

agricolae tutorial (Version 1.2-4)

Felipe de Mendiburu⁽¹⁾

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¹Profesor Principal del Departamento Académico de Estadística e Informática de la Facultad de Economía y Planificación. Universidad Nacional Agraria La Molina-PERU

Preface

The following document was developed to facilitate the use of agricolae package in R, it is understood that the user knows the statistical methodology for the design and analysis of experiments and through the use of the functions programmed in agricolae facilitate the generation of the field book experimental design and their analysis. The first part document describes the use of graph.freq role is complementary to the *hist* function of R functions to facilitate the collection of statistics and frequency table, statistics or grouped data histogram based training grouped data and graphics as frequency polygon or ogive; second part is the development of experimental plans and numbering of the units as used in an agricultural experiment; a third part corresponding to the comparative tests and finally provides agricolae miscellaneous additional functions applied in agricultural research and stability functions, soil consistency, late blight simulation and others.

1 Introduction

The package **agricolae** offers a broad functionality in the design of experiments, especially for experiments in agriculture and improvements of plants, which can also be used for other purposes. It contains the following designs: lattice, alpha, cyclic, balanced incomplete block designs, complete randomized blocks, Latin, Graeco-Latin, augmented block designs, split plot and strip plot. It also has several procedures of experimental data analysis, such as the comparisons of treatments of Waller-Duncan, Bonferroni, Duncan, Student-Newman-Keuls, Scheffe, or the classic LSD and Tukey; and non-parametric comparisons, such as Kruskal-Wallis, Friedman, Durbin, Median and Waerden, stability analysis, and other procedures applied in genetics, as well as procedures in biodiversity and descriptive statistics. reference [4]

1.1 Installation

The main program of **R** should be already installed in the platform of your computer (*Windows, Linux or MAC*). If it is not installed yet, you can download it from the R project (*www.r-project.org*) of a repository CRAN. Reference [14]

```
> install.packages("agricolae")
```

 Once the **agricolae** package is installed, it needs to be made accessible to the current **R** session by the command:

```
> library(agricolae)
```

For online help facilities or the details of a particular command (such as the function **waller.test**) you can type:

```
> help(package="agricolae")
> help(waller.test)
```

For a complete functionality, **agricolae** requires other packages.

MASS: for the generalized inverse used in the function *PBIB.test*

nlme: for the methods REML and LM in *PBIB.test*

klaR: for the function *triplot* used in the function *AMMI*

Cluster: for the use of the function *consensus*

spdep: for the between genotypes spatial relation in biplot of the function *AMMI*

algDesign: for the balanced incomplete block design *design.bib*

1.2 Use in R

Since **agricolae** is a package of functions, these are operational when they are called directly from the console of **R** and are integrated to all the base functions of **R**. The following orders are frequent:

```
> detach(package:agricolae) # detach package agricole
> library(agricolae) # Load the package to the memory
> designs<-apropos("design")
> print(designs[substr(designs,1,6)=="design"], row.names=FALSE)

[1] "design.ab"      "design.alpha"  "design.bib"
[4] "design.crd"    "design.cyclic" "design.dau"
[7] "design.graeco" "design.lattice" "design.lsd"
[10] "design.rcbd"   "design.split"  "design.strip"
[13] "design.youden"
```

For the use of symbols that do not appear in the keyboard in Spanish, such as:

~, [,], &, ^, |. <, >, {, }, \% or others, use the table ASCII code.

```
> library(agricolae) # Load the package to the memory:
```

In order to continue with the command line, do not forget to close the open windows with any R order. For help:

```
help(graph.freq)
? (graph.freq)
str(normal.freq)
example(join.freq)
```

1.3 Data set in agricolae

```
> A<-as.data.frame(data(package="agricolae")$results[,3:4])
> A[,2]<-paste(substr(A[,2],1,35),"..",sep="..")
> head(A)
```

	Item	Title
1	CIC	Data for late blight of potatoes...
2	Chz2006	Data amendment Carhuaz 2006...
3	ComasOxapampa	Data AUDPC Comas - Oxapampa...
4	DC	Data for the analysis of carolina g...
5	Glycoalkaloids	Data Glycoalkaloids...
6	Hco2006	Data amendment Huanuco 2006...

2 Descriptive statistics

The package **agricolae** provides some complementary functions to the **R** program, specifically for the management of the histogram and function *hist*.

2.1 Histogram

The histogram is constructed with the function *graph.freq* and is associated to other functions: *polygon.freq*, *table.freq*, *stat.freq*. See Figures: 1, 2 and 3 for more details.

Example. Data generated in **R** . (students' weight).

```
> weight<-c( 68, 53, 69.5, 55, 71, 63, 76.5, 65.5, 69, 75, 76, 57, 70.5, 71.5, 56, 81.5,  
+           69, 59, 67.5, 61, 68, 59.5, 56.5, 73, 61, 72.5, 71.5, 59.5, 74.5, 63)  
> print(summary(weight))
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   
  53.00  59.88   68.00   66.45  71.50   81.50
```

```
> par(mfrow=c(1,2),mar=c(4,3,0,1),cex=0.6)  
> h1<- graph.freq(weight,col="yellow",frequency=1,las=2,xlab="h1")  
> h2<- graph.freq (weight, frequency =2, axes= FALSE,las=2,xlab="h2")  
> polygon.freq(h2, col="blue", lwd=2, frequency =2)  
> TIC<- h2$breaks[2]- h2$breaks[1]  
> axis(1,c(h2$mids[1]-TIC, h2$mids, h2$mids[6]+TIC ),cex=0.6)  
> axis(2, cex=0.6,las=1)
```

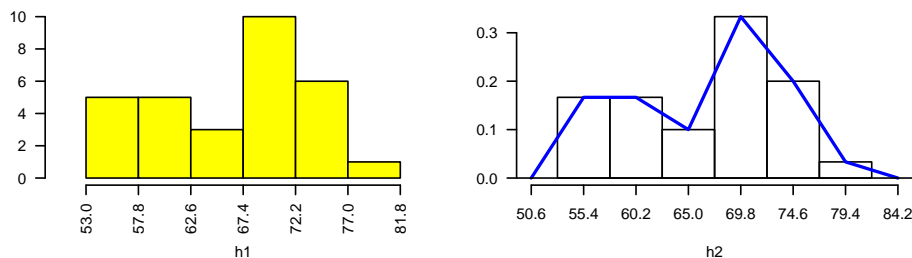


Figure 1: Absolute and relative frequency with polygon.

2.2 Statistics and Frequency tables

Statistics: mean, median, mode and standard deviation of the grouped data.

```
> stat.freq(h1)
```

```
$variance  
[1] 51.37655
```

```
$mean  
[1] 66.6
```

```
$median  
[1] 68.36
```

```
$mode
```

```
      [- -]      mode  
[1,] 67.4 72.2 70.45455
```

Frequency tables: Use *table.freq*, *stat.freq* and *summary*
The *table.freq* is equal to *summary()*

Limits class: **Lower and Upper**
Class point: **Main**
Frequency: **Frequency**
Percentage frequency: **Percentage**
Cumulative frequency: **CF**
Cumulative percentage frequency: **CPF**

```
> print(summary(h1), row.names=FALSE)
```

Lower	Upper	Main	Frequency	Percentage	CF	CPF
53.0	57.8	55.4	5	16.7	5	16.7
57.8	62.6	60.2	5	16.7	10	33.3
62.6	67.4	65.0	3	10.0	13	43.3
67.4	72.2	69.8	10	33.3	23	76.7
72.2	77.0	74.6	6	20.0	29	96.7
77.0	81.8	79.4	1	3.3	30	100.0

2.3 Histogram manipulation functions

You can extract information from a histogram such as class intervals *intervals.freq*, attract new intervals with the *sturges.freq* function or to join classes with *join.freq* function. It is also possible to reproduce the graph with the same creator *graph.freq* or function *plot* and overlay normal function with *normal.freq* be it a histogram in absolute scale, relative or density . The following examples illustrates these properties.

```
> sturges.freq(weight)
```

```
$maximum  
[1] 81.5
```

```
$minimum  
[1] 53
```

```
$amplitude  
[1] 29
```

```
$classes  
[1] 6
```

```
$interval  
[1] 4.8
```

```
$breaks  
[1] 53.0 57.8 62.6 67.4 72.2 77.0 81.8
```

```

> intervals.freq(h1)

      lower upper
[1,]  53.0  57.8
[2,]  57.8  62.6
[3,]  62.6  67.4
[4,]  67.4  72.2
[5,]  72.2  77.0
[6,]  77.0  81.8

> join.freq(h1,1:3) -> h3
> print(summary(h3))

  Lower Upper Main Frequency Percentage CF   CPF
1  53.0  67.4 60.2         13      43.3 13  43.3
2  67.4  72.2 69.8         10      33.3 23  76.7
3  72.2  77.0 74.6          6      20.0 29  96.7
4  77.0  81.8 79.4          1       3.3 30 100.0

> par(mfrow=c(1,2),mar=c(4,3,0,1),cex=0.6)
> plot(h3, frequency=2,col="magenta",ylim=c(0,0.6))
> normal.freq(h3,frequency=2,col="green")
> ogive.freq(h3,col="blue")

```

```

      x      RCF
1  53.0  0.0000
2  67.4  0.4333
3  72.2  0.7667
4  77.0  0.9667
5  81.8  1.0000
6  86.6  1.0000

```

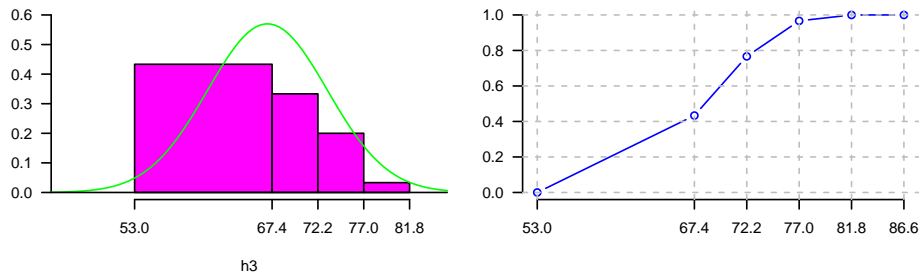


Figure 2: Join frequency and relative frequency with normal and Ogive.

2.4 hist() and graph.freq() based on grouped data

The *hist* and *graph.freq* have the same characteristics, only *f2* allows build histogram from grouped data.


```

0-10 (3)
10-20 (8)
20-30 (15)
30-40 (18)
40-50 (6)

> par(mfrow=c(1,2),mar=c(4,3,2,1),cex=0.6)
> h4<-hist(weight,xlab="Classes (h4)")
> table.freq(h4)
> # this is possible
> # hh<-graph.freq(h4,plot=FALSE)
> # summary(hh)
> # new class
> classes <- c(0, 10, 20, 30, 40, 50)
> freq <- c(3, 8, 15, 18, 6)
> h5 <- graph.freq(classes,counts=freq, xlab="Classes (h5)",main="Histogram grouped data")

```

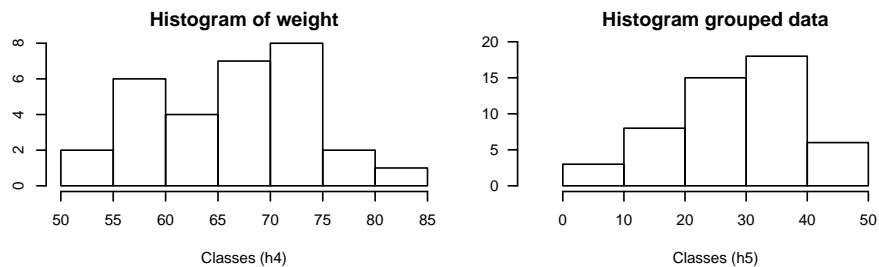


Figure 3: hist() function and histogram defined class

```

> print(summary(h5),row.names=FALSE)

```

Lower	Upper	Main	Frequency	Percentage	CF	CPF
0	10	5	3	6	3	6
10	20	15	8	16	11	22
20	30	25	15	30	26	52
30	40	35	18	36	44	88
40	50	45	6	12	50	100

3 Experiment designs

The package **agricolae** presents special functions for the creation of the field book for experimental designs. Due to the random generation, this package is quite used in agricultural research.

For this generation, certain parameters are required, as for example the name of each treatment, the number of repetitions, and others, according to the design references [1, 9, 10, 11]. There are other parameters of random generation, as the seed to reproduce the same random generation or the generation method (See the reference manual of **agricolae** .

<http://cran.at.r-project.org/web/packages/agricolae/agricolae.pdf>

Important parameters in the generation of design:

series: A constant that is used to set numerical tag blocks , eg number = 2, the labels will be : 101, 102, for the first row or block, 201, 202, for the following , in the case of completely randomized design, the numbering is sequential.

design: Some features of the design requested agricolae be applied specifically to design.ab(factorial) or design.split (split plot) and their possible values are: "rcbd", "crd" and "lsd".

seed: The seed for the random generation and its value is any real value, if the value is zero, it has no reproducible generation, in this case copy of value of the outdesign\$parameters.

kinds: the random generation method, by default "Super-Duper".

first: For some designs is not required random the first repetition, especially in the block design, if you want to switch to random, change to TRUE.

randomization: TRUE or FALSE. If false, randomization is not performed

Output design:

parameters: the input to generation design, include the seed to generation random, if seed=0, the program generate one value and it is possible reproduce the design.

book: field book

statistics: the information statistics the design for example efficiency index, number of treatments.

sketch: distribution of treatments in the field.

The enumeration of the plots

zigzag is a function that allows you to place the numbering of the plots in the direction of serpentine: The zigzag is output generated by one design: blocks, Latin square, graeco, split plot, strip plot, into blocks factorial, balanced incomplete block, cyclic lattice, alpha and augmented blocks.

fieldbook: output zigzag, contain field book.

3.1 Completely randomized design

They only require the names of the treatments and the number of their repetitions and its parameters are:

```
> str(design.crd)
```

```
function (trt, r, serie = 2, seed = 0, kinds = "Super-Duper",
         randomization = TRUE)
```

```
> trt <- c("A", "B", "C")
```

```
> repeticion <- c(4, 3, 4)
```

```
> outdesign <- design.crd(trt,r=repeticion,seed=777,serie=0)
```

```
> book1 <- outdesign$book
```

```
> head(book1)
```

```
plots r trt
1     1 1  B
2     2 1  A
3     3 2  A
4     4 1  C
```

```
5    5 2  C
6    6 3  A
```

```
Excel:write.csv(book1,"book1.csv",row.names=FALSE)
```

3.2 Randomized complete block design

They require the names of the treatments and the number of blocks and its parameters are:

```
> str(design.rcbd)

function (trt, r, serie = 2, seed = 0, kinds = "Super-Duper",
         first = TRUE, continue = FALSE, randomization = TRUE)

> trt <- c("A", "B", "C","D","E")
> repeticion <- 4
> outdesign <- design.rcbd(trt,r=repeticion, seed=-513, serie=2)
> # book2 <- outdesign$book
> book2<- zigzag(outdesign) # zigzag numeration
> print(outdesign$sketch)

      [,1] [,2] [,3] [,4] [,5]
[1,] "D"  "B"  "C"  "E"  "A"
[2,] "E"  "A"  "D"  "B"  "C"
[3,] "E"  "D"  "B"  "A"  "C"
[4,] "A"  "E"  "C"  "B"  "D"

> print(matrix(book2[,1],byrow = TRUE, ncol = 5))
```

```
      [,1] [,2] [,3] [,4] [,5]
[1,] 101 102 103 104 105
[2,] 205 204 203 202 201
[3,] 301 302 303 304 305
[4,] 405 404 403 402 401
```

3.3 Latin square design

They require the names of the treatments and its parameters are:

```
> str(design.lsd)

function (trt, serie = 2, seed = 0, kinds = "Super-Duper",
         first = TRUE, randomization = TRUE)

> trt <- c("A", "B", "C", "D")
> outdesign <- design.lsd(trt, seed=543, serie=2)
> print(outdesign$sketch)
```

```

      [,1] [,2] [,3] [,4]
[1,] "C"  "A"  "B"  "D"
[2,] "D"  "B"  "C"  "A"
[3,] "B"  "D"  "A"  "C"
[4,] "A"  "C"  "D"  "B"

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> print(matrix(book[,1],byrow = TRUE, ncol = 4))

```

```

      [,1] [,2] [,3] [,4]
[1,] 101 102 103 104
[2,] 204 203 202 201
[3,] 301 302 303 304
[4,] 404 403 402 401

```

3.4 Graeco-Latin designs

They require the names of the treatments of each factor of study and its parameters are:

```

> str(design.graeco)

function (trt1, trt2, serie = 2, seed = 0, kinds = "Super-Duper",
         randomization = TRUE)

> trt1 <- c("A", "B", "C", "D")
> trt2 <- 1:4
> outdesign <- design.graeco(trt1,trt2, seed=543, serie=2)
> print(outdesign$sketch)

```

```

      [,1] [,2] [,3] [,4]
[1,] "A 1" "D 4" "B 3" "C 2"
[2,] "D 3" "A 2" "C 1" "B 4"
[3,] "B 2" "C 3" "A 4" "D 1"
[4,] "C 4" "B 1" "D 2" "A 3"

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> print(matrix(book[,1],byrow = TRUE, ncol = 4))

```

```

      [,1] [,2] [,3] [,4]
[1,] 101 102 103 104
[2,] 204 203 202 201
[3,] 301 302 303 304
[4,] 404 403 402 401

```

3.5 Youden design

They require the names of the treatments of each factor of study and its parameters are:

```
> str(design.youden)

function (trt, r, serie = 2, seed = 0, kinds = "Super-Duper",
         first = TRUE, randomization = TRUE)

> varieties<-c("perricholi","yungay","maria bonita","tomasa")
> r<-3
> outdesign <-design.youden(varieties,r,serie=2,seed=23)
> print(outdesign$sketch)
```

```
      [,1]      [,2]      [,3]
[1,] "maria bonita" "perricholi" "tomasa"
[2,] "yungay"      "tomasa"      "maria bonita"
[3,] "tomasa"      "yungay"      "perricholi"
[4,] "perricholi"  "maria bonita" "yungay"
```

```
> book <- outdesign$book
> print(book) # field book.
```

```
   plots row col varieties
1    101  1  1 maria bonita
2    102  1  2  perricholi
3    103  1  3    tomasa
4    201  2  1    yungay
5    202  2  2    tomasa
6    203  2  3 maria bonita
7    301  3  1    tomasa
8    302  3  2    yungay
9    303  3  3  perricholi
10   401  4  1  perricholi
11   402  4  2 maria bonita
12   403  4  3    yungay
```

```
> print(matrix(as.numeric(book[,1]),byrow = TRUE, ncol = r))
```

```
      [,1] [,2] [,3]
[1,]  101  102  103
[2,]  201  202  203
[3,]  301  302  303
[4,]  401  402  403
```

Serpentine enumeration:

```
> book <- zigzag(outdesign)
> print(matrix(as.numeric(book[,1]),byrow = TRUE, ncol = r))
```

```

      [,1] [,2] [,3]
[1,] 101 102 103
[2,] 203 202 201
[3,] 301 302 303
[4,] 403 402 401

```

3.6 Balanced Incomplete Block Designs

They require the names of the treatments and the size of the block and its parameters are:

```

> str(design.bib)

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

> trt <- c("A", "B", "C", "D", "E" )
> k <- 4
> outdesign <- design.bib(trt,k, seed=543, serie=2)

```

Parameters BIB

```

=====
Lambda      : 3
treatmeans  : 5
Block size  : 4
Blocks      : 5
Replication : 4

```

Efficiency factor 0.9375

<<< Book >>>

```

> book5 <- outdesign$book
> outdesign$statistics

```

	lambda	treatmeans	blockSize	blocks	r	Efficiency
values	3	5	4	5	4	0.9375

```

> outdesign$parameters

```

```

$design
[1] "bib"

```

```

$trt
[1] "A" "B" "C" "D" "E"

```

```

$k
[1] 4

```

```

$serie

```

```
[1] 2

$seed
[1] 543

$kinds
[1] "Super-Duper"
```

According to the produced information, they are five blocks of size 4, being the matrix:

```
> outdesign$sketch

      [,1] [,2] [,3] [,4]
[1,] "D"  "B"  "E"  "C"
[2,] "B"  "A"  "C"  "E"
[3,] "D"  "C"  "E"  "A"
[4,] "D"  "A"  "B"  "C"
[5,] "B"  "D"  "E"  "A"
```

It can be observed that the treatments have four repetitions. The parameter lambda has three repetitions, which means that a couple of treatments are together on three occasions. For example, B and E are found in the blocks I, II and V.

Serpentine enumeration:

```
> book <- zigzag(outdesign)
> matrix(book[,1],byrow = TRUE, ncol = 4)

      [,1] [,2] [,3] [,4]
[1,] 101 102 103 104
[2,] 204 203 202 201
[3,] 301 302 303 304
[4,] 404 403 402 401
[5,] 501 502 503 504
```

3.7 Cyclic designs

They require the names of the treatments, the size of the block and the number of repetitions. This design is used for 6 to 30 treatments. The repetitions are a multiple of the size of the block; if they are six treatments and the size is 3, then the repetitions can be 6, 9, 12, etc. and its parameters are:

```
> str(design.cyclic)

function (trt, k, r, serie = 2, rowcol = FALSE, seed = 0,
  kinds = "Super-Duper", randomization = TRUE)

> trt <- c("A", "B", "C", "D", "E", "F" )
> outdesign <- design.cyclic(trt,k=3, r=6, seed=543, serie=2)
```

```
cyclic design
Generator block basic:
1 2 4
1 3 2
```

```
Parameters
```

```
=====
```

```
treatmeans : 6
Block size : 3
Replication: 6
```

```
> book6 <- outdesign$book
> outdesign$sketch[[1]]
```

```
      [,1] [,2] [,3]
[1,] "A"  "E"  "D"
[2,] "D"  "F"  "C"
[3,] "A"  "D"  "B"
[4,] "A"  "C"  "F"
[5,] "C"  "B"  "E"
[6,] "B"  "E"  "F"
```

```
> outdesign$sketch[[2]]
```

```
      [,1] [,2] [,3]
[1,] "B"  "D"  "C"
[2,] "C"  "A"  "B"
[3,] "F"  "A"  "B"
[4,] "C"  "D"  "E"
[5,] "E"  "A"  "F"
[6,] "F"  "E"  "D"
```

12 blocks of 4 treatments each have been generated. **Serpentine enumeration:**

```
> book <- zigzag(outdesign)
> array(book$plots,c(3,6,2))->X
> t(X[, ,1])
```

```
      [,1] [,2] [,3]
[1,] 101 102 103
[2,] 106 105 104
[3,] 107 108 109
[4,] 112 111 110
[5,] 113 114 115
[6,] 118 117 116
```

```
> t(X[, ,2])
```

```
      [,1] [,2] [,3]
[1,] 201 202 203
```



```
[2,] 206 205 204
[3,] 207 208 209
[4,] 212 211 210
[5,] 213 214 215
[6,] 218 217 216
```

3.8 Lattice designs

They require a number of treatments of a perfect square; for example 9, 16, 25, 36, 49, etc. and its parameters are:

```
> str(design.lattice)
```

```
function (trt, r = 3, serie = 2, seed = 0, kinds = "Super-Duper",
         randomization = TRUE)
```

They can generate a simple lattice (2 rep.) or a triple lattice (3 rep.) generating a triple lattice design for 9 treatments 3x3

```
> trt<-letters[1:9]
> outdesign <-design.lattice(trt, r = 3, serie = 2, seed = 33,
+   kinds = "Super-Duper")
```

```
Lattice design, triple 3 x 3
```

```
Efficiency factor
(E ) 0.7272727
```

```
<<< Book >>>
```

```
> book7 <- outdesign$book
> outdesign$parameters
```

```
$design
[1] "lattice"
```

```
$type
[1] "triple"
```

```
$trt
[1] "a" "b" "c" "d" "e" "f" "g" "h" "i"
```

```
$r
[1] 3
```

```
$serie
[1] 2
```

```
$seed
[1] 33
```

```

$kind
[1] "Super-Duper"

> outdesign$sketch

$rep1
  [,1] [,2] [,3]
[1,] "i" "d" "a"
[2,] "b" "c" "e"
[3,] "h" "f" "g"

$rep2
  [,1] [,2] [,3]
[1,] "c" "f" "d"
[2,] "b" "h" "i"
[3,] "e" "g" "a"

$rep3
  [,1] [,2] [,3]
[1,] "e" "h" "d"
[2,] "b" "f" "a"
[3,] "c" "g" "i"

> head(book7)

```

```

  plots r block trt
1  101 1     1  i
2  102 1     1  d
3  103 1     1  a
4  104 1     2  b
5  105 1     2  c
6  106 1     2  e

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> array(book$plots,c(3,3,3)) -> X
> t(X[, ,1])

```

```

  [,1] [,2] [,3]
[1,] 101 102 103
[2,] 106 105 104
[3,] 107 108 109

```

```

> t(X[, ,2])

```

```

  [,1] [,2] [,3]
[1,] 201 202 203
[2,] 206 205 204
[3,] 207 208 209

```

```
> t(X[, ,3])

      [,1] [,2] [,3]
[1,] 301 302 303
[2,] 306 305 304
[3,] 307 308 309
```

3.9 Alpha designs

These designs are generated by the alpha arrangements reference [12]. They are similar to the lattice designs, but the tables are rectangular, with s blocks \times k treatments. The number of treatments should be equal to $s*k$ and all the experimental units, $r*s*k$ and its parameters are:

```
> str(design.alpha)

function (trt, k, r, serie = 2, seed = 0, kinds = "Super-Duper",
  randomization = TRUE)

> trt <- letters[1:15]
> outdesign <- design.alpha(trt,k=3,r=2,seed=543)
```

alpha design (0,1) - Serie I

```
Parameters Alpha design
=====
treatmeans : 15
Block size : 3
Blocks      : 5
Replication: 2
```

```
Efficiency factor
(E ) 0.6363636
```

<<< Book >>>

```
> book8 <- outdesign$book
> outdesign$statistics
```

```
      treatments blocks Efficiency
values      15      5 0.6363636
```

```
> outdesign$sketch
```

```
$rep1
      [,1] [,2] [,3]
[1,] "l"  "m"  "e"
[2,] "g"  "c"  "i"
[3,] "o"  "k"  "d"
[4,] "h"  "f"  "j"
```

```
[5,] "a" "n" "b"
```

```
$rep2
```

```
      [,1] [,2] [,3]  
[1,] "o"  "a"  "m"  
[2,] "l"  "k"  "g"  
[3,] "d"  "n"  "h"  
[4,] "j"  "b"  "c"  
[5,] "f"  "i"  "e"
```

```
> # codification of the plots  
> A<-array(book8[,1], c(3,5,2))  
> t(A[,,1])
```

```
      [,1] [,2] [,3]  
[1,] 101 102 103  
[2,] 104 105 106  
[3,] 107 108 109  
[4,] 110 111 112  
[5,] 113 114 115
```

```
> t(A[,,2])
```

```
      [,1] [,2] [,3]  
[1,] 201 202 203  
[2,] 204 205 206  
[3,] 207 208 209  
[4,] 210 211 212  
[5,] 213 214 215
```

Serpentine enumeration:

```
> book <- zigzag(outdesign)  
> A<-array(book[,1], c(3,5,2))  
> t(A[,,1])
```

```
      [,1] [,2] [,3]  
[1,] 101 102 103  
[2,] 106 105 104  
[3,] 107 108 109  
[4,] 112 111 110  
[5,] 113 114 115
```

```
> t(A[,,2])
```

```
      [,1] [,2] [,3]  
[1,] 201 202 203  
[2,] 206 205 204  
[3,] 207 208 209  
[4,] 212 211 210  
[5,] 213 214 215
```

3.10 Augmented block designs

These are designs for two types of treatments: the control treatments (common) and the increased treatments. The common treatments are applied in complete randomized blocks, and the increased treatments, at random. Each treatment should be applied in any block once only. It is understood that the common treatments are of a greater interest; the standard error of the difference is much smaller than when between two increased ones in different blocks. The function `design.dau()` achieves this purpose and its parameters are:

```
> str(design.dau)

function (trt1, trt2, r, serie = 2, seed = 0, kinds = "Super-Duper",
        name = "trt", randomization = TRUE)

> rm(list=ls())
> trt1 <- c("A", "B", "C", "D")
> trt2 <- c("t", "u", "v", "w", "x", "y", "z")
> outdesign <- design.dau(trt1, trt2, r=5, seed=543, serie=2)
> book9 <- outdesign$book
> attach(book9)
> by(trt, block, as.character)

block: 1
[1] "D" "C" "A" "u" "B" "t"
-----
block: 2
[1] "D" "z" "C" "A" "v" "B"
-----
block: 3
[1] "C" "w" "B" "A" "D"
-----
block: 4
[1] "A" "C" "D" "B" "y"
-----
block: 5
[1] "C" "B" "A" "D" "x"

> detach(book9)
```

Serpentine enumeration:

```
> book <- zigzag(outdesign)
> attach(book)
> by(plots, block, as.character)

block: 1
[1] "101" "102" "103" "104" "105" "106"
-----
block: 2
[1] "206" "205" "204" "203" "202" "201"
```

```
-----
block: 3
[1] "301" "302" "303" "304" "305"
```

```
-----
block: 4
[1] "405" "404" "403" "402" "401"
```

```
-----
block: 5
[1] "501" "502" "503" "504" "505"
```

```
> detach(book)
> head(book)
```

```
plots block trt
1  101     1  D
2  102     1  C
3  103     1  A
4  104     1  u
5  105     1  B
6  106     1  t
```

For augmented completely randomized design, use the function `design.crd()`.

3.11 Split plot designs

These designs have two factors, one is applied in plots and is defined as A in a randomized complete block design; and a second factor, which is applied in the subplots of each plot applied at random. The function `design.split()` permits to find the experimental plan for this design and its parameters are:

```
> str(design.split)
```

```
function (trt1, trt2, r = NULL, design = c("rcbd",
      "crd", "lsd"), serie = 2, seed = 0, kinds = "Super-Duper",
      first = TRUE, randomization = TRUE)
```

Application

```
> trt1<-c("A","B","C","D")
> trt2<-c("a","b","c")
> outdesign <-design.split(trt1,trt2,r=3,serie=2,seed=543)
> book10 <- outdesign$book
> head(book10)
```

```
plots  splots  block  trt1  trt2
1  101      1      1      A      c
2  101      2      1      A      a
3  101      3      1      A      b
4  102      1      1      D      b
5  102      2      1      D      c
6  102      3      1      D      a
```

```

> p<-book10$trt1[seq(1,36,3)]
> q<-NULL
> for(i in 1:12)
+ q <- c(q,paste(book10$trt2[3*(i-1)+1],book10$trt2[3*(i-1)+2], book10$trt2[3*(i-1)+3]))

```

In plots:

```

> print(t(matrix(p,c(4,3))))

```

```

      [,1] [,2] [,3] [,4]
[1,] "A"  "D"  "B"  "C"
[2,] "A"  "C"  "B"  "D"
[3,] "A"  "C"  "B"  "D"

```

Ind sub plots (split plot)

```

> print(t(matrix(q,c(4,3))))

```

```

      [,1] [,2] [,3] [,4]
[1,] "c a b" "b c a" "b c a" "a b c"
[2,] "b a c" "a b c" "a c b" "b c a"
[3,] "a b c" "a c b" "a c b" "c a b"

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> head(book,5)

```

```

plots splots block trt1 trt2
1  101     1     1    A    c
2  101     2     1    A    a
3  101     3     1    A    b
4  102     1     1    D    b
5  102     2     1    D    c

```

3.12 Strip-plot designs

These designs are used when there are two types of treatments (factors) and are applied separately in large plots, called bands, in a vertical and horizontal direction of the block, obtaining the divided blocks. Each block constitutes a repetition and its parameters are:

```

> str(design.strip)

```

```

function (trt1, trt2, r, serie = 2, seed = 0, kinds = "Super-Duper",
         randomization = TRUE)

```

Aplication

```

> trt1<-c("A","B","C","D")
> trt2<-c("a","b","c")
> outdesign <-design.strip(trt1,trt2,r=3,serie=2,seed=543)
> book11 <- outdesign$book
> head(book11)

```

```

plots block trt1 trt2
1 101 1 A a
2 102 1 A b
3 103 1 A c
4 104 1 D a
5 105 1 D b
6 106 1 D c

```

```

> t3<-paste(book11$trt1, book11$trt2)
> B1<-t(matrix(t3[1:12],c(4,3)))
> B2<-t(matrix(t3[13:24],c(3,4)))
> B3<-t(matrix(t3[25:36],c(3,4)))
> print(B1)

```

```

      [,1] [,2] [,3] [,4]
[1,] "A a" "A b" "A c" "D a"
[2,] "D b" "D c" "B a" "B b"
[3,] "B c" "C a" "C b" "C c"

```

```

> print(B2)

```

```

      [,1] [,2] [,3]
[1,] "D a" "D b" "D c"
[2,] "A a" "A b" "A c"
[3,] "B a" "B b" "B c"
[4,] "C a" "C b" "C c"

```

```

> print(B3)

```

```

      [,1] [,2] [,3]
[1,] "B b" "B c" "B a"
[2,] "D b" "D c" "D a"
[3,] "C b" "C c" "C a"
[4,] "A b" "A c" "A a"

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> head(book)

```

```

plots block trt1 trt2
1 101 1 A a
2 102 1 A b
3 103 1 A c

```



```
4  106    1    D    a
5  105    1    D    b
6  104    1    D    c
```

```
> array(book$plots,c(3,4,3))->X
> t(X[, ,1])
```

```
      [,1] [,2] [,3]
[1,]  101  102  103
[2,]  106  105  104
[3,]  107  108  109
[4,]  112  111  110
```

```
> t(X[, ,2])
```

```
      [,1] [,2] [,3]
[1,]  201  202  203
[2,]  206  205  204
[3,]  207  208  209
[4,]  212  211  210
```

```
> t(X[, ,3])
```

```
      [,1] [,2] [,3]
[1,]  301  302  303
[2,]  306  305  304
[3,]  307  308  309
[4,]  312  311  310
```

3.13 Factorial

The full factorial of n factors applied to an experimental design (CRD, RCBD and LSD) is common and this procedure in **agricolae** applies the factorial to one of these three designs and its parameters are:

```
> str(design.ab)
```

```
function (trt, r = NULL, serie = 2, design = c("rcbd",
  "crd", "lsd"), seed = 0, kinds = "Super-Duper",
  first = TRUE, randomization = TRUE)
```

To generate the factorial, you need to create a vector of levels of each factor, the method automatically generates up to 25 factors and "r" repetitions.

```
> trt <- c(4,2,3) # three factors with 4,2 and 3 levels.
```

to crd and rcdb designs, it is necessary to value "r" as the number of repetitions, this can be a vector if unequal to equal or constant repetition (recommended).

```

> trt<-c(3,2) # factorial 3x2
> outdesign <-design.ab(trt, r=3, serie=2)
> book12 <- outdesign$book
> head(book12) # print of the field book

```

```

plots block A B
1  101      1 3 1
2  102      1 2 2
3  103      1 1 1
4  104      1 1 2
5  105      1 3 2
6  106      1 2 1

```

Serpentine enumeration:

```

> book <- zigzag(outdesign)
> head(book)

```

```

plots block A B
1  101      1 3 1
2  102      1 2 2
3  103      1 1 1
4  104      1 1 2
5  105      1 3 2
6  106      1 2 1

```

factorial 2 x 2 x 2 with 5 replications in completely randomized design.

```

> trt<-c(2,2,2)
> crd<-design.ab(trt, r=5, serie=2,design="crd")
> names(crd)

```

```
[1] "parameters" "book"
```

```
> crd$parameters
```

```
$design
[1] "factorial"
```

```
$trt
[1] "1 1 1" "1 1 2" "1 2 1" "1 2 2" "2 1 1" "2 1 2" "2 2 1"
[8] "2 2 2"
```

```
$r
[1] 5 5 5 5 5 5 5 5
```

```
$serie
[1] 2
```

```
$seed
```

```

[1] 970386955

$kind
[1] "Super-Duper"

[[7]]
[1] TRUE

$applied
[1] "crd"

> head(crd$book)

  plots r A B C
1   101 1 2 2 1
2   102 1 1 1 2
3   103 1 2 1 2
4   104 1 2 1 1
5   105 1 2 2 2
6   106 2 2 1 2

```

4 Multiple comparisons

For the analyses, the following functions of **agricolae** are used: *LSD.test*, *HSD.test*, *duncan.test*, *scheffe.test*, *waller.test*, *SNK.test*, *REGW.test* reference [17, 6] and *durbin.test*, *kruskal*, *friedman*, *waerden.test* and *Median.test* reference [2].

For every statistical analysis, the data should be organized in columns. For the demonstration, the **agricolae** database will be used.

The *sweetpotato* data correspond to a completely random experiment in field with plots of 50 sweet potato plants, subjected to the virus effect and to a control without virus (See the reference manual of the package).

```

> data(sweetpotato)
> model<-aov(yield~virus, data=sweetpotato)
> cv.model(model)

[1] 17.1666

> attach(sweetpotato)
> mean(yield)

[1] 27.625

> detach(sweetpotato)

```

Model parameters: Degrees of freedom and variance of the error:

```

> df<-df.residual(model)
> MSerror<-deviance(model)/df

```

4.1 The Least Significant Difference (LSD)

It includes the multiple comparison through the method of the minimum significant difference (Least Significant Difference), reference [17].

```
> # comparison <- LSD.test(yield,virus,df,MSerror)
> LSD.test(model, "virus",console=TRUE)
```

```
Study: model ~ "virus"
```

```
LSD t Test for yield
```

```
Mean Square Error: 22.48917
```

```
virus, means and individual ( 95 %) CI
```

	yield	std r	LCL	UCL	Min	Max
cc	24.40000	3.609709	3 18.086268	30.71373	21.7	28.5
fc	12.86667	2.159475	3 6.552935	19.18040	10.6	14.9
ff	36.33333	7.333030	3 30.019601	42.64707	28.0	41.8
oo	36.90000	4.300000	3 30.586268	43.21373	32.1	40.4

```
alpha: 0.05 ; Df Error: 8
```

```
Critical Value of t: 2.306004
```

```
t-Student: 2.306004
```

```
Alpha : 0.05
```

```
Least Significant Difference 8.928965
```

```
Means with the same letter are not significantly different
```

```
Groups, Treatments and means
```

a	oo	36.9
a	ff	36.33333
b	cc	24.4
c	fc	12.86667

In the function *LSD.test*, the multiple comparison was carried out. In order to obtain the probabilities of the comparisons, it should be indicated that groups are not required; thus:

```
> # comparison <- LSD.test(yield, virus,df, MSerror, group=F)
> outLSD <-LSD.test(model, "virus", group=F,console=TRUE)
```

```
Study: model ~ "virus"
```

```
LSD t Test for yield
```

```
Mean Square Error: 22.48917
```

```
virus, means and individual ( 95 %) CI
```

	yield	std r		LCL	UCL	Min	Max
cc	24.40000	3.609709	3	18.086268	30.71373	21.7	28.5
fc	12.86667	2.159475	3	6.552935	19.18040	10.6	14.9
ff	36.33333	7.333030	3	30.019601	42.64707	28.0	41.8
oo	36.90000	4.300000	3	30.586268	43.21373	32.1	40.4

alpha: 0.05 ; Df Error: 8
Critical Value of t: 2.306004

Minimum difference changes for each comparison

Means with the same letter are not significantly different

Groups, Treatments and means

Comparison between treatments means

	Difference	pvalue	sig.	LCL	UCL
cc - fc	11.5333333	0.0176	*	2.604368	20.462299
cc - ff	-11.9333333	0.0151	*	-20.862299	-3.004368
cc - oo	-12.5000000	0.0121	*	-21.428965	-3.571035
fc - ff	-23.4666667	0.0003	***	-32.395632	-14.537701
fc - oo	-24.0333333	0.0003	***	-32.962299	-15.104368
ff - oo	-0.5666667	0.8873		-9.495632	8.362299

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> print(outLSD)

\$statistics

Mean	CV	MSerror
27.625	17.1666	22.48917

\$parameters

Df	ntr	t.value	alpha	test name	t
8	4	2.306004	0.05	Fisher-LSD	virus

\$means

	yield	std r		LCL	UCL	Min	Max
cc	24.40000	3.609709	3	18.086268	30.71373	21.7	28.5
fc	12.86667	2.159475	3	6.552935	19.18040	10.6	14.9
ff	36.33333	7.333030	3	30.019601	42.64707	28.0	41.8
oo	36.90000	4.300000	3	30.586268	43.21373	32.1	40.4

\$comparison

	Difference	pvalue	sig.	LCL	UCL
cc - fc	11.5333333	0.0176	*	2.604368	20.462299

```

cc - ff -11.9333333 0.0151      * -20.862299  -3.004368
cc - oo -12.5000000 0.0121      * -21.428965  -3.571035
fc - ff -23.4666667 0.0003     *** -32.395632 -14.537701
fc - oo -24.0333333 0.0003     *** -32.962299 -15.104368
ff - oo  -0.5666667 0.8873      -9.495632   8.362299

```

```

$groups
NULL

```

4.2 holm, hommel, hochberg, bonferroni, BH, BY, fdr

With the function *LSD.test* we can make adjustments to the probabilities found, as for example the adjustment by Bonferroni, holm.

```
> LSD.test(model, "virus", group=F, p.adj= "bon",console=TRUE)
```

```
Study: model ~ "virus"
```

```
LSD t Test for yield
P value adjustment method: bonferroni
```

```
Mean Square Error: 22.48917
```

```
virus, means and individual ( 95 %) CI
```

	yield	std r		LCL	UCL	Min	Max
cc	24.40000	3.609709	3	18.086268	30.71373	21.7	28.5
fc	12.86667	2.159475	3	6.552935	19.18040	10.6	14.9
ff	36.33333	7.333030	3	30.019601	42.64707	28.0	41.8
oo	36.90000	4.300000	3	30.586268	43.21373	32.1	40.4

```
alpha: 0.05 ; Df Error: 8
Critical Value of t: 3.478879
```

```
Minimum difference changes for each comparison
```

```
Means with the same letter are not significantly different
```

```
Groups, Treatments and means
```

```
Comparison between treatments means
```

	Difference	pvalue	sig.	LCL	UCL
cc - fc	11.5333333	0.1058		-1.937064	25.0037305
cc - ff	-11.9333333	0.0904	.	-25.403730	1.5370638
cc - oo	-12.5000000	0.0725	.	-25.970397	0.9703971
fc - ff	-23.4666667	0.0018	**	-36.937064	-9.9962695
fc - oo	-24.0333333	0.0015	**	-37.503730	-10.5629362
ff - oo	-0.5666667	1.0000		-14.037064	12.9037305

```
> out<-LSD.test(model, "virus", group=TRUE, p.adj= "holm")
> print(out$group)
```

```
trt      means M
1 oo 36.90000 a
2 ff 36.33333 a
3 cc 24.40000 b
4 fc 12.86667 c
```

```
> out<-LSD.test(model, "virus", group=FALSE, p.adj= "holm")
> print(out$comparison)
```

```
          Difference pvalue sig.
cc - fc  11.5333333 0.0484    *
cc - ff -11.9333333 0.0484    *
cc - oo -12.5000000 0.0484    *
fc - ff -23.4666667 0.0015   **
fc - oo -24.0333333 0.0015   **
ff - oo  -0.5666667 0.8873
```

Other comparison tests can be applied, such as *duncan*, *Student-Newman-Keuls*, *tukey* and *waller-duncan*.

For *Duncan*, use the function *duncan.test*; for *Student-Newman-Keuls*, the function *SNK.test*; for *Tukey*, the function *HSD.test()*; for *Scheffe*, the function *scheffe.test*; and for *Waller-Duncan*, the function *waller.test*. The parameters are the same. *Waller* also requires the value of F-calculated of the ANOVA treatments. If the model is used as a parameter, this is no longer necessary.

4.3 Duncan's New Multiple-Range Test

It corresponds to the Duncan's Test reference [17].

```
> duncan.test(model, "virus", console=TRUE)
```

```
Study: model ~ "virus"
```

```
Duncan's new multiple range test
for yield
```

```
Mean Square Error: 22.48917
```

```
virus, means
```

```
          yield      std r  Min  Max
cc 24.40000 3.609709 3 21.7 28.5
fc 12.86667 2.159475 3 10.6 14.9
ff 36.33333 7.333030 3 28.0 41.8
oo 36.90000 4.300000 3 32.1 40.4
```

alpha: 0.05 ; Df Error: 8

Critical Range

	2	3	4
	8.928965	9.304825	9.514910

Means with the same letter are not significantly different.

Groups, Treatments and means

a	oo	36.9
a	ff	36.33
b	cc	24.4
c	fc	12.87

4.4 Student-Newman-Keuls

Student, Newman and Keuls helped to improve the Newman-Keuls test of 1939, which was known as the Keuls method reference [17]

```
> # SNK.test(model, "virus", alpha=0.05,console=TRUE)
> SNK.test(model, "virus", group=FALSE,console=TRUE)
```

```
Study: model ~ "virus"
```

```
Student Newman Keuls Test
for yield
```

```
Mean Square Error: 22.48917
```

```
virus, means
```

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

alpha: 0.05 ; Df Error: 8

Critical Range

	2	3	4
	8.928965	11.064170	12.399670

Comparison between treatments means

	Difference	pvalue	sig.	LCL	UCL
cc-fc	11.5333333	0.0176	*	2.604368	20.462299
cc-ff	-11.9333333	0.0151	*	-20.862299	-3.004368
cc-oo	-12.5000000	0.0291	*	-23.564170	-1.435830
fc-ff	-23.4666667	0.0008	***	-34.530836	-12.402497


```
fc-oo -24.0333333 0.0012 ** -36.433003 -11.633664
ff-oo -0.5666667 0.8873 -9.495632 8.362299
```

4.5 Ryan, Einot and Gabriel and Welsch

Multiple range tests for all pairwise comparisons, to obtain a confident inequalities multiple range tests. Reference [6]

```
> # REGW.test(model, "virus", alpha=0.05,console=TRUE)
> REGW.test(model, "virus", group=FALSE,console=TRUE)
```

```
Study: model ~ "virus"
```

```
Ryan, Einot and Gabriel and Welsch multiple range test
for yield
```

```
Mean Square Error: 22.48917
```

```
virus, means
```

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

```
alpha: 0.05 ; Df Error: 8
```

```
Critical Range
```

	2	3	4
	10.62212	11.06417	12.39967

```
Comparison between treatments means
```

	Difference	pvalue	sig.	LCL	UCL
cc - fc	11.5333333	0.0350	*	0.9112173	22.155449
cc - ff	-11.9333333	0.0299	*	-22.5554494	-1.311217
cc - oo	-12.5000000	0.0291	*	-23.5641696	-1.435830
fc - ff	-23.4666667	0.0008	***	-34.5308363	-12.402497
fc - oo	-24.0333333	0.0012	**	-36.4330031	-11.633664
ff - oo	-0.5666667	0.9873		-11.1887827	10.055449

4.6 Tukey's W Procedure (HSD)

This studentized range test, created by Tukey in 1953, is known as the Tukey's HSD (Honestly Significant Differences) Test reference [17]

```
> outHSD<- HSD.test(model, "virus",console=TRUE)
```

Study: model ~ "virus"

HSD Test for yield

Mean Square Error: 22.48917

virus, means

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

alpha: 0.05 ; Df Error: 8

Critical Value of Studentized Range: 4.52881

Honestly Significant Difference: 12.39967

Means with the same letter are not significantly different.

Groups, Treatments and means

a	oo	36.9
ab	ff	36.33
bc	cc	24.4
c	fc	12.87

> outHSD

\$statistics

Mean	CV	MSerror	HSD
27.625	17.1666	22.48917	12.39967

\$parameters

Df	ntr	StudentizedRange	alpha	test	name.t
8	4	4.52881	0.05	Tukey	virus

\$means

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

\$comparison

NULL

\$groups

trt	means	M
1 oo	36.90000	a
2 ff	36.33333	ab

```
3 cc 24.40000 bc
4 fc 12.86667 c
```

4.7 Waller-Duncan's Bayesian K-Ratio T-Test

In 1975, Duncan continued the multiple comparison procedures, introducing the criterion of minimizing both experimental errors; for this, he used the Bayes' theorem, obtaining one new test called Waller-Duncan reference [17]

```
> # variance analysis:
> anova(model)
```

Analysis of Variance Table

```
Response: yield
      Df Sum Sq Mean Sq F value    Pr(>F)
virus   3 1170.21  390.07  17.345 0.0007334 ***
Residuals 8  179.91   22.49
```

```
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> attach(sweetpotato)
> waller.test(yield,virus,df,MSerror,Fc= 17.345, group=F,console=TRUE)
```

Study: yield ~ virus

Waller-Duncan K-ratio t Test for yield

This test minimizes the Bayes risk under additive loss and certain other assumptions.

```
.....
K ratio                100.00000
Error Degrees of Freedom  8.00000
Error Mean Square         22.48917
F value                   17.34500
Critical Value of Waller  2.23600
```

virus, means

```
      yield      std r  Min  Max
cc 24.40000 3.609709 3 21.7 28.5
fc 12.86667 2.159475 3 10.6 14.9
ff 36.33333 7.333030 3 28.0 41.8
oo 36.90000 4.300000 3 32.1 40.4
```

Minimum Significant Difference 8.657906
Comparison between treatments means

Difference significant

```

cc - fc  11.5333333      TRUE
cc - ff -11.9333333     TRUE
cc - oo -12.5000000     TRUE
fc - ff -23.4666667     TRUE
fc - oo -24.0333333     TRUE
ff - oo  -0.5666667     FALSE

```

```
> detach(sweetpotato)
```

In another case with only invoking the model object:

```
> outWaller <- waller.test(model, "virus", group=FALSE, console=FALSE)
```

The found object *outWaller* has information to make other procedures.

```
> names(outWaller)
```

```

[1] "statistics" "parameters" "means"      "comparison"
[5] "groups"

```

```
> print(outWaller$comparison)
```

```

          Difference significant
cc - fc  11.5333333      TRUE
cc - ff -11.9333333     TRUE
cc - oo -12.5000000     TRUE
fc - ff -23.4666667     TRUE
fc - oo -24.0333333     TRUE
ff - oo  -0.5666667     FALSE

```

It is indicated that the virus effect "ff" is not significant to the control "oo".

```
> outWaller$statistics
```

```

      Mean      CV  MSerror  F.Value  CriticalDifference
27.625  17.1666  22.48917  17.34478      8.657906

```

4.8 Scheffe's Test

This method, created by Scheffe in 1959, is very general for all the possible contrasts and their confidence intervals. The confidence intervals for the averages are very broad, resulting in a very conservative test for the comparison between treatment averages reference [17]

```

> # analysis of variance:
> scheffe.test(model, "virus", group=TRUE, console=TRUE,
+ main="Yield of sweetpotato\nDealt with different virus")

```

```

Study: Yield of sweetpotato
Dealt with different virus

```

Scheffe Test for yield

Mean Square Error : 22.48917

virus, means

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

alpha: 0.05 ; Df Error: 8

Critical Value of F: 4.066181

Minimum Significant Difference: 13.52368

Means with the same letter are not significantly different.

Groups, Treatments and means

a	oo	36.9
a	ff	36.33
ab	cc	24.4
b	fc	12.87

The minimum significant value is very high. If you require the approximate probabilities of comparison, you can use the option *group=FALSE*.

```
> outScheffe <- scheffe.test(model,"virus", group=FALSE, console=TRUE)
```

```
Study: model ~ "virus"
```

Scheffe Test for yield

Mean Square Error : 22.48917

virus, means

	yield	std r	Min	Max
cc	24.40000	3.609709	3 21.7	28.5
fc	12.86667	2.159475	3 10.6	14.9
ff	36.33333	7.333030	3 28.0	41.8
oo	36.90000	4.300000	3 32.1	40.4

alpha: 0.05 ; Df Error: 8

Critical Value of F: 4.066181

Comparison between treatments means

Difference	pvalue	sig	LCL	UCL
------------	--------	-----	-----	-----

```

cc - fc  11.5333333 0.0978   .  -1.000348  24.0670149
cc - ff -11.9333333 0.0855   . -24.467015   0.6003483
cc - oo -12.5000000 0.0706   . -25.033682   0.0336816
fc - ff -23.4666667 0.0023  ** -36.000348 -10.9329851
fc - oo -24.0333333 0.0020  ** -36.567015 -11.4996517
ff - oo  -0.5666667 0.9991   . -13.100348  11.9670149

```

4.9 Multiple comparison in factorial treatments

In a factorial combined effects of the treatments. Comparative tests: *LSD*, *HSD*, *Waller-Duncan*, *Duncan*, *Scheffé*, *SNK* can be applied.

```

> # modelABC <-aov (y ~ A * B * C, data)
> # compare <-LSD.test (modelABC, c ("A", "B", "C"),console=TRUE)

```

The comparison is the combination of A:B:C.

Data RCBD design with a factorial clone x nitrogen. The response variable yield.

```

> yield <-scan (text =
+ "6 7 9 13 16 20 8 8 9
+ 7 8 8 12 17 18 10 9 12
+ 9 9 9 14 18 21 11 12 11
+ 8 10 10 15 16 22 9 9 9 "
+ )
> block <-gl (4, 9)
> clone <-rep (gl (3, 3, labels = c ("c1", "c2", "c3")), 4)
> nitrogen <-rep (gl (3, 1, labels = c ("n1", "n2", "n3")), 12)
> A <-data.frame (block, clone, nitrogen, yield)
> head (A)

```

```

      block clone nitrogen yield
1         1   c1         n1      6
2         1   c1         n2      7
3         1   c1         n3      9
4         1   c2         n1     13
5         1   c2         n2     16
6         1   c2         n3     20

```

```

> outAOV <-aov (yield ~ block + clone * nitrogen, data = A)
> anova (outAOV)

```

Analysis of Variance Table

Response: yield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
block	3	20.75	6.917	5.8246	0.0038746	**
clone	2	497.72	248.861	209.5673	6.370e-16	***
nitrogen	2	54.06	27.028	22.7602	2.865e-06	***
clone:nitrogen	4	43.28	10.819	9.1111	0.0001265	***
Residuals	24	28.50	1.187			

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> outFactorial <-LSD.test (outAOV, c("clone", "nitrogen"),
+ main = "Yield ~ block + nitrogen + clone + clone:nitrogen",console=TRUE)
```

Study: Yield ~ block + nitrogen + clone + clone:nitrogen

LSD t Test for yield

Mean Square Error: 1.1875

clone:nitrogen, means and individual (95 %) CI

	yield	std r	LCL	UCL	Min	Max
c1:n1	7.50	1.2909944	4 6.375459	8.624541	6	9
c1:n2	8.50	1.2909944	4 7.375459	9.624541	7	10
c1:n3	9.00	0.8164966	4 7.875459	10.124541	8	10
c2:n1	13.50	1.2909944	4 12.375459	14.624541	12	15
c2:n2	16.75	0.9574271	4 15.625459	17.874541	16	18
c2:n3	20.25	1.7078251	4 19.125459	21.374541	18	22
c3:n1	9.50	1.2909944	4 8.375459	10.624541	8	11
c3:n2	9.50	1.7320508	4 8.375459	10.624541	8	12
c3:n3	10.25	1.5000000	4 9.125459	11.374541	9	12

alpha: 0.05 ; Df Error: 24

Critical Value of t: 2.063899

t-Student: 2.063899

Alpha : 0.05

Least Significant Difference 1.590341

Means with the same letter are not significantly different

Groups, Treatments and means

a	c2:n3	20.25
b	c2:n2	16.75
c	c2:n1	13.5
d	c3:n3	10.25
de	c3:n1	9.5
de	c3:n2	9.5
def	c1:n3	9
ef	c1:n2	8.5
f	c1:n1	7.5

```
> par(mar=c(3,3,2,0))
```

```
> pic1<-bar.err(outFactorial$means,variation="range",ylim=c(5,25), bar=FALSE,col=0,las=1)
```

```
> points(pic1$index,pic1$means,pch=18,cex=1.5,col="blue")
```

```
> axis(1,pic1$index,labels=FALSE)
```

```
> title(main="average and range\nclon:nitrogen")
```

4.10 Analysis of Balanced Incomplete Blocks

This analysis can come from balanced or partially balanced designs. The function *BIB.test* is for balanced designs, and *BIB.test*, for partially balanced designs. In the following example, the **agricolae** data will be used, reference [7].

```
> #Example linear estimation and design of experiments. (Joshi)
> # Profesor de Estadística, Institute of Social Sciences Agra, India
> # 6 variedades de trigo en 10 bloques de 3 parcelas cada una.
> block<-gl(10,3)
> variety<-c(1,2,3,1,2,4,1,3,5,1,4,6,1,5,6,2,3,6,2,4,5,2,5,6,3,4,5,3, 4,6)
> y<-c(69,54,50,77,65,38,72,45,54,63,60,39,70,65,54,65,68,67,57,60,62,
+ 59,65,63,75,62,61,59,55,56)
> BIB.test(block, variety, y,console=TRUE)
```

ANALYSIS BIB: y

Class level information

```
Block:  1 2 3 4 5 6 7 8 9 10
Trt   :  1 2 3 4 5 6
```

Number of observations: 30

Analysis of Variance Table

Response: y

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
block.unadj	9	466.97	51.885	0.9019	0.54712
trt.adj	5	1156.44	231.289	4.0206	0.01629 *
Residuals	15	862.89	57.526		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 12.6 %

y Means: 60.3

variety, statistics

	y	mean.adj	SE	r	std	Min	Max
1	70.2	75.13333	3.728552	5	5.069517	63	77
2	60.0	58.71667	3.728552	5	4.898979	54	65
3	59.4	58.55000	3.728552	5	12.381438	45	75
4	55.0	54.96667	3.728552	5	9.848858	38	62
5	61.4	60.05000	3.728552	5	4.505552	54	65
6	55.8	54.38333	3.728552	5	10.756393	39	67

LSD test

Std.diff : 5.363111

Alpha : 0.05

LSD : 11.4312

Parameters BIB
Lambda : 2
treatmeans : 6
Block size : 3
Blocks : 10
Replication: 5

Efficiency factor 0.8

<<< Book >>>

Means with the same letter are not significantly different.

Comparison of treatments

Groups, Treatments and means

a	1	75.13
b	5	60.05
b	2	58.72
b	3	58.55
b	4	54.97
b	6	54.38

function (block, trt, y, test = c("lsd", "tukey", "duncan", "waller", "snk"), alpha = 0.05, group = TRUE) LSD, Tukey Duncan, Waller-Duncan and SNK, can be used. The probabilities of the comparison can also be obtained. It should only be indicated: group=FALSE, thus:

```
> out <-BIB.test(block, trt=variety, y, test="tukey", group=FALSE, console=TRUE)
```

ANALYSIS BIB: y

Class level information

Block: 1 2 3 4 5 6 7 8 9 10
Trt : 1 2 3 4 5 6

Number of observations: 30

Analysis of Variance Table

Response: y

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
block.unadj	9	466.97	51.885	0.9019	0.54712
trt.adj	5	1156.44	231.289	4.0206	0.01629 *
Residuals	15	862.89	57.526		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 12.6 %

y Means: 60.3

variety, statistics

	y	mean.adj	SE	r	std	Min	Max
1	70.2	75.13333	3.728552	5	5.069517	63	77
2	60.0	58.71667	3.728552	5	4.898979	54	65
3	59.4	58.55000	3.728552	5	12.381438	45	75
4	55.0	54.96667	3.728552	5	9.848858	38	62
5	61.4	60.05000	3.728552	5	4.505552	54	65
6	55.8	54.38333	3.728552	5	10.756393	39	67

Tukey

Alpha : 0.05
Std.err : 3.792292
HSD : 17.42458
Parameters BIB
Lambda : 2
treatmeans : 6
Block size : 3
Blocks : 10
Replication: 5

Efficiency factor 0.8

<<< Book >>>

Comparison between treatments means

	Difference	pvalue	sig.
1 - 2	16.4166667	0.0705	.
1 - 3	16.5833333	0.0666	.
1 - 4	20.1666667	0.0191	*
1 - 5	15.0833333	0.1096	
1 - 6	20.7500000	0.0155	*
2 - 3	0.1666667	1.0000	
2 - 4	3.7500000	0.9792	
2 - 5	-1.3333333	0.9998	
2 - 6	4.3333333	0.9616	
3 - 4	3.5833333	0.9829	
3 - 5	-1.5000000	0.9997	
3 - 6	4.1666667	0.9674	
4 - 5	-5.0833333	0.9273	
4 - 6	0.5833333	1.0000	
5 - 6	5.6666667	0.8908	

> names(out)

```
[1] "parameters" "statistics" "comparison" "means"  
[5] "groups"
```

> rm(block, variety)

bar.group: out\$groups
bar.err: out\$means

4.11 Partially Balanced Incomplete Blocks

The function *PBIB.test*, reference [7], can be used for the lattice and alpha designs.

Consider the following case: Construct the alpha design with 30 treatments, 2 repetitions, and a block size equal to 3.

```
> # alpha design
> Genotype<-paste("geno",1:30,sep="")
> r<-2
> k<-3
> plan<-design.alpha(Genotype,k,r,seed=5)
```

alpha design (0,1) - Serie I

Parameters Alpha design

=====

```
treatmeans : 30
Block size : 3
Blocks      : 10
Replication: 2
```

Efficiency factor

(E) 0.6170213

<<< Book >>>

The generated plan is plan\$book.

Suppose that the corresponding observation to each experimental unit is:

```
> yield <-c(5,2,7,6,4,9,7,6,7,9,6,2,1,1,3,2,4,6,7,9,8,7,6,4,3,2,2,1,1,
+          2,1,1,2,4,5,6,7,8,6,5,4,3,1,1,2,5,4,2,7,6,6,5,6,4,5,7,6,5,5,4)
```

The data table is constructed for the analysis. In theory, it is presumed that a design is applied and the experiment is carried out; subsequently, the study variables are observed from each experimental unit.

```
> data<-data.frame(plan$book,yield)
> rm(yield,Genotype)
> # The analysis:
> attach(data)
> modelPBIB <- PBIB.test(block, Genotype, replication, yield, k=3, group=TRUE,
+ console=TRUE)
```

ANALYSIS PBIB: yield

Class level information

```
block : 20
Genotype : 30
```

Number of observations: 60

Estimation Method: Residual (restricted) maximum likelihood

Parameter Estimates

	Variance
block:replication	2.834033e+00
replication	8.045171e-09
Residual	2.003098e+00

Fit Statistics

AIC	213.65937
BIC	259.89888
-2 Res Log Likelihood	-73.82968

Analysis of Variance Table

Response: yield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Genotype	29	72.006	2.4830	1.2396	0.3668
Residuals	11	22.034	2.0031		

coefficient of variation: 31.2 %

yield Means: 4.533333

Parameters PBIB

Genotype	30
block size	3
block/replication	10
replication	2

Efficiency factor 0.6170213

Comparison test lsd

<<< to see the objects: means, comparison and groups. >>>

> detach(data)

The adjusted averages can be extracted from the modelPBIB.

head(modelPBIB\$means)

The comparisons:

head(modelPBIB\$comparison)

The data on the adjusted averages and their variation can be illustrated see Figure ??, since the created object is very similar to the objects generated by the multiple comparisons.

Analysis of balanced lattice 3x3, 9 treatments, 4 repetitions.

Create the data in a text file: lattice3x3.txt and read with R:

sqr block trt yield		
1 1 1 48.76	1 1 4 14.46	1 1 3 19.68
1 2 8 10.83	1 2 6 30.69	1 2 7 31.00
1 3 5 12.54	1 3 9 42.01	1 3 2 23.00
2 4 5 11.07	2 4 8 22.00	2 4 1 41.00
2 5 2 22.00	2 5 7 42.80	2 5 3 12.90
2 6 9 47.43	2 6 6 28.28	2 6 4 49.95
3 7 2 27.67	3 7 1 50.00	3 7 6 25.00
3 8 7 30.00	3 8 5 24.00	3 8 4 45.57
3 9 3 13.78	3 9 8 24.00	3 9 9 30.00
4 10 6 37.00	4 10 3 15.42	4 10 5 20.00
4 11 4 42.37	4 11 2 30.00	4 11 8 18.00
4 12 9 39.00	4 12 7 23.80	4 12 1 43.81

```

> trt<-c(1,8,5,5,2,9,2,7,3,6,4,9,4,6,9,8,7,6,1,5,8,3,2,7,3,7,2,1,3,4,6,4,9,5,8,1)
> yield<-c(48.76,10.83,12.54,11.07,22,47.43,27.67,30,13.78,37,42.37,39,14.46,30.69,42.01,
+ 22,42.8,28.28,50,24,24,15.42,30,23.8,19.68,31,23,41,12.9,49.95,25,45.57,30,20,18,43.81)
> sqr<-rep(gl(4,3),3)
> block<-rep(1:12,3)
> modelLattice<-PBIB.test(block,trt,sqr,yield,k=3,console=TRUE)

```

ANALYSIS PBIB: yield

Class level information

block : 12

trt : 9

Number of observations: 36

Estimation Method: Residual (restricted) maximum likelihood

Parameter Estimates

	Variance
block:sqr	1.618725e-08
sqr	1.681070e-07
Residual	5.693724e+01

Fit Statistics

AIC	222.23197
BIC	237.78201
-2 Res Log Likelihood	-99.11599

Analysis of Variance Table

Response: yield

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
trt	8	3749.4	468.68	8.2315	0.0001987 ***
Residuals	16	911.0	56.94		

Signif. codes:

0 '***' 0.001 '***' 0.01 'S*' 0.05 'S.' 0.1 'S' 1

```
coefficient of variation: 25.9 %
yield Means: 29.16167
```

```
Parameters PBIB
```

```
      .
trt    9
block size 3
block/sqr 3
sqr    4
```

```
Efficiency factor 0.75
```

```
Comparison test lsd
```

```
<<< to see the objects: means, comparison and groups. >>>
```

The adjusted averages can be extracted from the modelLattice.

```
print(modelLattice$means)
```

The comparisons:

```
head(modelLattice$comparison)
```

4.12 Augmented Blocks

The function *DAU.test* can be used for the analysis of the augmented block design.

The data should be organized in a table, containing the blocks, treatments, and the response.

```
> block<-c(rep("I",7),rep("II",6),rep("III",7))
> trt<-c("A","B","C","D","g","k","l","A","B","C","D","e","i","A","B","C",
+ "D","f","h","j")
> yield<-c(83,77,78,78,70,75,74,79,81,81,91,79,78,92,79,87,81,89,96, 82)
> head(data.frame(block, trt, yield))
```

```
  block trt yield
1     I  A    83
2     I  B    77
3     I  C    78
4     I  D    78
5     I  g    70
6     I  k    75
```

The treatments are in each block:

```
> by(trt,block,as.character)
```

```
block: I
[1] "A" "B" "C" "D" "g" "k" "l"
```

```
-----
block: II
```

```
[1] "A" "B" "C" "D" "e" "i"
-----
block: III
[1] "A" "B" "C" "D" "f" "h" "j"
```

With their respective responses:

```
> by(yield,block,as.character)

block: I
[1] "83" "77" "78" "78" "70" "75" "74"
-----
block: II
[1] "79" "81" "81" "91" "79" "78"
-----
block: III
[1] "92" "79" "87" "81" "89" "96" "82"
```

Analysis:

```
> modelDAU<- DAU.test(block,trt,yield,method="lsd",console=TRUE)
```

```
ANALYSIS DAU: yield
Class level information
```

```
Block: I II III
Trt : A B C D e f g h i j k l
```

```
Number of observations: 20
```

```
ANOVA, Treatment Adjusted
Analysis of Variance Table
```

```
Response: yield
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
block.unadj	2	360.07	180.036		
trt.adj	11	285.10	25.918	0.9609	0.5499
Control	3	52.92	17.639	0.6540	0.6092
Control + control.VS.aug.	8	232.18	29.022	1.0760	0.4779
Residuals	6	161.83	26.972		

```
ANOVA, Block Adjusted
Analysis of Variance Table
```

```
Response: yield
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
trt.unadj	11	575.67	52.333		
block.adj	2	69.50	34.750	1.2884	0.3424
Control	3	52.92	17.639	0.6540	0.6092
Augmented	7	505.87	72.268	2.6793	0.1253
Control vs augmented	1	16.88	16.875	0.6256	0.4591

Residuals 6 161.83 26.972

coefficient of variation: 6.4 %

yield Means: 81.5

Critical Differences (Between)

	Std Error Diff.
Two Control Treatments	4.240458
Two Augmented Treatments (Same Block)	7.344688
Two Augmented Treatments(Different Blocks)	8.211611
A Augmented Treatment and A Control Treatment	6.360687

Means with the same letter are not significantly different.

Groups, Treatments and means

a	h	93.5
ab	f	86.5
ab	A	84.67
ab	D	83.33
ab	C	82
ab	j	79.5
ab	B	79
ab	e	78.25
ab	k	78.25
ab	i	77.25
ab	l	77.25
b	g	73.25

Comparison between treatments means

<<< to see the objects: comparison and means >>>

> *modelDAU\$means*

	yield	std	r	Min	Max	mean.adj	SE	block
A	84.66667	6.658328	3	79	92	84.66667	2.998456	
B	79.00000	2.000000	3	77	81	79.00000	2.998456	
C	82.00000	4.582576	3	78	87	82.00000	2.998456	
D	83.33333	6.806859	3	78	91	83.33333	2.998456	
e	79.00000	NA	1	79	79	78.25000	5.193479	II
f	89.00000	NA	1	89	89	86.50000	5.193479	III
g	70.00000	NA	1	70	70	73.25000	5.193479	I
h	96.00000	NA	1	96	96	93.50000	5.193479	III
i	78.00000	NA	1	78	78	77.25000	5.193479	II
j	82.00000	NA	1	82	82	79.50000	5.193479	III
k	75.00000	NA	1	75	75	78.25000	5.193479	I
l	74.00000	NA	1	74	74	77.25000	5.193479	I


```
> modelDAU<- DAU.test(block,trt,yield,method="lsd",group=F,console=FALSE)
> head(modelDAU$comparison,8)
```

```
      Difference pvalue sig.
A - B    5.666667 0.2298
A - C    2.666667 0.5526
A - D    1.333333 0.7638
A - e    6.416667 0.3520
A - f   -1.833333 0.7828
A - g   11.416667 0.1228
A - h   -8.833333 0.2142
A - i    7.416667 0.2878
```

5 Non-parametric comparisons

The functions for non-parametric multiple comparisons included in **agricolae** are: *kruskal*, *waerden.test*, *friedman* and *durbin.test*, reference [2].

The function *kruskal* is used for N samples (N>2), populations or data coming from a completely random experiment (populations = treatments).

The function *waerden.test*, similar to kruskal-wallis, uses a normal score instead of ranges as kruskal does.

The function *friedman* is used for organoleptic evaluations of different products, made by judges (every judge evaluates all the products). It can also be used for the analysis of treatments of the randomized complete block design, where the response cannot be treated through the analysis of variance.

The function *durbin.test* for the analysis of balanced incomplete block designs is very used for sampling tests, where the judges only evaluate a part of the treatments.

Montgomery book data, reference [11]. Included in the **agricolae** package

```
> data(corn)
> str(corn)

'data.frame':      34 obs. of  3 variables:
 $ method      : int  1 1 1 1 1 1 1 1 2 ...
 $ observation: int  83 91 94 89 89 96 91 92 90 91 ...
 $ rx          : num  11 23 28.5 17 17 31.5 23 26 19.5 23 ...
```

For the examples, the **agricolae** package data will be used

5.1 Kruskal-Wallis

It makes the multiple comparison with Kruskal-Wallis. The parameters by default are alpha = 0.05.

```
> str(kruskal)

function (y, trt, alpha = 0.05, p.adj = c("none", "holm",
      "hommel", "hochberg", "bonferroni", "BH", "BY",
      "fdr"), group = TRUE, main = NULL, console = FALSE)
```

Analysis

```
> outKruskal<-with(corn,kruskal(observation,method,group=TRUE, main="corn", console=TRUE))
```

```
Study: corn  
Kruskal-Wallis test's  
Ties or no Ties
```

```
Value: 25.62884  
degrees of freedom: 3  
Pvalue chisq : 1.140573e-05
```

```
method, means of the ranks
```

```
  observation  r  
1    21.83333  9  
2    15.30000 10  
3    29.57143  7  
4     4.81250  8
```

```
t-Student: 2.042272  
Alpha      : 0.05  
Minimum difference changes for each comparison
```

```
Means with the same letter are not significantly different
```

```
Groups, Treatments and mean of the ranks
```

```
a      3      29.57143  
b      1      21.83333  
c      2       15.3  
d      4       4.8125
```

The object output has the same structure of the comparisons see [Figure 8](#).

5.2 Kruskal-Wallis: adjust P-values

To see `p.adjust.methods()`

```
> out<-with(corn,kruskal(observation,method,group=TRUE, main="corn", p.adj="holm"))  
> print(out$group)
```

```
  trt  means M  
1  3 29.57143 a  
2  1 21.83333 b  
3  2 15.30000 c  
4  4  4.81250 d
```

```
> out<-with(corn,kruskal(observation,method,group=FALSE, main="corn", p.adj="holm"))  
> print(out$comparison)
```

```

      Difference pvalue sig.
1 - 2   6.533333 0.0079  **
1 - 3  -7.738095 0.0079  **
1 - 4  17.020833 0.0000  ***
2 - 3 -14.271429 0.0000  ***
2 - 4   10.487500 0.0003  ***
3 - 4   24.758929 0.0000  ***

```

5.3 Friedman

```
> str(friedman)
```

```
function (judge, trt, evaluation, alpha = 0.05, group = TRUE,
         main = NULL, console = FALSE)
```

Analysis

```

> rm(trt)
> data(grass)
> attach(grass)
> out<-friedman(judge,trt, evaluation,alpha=0.05, group=FALSE,
+ main="Data of the book of Conover",console=TRUE)

```

Study: Data of the book of Conover

trt, Sum of the ranks

```

      evaluation r
t1         38.0 12
t2         23.5 12
t3         24.5 12
t4         34.0 12

```

Friedman's Test

=====

Adjusted for ties

Value: 8.097345

Pvalue chisq : 0.04404214

F value : 3.192198

Pvalue F: 0.03621547

Alpha : 0.05

t-Student : 2.034515

Comparison between treatments

Sum of the ranks

```

      Difference pvalue sig.   LCL   UCL
t1 - t2         14.5 0.0149  *   3.02 25.98
t1 - t3         13.5 0.0226  *   2.02 24.98

```

```

t1 - t4      4.0 0.4834      -7.48 15.48
t2 - t3      -1.0 0.8604     -12.48 10.48
t2 - t4     -10.5 0.0717     . -21.98  0.98
t3 - t4      -9.5 0.1017     -20.98  1.98

```

```
> detach(grass)
```

5.4 Waerden

A nonparametric test for several independent samples. Example applied with the sweet potato data in the `agricolae` basis.

```
> str(waerden.test)
```

```
function (y, trt, alpha = 0.05, group = TRUE, main = NULL,
         console = FALSE)
```

Analysis

```

> rm(yield)
> data(sweetpotato)
> attach(sweetpotato)
> outWaerden<-waerden.test(yield,virus,alpha=0.01,group=TRUE,console=TRUE)

```

```
Study: yield ~ virus
Van der Waerden (Normal Scores) test's
```

```
Value : 8.409979
Pvalue: 0.03825667
Degrees of freedom: 3
```

```
virus, means of the normal score
```

	yield	std	r
cc	-0.2328353	0.3028832	3
fc	-1.0601764	0.3467934	3
ff	0.6885684	0.7615582	3
oo	0.6044433	0.3742929	3

```

t-Student: 3.355387
Alpha      : 0.01
LSD        : 1.322487

```

Means with the same letter are not significantly different

Groups, Treatments and means of the normal score

a	ff	0.6886
a	oo	0.6044
ab	cc	-0.2328
b	fc	-1.06

The comparison probabilities are obtained with the parameter group = **FALSE**

```
> names(outWaerden)
```

```
[1] "statistics" "parameters" "means"      "comparison"  
[5] "groups"
```

To see `outWaerden$comparison`

```
> out<-waerden.test(yield,virus,group=F,console=TRUE)
```

```
Study: yield ~ virus  
Van der Waerden (Normal Scores) test's
```

```
Value : 8.409979  
Pvalue: 0.03825667  
Degrees of freedom: 3
```

```
virus, means of the normal score
```

```
      yield      std r  
cc -0.2328353 0.3028832 3  
fc -1.0601764 0.3467934 3  
ff  0.6885684 0.7615582 3  
oo  0.6044433 0.3742929 3
```

```
Comparison between treatments means  
mean of the normal score
```

	Difference	pvalue	sig.	LCL	UCL
cc - fc	0.8273411	0.0690	.	-0.08154345	1.73622564
cc - ff	-0.9214037	0.0476	*	-1.83028827	-0.01251917
cc - oo	-0.8372786	0.0664	.	-1.74616316	0.07160593
fc - ff	-1.7487448	0.0022	**	-2.65762936	-0.83986026
fc - oo	-1.6646197	0.0029	**	-2.57350426	-0.75573516
ff - oo	0.0841251	0.8363		-0.82475944	0.99300965

```
> detach(sweetpotato)
```

5.5 Median test

A nonparametric test for several independent samples. The median test is designed to examine whether several samples came from populations having the same median, reference [2].

```
> str(Median.test)
```

```
function (y, trt, correct = TRUE, simulate.p.value = FALSE,  
         console = TRUE)
```

Analysis

```

> data(sweetpotato)
> attach(sweetpotato)
> outMedian<-Median.test(yield,virus,console=TRUE)

```

The Median Test for yield ~ virus

```

Chi-square = 6.666667   DF = 3   P.value 0.08331631
Median = 28.25

```

	Median	Chisq	pvalue	sig
cc and fc	18.30	6.0000000	0.0143	*
cc and ff	28.25	0.6666667	0.4142	
cc and oo	30.30	6.0000000	0.0143	*
fc and ff	21.45	6.0000000	0.0143	*
fc and oo	23.50	6.0000000	0.0143	*
ff and oo	38.70	0.6666667	0.4142	

```

> detach(sweetpotato)
> names(outMedian)

```

```

[1] "statistics" "parameters" "Medians"    "comparison"
[5] "data"

```

```

> outMedian$statistics

```

Chisq	p.chisq	Median
6.666667	0.08331631	28.25

```

> outMedian$Medians

```

trt	Median	grather	lessEqual
1 cc	23.0	1	2
2 fc	13.1	0	3
3 ff	39.2	2	1
4 oo	38.2	3	0

5.6 Durbin

durbin.test; example: Myles Hollander (p. 311) Source: W. Moore and C.I. Bliss. (1942) A multiple comparison of the Durbin test for the balanced incomplete blocks for sensorial or categorical evaluation. It forms groups according to the demanded ones for level of significance (alpha); by default, 0.05.

```

> str(durbin.test)

```

```

function (judge, trt, evaluation, alpha = 0.05, group = TRUE,
         main = NULL, console = FALSE)

```

Analysis

```

> days <-gl(7,3)
> chemical<-c("A","B","D","A","C","E","C","D","G","A","F","G", "B","C","F",
+ "B","E","G","D","E","F")
> toxic<-c(0.465,0.343,0.396,0.602,0.873,0.634,0.875,0.325,0.330, 0.423,0.987,0.426,
+ 0.652,1.142,0.989,0.536,0.409,0.309, 0.609,0.417,0.931)
> out<-durbin.test(days,chemical,toxic,group=F,console=TRUE,
+ main="Logarithm of the toxic dose")

```

Study: Logarithm of the toxic dose
chemical, Sum of ranks

```

      sum
A      5
B      5
C      9
D      5
E      5
F      8
G      5

```

Durbin Test

=====

```

Value      : 7.714286
Df 1      : 6
P-value    : 0.2597916
Alpha     : 0.05
Df 2      : 8
t-Student  : 2.306004

```

Least Significant Difference
between the sum of ranks: 5.00689

Parameters BIB

```

Lambda     : 1
treatmeans : 7
Block size : 3
Blocks     : 7
Replication: 3

```

Comparison between treatments sum of the ranks

```

      Difference pvalue sig.
A - B          0 1.0000
A - C         -4 0.1026
A - D          0 1.0000
A - E          0 1.0000
A - F         -3 0.2044
A - G          0 1.0000
B - C         -4 0.1026
B - D          0 1.0000
B - E          0 1.0000

```

```

B - F      -3 0.2044
B - G      0 1.0000
C - D      4 0.1026
C - E      4 0.1026
C - F      1 0.6574
C - G      4 0.1026
D - E      0 1.0000
D - F     -3 0.2044
D - G      0 1.0000
E - F     -3 0.2044
E - G      0 1.0000
F - G      3 0.2044

```

```
> names(out)
```

```

[1] "statistics" "parameters" "means"      "rank"
[5] "comparison" "groups"

```

```
> out$statistics
```

```

chisq.value  p.value  t.value    LSD
    7.714286 0.2597916 2.306004 5.00689

```

6 Graphics of the multiple comparison

The results of a comparison can be graphically seen with the functions *bar.group*, *bar.err* and *diffograph*.

6.1 bar.group

A function to plot horizontal or vertical bar, where the letters of groups of treatments is expressed. The function applies to all functions comparison treatments. Each object must use the group object previously generated by comparative function in indicating that `group = TRUE`.

example:

```

> # model <-aov (yield ~ fertilizer, data = field)
> # out <-LSD.test (model, "fertilizer", group = TRUE)
> # bar.group (out $ group)
> str(bar.group)

```

```
function (x, horiz = FALSE, ...)
```

The found object of one comparison is the entry for these functions, see Figure 4. The objects `outHSD` and `outWaller` are used in the following exercise:

`outHSD`, for the functions *bar.group* and *bar.err*
`outWaller`, for the function *bar.err*

6.2 bar.err

A function to plot horizontal or vertical bar, where the variation of the error is expressed in every treatments. The function applies to all functions comparison treatments. Each object must use the means object previously generated by the comparison function, see Figure 4

```
> # model <-aov (yield ~ fertilizer, data = field)
> # out <-LSD.test (model, "fertilizer", group = TRUE)
> # bar.err(out$means)
> str(bar.err)
```

```
function (x, variation = c("SE", "SD", "range"), horiz = FALSE,
         bar = TRUE, ...)
```

variation SE: Standard error

SD: standard deviation

range: max-min)

```
> par(mfrow=c(1,2),mar=c(3,3,2,0),cex=0.7)
> c1<-colors()[480]; c2=colors()[65]; c3=colors()[15]; c4=colors()[140]
> G1<-bar.group(outHSD$groups, ylim=c(0,45), main="Tukey\nG1",col=c1,las=1)
> # G2<-bar.group(outHSD$groups, horiz=T, xlim=c(0,45), main="Tukey\nG2",col=c2,las=1)
> # G3<-bar.err(outWaller$means, variation="range",ylim=c(0,45), col=c3,main="Range\nG3",las=1)
> G4<-bar.err(outWaller$means, horiz=T, xlim=c(0,45), col=c4, variation="SE",
+ main="Standard error \nG4",las=1)
```

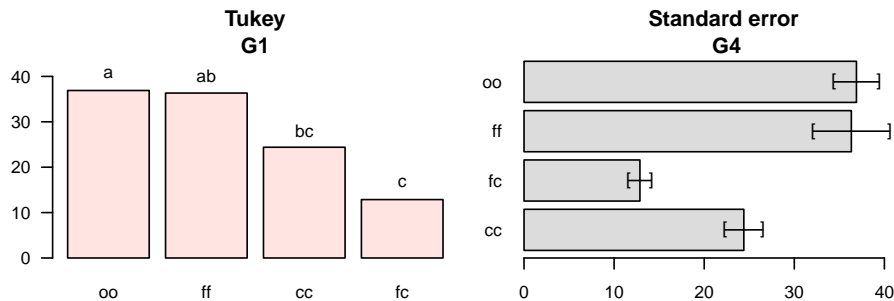


Figure 4: Comparison between treatments

```
> par(mfrow=c(2,2),cex=0.7,mar=c(3.5,1.5,3,0))
> C1<-bar.err(modelPBIB$means[1:7, ], ylim=c(0,9), col=0, main="C1",
+ variation="range",border=3,las=2)
> C2<-bar.err(modelPBIB$means[8:15, ], ylim=c(0,9), col=0, main="C2",
+ variation="range", border =4,las=2)
> # Others graphic
> C3<-bar.err(modelPBIB$means[16:22, ], ylim=c(0,9), col=0, main="C3",
+ variation="range",border =2,las=2)
> C4<-bar.err(modelPBIB$means[23:30, ], ylim=c(0,9), col=0, main="C4",
+ variation="range", border =6,las=2)
> # Lattice graphics
```

```
> par(mar=c(2.5,2.5,1,0),cex=0.6)
> bar.group(modelLattice$group,ylim=c(0,55),density=10,las=1)
```

6.3 diffograph

It plots bars of the averages of treatments to compare. It uses the objects generated by a procedure of comparison like LSD (Fisher), duncan, Tukey (HSD), Student Newman Keul (SNK), Scheffe, Ryan, Einot and Gabriel and Welsch (REGW), Kruskal Wallis, Friedman and Waerden. Reference [6], see Figure 6

```
> # function (x, main = NULL, color1 = "red", color2 = "blue",
> #   color3 = "black", cex.axis = 0.8, las = 1, pch = 20,
> #   bty = "l", cex = 0.8, lwd = 1, xlab = "", ylab = "",
> #   ...)
> # model : yield ~ virus
> # Important group=FALSE
> x<-HSD.test(model, "virus", group=FALSE)
> diffograph(x,cex.axis=0.9,xlab="Yield",ylab="Yield",cex=0.9)
```

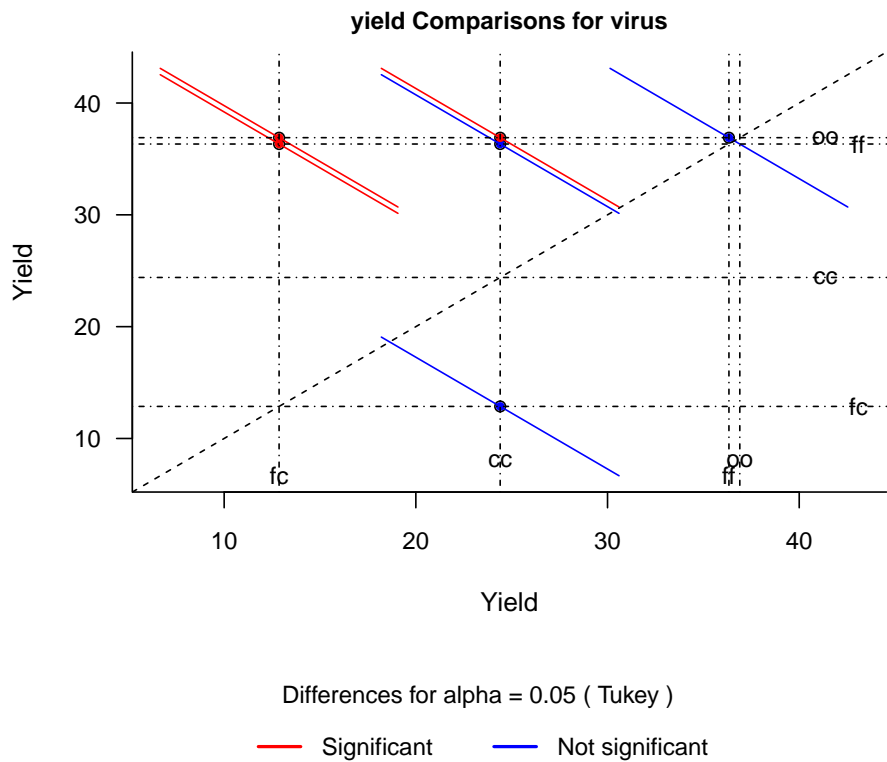


Figure 5: Mean-Mean scatter plot representation of the Tukey method

7 Stability Analysis

In *agricolae* there are two methods for the study of stability and the AMMI model. These are: a parametric model for a simultaneous selection in yield and stability "SHUKLA'S STABILITY VARIANCE AND KANG'S", reference [8] and a non-parametric method of Haynes, based on the data range.

7.1 Parametric Stability

Use the parametric model, function *stability.par*.

Prepare a data table where the rows and the columns are the genotypes and the environments, respectively. The data should correspond to yield averages or to another measured variable. Determine the variance of the common error for all the environments and the number of repetitions that was evaluated for every genotype. If the repetitions are different, find a harmonious average that will represent the set. Finally, assign a name to each row that will represent the genotype. Reference [8] We will consider five environments in the following example:

```
> options(digit=2)
> v1 <- c(10.2,8.8,8.8,9.3,9.6,7.2,8.4,9.6,7.9,10,9.3,8.0,10.1,9.4,10.8,6.3,7.4)
> v2 <- c(7,7.8,7.0,6.9,7,8.3,7.4,6.5,6.8,7.9,7.3,6.8,8.1,7.1,7.1,6.4,4.1)
> v3 <- c(5.3,4.4,5.3,4.4,5.5,4.6,6.2,6.0,6.5,5.3,5.7,4.4,4.2,5.6,5.8,3.9,3.8)
> v4 <- c(7.8,5.9,7.3,5.9,7.8,6.3,7.9,7.5,7.6,5.4,5.6,7.8,6.5,8.1,7.5,5.0,5.4)
> v5 <- c(9,9.2,8.8,10.6,8.3,9.3,9.6,8.8,7.9, 9.1,7.7,9.5,9.4,9.4,10.3,8.8,8.7)
```

For 17 genotypes, the identification is made by letters.

```
> study <- data.frame(v1, v2, v3, v4, v5)
> rownames(study) <- LETTERS[1:17]
```

An error variance of 2 and 4 repetitions is assumed.

Analysis

```
> output <- stability.par(study, rep=4, MSError=2)
> names(output)
```

```
[1] "analysis" "statistics" "stability"
```

```
> print(output$stability)
```

	Yield	Rank	Adj.rank	Adjusted	Stab.var	Stab.rating	YSi	...
A	7.86	14	1	15	1.671833	0	15	+
B	7.22	5	-1	4	1.822233	0	4	
C	7.44	9	1	10	0.233967	0	10	+
D	7.42	8	1	9	4.079567	-2	7	
E	7.64	11	1	12	2.037967	0	12	+
F	7.14	4	-1	3	5.161967	-4	-1	
G	7.90	15	1	16	1.759300	0	16	+
H	7.68	13	1	14	1.757167	0	14	+
I	7.34	7	-1	6	5.495300	-4	2	
J	7.54	10	1	11	4.129967	-2	9	+

K	7.12	3	-1	2	3.848900	0	2	
L	7.30	6	-1	5	2.675300	0	5	
M	7.66	12	1	13	3.473167	0	13	+
N	7.92	16	1	17	0.806233	0	17	+
O	8.30	17	2	19	1.951300	0	19	+
P	6.08	2	-2	0	3.647833	0	0	
Q	5.88	1	-3	-2	3.598500	0	-2	

The selected genotypes are: A, C, E, G, H, J, M, N and O. These genotypes have a higher yield and a lower variation. to see `output$analysis`, the interaction is significant.

If for example there is an environmental index, it can be added as a covariate. For this case, the altitude of the localities is included.

```
> altitude<-c(1200, 1300, 800, 1600, 2400)
> stability <- stability.par(study,rep=4,MSerror=2, cova=TRUE, name.cov= "altitude",
+ file.cov=altitude)
```

7.2 Non-parametric Stability

For non-parametric stability, the function in 'agricolae' is `stability.nonpar()`. The names of the genotypes should be included in the first column, and in the other columns, the response by environments. Reference [5]

Analysis

```
> data <- data.frame(name=row.names(study), study)
> output<-stability.nonpar(data, "YIELD", ranking=TRUE)
> names(output)
```

```
[1] "ranking"      "statistics"
```

```
> output$statistics
```

	MEAN	es1	es2	vs1	vs2	chi.ind	chi.sum
1	7.378824	5.647059	24	2.566667	148.8	8.843605	27.58711

7.3 AMMI

The model AMMI uses the biplot constructed through the principal components generated by the interaction environment-genotype. If there is such interaction, the percentage of the two principal components would explain more than the 50% of the total variation; in such case, the biplot would be a good alternative to study the interaction environment-genotype. Reference [3]

The data for AMMI should come from similar experiments conducted in different environments. Homogeneity of variance of the experimental error, produced in the different environments, is required. The analysis is done by combining the experiments.

The data can be organized in columns, thus: environment, genotype, repetition, and variable.

The data can also be the averages of the genotypes in each environment, but it is necessary to consider a harmonious average for the repetitions and a common variance of the error. The data should be organized in columns: environment, genotype, and variable.

When performing AMMI, this generates the Biplot, Triplot and Influence graphics, see Figures ??

For the application, we consider the data used in the example of parametric stability (study):

AMMI structure

```
> str(AMMI)
```

```
function (ENV, GEN, REP, Y, MSE = 0, console = FALSE,
         PC = FALSE)
```

plot.AMMI structure, plot()

```
> str(plot.AMMI)
```

```
function (x, first = 1, second = 2, third = 3, type = 1,
         number = FALSE, gcol = NULL, ecol = NULL, icol = NULL,
         angle = 25, lwd = 1.8, length = 0.1, xlab = NULL,
         ylab = NULL, xlim = NULL, ylim = NULL, ...)
```

type: 1=biplot, 2= triplot 3=influence genotype

```
> rdto <- c(study[,1], study[,2], study[,3], study[,4], study[,5])
> environment <- gl(5,17)
> genotype <- rep(rownames(study),5)
> model<-AMMI(ENV=environment, GEN=genotype, REP=4, Y=rdto, MSE=2, console=TRUE)
```

```
ANALYSIS AMMI: rdto
Class level information
```

```
ENV:  1 2 3 4 5
GEN:  A B C D E F G H I J K L M N O P Q
REP:  4
```

```
Number of means:  85
```

```
Dependent Variable: rdto
```

```
Analysis of variance
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ENV	4	734.2475	183.561882		
REP(ENV)	15				
GEN	16	120.0875	7.505471	3.752735	3.406054e-06
ENV:GEN	64	181.2725	2.832382	1.416191	3.279630e-02
Residuals	240	480.0000	2.000000		

Coeff var	Mean rdto
19.16584	7.378824

```
Analysis
```

	percent	acum	Df	Sum.Sq	Mean.Sq	F.value	Pr.F
PC1	38.0	38.0	19	68.96258	3.629609	1.81	0.0225

```

PC2    29.8  67.8 17 54.02864 3.178155    1.59 0.0675
PC3    22.5  90.4 15 40.84756 2.723170    1.36 0.1680
PC4     9.6 100.0 13 17.43370 1.341054    0.67 0.7915

```

```

> pc <- model$analysis[, 1]
> pc12<-sum(pc[1:2])
> pc123<-sum(pc[1:3])
> rm(rdto,environment,genotype)

```

```

> par(cex=0.8,mar=c(4,4,1,0))
> plot(model,type=1,las=1)

```

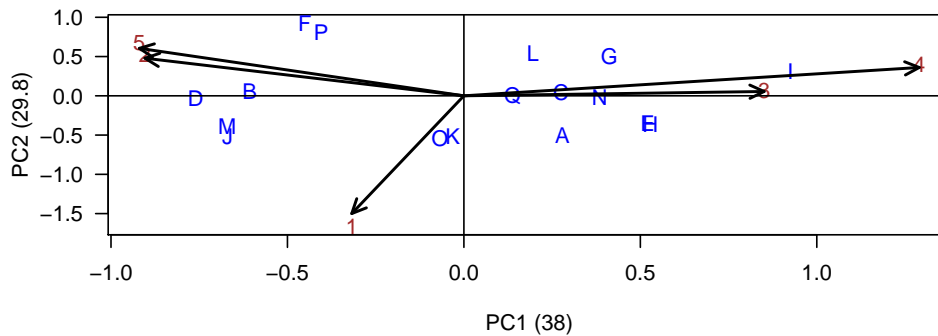


Figure 6: Biplot

In this case, the interaction is significant. The first two components explain 67.8 %; then the biplot can provide information about the interaction genotype-environment. With the triplot, 90.3% would be explained.

To triplot require klaR package. in R execute:

```
plot(model,type=2,las=1)
```

To Influence graphics genotype require spdep package, in R execute:

```
plot(model,type=3,las=1)
```

7.4 AMMI index and yield stability

Calculate AMMI stability value (ASV) and Yield stability index (YSI). References [15, 13]

```

> data(plrv)
> attach(plrv)
> model<- AMMI(Locality, Genotype, Rep, Yield, console=FALSE)
> detach(plrv)
> index<-index.AMMI(model)
> # Crops with improved stability according AMMI.
> print(index[order(index[,3]),])

```

	ASV	YSI	rASV	rYSI	means
402.7	0.2026430	20	1	19	27.47748

506.2	0.5646275	13	2	11	33.26623
364.21	0.5966506	13	3	10	34.05974
427.7	0.9507170	11	4	7	36.19020
233.11	1.0521529	22	5	17	28.66655
241.2	1.1739456	28	6	22	26.34039
221.19	1.2740344	33	7	26	22.98480
104.22	1.3792025	21	8	13	31.28887
317.6	1.5167528	18	9	9	35.32583
121.31	1.7912464	25	10	15	30.10174
314.12	2.0368354	29	11	18	28.17335
342.15	2.0954103	36	12	24	26.01336
Canchan	2.1652861	33	13	20	27.00126
406.12	2.1722949	26	14	12	32.68323
351.26	2.3436592	23	15	8	36.11581
320.16	2.3623790	37	16	21	26.34808
450.3	2.3663500	23	17	6	36.19602
255.7	2.4615460	32	18	14	30.58975
102.18	2.5131813	42	19	23	26.31947
405.2	2.7709324	36	20	16	28.98663
157.26	2.8907699	26	21	5	36.95181
163.9	3.0764673	49	22	27	21.41747
141.28	3.1531170	24	23	1	39.75624
235.6	3.3065468	28	24	4	38.63477
Unica	3.3470545	27	25	2	39.10400
346.2	3.6050812	51	26	25	23.84175
319.20	4.8741897	30	27	3	38.75767
Desiree	5.5374138	56	28	28	16.15569

```
> # Crops with better response and improved stability according AMMI.
> print(index[order(index[,4]),])
```

	ASV	YSI	rASV	rYSI	means
141.28	3.1531170	24	23	1	39.75624
Unica	3.3470545	27	25	2	39.10400
319.20	4.8741897	30	27	3	38.75767
235.6	3.3065468	28	24	4	38.63477
157.26	2.8907699	26	21	5	36.95181
450.3	2.3663500	23	17	6	36.19602
427.7	0.9507170	11	4	7	36.19020
351.26	2.3436592	23	15	8	36.11581
317.6	1.5167528	18	9	9	35.32583
364.21	0.5966506	13	3	10	34.05974
506.2	0.5646275	13	2	11	33.26623
406.12	2.1722949	26	14	12	32.68323
104.22	1.3792025	21	8	13	31.28887
255.7	2.4615460	32	18	14	30.58975
121.31	1.7912464	25	10	15	30.10174
405.2	2.7709324	36	20	16	28.98663
233.11	1.0521529	22	5	17	28.66655
314.12	2.0368354	29	11	18	28.17335
402.7	0.2026430	20	1	19	27.47748

Canchan	2.1652861	33	13	20	27.00126
320.16	2.3623790	37	16	21	26.34808
241.2	1.1739456	28	6	22	26.34039
102.18	2.5131813	42	19	23	26.31947
342.15	2.0954103	36	12	24	26.01336
346.2	3.6050812	51	26	25	23.84175
221.19	1.2740344	33	7	26	22.98480
163.9	3.0764673	49	22	27	21.41747
Desiree	5.5374138	56	28	28	16.15569

8 Special functions

8.1 Consensus of dendrogram

Consensus is the degree or similarity of the vertexes of a tree regarding its branches of the constructed dendrogram. The function to apply is `consensus()`.

The data correspond to a table, with the name of the individuals and the variables in the rows and columns respectively. For the demonstration, we will use the "pamCIP" data of 'agricolae', which correspond to molecular markers of 43 entries of a germplasm bank (rows) and 107 markers (columns).

The program identifies duplicates in the rows and can operate in both cases. The result is a dendrogram, in which the consensus percentage is included, see Figure 7.

When the dendrogram is complex, it is convenient to extract part of it with the function `hcut()`, see Figure 8.

The obtained object "output" contains information about the process:

```
> names(output)

[1] "table.dend" "dendrogram" "duplicates"
```

Construct a classic dendrogram, execute procedure in R

use the previous result 'output'

```
> dend <- as.dendrogram(output$dendrogram)
> data <- output$table.dend
> head(output$table.dend)

  X1 X2 axis      height percentage groups
1 -6 -24 7.50 0.02857143          60 6-24
2 -3 -4 19.50 0.03571429          40 3-4
3 -2 -8 22.50 0.03846154          60 2-8
4 -7 -10 10.50 0.03846154          60 7-10
5 -21 2 18.75 0.07142857          60 3-4-21
6 -16 3 21.75 0.07407407          40 2-8-16

> par(mar=c(3,3,1,1),cex=0.6)
> plot(dend,type="r",edgePar = list(lty=1:2, col=colors()[c(42,84)]),las=1)
> text(data[,3],data[,4],data[,5],col="blue",cex=1)
```



```

> par(cex=0.6,mar=c(3,3,2,0))
> data(pamCIP)
> rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
> output<-consensus(pamCIP,distance="binary", method="complete", nboot=5)

```

Duplicates: 18

New data : 25 Records

Consensus hclust

Method distance: binary

Method cluster : complete

rows and cols : 25 107

n-bootstrap : 5

Run time : 1.636606 secs

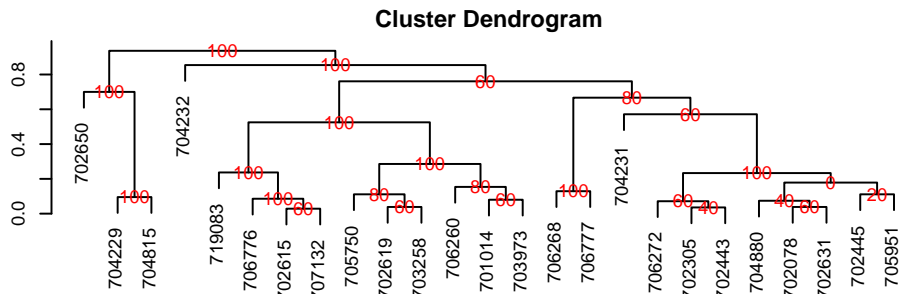


Figure 7: Dendrogram, production by consensus

```

> par(cex=0.6,mar=c(3,3,1.5,0))
> out1<- hcut(output,h=0.4,group=8,type="t",edgePar = list(lty=1:2, col=colors()[c(42,84)]),
+ main="group 8" ,col.text="blue",cex.text=1,las=1)

```

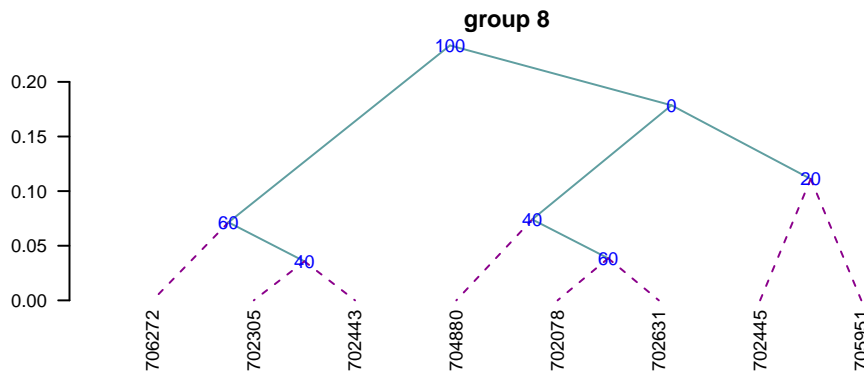


Figure 8: Dendrogram, production by hcut()

8.2 Montecarlo

It is a method for generating random numbers of an unknown distribution. It uses a data set and, through the cumulative behavior of its relative frequency, generates the possible random values that follow the data distribution. These new numbers are used in some simulation process.

The probability density of the original and simulated data can be compared, see Figure 9.

```
> data(soil)
> # set.seed(9473)
> simulated <- montecarlo(soil$pH,1000)
> h<-graph.freq(simulated,nclass=7,plot=FALSE)

> par(mar=c(2,0,2,1),cex=0.6)
> plot(density(soil$pH),axes=F,main="pH density of the soil\ncon Ralstonia",xlab="",lwd=4)
> lines(density(simulated), col="blue", lty=4,lwd=4)
> axis(1,0:12)
> legend("topright",c("Original","Simulated"),lty=c(1,4),col=c("black","blue"), lwd=4)
```

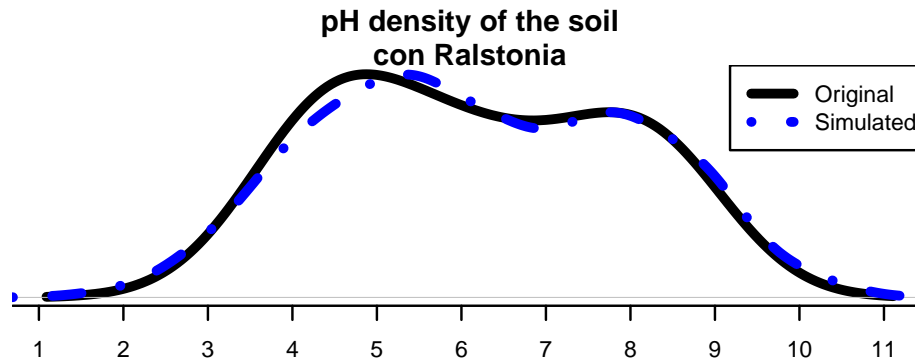


Figure 9: Distribution of the simulated and the original data

1000 data was simulated, being the frequency table:

```
> round(table.freq(h),2)
```

	Lower	Upper	Main	Frequency	Percentage	CF	CPF
1	1.50	2.81	2.16	20	2.0	20	2.0
2	2.81	4.12	3.47	120	12.0	140	14.0
3	4.12	5.43	4.78	238	23.8	378	37.8
4	5.43	6.74	6.09	225	22.5	603	60.3
5	6.74	8.05	7.40	198	19.8	801	80.1
6	8.05	9.36	8.70	168	16.8	969	96.9
7	9.36	10.67	10.02	31	3.1	1000	100.0

Some statistics, original data:

```
> summary(soil$pH)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
3.800	4.700	6.100	6.154	7.600	8.400

Some statistics, `montecarlo` simulate data:

```
> summary(simulated)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.600	4.776	6.090	6.218	7.737	10.660

8.3 Re-Sampling in linear model

It uses the permutation method for the calculation of the probabilities of the sources of variation of ANOVA according to the linear regression model or the design used. The principle is that the Y response does not depend on the averages proposed in the model; hence, the Y values can be permuted and many model estimates can be constructed. On the basis of the patterns of the random variables of the elements under study, the probability is calculated in order to measure the significance.

For a variance analysis, the data should be prepared similarly. The function to use is: `resampling.model()`

```
> data(potato)
> potato[,1]<-as.factor(potato[,1])
> potato[,2]<-as.factor(potato[,2])
> model<-"cutting~variety + date + variety:date"
> analysis<-resampling.model(model, potato, k=100)
> Xsol<-as.matrix(round(analysis$solution,2))
> print(Xsol,na.print = "")
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	Resampling
variety	1	25.09	25.09	7.26	0.02	0.01
date	2	13.89	6.95	2.01	0.18	0.16
variety:date	2	4.85	2.43	0.70	0.51	0.61
Residuals	12	41.48	3.46			

The function `resampling.model()` can be used when the errors have a different distribution from normal

8.4 Simulation in linear model

Under the assumption of normality, the function generates pseudo experimental errors under the proposed model, and determines the proportion of valid results according to the analysis of variance found.

The function is: `simulation.model()`. The data are prepared in a table, similarly to an analysis of variance.

Considering the example proposed in the previous procedure:

```
> simModel <- simulation.model(model, potato, k=100,console=TRUE)
```

Simulation of experiments
Under the normality assumption

```

-----
Proposed model: cutting~variety + date + variety:date
Analysis of Variance Table

```

```

Response: cutting
          Df Sum Sq Mean Sq F value Pr(>F)
variety    1 25.087  25.0868   7.2580 0.01952 *
date       2  13.892   6.9459   2.0096 0.17671
variety:date 2   4.853   2.4265   0.7020 0.51484
Residuals 12  41.477   3.4564

```

```

---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

---
Validation of the analysis of variancia for the proposed model
Simulations: 100

```

	Df	F value	% Acceptance	% Rejection
variety	1	7.2580377	49	51
date	2	2.0095604	60	40
variety:date	2	0.7020312	61	39

```

          Criterion
variety    nonacceptable
date       acceptable
variety:date acceptable

```

The validation is referred to the percentage of decision results equal to the result of the ANOVA decision. Thus, 61% of the results simulated on the interaction variety*date gave the same result of acceptance or rejection obtained in the ANOVA.

8.5 Path Analysis

It corresponds to the "path analysis" method. The data correspond to correlation matrices of the independent ones with the dependent matrix (XY) and between the independent ones (XX).

It is necessary to assign names to the rows and columns in order to identify the direct and indirect effects.

```

> corr.x<- matrix(c(1,0.5,0.5,1),c(2,2))
> corr.y<- rbind(0.6,0.7)
> names<-c("X1", "X2")
> dimnames(corr.x)<-list(names,names)
> dimnames(corr.y)<-list(names,"Y")
> output<-path.analysis(corr.x,corr.y)

```

Direct(Diagonal) and indirect effect path coefficients

```

=====
          X1          X2
X1 0.3333333 0.2666667
X2 0.1666667 0.5333333

```

```
Residual Effect^2 = 0.4266667
```

```
> output
```

```
$Coeff
      X1      X2
X1 0.3333333 0.2666667
X2 0.1666667 0.5333333

$Residual
[1] 0.4266667
```

8.6 Line X Tester

It corresponds to a crossbreeding analysis of a genetic design. The data should be organized in a table. Only four columns are required: repetition, females, males, and response. In case it corresponds to progenitors, the females or males field will only be filled with the corresponding one. See the heterosis data. Reference [16].

Example with the heterosis data, locality 2.

	Replication	Female	Male	v2
109	1	LT-8	TS-15	2.65
110	1	LT-8	TPS-13	2.26
...				
131	1	Achirana	TPS-13	3.55
132	1	Achirana	TPS-67	3.05
...				
140	1	Achirana	<NA>	3.35
...				
215	3	<NA>	TPS-67	2.91

where <NA> is empty.

If it is a progeny, it comes from a "Female" and a "Male." If it is a progenitor, it will only be "Female" or "Male."

The following example corresponds to data of the locality 2:

24 progenies 8 females 3 males 3 repetitions

They are 35 treatments (24, 8, 3) applied to three blocks.

```
> rm(list=ls())
> data(heterosis)
> site2<-subset(heterosis,heterosis[,1]==2)
> site2<-subset(site2[,c(2,5,6,8)],site2[,4]!="Control")
> attach(site2)
> output1<-lineXtester(Replication, Female, Male, v2)
```

```
ANALYSIS LINE x TESTER: v2
```

ANOVA with parents and crosses

=====

	Df	Sum Sq	Mean Sq	F value	
Replications	2	0.519190476	0.259595238	9.801	
Treatments	34	16.101605714	0.473576639	17.879	
Parents	10	7.731490909	0.773149091	29.189	
Parents vs. Crosses	1	0.005082861	0.005082861	0.192	
Crosses	23	8.365031944	0.363697041	13.731	
Error	68	1.801142857	0.026487395		
Total	104	18.421939048			
		Pr(>F)			
Replications		0.0002			
Treatments		0.0000			
Parents		0.0000			
Parents vs. Crosses		0.6626			
Crosses		0.0000			
Error					
Total					

ANOVA for line X tester analysis

=====

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Lines	7	4.9755431	0.71079187	3.632	0.0191
Testers	2	0.6493861	0.32469306	1.659	0.2256
Lines X Testers	14	2.7401028	0.19572163	7.389	0.0000
Error	68	1.8011429	0.02648739		

ANOVA for line X tester analysis including parents

=====

	Df	Sum Sq	Mean Sq	F value	
Replications	2	0.519190476	0.259595238	9.801	
Treatments	34	16.101605714	0.473576639	17.879	
Parents	10	7.731490909	0.773149091	29.189	
Parents vs. Crosses	1	0.005082861	0.005082861	0.192	
Crosses	23	8.365031944	0.363697041	13.731	
Lines	7	4.975543056	0.710791865	3.632	
Testers	2	0.649386111	0.324693056	1.659	
Lines X Testers	14	2.740102778	0.195721627	7.389	
Error	68	1.801142857	0.026487395		
Total	104	18.421939048			
		Pr(>F)			
Replications		0.0002			
Treatments		0.0000			
Parents		0.0000			
Parents vs. Crosses		0.6626			
Crosses		0.0000			
Lines		0.0191			
Testers		0.2256			
Lines X Testers		0.0000			
Error					
Total					

GCA Effects:

=====

Lines Effects:

Achirana	LT-8	MF-I	MF-II	Serrana	TPS-2
0.022	-0.338	0.199	-0.449	0.058	-0.047
TPS-25	TPS-7				
0.414	0.141				

Testers Effects:

TPS-13	TPS-67	TS-15
0.087	0.046	-0.132

SCA Effects:

=====

Lines	Testers		
	TPS-13	TPS-67	TS-15
Achirana	0.061	0.059	-0.120
LT-8	-0.435	0.519	-0.083
MF-I	-0.122	-0.065	0.187
MF-II	-0.194	0.047	0.148
Serrana	0.032	-0.113	0.081
TPS-2	0.197	-0.072	-0.124
TPS-25	0.126	-0.200	0.074
TPS-7	0.336	-0.173	-0.162

Standard Errors for Combining Ability Effects:

=====

S.E. (gca for line) : 0.05424983
S.E. (gca for tester) : 0.0332211
S.E. (sca effect) : 0.09396346
S.E. (gi - gj)line : 0.07672084
S.E. (gi - gj)tester : 0.04698173
S.E. (sij - skl)tester: 0.1328844

Genetic Components:

=====

Cov H.S. (line) : 0.05723003
Cov H.S. (tester) : 0.00537381
Cov H.S. (average): 0.003867302
Cov F.S. (average): 0.1279716
F = 0, Additive genetic variance: 0.01546921
F = 1, Additive genetic variance: 0.007734604
F = 0, Variance due to Dominance: 0.1128228
F = 1, Variance due to Dominance: 0.05641141

Proportional contribution of lines, testers
and their interactions to total variance

=====

Contributions of lines : 59.48026
Contributions of testers: 7.763104

```
Contributions of lxt      : 32.75663
```

```
> detach(site2)
```

8.7 Soil Uniformity

The Smith index is an indicator of the uniformity, used to determine the parcel size for research purposes. The data correspond to a matrix or table that contains the response per basic unit, a number of n rows \times m columns, and a total of $n \times m$ basic units.

For the test, we will use the rice file. The graphic is a result with the adjustment of a model for the plot size and the coefficient of variation, see Figure 10.

```
> par(mar=c(3,3,4,0),cex=0.7)
> data(rice)
> table<-index.smith(rice,pch=19, col="blue",
+ main="Interaction between the CV and the plot size",type="l",xlab="Size")
```

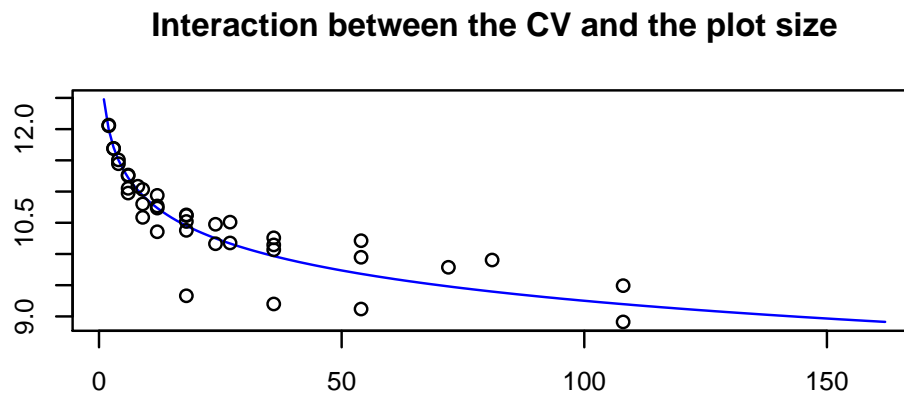


Figure 10: Adjustment curve for the optimal size of plot

```
> uniformity <- data.frame(table$uniformity)
> head(uniformity)
```

	Size	Width	Length	plots	Vx	CV
1	1	1	1	648	9044.539	13.0
2	2	1	2	324	7816.068	12.1
3	2	2	1	324	7831.232	12.1
4	3	1	3	216	7347.975	11.7
5	3	3	1	216	7355.216	11.7
6	4	1	4	162	7047.717	11.4

8.8 Confidence Limits In Biodiversity Indices

The biodiversity indices are widely used for measuring the presence of living things in an ecological area. Many programs indicate their value. The function of 'agricolae' is also to show the confidence intervals, which can be used for a statistical comparison. Use the bootstrap procedure. The data are organized in a table; the species are placed in a column; and in another one, the number of individuals. The indices that can be calculated with the function `index.bio()` of 'agricolae' are: "Margalef", "Simpson.Dom", "Simpson.Div", "Berger.Parker", "McIntosh", and "Shannon."

In the example below, we will use the data obtained in the locality of Paracsho, district of Huasahuasi, province of Tarma in the department of Junin.

The evaluation was carried out in the parcels on 17 November 2005, without insecticide application. The counted specimens were the following:

```
> data(paracsho)
> species <- paracsho[79:87,4:6]
> species
```

	Orden	Family	Number.of.specimens
79	DIPTERA	TIPULIDAE	3
80	LEPIDOPTERA	NOCTUIDAE	1
81	NOCTUIDAE	PYRALIDAE	3
82	HEMIPTERA	ANTHOCORIDAE	1
83	DIPTERA	TACHINIDAE	16
84	DIPTERA	ANTHOCORIDAE	3
85	DIPTERA	SCATOPHAGIDAE	5
86	DIPTERA	SYRPHIDAE	1
87	DIPTERA	MUSCIDAE	3

The Shannon index is:

```
> output <- index.bio(species[,3],method="Shannon",level=95,nboot=200)
```

Method: Shannon

The index: 3.52304

95 percent confidence interval:
3.180131 ; 4.260501

8.9 Correlation

The function `correlation()` of 'agricolae' makes the correlations through the methods of Pearson, Spearman and Kendall for vectors and/or matrices. If they are two vectors, the test is carried out for one or two lines; if it is a matrix one, it determines the probabilities for a difference, whether it is greater or smaller.

For its application, consider the soil data: `data(soil)`

```
> data(soil)
> correlation(soil[,2:4],method="pearson")
```

```

$correlation
      pH  EC CaCO3
pH    1.00 0.55  0.73
EC    0.55 1.00  0.32
CaCO3 0.73 0.32  1.00

$pvalue
      pH      EC      CaCO3
pH    1.000000000 0.0525330 0.004797027
EC    0.052532997 1.0000000 0.294159813
CaCO3 0.004797027 0.2941598 1.000000000

$n.obs
[1] 13

> attach(soil)
> correlation(pH,soil[,3:4],method="pearson")

```

```

$correlation
      EC CaCO3
pH 0.55  0.73

```

```

$pvalue
      EC CaCO3
pH 0.0525 0.0048

```

```

$n.obs
[1] 13

```

```

> correlation(pH,CaCO3,method="pearson")

```

Pearson's product-moment correlation

```

data: pH and CaCO3
t = 3.520169 , df = 11 , p-value = 0.004797027
alternative hypothesis: true rho is not equal to 0
sample estimates:

```

```

cor
 0.7278362

```

```

> detach(soil)

```

8.10 tapply.stat()

Gets a functional calculation of variables grouped by study factors.

Application with 'agricolae' data:

max(yield)-min(yield) by farmer

```

> data(RioChillon)
> attach(RioChillon$babies)
> tapply.stat(yield,farmer,function(x) max(x)-min(x))

```

```

          farmer yield
1 AugustoZambrano  7.5
2      Caballero  13.4
3      ChocasAlto  14.1
4      FelixAndia  19.4
5      Huarangal-1  9.8
6      Huarangal-2  9.1
7      Huarangal-3  9.4
8      Huatocay   19.4
9 IgnacioPolinario 13.1

```

```
> detach(RioChillon$babies)
```

It corresponds to the range of variation in the farmers' yield.

The function "tapply" can be used directly or with function.

If A is a table with columns 1,2 and 3 as category, and 5,6 and 7 as variables, then the following procedures are valid:

```

tapply.stat(A[,5:7], A[,1:3],mean)
tapply.stat(A[,5:7], A[,1:3],function(x) mean(x,na.rm=TRUE))
tapply.stat(A[,c(7,6)], A[,1:2],function(x) sd(x)*100/mean(x))

```

8.11 Coefficient of variation of an experiment

If "model" is the object resulting from an analysis of variance of the function aov() or lm() of R, then the function cv.model() calculates the coefficient of variation.

```

> data(sweetpotato)
> model <- aov(yield ~ virus, data=sweetpotato)
> cv.model(model)

```

```
[1] 17.1666
```

8.12 Skewness and kurtosis

The skewness and kurtosis results, obtained by 'agricolae', are equal to the ones obtained by SAS, MiniTab, SPSS, InfoStat, and Excel.

If x represents a data set:

```
> x<-c(3,4,5,2,3,4,5,6,4,NA,7)
```

skewness is calculated with:

```
> skewness(x)
```

```
[1] 0.3595431
```

and kurtosis with:

```
> kurtosis(x)
```

```
[1] -0.1517996
```

8.13 Tabular value of Waller-Duncan

The function Waller determines the tabular value of Waller-Duncan. For the calculation, value F is necessary, calculated from the analysis of variance of the study factor, with its freedom degrees and the estimate of the variance of the experimental error. Value K, parameter of the function is the ratio between the two types of errors (I and II). To use it, a value associated with the alpha level is assigned. When the alpha level is 0.10, 50 is assigned to K; for 0.05, K=100; and for 0.01, K=500. K can take any value.

```
> q<-5
> f<-15
> K<-seq(10,1000,100)
> n<-length(K)
> y<-rep(0,3*n)
> dim(y)<-c(n,3)
> for(i in 1:n) y[i,1]<-waller(K[i],q,f,Fc=2)
> for(i in 1:n) y[i,2]<-waller(K[i],q,f,Fc=4)
> for(i in 1:n) y[i,3]<-waller(K[i],q,f,Fc=8)
```

Function of Waller to different value of parameters K and Fc The next procedure illustrates the function for different values of K with freedom degrees of 5 for the numerator and 15 for the denominator, and values of calculated F, equal to 2, 4, and 8.

```
> par(mar=c(3,3,4,0),cex=0.7)
> plot(K,y[,1],type="l",col="blue",ylab="waller",bty="l")
> lines(K,y[,2],type="l",col="brown",lty=2,lwd=2)
> lines(K,y[,3],type="l",col="green",lty=4,lwd=2)
> legend("topleft",c("2","4","8"),col=c("blue","brown","green"),lty=c(1,8,20),
+ lwd=2,title="Fc")
> title(main="Waller in function of K")
```

Generating table Waller-Duncan

```
> K<-100
> Fc<-1.2
> q<-c(seq(6,20,1),30,40,100)
> f<-c(seq(4,20,2),24,30)
> n<-length(q)
> m<-length(f)
> W.D <-rep(0,n*m)
> dim(W.D)<-c(n,m)
> for (i in 1:n) {
+ for (j in 1:m) {
+ W.D[i,j]<-waller(K, q[i], f[j], Fc)
+ }}
> W.D<-round(W.D,2)
> dimnames(W.D)<-list(q,f)
> cat("table: Waller Duncan k=100, F=1.2")
```

table: Waller Duncan k=100, F=1.2

```
> print(W.D)
```

```
      4    6    8   10   12   14   16   18   20   24   30
6  2.85 2.87 2.88 2.89 2.89 2.89 2.89 2.88 2.88 2.88 2.88
7  2.85 2.89 2.92 2.93 2.94 2.94 2.94 2.94 2.94 2.94 2.94
8  2.85 2.91 2.94 2.96 2.97 2.98 2.99 2.99 2.99 3.00 3.00
9  2.85 2.92 2.96 2.99 3.01 3.02 3.03 3.03 3.04 3.04 3.05
10 2.85 2.93 2.98 3.01 3.04 3.05 3.06 3.07 3.08 3.09 3.10
11 2.85 2.94 3.00 3.04 3.06 3.08 3.09 3.10 3.11 3.12 3.14
12 2.85 2.95 3.01 3.05 3.08 3.10 3.12 3.13 3.14 3.16 3.17
13 2.85 2.96 3.02 3.07 3.10 3.12 3.14 3.16 3.17 3.19 3.20
14 2.85 2.96 3.03 3.08 3.12 3.14 3.16 3.18 3.19 3.21 3.23
15 2.85 2.97 3.04 3.10 3.13 3.16 3.18 3.20 3.21 3.24 3.26
16 2.85 2.97 3.05 3.11 3.15 3.18 3.20 3.22 3.24 3.26 3.29
17 2.85 2.98 3.06 3.12 3.16 3.19 3.22 3.24 3.25 3.28 3.31
18 2.85 2.98 3.07 3.13 3.17 3.21 3.23 3.25 3.27 3.30 3.33
19 2.85 2.98 3.07 3.13 3.18 3.22 3.25 3.27 3.29 3.32 3.35
20 2.85 2.99 3.08 3.14 3.19 3.23 3.26 3.28 3.30 3.33 3.37
30 2.85 3.01 3.11 3.19 3.26 3.31 3.35 3.38 3.41 3.45 3.50
40 2.85 3.02 3.13 3.22 3.29 3.35 3.39 3.43 3.47 3.52 3.58
100 2.85 3.04 3.17 3.28 3.36 3.44 3.50 3.55 3.59 3.67 3.76
```

8.14 AUDPC

The area under the disease progress curve (AUDPC), see Figure 10 calculates the absolute and relative progress of the disease. It is required to measure the disease in percentage terms during several dates, preferably equidistantly.

```
> days<-c(7,14,21,28,35,42)
> evaluation<-data.frame(E1=10,E2=40,E3=50,E4=70,E5=80,E6=90)
> print(evaluation)
```

```
  E1 E2 E3 E4 E5 E6
1 10 40 50 70 80 90
```

```
> absolute1 <-audpc(evaluation,days)
> relative1 <-round(audpc(evaluation,days,"relative"),2)
```

8.15 AUDPS

The Area Under the Disease Progress Stairs (AUDPS), see Figure 11. A better estimate of disease progress is the area under the disease progress stairs (AUDPS). The AUDPS approach improves the estimation of disease progress by giving a weight closer to optimal to the first and last observations..

```
> absolute2 <-audps(evaluation,days)
> relative2 <-round(audps(evaluation,days,"relative"),2)
```

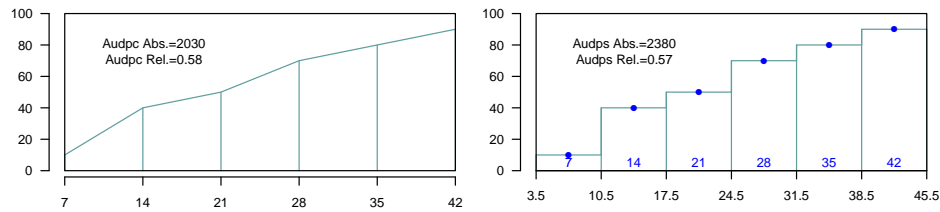


Figure 11: Area under the curve (AUDPC) and Area under the Stairs (AUDPS)

8.16 Non-Additivity

Tukey's test for non-additivity is used when there are doubts about the additivity veracity of a model. This test confirms such assumption and it is expected to accept the null hypothesis of the non-additive effect of the model.

For this test, all the experimental data used in the estimation of the linear additive model are required. Use the function `nonadditivity()` of 'agricolae'. For its demonstration, the experimental data "potato", of the package 'agricolae', will be used. In this case, the model corresponds to the randomized complete block design, where the treatments are the varieties.

```
> data(potato)
> potato[,1]<-as.factor(potato[,1])
> model<-lm(cutting ~ date + variety,potato)
> df<-df.residual(model)
> MSerror<-deviance(model)/df
> attach(potato)
> analysis<-nonadditivity(cutting, date, variety, df, MSerror)
```

Tukey's test of nonadditivity
cutting

P : 15.37166
Q : 77.44441

Analysis of Variance Table

```
Response: residual
      Df Sum Sq Mean Sq F value Pr(>F)
Nonadditivity  1  3.051  3.0511  0.922 0.3532
Residuals    14 46.330  3.3093
```

```
> detach(potato)
```

According to the results, the model is additive because the p.value 0.35 is greater than 0.05.

8.17 LATEBLIGHT

LATEBLIGHT is a mathematical model that simulates the effect of weather, host growth and resistance, and fungicide use on asexual development and growth of *Phytophthora infestans* on potato

foliage, see Figure 12

LATEBLIGHT Version LB2004 was created in October 2004 (Andrade-Piedra et al., 2005a, b and c), based on the C-version written by B.E. Ticknor ('BET 21191 modification of cbm8d29.c'), reported by Doster et al. (1990) and described in detail by Fry et al. (1991) (This version is referred as LB1990 by Andrade-Piedra et al. [2005a]). The first version of LATEBLIGHT was developed by Bruhn and Fry (1981) and described in detail by Bruhn et al. (1980).

```
> f <- system.file("external/weather.csv", package="agricolae")
> weather <- read.csv(f,header=FALSE)
> f <- system.file("external/severity.csv", package="agricolae")
> severity <- read.csv(f)
> weather[,1]<-as.Date(weather[,1],format = "%m/%d/%Y")
> # Parameters dates
> dates<-c("2000-03-25", "2000-04-09", "2000-04-12", "2000-04-16", "2000-04-22")
> dates<-as.Date(dates)
> EmergDate <- as.Date("2000/01/19")
> EndEpidDate <- as.Date("2000-04-22")
> dates<-as.Date(dates)
> NoReadingsH<- 1
> RHthreshold <- 90
> WS<-weatherSeverity(weather,severity,dates,EmergDate,EndEpidDate,
+ NoReadingsH,RHthreshold)
> # Parameters to Lateblight function
> InocDate<-"2000-03-18"
> LGR <- 0.00410
> IniSpor <- 0
> SR <- 292000000
> IE <- 1.0
> LP <- 2.82
> InMicCol <- 9
> Cultivar <- "NICOLA"
> ApplSys <- "NOFUNGICIDE"
> main<-"Cultivar: NICOLA"
```

```

> par(mar=c(3,3,4,0),cex=0.7)
> #-----
> model<-lateblight(WS, Cultivar,ApplSys, InocDate, LGR,IniSpor,SR,IE,
+ LP,MatTime='LATESEASON',InMicCol,main=main,type="1",xlim=c(65,95),lwd=1.5,
+ xlab="Time (days after emergence)", ylab="Severity (Percentage)")

```

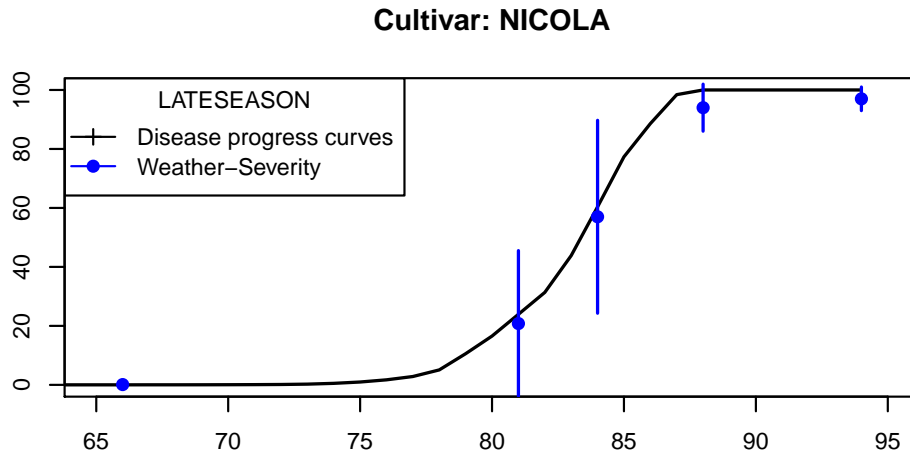


Figure 12: lateblight: LATESEASON

```

> head(model$Gfile)

```

	dates	nday	MeanSeverity	StDevSeverity	MinObs
Eval1	2000-03-25	66	0.1	0.000000	0.100000
Eval2	2000-04-09	81	20.8	24.722459	-3.922459
Eval3	2000-04-12	84	57.0	32.710854	24.289146
Eval4	2000-04-16	88	94.0	7.968689	86.031311
Eval5	2000-04-22	94	97.0	4.000000	93.000000

	MaxObs
Eval1	0.10000
Eval2	45.52246
Eval3	89.71085
Eval4	101.96869
Eval5	101.00000

```

> str(model$Ofile)

```

```

'data.frame':      94 obs. of  13 variables:
 $ Date       : Date, format: "2000-01-20" ...
 $ nday       : num  1 2 3 4 5 6 7 8 9 10 ...
 $ MicCol     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ SimSeverity: num  0 0 0 0 0 0 0 0 0 0 ...
 $ LAI        : num  0.01 0.0276 0.0384 0.0492 0.06 0.086 0.112 0.138 0.164 0.19 ...
 $ LatPer     : num  0 2 2 2 2 2 2 2 2 2 ...

```



```

$ LesExInc : num 0 0 0 0 0 0 0 0 0 0 ...
$ AttchSp  : num 0 0 0 0 0 0 0 0 0 0 ...
$ AUDPC    : num 0 0 0 0 0 0 0 0 0 0 ...
$ rLP      : num 0 0 0 0 0 0 0 0 0 0 ...
$ InvrLP   : num 0 0 0 0 0 0 0 0 0 0 ...
$ BlPr     : num 0 0 0 0 0 0 0 0 0 0 ...
$ Defol    : num 0 0 0 0 0 0 0 0 0 0 ...

```

```
> head(model$Ofile[,1:7])
```

	Date	nday	MicCol	SimSeverity	LAI	LatPer	LesExInc
1	2000-01-20	1	0	0	0.0100	0	0
2	2000-01-21	2	0	0	0.0276	2	0
3	2000-01-22	3	0	0	0.0384	2	0
4	2000-01-23	4	0	0	0.0492	2	0
5	2000-01-24	5	0	0	0.0600	2	0
6	2000-01-25	6	0	0	0.0860	2	0

Repeating graphic

```

> x<- model$Ofile$nday
> y<- model$Ofile$SimSeverity
> w<- model$Gfile$nday
> z<- model$Gfile$MeanSeverity
> Min<-model$Gfile$MinObs
> Max<-model$Gfile$MaxObs

> par(mar=c(3,2.5,1,0),cex=0.7)
> plot(x,y,type="l",xlim=c(65,95),lwd=1.5,xlab="Time (days after emergence)",
+ ylab="Severity (Percentage)")
> points(w,z,col="red",cex=1,pch=19); npoints <- length(w)
> for ( i in 1:npoints)segments(w[i],Min[i],w[i],Max[i],lwd=1.5,col="red")
> legend("topleft",c("Disease progress curves","Weather-Severity"),
+ title="Description",lty=1,pch=c(3,19),col=c("black","red"))

```

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