is therefore necessary to block experimental units into groups smaller than complete replicate of all treatments with RCBD or Latin Square designs
- ❖ i.e. plots are grouped into blocks that are not large enough to contain all treatments (entries)

# Introduction to IBD

Incomplete block designs may be classified into based on

- 1) Number of blocking factors (One vs two Blocking factors)
- 2) Precision of comparison of treatments (Balanced vs Partially Balanced)

# Introduction to IBD

## Classification based number of blocking factors

- Randomized Incomplete Block Design – one blocking factor
- In complete Latin Square – two blocking factors

# Introduction to IBD

## Classification based on precision of treatment comparison

- **Balanced Incomplete Block design:** Each pair of treatment occur equal number of times in the same block (eq)
- **Partially balanced Incomplete Block design** – pairs of treatments don't occur in equal frequency

# Balanced Incomplete Block Design

- ❖ All treatments are equally replicated
- ❖ Each pair of treatments in the same block equal number of times
- ❖ All pairs are compared with the same precision even though differences between blocks may be large



# Balanced Incomplete Block Design

- **Balanced Incomplete Block Designs**

- ❖ Can balance any number of treatments and any size of block  
but...**treatments** and **block size** determine the number of  
replications required for balance
- ❖ Often the minimum number of replications required for balance  
is too large to be practical

# Balanced Incomplete Block Design

- Example BIB: Tomato Seed Germination Experiment (Kuehl)
  - Effect of temperature inhibition on seed germination
  - **Treatment**: Four temperature (25° C, 30° C, 35° and 40° C). Seed subjected to a constant temperature in a controlled environment chamber
  - **Design**: A single chamber constitute an experimental unit and **each run of the experiment constitute a block**
  - One complete block/replication would require 4 chambers but only three chambers were available to the scientist - **Incomplete Block**

# Balanced Incomplete Block Design

- Example BIB: Tomato Seed Germination Experiment (Kuehl)

Chamber				Chamber			
	1	2	3		1	2	3
Run 1	25°C	30°C	40°C	Run 2	35°C	30°C	25°C
Chamber				Chamber			
	1	2	3		1	2	3
Run 3	40°C	25°C	35°C	Run 4	40°C	30°C	35°C

# Balanced Incomplete Block Design

- Designing BIB using agricolae
- library(agricolae)

```
design.bib(trt, k, r=NULL, serie = 2, seed = 0, kinds = "Super-  
Duper", maxRep=20,randomization=TRUE)
```

# Balanced Incomplete Block Design

#BIB

```
trt<-c("25C", "30C", "35C", "40C")
```

```
design.bib(trt, k=3, r=NULL, serie = 2, seed = 30, kinds = "Super-Duper",  
maxRep=20, randomization=TRUE)
```

*#trt= number of treatments, k= block size, r= number of rep  
(calculate)*

# Balanced Incomplete Block Design

#BIB

```
trt<-c("25C", "30C", "35C", "40C")  
design.bib(trt, k=3, r=NULL, serie = 2, seed = 30, kinds = "Super-Duper",  
maxRep=20,randomization=TRUE)
```

*\$book*

	<i>plots</i>	<i>block</i>	<i>trt</i>
1	101	1	40C
2	102	1	35C
3	103	1	30C
4	201	2	25C
5	202	2	30C
6	203	2	35C
7	301	3	40C
8	302	3	35C
9	303	3	25C
10	401	4	30C
11	402	4	25C
12	403	4	40C

# Partially balanced incomplete block designs

- BIB designs can not be constructed for every experimental situation requiring incomplete block
- **Required number of replications may become prohibitive**
- Partially balanced incomplete designs requiring much less replication can be constructed

# Partially balanced incomplete block designs

- Different treatment pairs occur in the same blocks an unequal number of times or some treatment pairs never occur together in the same block
- Mean comparisons have differing levels of precision



# Partially balanced incomplete block designs

Partially Balanced Incomplete Block Design with six treatments in  
Blocks of size 4 (Kuel page 323)

Block 1	1	4	2	5
Block 2	2	5	3	6
Block 3	3	6	1	4

- Pairs (1,4), (2,5) and (3,6) occur together in 3 blocks
- All other treatments occur together in only one block
- Different pairs are compared with different levels of precision
- For application ensure that there is reasonable precision for all pair-wise comparison

# Row-Column Designs for Two Blocking Criteria

- Latin Square is a complete Block Design used to control variation in two directions
- Latin Square may be impractical because large number of experimental units required  $N = t^2$
- There are incomplete block designs derived from Latin Squares
  - Row-Column Designs – either rows or columns or both as incomplete blocks
  - Youden Squares – two or more rows omitted from the Latin Square

# Row-Column Designs for Two Blocking Criteria

- The designs are arranged in  $p$  rows and  $q$  column of experimental units

4 X7 Row-Column Balanced Incomplete Block Design (Kuel page 321)

	Automobiles						
Position	(1)	(2)	(3)	(4)	(5)	(6)	(7)
(1)	3	4	5	6	7	1	2
(2)	5	6	7	1	2	3	4
(3)	6	7	1	2	3	4	5
(4)	7	1	2	3	4	5	6

Row-Column design with seven treatments evaluated on the four car tire positions (Row) and 7 automobiles (Column).

Position – Complete block (all seven treatment)

Automobile – Incomplete Block (only take 4 tires – test only 4 out of 7)

# Row-Column Designs for Two Blocking Criteria

## **Youden Squares**

- Are incomplete Latin Squares with two or more rows from the Latin squares omitted.

# RESOLVABLE and CYCLIC INCOMPLETE BLOCK DESIGNS

# Resolvable incomplete block designs

- **Resolvable designs** - blocks are grouped so that each group of blocks constitute one complete replication of the treatments
  - Useful for trial management - replication-by-replication basis
  - Field operations can be conducted in stages (planting, weeding, data collection, harvest)
  - Complete replicates can be lost without losing the whole experiment
  - If you have two or more complete replications, you can analyze as a RCBD if the blocking turns out to be ineffective

# Resolvable incomplete block designs

- Resolvable designs are arranged in  $r$  replicate groups of  $s$  blocks with  $k$  units per blocks
- The number of treatments is a multiple of the number of unit per block  $t = sk$
- The total number of blocks satisfies the relationship

$$b = rs \geq t + r - 1$$

for balanced resolvable incomplete block designs

# Alpha designs

- Resolvable designs developed by Patterson and Williams, 1976
  - Number of varieties and replications were fixed by statutory requirements
  - Large number of varieties necessitate incomplete block designs
  - Resolvable design were required for proper management in the field
  - Existing resolvable designs did not always accommodate the number varieties and block sizes required by the trials



# Alpha designs

- Alpha designs have no limitation on block size
- except for constraint that the number of treatments  $t$  is a multiple of block size  $k$ , so that  $t=sk$  to have resolvable design with equal block sizes
  - Alpha designs are available for many  $(r,k,s)$  combinations where  $r$  is the number of replicates,  $k$  is the block size and  $s$  is the number of blocks per replicate (the number of treatments  $t=ks$ ).

# Alpha designs

- Alpha designs have no limitation on block size
  - Efficient alpha designs exist for some combinations for which conventional lattices do not exist. Can also accommodate unequal block sizes.

# Alpha designs

```
#alpha lattice design
```

```
trt<-1:100
```

```
t<-length(trt)
```

```
k<-5 #number of blocks
```

```
s<-t/k # number of blocks that constitute a complete replicate
```

```
r<-2 #number of replications
```

```
outdesign<-design.alpha(trt, k=5, r=2, serie = 2, seed = 0, kinds = "Super-Duper",randomization=TRUE)
```

```
class(outdesign) #finding out the type of object
```

```
str(outdesign) #finding out the structure of the object outdesign
```

```
book<-outdesign$book # picking one element from our list called book
```

```
plots<-book[,1] #creating an object called plot showing experimental units/plots
```

```
dim(plots)<-c(k,s,r) #showing plot labels with respect to k, s, r
```

```
for (i in 1:r) print(t(plots[,i]))
```

```
outdesign$sketch #show a field sketch
```