agricolae tutorial (Version 1.3-7)

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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, Ryan, Einot and Gabriel and Welsch multiple range test 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, De Mendiburu (2009)

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 `http://www.R-project.org` of a repository CRAN, R Core Team (2020).

`> install.packages("agricolae")` Once the `agricolae` package is installed, it needs to be made accessible to the current **R** session by the command:

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```
> 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*
Cluster: for the use of the function *consensus*
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")
> designs[substr(designs,1,6)=="design"]

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

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()

```
> oldpar<-par(mfrow=c(1,2),mar=c(4,4,0,1),cex=0.6)
> h1<- graph.freq(weight,col=colors()[84],frequency=1,las=2,density=20,ylim=c(0,12),
+                 ylab="Frequency")
> x<-h1$breaks
> h2<- plot(h1, frequency =2, axes= FALSE,ylim=c(0,0.4),xlab="weight",ylab="Relative (%)")
> polygon.freq(h2, col=colors()[84], lwd=2, frequency =2)
> axis(1,x,cex=0.6,las=2)
> y<-seq(0,0.4,0.1)
> axis(2, y,y*100,cex=0.6,las=1)
> par(oldpar)
```

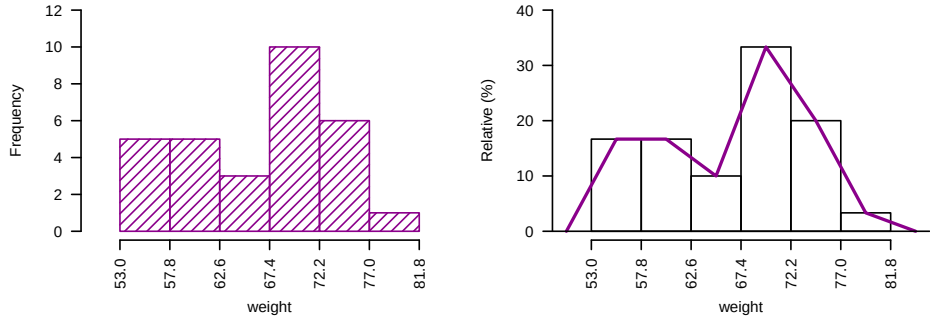

Figure 1: Absolute and relative frequency with polygon.

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 *inter.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

> inter.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
```

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)
```

```
> oldpar<-par(mfrow=c(1,2),mar=c(4,4,0,1),cex=0.8)
> plot(h3, frequency=2,col=colors()[84],ylim=c(0,0.6),axes=FALSE,xlab="weight",ylab="%",border=0)
> y<-seq(0,0.6,0.2)
> axis(2,y,y*100,las=2)
> axis(1,h3$breaks)
> normal.freq(h3,frequency=2,col=colors()[90])
> ogive.freq(h3,col=colors()[84],xlab="weight")

  weight    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

> par(oldpar)
```

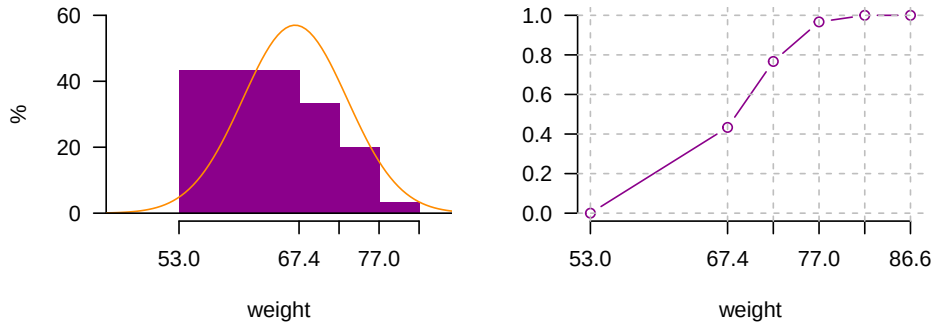

Figure 2: Join frequency and relative frequency with normal and Ogive.

```
> oldpar<-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")
> par(oldpar)
```

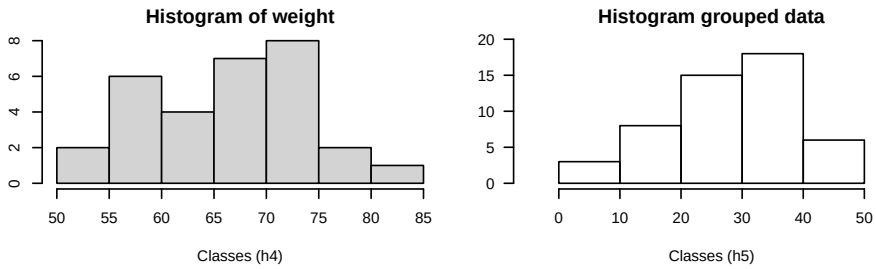

Figure 3: hist() function and histogram defined class

```
> 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, Cochran and Cox (1957); kueh (2000); Le Clerg and Leonard and Erwin and Warren and Andrew (1992); Montgomery (2002). 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 sequencial.

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

It generates completely a randomized design with equal or different repetition. "Random" uses the methods of number generation in R.The seed is by set.seed(seed, kinds). 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   C
2     2 1   A
3     3 1   B
4     4 2   A
5     5 3   A
6     6 2   C
```

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

3.2 Randomized complete block design

It generates field book and sketch to Randomized Complete Block Design. "Random" uses the methods of number generation in R.The seed is by set.seed(seed, kinds). 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,] "E"  "B"  "D"  "A"  "C"
[2,] "B"  "A"  "D"  "C"  "E"
[3,] "C"  "E"  "A"  "B"  "D"
[4,] "D"  "C"  "E"  "B"  "A"

> 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

It generates Latin Square Design. "Random" uses the methods of number generation in R.The seed is by set.seed(seed, kinds). 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,] "B"  "C"  "A"  "D"
[2,] "D"  "A"  "C"  "B"
[3,] "C"  "D"  "B"  "A"
[4,] "A"  "B"  "D"  "C"
```

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

A graeco - latin square is a KxK pattern that permits the study of k treatments simultaneously with three different blocking variables, each at k levels. The function is only for squares of the odd numbers and even numbers (4, 8, 10 and 12). 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,] "D 2" "B 4" "A 3" "C 1"
[2,] "B 3" "D 1" "C 2" "A 4"
[3,] "A 1" "C 3" "D 4" "B 2"
[4,] "C 4" "A 2" "B 1" "D 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

Such designs are referred to as Youden squares since they were introduced by Youden (1937) after Yates (1936) considered the special case of column equal to number treatment minus 1. "Random" uses the methods of number generation in R. The seed is by set.seed(seed, kinds). 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" "tomasa"       "perricholi"
[2,] "yungay"       "maria bonita" "tomasa"
[3,] "perricholi"   "yungay"       "maria bonita"
[4,] "tomasa"       "perricholi"   "yungay"

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

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

Creates Randomized Balanced Incomplete Block Design. "Random" uses the methods of number generation in R. The seed is by set.seed(seed, kinds). 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,] "B"  "C"  "E"  "A"
[2,] "C"  "D"  "B"  "A"
[3,] "A"  "D"  "E"  "B"
[4,] "E"  "C"  "D"  "B"
[5,] "D"  "C"  "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,] "F"  "D"  "C"
[2,] "C"  "B"  "E"
[3,] "D"  "E"  "A"
[4,] "B"  "E"  "F"
[5,] "A"  "F"  "C"
[6,] "B"  "A"  "D"

> outdesign$sketch[[2]]

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

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

SIMPLE and TRIPLE lattice designs. It randomizes treatments in k x k lattice. 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

$kinds
[1] "Super-Duper"

> outdesign$sketch

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

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

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

```
> head(book7)

  plots r block trt
1   101 1     1   g
2   102 1     1   c
3   103 1     1   a
4   104 1     2   f
5   105 1     2   b
6   106 1     2   h
```

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

Generates an alpha designs starting from the alpha design fixing under the series formulated by Patterson and Williams. These designs are generated by the alpha arrangements. They are similar to the lattice designs, but the tables are rectangular s by k (with s blocks and k<s columns. The number of treatments should be equal to s*k and all the experimental units r*s*k (r replications) 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,] "i"  "g"  "m"
[2,] "f"  "o"  "h"
[3,] "n"  "j"  "b"
[4,] "a"  "c"  "k"
[5,] "e"  "l"  "d"

$rep2
     [,1] [,2] [,3]
[1,] "g"  "f"  "k"
[2,] "e"  "j"  "a"
```

```
[3,] "m"  "c"  "l"
[4,] "n"  "d"  "o"
[5,] "i"  "h"  "b"

> # 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
> with(book9,by(trt, block,as.character))

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

Serpentine enumeration:

```
> book <- zigzag(outdesign)
> with(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"
```

```
> head(book)

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

For augmented ompletely 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 **trt1** in a randomized complete block design; and a second factor as **trt2** , 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)
```

Aplication

```
> 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    D    b
2   101      2     1    D    a
3   101      3     1    D    c
4   102      1     1    B    a
5   102      2     1    B    b
6   102      3     1    B    c

> 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,] "D"  "B"  "A"  "C"
[2,] "B"  "C"  "A"  "D"
[3,] "D"  "B"  "A"  "C"
```

In sub plots (split plot)

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

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

Serpentine enumeration:

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

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

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    D    b
2   102     1    D    a
3   103     1    D    c
4   104     1    B    b
5   105     1    B    a
6   106     1    B    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,] "D b" "D a" "D c" "B b"
[2,] "B a" "B c" "A b" "A a"
[3,] "A c" "C b" "C a" "C c"

> print(B2)

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

> print(B3)

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

Serpentine enumeration:

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

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

Serpentine enumeration:

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

  plots block A B
1   101     1 2 2
2   102     1 2 1
3   103     1 3 2
4   104     1 1 2
5   105     1 1 1
6   106     1 3 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] 1923434691

$kinds
[1] "Super-Duper"

[[7]]
[1] TRUE

$applied
[1] "crd"

> head(crd$book)

  plots r A B C
1   101 1 2 2 2
```

```
2   102 2 2 2 2
3   103 1 2 1 1
4   104 1 1 2 1
5   105 1 1 1 1
6   106 2 1 2 1
```

3.14 Experimental design matrix

Generate the design matrix from the field book generated by an experimental plan or a data table for analysis and its parameters are:

```
> str(design.mat)

function (book, locations)
```

To generate the matrix, it is necessary to extract the field book of the design generated by agricolae. The matrix can also be generated if you have a table for experimental analysis.

For example, analyze the sweetpotato experiment using the design matrix.

```
> data(sweetpotato)
> X <- design.mat(sweetpotato,1)
> n<-nrow(X)
> print(X)

   constant cc fc ff oo
1         1  1  0  0  0
2         1  1  0  0  0
3         1  1  0  0  0
4         1  0  1  0  0
5         1  0  1  0  0
6         1  0  1  0  0
7         1  0  0  1  0
8         1  0  0  1  0
9         1  0  0  1  0
10        1  0  0  0  1
11        1  0  0  0  1
12        1  0  0  0  1
```

Matrix X is of incomplete range, to find an estimate, the restriction of condition of the effects is added, for example the weighted sum for repetitions of the effects is zero to the matrix X and thus it is complete, in this way the estimators are found.

```
> X<- rbind(X,c(0,3,3,3,3))
> y<-sweetpotato[,2]
> Y<- c(y,0)
> XX<-t(X)%*%X
> XY<-t(X)%*%Y
> YY<-t(Y)%*%Y
> beta<-solve(XX,XY)
```

```
> e<-Y-X%*%beta
> tau<- beta[-1,]
> print(tau) #Efectos de tratamientos

        cc         fc         ff         oo
 -3.225000 -14.758333   8.708333   9.275000
```

Unadjusted sums of squares

```
> SCtot<-t(Y)%*%Y
> SCb<-t(beta)%*%XX%*%beta
> SCe<-t(e)%*%e
> SS<-rbind(SCtot,SCb,SCe)
> dimnames(SS)<-list(c("Total","model","Error"),"SC")
> print(SS)

              SC
Total 10507.8100
model 10327.8967
Error   179.9133
```

Adjusted sum of squares and mean square

```
> trt<-tau
> t<-length(trt)
> XX1<-XX[2:5,2:5]
> SCtot<-t(Y)%*%Y-beta[1,1]%*%XX[1,1]%*%beta[1,1] ; GLtotal<- n-1
> SCt<-trt%*%XX1%*%trt ; GLt <- t-1; GLe<-GLtotal - GLt
> SC<-cbind(c(GLtotal,GLt,GLe),c(SCtot,SCt,SCe))
> MS<-cbind(SC,SC[,2]/SC[,1])
> dimnames(MS)<-list(c("Total","trt","Error"),c("Gl","SC","CM"))
> print(MS)

      Gl        SC        CM
Total 11 1350.1225 122.73841
trt    3 1170.2092 390.06972
Error  8  179.9133  22.48917
```

4 Multiple comparisons

For the analyses, the following functions of **agricolae** are used: *L*SD.test, HSD.test, duncan.test, scheffe.test, waller.test, SNK.test, REGW.test, Steel and Torry and Dickey (1997); Hsu (1996) and *d*urbin.test, kruskal, friedman, waerden.test and Median.test, Conover (1999).

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

The *s*weetpotato 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

> with(sweetpotato,mean(yield))

[1] 27.625
```

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), Steel and Torry and Dickey (1997).

```
> # 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       se       LCL      UCL  Min
cc 24.40000 3.609709 3 2.737953 18.086268 30.71373 21.7
fc 12.86667 2.159475 3 2.737953  6.552935 19.18040 10.6
ff 36.33333 7.333030 3 2.737953 30.019601 42.64707 28.0
oo 36.90000 4.300000 3 2.737953 30.586268 43.21373 32.1
    Max   Q25  Q50   Q75
cc 28.5 22.35 23.0 25.75
fc 14.9 11.85 13.1 14.00
ff 41.8 33.60 39.2 40.50
oo 40.4 35.15 38.2 39.30

Alpha: 0.05 ; DF Error: 8
Critical Value of t: 2.306004

least Significant Difference: 8.928965

Treatments with the same letter are not significantly different.
```

```
      yield groups
oo 36.90000      a
ff 36.33333      a
cc 24.40000      b
fc 12.86667      c
```

In the function *L*SD.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=FALSE)
> outLSD <-LSD.test(model, "virus", group=FALSE,console=TRUE)

Study: model ~ "virus"

LSD t Test for yield

Mean Square Error:  22.48917

virus,  means and individual ( 95 %) CI

      yield      std r       se       LCL      UCL  Min
cc 24.40000 3.609709 3 2.737953 18.086268 30.71373 21.7
fc 12.86667 2.159475 3 2.737953  6.552935 19.18040 10.6
ff 36.33333 7.333030 3 2.737953 30.019601 42.64707 28.0
oo 36.90000 4.300000 3 2.737953 30.586268 43.21373 32.1
    Max   Q25  Q50   Q75
cc 28.5 22.35 23.0 25.75
fc 14.9 11.85 13.1 14.00
ff 41.8 33.60 39.2 40.50
oo 40.4 35.15 38.2 39.30

Alpha: 0.05 ; DF Error: 8
Critical Value of t: 2.306004

Comparison between treatments means

         difference pvalue signif.        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**

```
> options(digits=2)
> print(outLSD)
```

```
$statistics
  MSerror Df Mean CV t.value LSD
       22  8   28 17     2.3 8.9

$parameters
        test p.ajusted name.t ntr alpha
  Fisher-LSD      none  virus   4  0.05

$means
   yield std r  se  LCL UCL Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7 18.1  31  22  28  22  23  26
fc    13 2.2 3 2.7  6.6  19  11  15  12  13  14
ff    36 7.3 3 2.7 30.0  43  28  42  34  39  40
oo    37 4.3 3 2.7 30.6  43  32  40  35  38  39

$comparison
        difference pvalue signif.   LCL   UCL
cc - fc      11.53 0.0176       *   2.6  20.5
cc - ff     -11.93 0.0151       * -20.9  -3.0
cc - oo     -12.50 0.0121       * -21.4  -3.6
fc - ff     -23.47 0.0003     *** -32.4 -14.5
fc - oo     -24.03 0.0003     *** -33.0 -15.1
ff - oo      -0.57 0.8873          -9.5   8.4

$groups
NULL

attr(,"class")
[1] "group"
```

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 and other options see Adjust P-values for Multiple Comparisons, function p.adjust(stats), **?**.

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

Study: model ~ "virus"

LSD t Test for yield
P value adjustment method: bonferroni

Mean Square Error:  22

virus,  means and individual ( 95 %) CI

   yield std r  se  LCL UCL Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7 18.1  31  22  28  22  23  26
fc    13 2.2 3 2.7  6.6  19  11  15  12  13  14
```

```
ff    36 7.3 3 2.7 30.0  43  28  42  34  39  40
oo    37 4.3 3 2.7 30.6  43  32  40  35  38  39

Alpha: 0.05 ; DF Error: 8
Critical Value of t: 3.5

Comparison between treatments means

        difference pvalue signif.   LCL    UCL
cc - fc      11.53 0.1058          -1.9  25.00
cc - ff     -11.93 0.0904       . -25.4   1.54
cc - oo     -12.50 0.0725       . -26.0   0.97
fc - ff     -23.47 0.0018      ** -36.9 -10.00
fc - oo     -24.03 0.0015      ** -37.5 -10.56
ff - oo      -0.57 1.0000         -14.0  12.90
```

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

```
   yield groups
oo    37      a
ff    36      a
cc    24      b
fc    13      c
```

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

```
        difference pvalue signif.
cc - fc      11.53 0.0484       *
cc - ff     -11.93 0.0484       *
cc - oo     -12.50 0.0484       *
fc - ff     -23.47 0.0015      **
fc - oo     -24.03 0.0015      **
ff - oo      -0.57 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 arguments 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, Steel and Torry and Dickey (1997).

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

```
Study: model ~ "virus"

Duncan's new multiple range test
for yield

Mean Square Error:  22

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

Alpha: 0.05 ; DF Error: 8

Critical Range
  2   3   4
8.9 9.3 9.5

Means with the same letter are not significantly different.

   yield groups
oo    37      a
ff    36      a
cc    24      b
fc    13      c
```

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, Steel and Torry and Dickey (1997).

```
> # 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

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
```

```
oo    37 4.3 3 2.7  32  40  35  38  39

Comparison between treatments means

        difference pvalue signif.   LCL   UCL
cc - fc      11.53 0.0176       *   2.6  20.5
cc - ff     -11.93 0.0151       * -20.9  -3.0
cc - oo     -12.50 0.0291       * -23.6  -1.4
fc - ff     -23.47 0.0008     *** -34.5 -12.4
fc - oo     -24.03 0.0012      ** -36.4 -11.6
ff - oo      -0.57 0.8873          -9.5   8.4
```

4.5 Ryan, Einot and Gabriel and Welsch

Multiple range tests for all pairwise comparisons, to obtain a confident inequalities multiple range tests, Hsu (1996).

```
> # 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

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

Comparison between treatments means

        difference pvalue signif.    LCL    UCL
cc - fc      11.53 0.0350       *   0.91  22.16
cc - ff     -11.93 0.0360       * -23.00  -0.87
cc - oo     -12.50 0.0482       * -24.90  -0.10
fc - ff     -23.47 0.0006     *** -34.09 -12.84
fc - oo     -24.03 0.0007     *** -35.10 -12.97
ff - oo      -0.57 0.9873         -11.19  10.06
```

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), Steel and Torry and Dickey (1997).

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

Study: model ~ "virus"

HSD Test for yield

Mean Square Error:  22

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

Alpha: 0.05 ; DF Error: 8
Critical Value of Studentized Range: 4.5

Minimun Significant Difference: 12

Treatments with the same letter are not significantly different.

   yield groups
oo    37      a
ff    36     ab
cc    24     bc
fc    13      c

> outHSD

$statistics
  MSerror Df Mean CV MSD
       22  8   28 17  12

$parameters
   test name.t ntr StudentizedRange alpha
  Tukey  virus   4              4.5  0.05

$means
   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

$comparison
NULL

$groups
   yield groups
```

```
oo    37      a
ff    36     ab
cc    24     bc
fc    13      c

attr(,"class")
[1] "group"
```

4.7 Tukey (HSD) for different repetition

Include the argument **unbalanced = TRUE** in the function. Valid for group = TRUE/FALSE

```
> A<-sweetpotato[-c(4,5,7),]
> modelUnbalanced <- aov(yield ~ virus, data=A)
> outUn <-HSD.test(modelUnbalanced, "virus",group=FALSE, unbalanced = TRUE)
> print(outUn$comparison)

        difference pvalue signif. LCL  UCL
cc - fc       11.3  0.252          -8 30.6
cc - ff       -9.2  0.386         -28 10.1
cc - oo      -12.5  0.196         -32  6.8
fc - ff      -20.5  0.040       * -40 -1.2
fc - oo      -23.8  0.022       * -43 -4.5
ff - oo       -3.3  0.917         -23 16.0

> outUn <-HSD.test(modelUnbalanced, "virus",group=TRUE, unbalanced = TRUE)
> print(outUn$groups)

   yield groups
oo    37      a
ff    34      a
cc    24     ab
fc    13      b
```

If this argument is not included, the probabilities of significance will not be consistent with the choice of groups.

Illustrative example of this inconsistency:

```
> outUn <-HSD.test(modelUnbalanced, "virus",group=FALSE)
> print(outUn$comparison[,1:2])

        difference pvalue
cc - fc       11.3  0.317
cc - ff       -9.2  0.297
cc - oo      -12.5  0.096
fc - ff      -20.5  0.071
fc - oo      -23.8  0.033
ff - oo       -3.3  0.885
```

```
> outUn <-HSD.test(modelUnbalanced, "virus",group=TRUE)
> print(outUn$groups)

   yield groups
oo    37      a
ff    34     ab
cc    24     ab
fc    13      b
```

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

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, Waller and Duncan (1969); Steel and Torry and Dickey (1997).

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

Analysis of Variance Table

Response: yield
          Df Sum Sq Mean Sq F value  Pr(>F)
virus      3   1170     390    17.3 0.00073 ***
Residuals  8    180      22
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(sweetpotato,waller.test(yield,virus,df,MSerror,Fc= 17.345, group=FALSE,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                    100.0
Error Degrees of Freedom     8.0
Error Mean Square           22.5
F value                     17.3
Critical Value of Waller     2.2

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39
```

```
Comparison between treatments means

        Difference significant
cc - fc      11.53        TRUE
cc - ff     -11.93        TRUE
cc - oo     -12.50        TRUE
fc - ff     -23.47        TRUE
fc - oo     -24.03        TRUE
ff - oo      -0.57       FALSE
```

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      11.53        TRUE
cc - ff     -11.93        TRUE
cc - oo     -12.50        TRUE
fc - ff     -23.47        TRUE
fc - oo     -24.03        TRUE
ff - oo      -0.57       FALSE
```

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

```
> outWaller$statistics

  Mean Df CV MSerror F.Value Waller CriticalDifference
    28  8 17      22      17    2.2                8.7
```

4.9 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, Steel and Torry and Dickey (1997).

```
> # 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

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

Alpha: 0.05 ; DF Error: 8
Critical Value of F: 4.1

Minimum Significant Difference: 14

Means with the same letter are not significantly different.

   yield groups
oo    37      a
ff    36      a
cc    24     ab
fc    13      b
```

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

virus,  means

   yield std r  se Min Max Q25 Q50 Q75
cc    24 3.6 3 2.7  22  28  22  23  26
fc    13 2.2 3 2.7  11  15  12  13  14
ff    36 7.3 3 2.7  28  42  34  39  40
oo    37 4.3 3 2.7  32  40  35  38  39

Alpha: 0.05 ; DF Error: 8
Critical Value of F: 4.1

Comparison between treatments means
```

```
        Difference pvalue sig LCL   UCL
cc - fc      11.53 0.0978   .  -2  25.1
cc - ff     -11.93 0.0855   . -25   1.6
cc - oo     -12.50 0.0706   . -26   1.0
fc - ff     -23.47 0.0023  ** -37  -9.9
fc - oo     -24.03 0.0020  ** -38 -10.5
ff - oo      -0.57 0.9991     -14  13.0
```

4.10 Multiple comparison in factorial treatments

In a factorial combined effects of the treatments. Comparetive 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     21     6.9    5.82 0.00387 **
```

```
clone           2    498   248.9  209.57 6.4e-16 ***
nitrogen        2     54    27.0   22.76 2.9e-06 ***
clone:nitrogen  4     43    10.8    9.11 0.00013 ***
Residuals      24     29     1.2
---
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:  1.2

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

      yield  std r   se  LCL  UCL Min Max  Q25  Q50  Q75
c1:n1   7.5 1.29 4 0.54  6.4  8.6   6   9  6.8  7.5  8.2
c1:n2   8.5 1.29 4 0.54  7.4  9.6   7  10  7.8  8.5  9.2
c1:n3   9.0 0.82 4 0.54  7.9 10.1   8  10  8.8  9.0  9.2
c2:n1  13.5 1.29 4 0.54 12.4 14.6  12  15 12.8 13.5 14.2
c2:n2  16.8 0.96 4 0.54 15.6 17.9  16  18 16.0 16.5 17.2
c2:n3  20.2 1.71 4 0.54 19.1 21.4  18  22 19.5 20.5 21.2
c3:n1   9.5 1.29 4 0.54  8.4 10.6   8  11  8.8  9.5 10.2
c3:n2   9.5 1.73 4 0.54  8.4 10.6   8  12  8.8  9.0  9.8
c3:n3  10.2 1.50 4 0.54  9.1 11.4   9  12  9.0 10.0 11.2

Alpha: 0.05 ; DF Error: 24
Critical Value of t: 2.1

least Significant Difference: 1.6

Treatments with the same letter are not significantly different.

      yield groups
c2:n3  20.2      a
c2:n2  16.8      b
c2:n1  13.5      c
c3:n3  10.2      d
c3:n1   9.5     de
c3:n2   9.5     de
c1:n3   9.0    def
c1:n2   8.5     ef
c1:n1   7.5      f
```

```
> oldpar<-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")
> par(oldpar)
```

4.11 Analysis of Balanced Incomplete Blocks

This analysis can come from balanced or partially balanced designs. The function *B*IB.test is for balanced designs, and *B*IB.test, for partially balanced designs. In the following example, the **agricolae** data will be used, Joshi (1987).

```
> # Example linear estimation and design of experiments. (Joshi)
> # Institute of Social Sciences Agra, India
> # 6 varieties of wheat in 10 blocks of 3 plots each.
> 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)
> head(cbind(block,variety,Y))

     block variety  Y
[1,]     1       1 69
[2,]     1       2 54
[3,]     1       3 50
[4,]     2       1 77
[5,]     2       2 65
[6,]     2       4 38

> 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    467    51.9    0.90  0.547
trt.adj      5   1156   231.3    4.02  0.016 *
Residuals   15    863    57.5
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 13 %
Y Means: 60
```

```
variety,  statistics

   Y mean.adj  SE r  std Min Max
1 70       75 3.7 5  5.1  63  77
2 60       59 3.7 5  4.9  54  65
3 59       59 3.7 5 12.4  45  75
4 55       55 3.7 5  9.8  38  62
5 61       60 3.7 5  4.5  54  65
6 56       54 3.7 5 10.8  39  67

LSD test
Std.diff   : 5.4
Alpha      : 0.05
LSD        : 11
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      16.42 0.0080   **
1 - 3      16.58 0.0074   **
1 - 4      20.17 0.0018   **
1 - 5      15.08 0.0132    *
1 - 6      20.75 0.0016   **
2 - 3       0.17 0.9756
2 - 4       3.75 0.4952
2 - 5      -1.33 0.8070
2 - 6       4.33 0.4318
3 - 4       3.58 0.5142
3 - 5      -1.50 0.7836
3 - 6       4.17 0.4492
4 - 5      -5.08 0.3582
4 - 6       0.58 0.9148
5 - 6       5.67 0.3074

Treatments with the same letter are not significantly different.

   Y groups
1 75      a
5 60      b
2 59      b
3 59      b
```

```
4 55      b
6 54      b
```

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    467    51.9    0.90  0.547
trt.adj      5   1156   231.3    4.02  0.016 *
Residuals   15    863    57.5
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 13 %
Y Means: 60

variety,  statistics

   Y mean.adj  SE r  std Min Max
1 70       75 3.7 5  5.1  63  77
2 60       59 3.7 5  4.9  54  65
3 59       59 3.7 5 12.4  45  75
4 55       55 3.7 5  9.8  38  62
5 61       60 3.7 5  4.5  54  65
6 56       54 3.7 5 10.8  39  67

Tukey
Alpha      : 0.05
Std.err    : 3.8
HSD        : 17
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      16.42  0.070    .
1 - 3      16.58  0.067    .
1 - 4      20.17  0.019    *
1 - 5      15.08  0.110
1 - 6      20.75  0.015    *
2 - 3       0.17  1.000
2 - 4       3.75  0.979
2 - 5      -1.33  1.000
2 - 6       4.33  0.962
3 - 4       3.58  0.983
3 - 5      -1.50  1.000
3 - 6       4.17  0.967
4 - 5      -5.08  0.927
4 - 6       0.58  1.000
5 - 6       5.67  0.891
```

```
> names(out)

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

> rm(block,variety)
```

bar.group: out$groups

bar.err: out$means

4.12 Partially Balanced Incomplete Blocks

The function *PBIB.test* Joshi (1987), 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 ) 0.62

<<< 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)
> # The analysis:
> modelPBIB <- with(data,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  3.8e+00
replication        6.1e-09
Residual           1.7e+00

                     Fit Statistics
AIC                             214
BIC                             260
-2 Res Log Likelihood           -74

Analysis of Variance Table

Response: yield
          Df Sum Sq Mean Sq F value Pr(>F)
```

```
Genotype  29   69.2    2.39     1.4   0.28
Residuals 11   18.7    1.70

Coefficient of variation: 29 %
yield Means: 4.5

Parameters PBIB
                   .
Genotype          30
block size         3
block/replication 10
replication        2

Efficiency factor 0.62

Comparison test lsd

Treatments with the same letter are not significantly different.

       yield.adj groups
geno10       7.7      a
geno19       6.7     ab
geno1        6.7     ab
geno9        6.4    abc
geno18       6.1    abc
geno16       5.7   abcd
geno26       5.2   abcd
geno8        5.2   abcd
geno17       5.2   abcd
geno29       4.9   abcd
geno27       4.9   abcd
geno11       4.9   abcd
geno30       4.8   abcd
geno22       4.5   abcd
geno28       4.5   abcd
geno5        4.2   abcd
geno14       4.1   abcd
geno23       4.0   abcd
geno15       3.9   abcd
geno2        3.8    bcd
geno4        3.8    bcd
geno3        3.7    bcd
geno25       3.6    bcd
geno12       3.6    bcd
geno6        3.6    bcd
geno21       3.4    bcd
geno24       3.0    bcd
geno13       2.8     cd
geno20       2.7     cd
geno7        2.3      d
```

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

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 with the functions plot.group and bar.err. 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: latice3x3.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, method="VC")

ANALYSIS PBIB:  yield

Class level information
block : 12
trt : 9

Number of observations:  36

Estimation Method:  Variances component model

    Fit Statistics
AIC            265
BIC            298

Analysis of Variance Table
```

```
Response: yield
          Df Sum Sq Mean Sq F value  Pr(>F)
sqr        3    133      44    0.69 0.57361
trt.unadj  8   3749     469    7.24 0.00042 ***
block/sqr  8    368      46    0.71 0.67917
Residual  16   1036      65
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Coefficient of variation: 28 %
yield Means: 29

Parameters PBIB
           .
trt        9
block size 3
block/sqr  3
sqr        4

Efficiency factor 0.75

Comparison test lsd

Treatments with the same letter are not significantly different.

  yield.adj groups
1        44      a
9        39     ab
4        39     ab
7        32     bc
6        31     bc
2        26     cd
8        18      d
5        17      d
3        15      d

<<< 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)

4.13 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   180.0
trt.adj                   11    285    25.9    0.96   0.55
Control                    3     53    17.6    0.65   0.61
Control + control.VS.aug.  8    232    29.0    1.08   0.48
Residuals                  6    162    27.0

ANOVA, Block Adjusted
Analysis of Variance Table

Response: yield
                     Df Sum Sq Mean Sq F value Pr(>F)
trt.unadj            11    576    52.3
block.adj             2     70    34.8    1.29   0.34
Control               3     53    17.6    0.65   0.61
Augmented             7    506    72.3    2.68   0.13
Control vs augmented  1     17    16.9    0.63   0.46
Residuals             6    162    27.0

coefficient of variation: 6.4 %
yield Means: 82

Critical Differences (Between)
                                                 Std Error Diff.
Two Control Treatments                                       4.2
Two Augmented Treatments (Same Block)                        7.3
Two Augmented Treatments(Different Blocks)                   8.2
A Augmented Treatment and A Control Treatment                6.4


Treatments with the same letter are not significantly different.

  yield groups
h    94      a
f    86     ab
A    85     ab
D    83     ab
C    82     ab
j    80     ab
B    79     ab
e    78     ab
k    78     ab
i    77     ab
l    77     ab
g    73      b
```

```
Comparison between treatments means

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

> options(digits = 2)
> modelDAU$means

  yield std r Min Max Q25 Q50 Q75 mean.adj  SE block
A    85 6.7 3  79  92  81  83  88       85 3.0
B    79 2.0 3  77  81  78  79  80       79 3.0
C    82 4.6 3  78  87  80  81  84       82 3.0
D    83 6.8 3  78  91  80  81  86       83 3.0
e    79  NA 1  79  79  79  79  79       78 5.2    II
f    89  NA 1  89  89  89  89  89       86 5.2   III
g    70  NA 1  70  70  70  70  70       73 5.2     I
h    96  NA 1  96  96  96  96  96       94 5.2   III
i    78  NA 1  78  78  78  78  78       77 5.2    II
j    82  NA 1  82  82  82  82  82       80 5.2   III
k    75  NA 1  75  75  75  75  75       78 5.2     I
l    74  NA 1  74  74  74  74  74       77 5.2     I

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

      Difference pvalue sig.
A - B        5.7   0.23
A - C        2.7   0.55
A - D        1.3   0.76
A - e        6.4   0.38
A - f       -1.8   0.79
A - g       11.4   0.14
A - h       -8.8   0.24
A - i        7.4   0.31
```

5 Non-parametric comparisons

The functions for non-parametric multiple comparisons included in **agricolae** are: *kruskal, waerden.test, friedman and durbin.test*, Conover (1999).

The post hoc nonparametrics tests (kruskal, friedman, durbin and waerden) are using the criterium Fisher's least significant difference (LSD).

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.

The function *Median.test* for the analysis the distribution is approximate with chi-squared ditribution with degree free number of groups minus one. In each comparison a table of 2x2 (pair of groups) and the criterion of greater or lesser value than the median of both are formed, the chi-square test is applied for the calculation of the probability of error that both are independent. This value is compared to the alpha level for group formation.

Montgomery book data, Montgomery (2002). 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

Critical Value: 26
Degrees of freedom: 3
Pvalue Chisq  : 1.1e-05

method,  means of the ranks

  observation  r
1        21.8  9
2        15.3 10
3        29.6  7
4         4.8  8
```

```
Post Hoc Analysis

t-Student: 2
Alpha    : 0.05
Groups according to probability of treatment differences and alpha level.

Treatments with the same letter are not significantly different.

  observation groups
3        29.6      a
1        21.8      b
2        15.3      c
4         4.8      d
```

The object output has the same structure of the comparisons see the functions plot.group(agricolae), bar.err(agricolae) and bar.group(agricolae).

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)

  observation groups
3        29.6      a
1        21.8      b
2        15.3      c
4         4.8      d

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

      Difference pvalue Signif.
1 - 2        6.5 0.0079      **
1 - 3       -7.7 0.0079      **
1 - 4       17.0 0.0000     ***
2 - 3      -14.3 0.0000     ***
2 - 4       10.5 0.0003     ***
3 - 4       24.8 0.0000     ***
```

5.3 Friedman

The data consist of b mutually independent k-variate random variables called b blocks. The random variable is in a block and is associated with treatment. It makes the multiple comparison of the Friedman test with or without ties. A first result is obtained by friedman.test of R.

```
> str(friedman)
```

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

Analysis

```
> data(grass)
> out<-with(grass,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 12
t2         24 12
t3         24 12
t4         34 12

Friedman's Test
===============
Adjusted for ties
Critical Value: 8.1
P.Value Chisq: 0.044
F Value: 3.2
P.Value F: 0.036

Post Hoc Analysis

Comparison between treatments
Sum of the ranks

        difference pvalue signif.   LCL   UCL
t1 - t2       14.5  0.015       *   3.0 25.98
t1 - t3       13.5  0.023       *   2.0 24.98
t1 - t4        4.0  0.483          -7.5 15.48
t2 - t3       -1.0  0.860         -12.5 10.48
t2 - t4      -10.5  0.072       . -22.0  0.98
t3 - t4       -9.5  0.102         -21.0  1.98
```

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

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

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

Value : 8.4
Pvalue: 0.038
Degrees of Freedom:  3

virus,  means of the normal score

   yield  std r
cc -0.23 0.30 3
fc -1.06 0.35 3
ff  0.69 0.76 3
oo  0.60 0.37 3

Post Hoc Analysis

Alpha: 0.01 ; DF Error: 8

Minimum Significant Difference: 1.3

Treatments with the same letter are not significantly different.

Means of the normal score

   score groups
ff  0.69      a
oo  0.60      a
cc -0.23     ab
fc -1.06      b
```

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

```
> names(outWaerden)

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

>
```

To see outWaerden$comparison

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

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

```
Value : 8.4
Pvalue: 0.038
Degrees of Freedom:  3

virus,  means of the normal score

   yield  std r
cc -0.23 0.30 3
fc -1.06 0.35 3
ff  0.69 0.76 3
oo  0.60 0.37 3

Post Hoc Analysis

Comparison between treatments
mean of the normal score

        difference pvalue signif.    LCL    UCL
cc - fc      0.827 0.0690       . -0.082  1.736
cc - ff     -0.921 0.0476       * -1.830 -0.013
cc - oo     -0.837 0.0664       . -1.746  0.072
fc - ff     -1.749 0.0022      ** -2.658 -0.840
fc - oo     -1.665 0.0029      ** -2.574 -0.756
ff - oo      0.084 0.8363         -0.825  0.993
```

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, Conover (1999). See also Figure 4.

In each comparison a table of 2x2 (pair of groups) and the criterion of greater or lesser value than the median of both are formed, the chi-square test is applied for the calculation of the probability of error that both are independent. This value is compared to the alpha level for group formation.

```
> str(Median.test)

function (y, trt, alpha = 0.05, correct = TRUE, simulate.p.value = FALSE,
    group = TRUE, main = NULL, console = TRUE)

> str(Median.test)

function (y, trt, alpha = 0.05, correct = TRUE, simulate.p.value = FALSE,
    group = TRUE, main = NULL, console = TRUE)
```

Analysis

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

```
The Median Test for yield ~ virus

Chi Square = 6.7   DF = 3   P.Value 0.083
Median = 28

   Median r Min Max Q25 Q75
cc     23 3  22  28  22  26
fc     13 3  11  15  12  14
ff     39 3  28  42  34  40
oo     38 3  32  40  35  39

Post Hoc Analysis

Groups according to probability of treatment differences and alpha level.

Treatments with the same letter are not significantly different.

   yield groups
ff    39      a
oo    38      a
cc    23      a
fc    13      b

> names(outMedian)

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

> outMedian$statistics

  Chisq Df p.chisq Median
    6.7  3   0.083     28

> outMedian$medians

   Median r Min Max Q25 Q75
cc     23 3  22  28  22  26
fc     13 3  11  15  12  14
ff     39 3  28  42  34  40
oo     38 3  32  40  35  39
```

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)
```

```
> oldpar<-par(mfrow=c(2,2),mar=c(3,3,1,1),cex=0.8)
> # Graphics
> bar.group(outMedian$groups,ylim=c(0,50))
> bar.group(outMedian$groups,xlim=c(0,50),horiz = TRUE)
> plot(outMedian)
> plot(outMedian,variation="IQR",horiz = TRUE)
> par(oldpar)
```

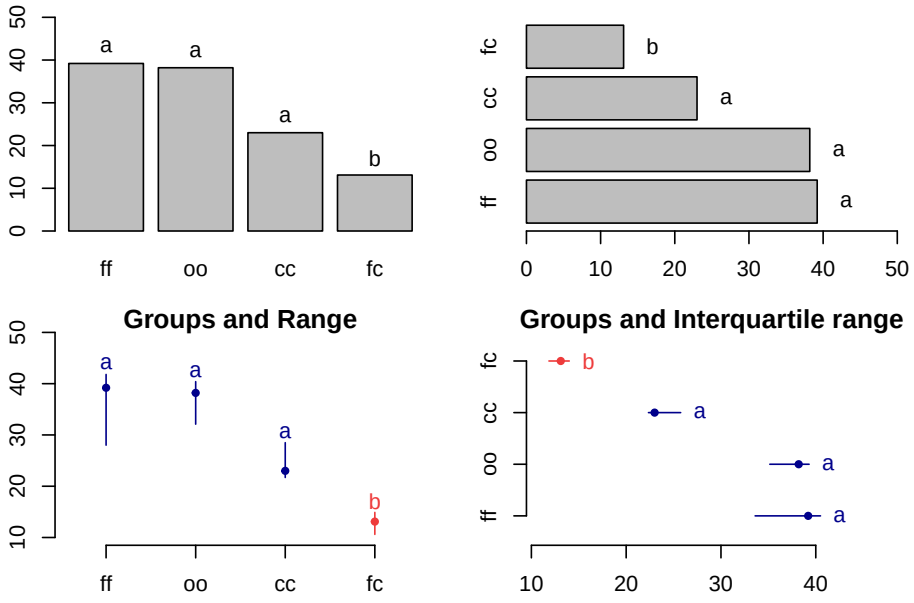

Figure 4: Grouping of treatments and its variation, Median method

```
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)
> head(data.frame(days,chemical,toxic))

  days chemical toxic
1    1        A  0.47
2    1        B  0.34
3    1        D  0.40
4    2        A  0.60
5    2        C  0.87
6    2        E  0.63

> out<-durbin.test(days,chemical,toxic,group=FALSE,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      : 7.7
DF 1       : 6
P-value    : 0.26
Alpha      : 0.05
DF 2       : 8
t-Student  : 2.3

Least Significant Difference
between the sum of ranks:  5

Parameters BIB
Lambda     : 1
Treatmeans : 7
```

```
Block size : 3
Blocks     : 7
Replication: 3

Comparison between treatments
Sum of the ranks

      difference pvalue signif.
A - B          0   1.00
A - C         -4   0.10
A - D          0   1.00
A - E          0   1.00
A - F         -3   0.20
A - G          0   1.00
B - C         -4   0.10
B - D          0   1.00
B - E          0   1.00
B - F         -3   0.20
B - G          0   1.00
C - D          4   0.10
C - E          4   0.10
C - F          1   0.66
C - G          4   0.10
D - E          0   1.00
D - F         -3   0.20
D - G          0   1.00
E - F         -3   0.20
E - G          0   1.00
F - G          3   0.20
```

```
> names(out)

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

> out$statistics

  chisq.value p.value t.value LSD
          7.7    0.26     2.3   5
```

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, decreasing = TRUE, ...)
```

See Figure 4. The Median test with option group=TRUE (default) is used in the exercise.

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 5

```
> # 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", "IQR"),
    horiz = FALSE, bar = TRUE, ...)
```

variation

SE: Standard error

SD: standard deviation

range: max-min

```
> oldpar<-par(mfrow=c(2,2),cex=0.7,mar=c(3.5,1.5,3,1))
> 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(oldpar)
> oldpar<-par(mar=c(2.5,2.5,1,0),cex=0.6)
> bar.group(modelLattice$group,ylim=c(0,55),density=10,las=1)
> par(oldpar)
```

```
> oldpar<-par(mfrow=c(2,2),mar=c(3,3,2,1),cex=0.7)
> c1<-colors()[480]; c2=colors()[65]
> bar.err(outHSD$means, variation="range",ylim=c(0,50),col=c1,las=1)
> bar.err(outHSD$means, variation="IQR",horiz=TRUE, xlim=c(0,50),col=c2,las=1)
> plot(outHSD, variation="range",las=1)
> plot(outHSD, horiz=TRUE, variation="SD",las=1)
> par(oldpar)
```

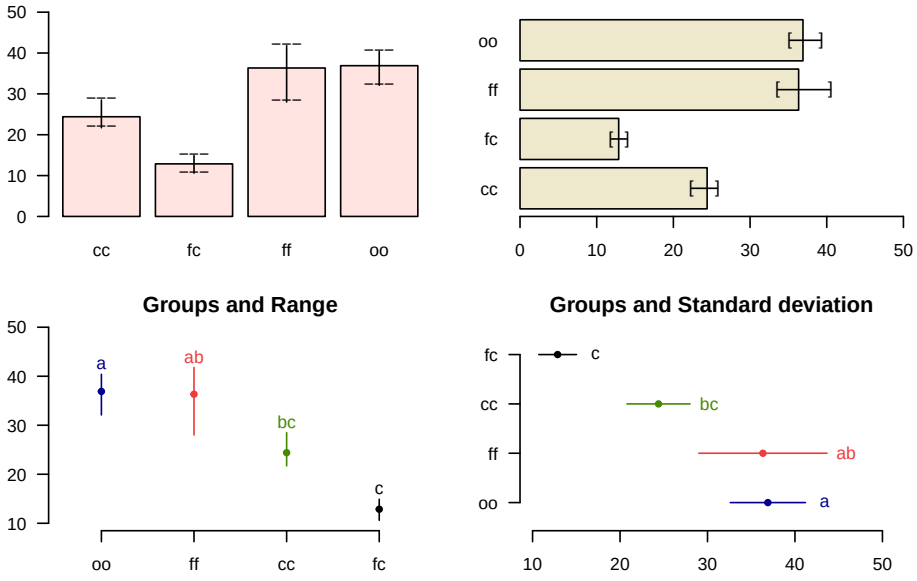

Figure 5: Comparison between treatments

```
> # model : yield ~ virus
> # Important group=TRUE
> oldpar<-par(mfrow=c(1,2),mar=c(3,3,1,1),cex=0.8)
> x<-duncan.test(model, "virus", group=TRUE)
> plot(x,las=1)
> plot(x,variation="IQR",horiz=TRUE,las=1)
> par(oldpar)
```

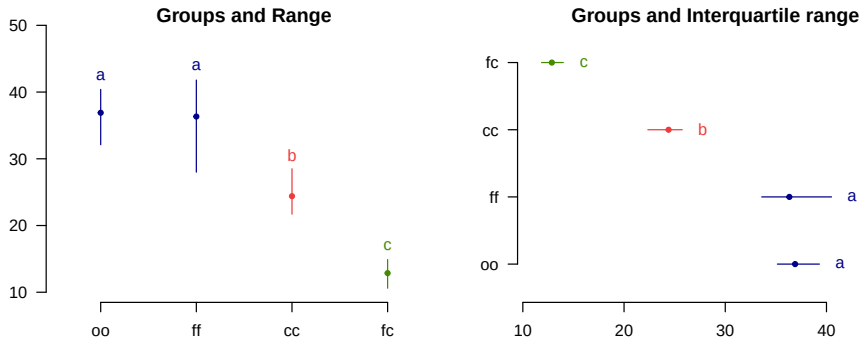

Figure 6: Grouping of treatments and its variation, Duncan method

6.3 plot.group

It plot groups and variation of the treatments to compare. It uses the objects generated by a procedure of comparison like LSD (Fisher), duncan, Tukey (HSD), Student Newman Keul (SNK), Scheffe, Waller-Duncan, Ryan, Einot and Gabriel and Welsch (REGW), Kruskal Wallis, Friedman, Median, Waerden and other tests like Durbin, DAU, BIB, PBIB. The variation types are range (maximun and minimun), IQR (interquartile range), SD (standard deviation) and SE (standard error), see Figure 6.

The function: plot.group() and their arguments are x (output of test), variation = c("range", "IQR", "SE", "SD"), horiz (TRUE or FALSE), xlim, ylim and main are optional plot() parameters and others plot parameters.

6.4 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, Hsu (1996), see Figure 7

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", Kang (1993) and a non-parametric method of Haynes, based on the data range.

```
> # 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)
```

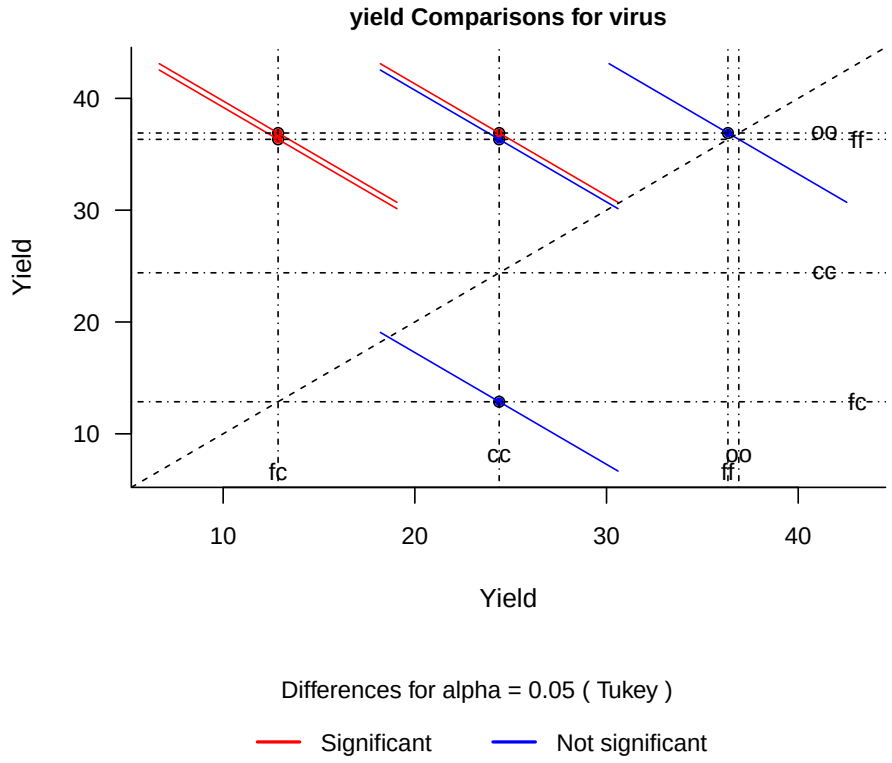

Figure 7: Mean-Mean scatter plot representation of the Tukey method

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, Kang (1993). We will consider five environments in the following example:

```
> options(digit=2)
> f <- system.file("external/dataStb.csv", package="agricolae")
> dataStb<-read.csv(f)
> stability.par(dataStb, rep=4, MSerror=1.8, alpha=0.1, main="Genotype",console=TRUE)

 INTERACTIVE PROGRAM FOR CALCULATING SHUKLA'S STABILITY VARIANCE AND KANG'S
                      YIELD - STABILITY (YSi) STATISTICS
 Genotype
 Environmental index  - covariate

 Analysis of Variance

               Df    Sum Sq  Mean Sq F value Pr(>F)
Total         203 2964.1716
Genotypes      16  186.9082  11.6818    4.17 <0.001
Environments   11 2284.0116 207.6374  115.35 <0.001
Interaction   176  493.2518   2.8026    1.56 <0.001
Heterogeneity  16   44.8576   2.8036       1  0.459
Residual      160  448.3942   2.8025    1.56 <0.001
Pooled Error  576               1.8

 Genotype. Stability statistics

  Mean Sigma-square  . s-square  . Ecovalence
A  7.4         2.47 ns     2.45 ns       25.8
B  6.8         1.60 ns     1.43 ns       17.4
C  7.2         0.57 ns     0.63 ns        7.3
D  6.8         2.61 ns     2.13 ns       27.2
E  7.1         1.86 ns     2.05 ns       19.9
F  6.9         3.58  *     3.95  *       36.5
G  7.8         3.58  *     3.96  *       36.6
H  7.9         2.72 ns     2.12 ns       28.2
I  7.3         4.25 **     3.94  *       43.0
J  7.1         2.27 ns     2.51 ns       23.9
K  6.4         2.56 ns     2.55 ns       26.7
L  6.9         1.56 ns     1.73 ns       16.9
M  6.8         3.48  *     3.28 ns       35.6
N  7.5         5.16 **     4.88 **       51.9
O  7.7         2.38 ns     2.64 ns       24.9
P  6.4         3.45  *     3.71  *       35.3
Q  6.2         3.53  *     3.69  *       36.1
```

```
Signif. codes:  0 '**' 0.01 '*' 0.05 'ns' 1

Simultaneous selection for yield and stability  (++)

  Yield Rank Adj.rank Adjusted Stab.var Stab.rating YSi ...
A   7.4   13        1       14     2.47           0  14   +
B   6.8    4       -1        3     1.60           0   3
C   7.2   11        1       12     0.57           0  12   +
D   6.8    4       -1        3     2.61           0   3
E   7.1    9        1       10     1.86           0  10   +
F   6.9    8       -1        7     3.58          -4   3
G   7.8   16        2       18     3.58          -4  14   +
H   7.9   17        2       19     2.72           0  19   +
I   7.3   12        1       13     4.25          -8   5
J   7.1   10        1       11     2.27           0  11   +
K   6.4    3       -2        1     2.56           0   1
L   6.9    7       -1        6     1.56           0   6
M   6.8    6       -1        5     3.48          -4   1
N   7.5   14        1       15     5.16          -8   7   +
O   7.7   15        2       17     2.38           0  17   +
P   6.4    2       -2        0     3.45          -4  -4
Q   6.2    1       -3       -2     3.53          -4  -6

 Yield Mean: 7.1
 YS    Mean: 6.8
 LSD (0.05): 0.45
 - - - - - - - - - - -
 +   selected genotype
 ++  Reference: Kang, M. S. 1993. Simultaneous selection for yield
 and stability: Consequences for growers. Agron. J. 85:754-757.
```

For 17 genotypes, the identification is made by letters. An error variance of 2 and 4 repetitions is assumed.

Analysis

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

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

> print(output$stability)

  Yield Rank Adj.rank Adjusted Stab.var Stab.rating YSi ...
A   7.4   13        1       14     2.47           0  14   +
B   6.8    4       -1        3     1.60           0   3
C   7.2   11        1       12     0.57           0  12   +
D   6.8    4       -1        3     2.61           0   3
E   7.1    9        1       10     1.86           0  10   +
```

```
F   6.9    8       -1        7     3.58          -2   5
G   7.8   16        2       18     3.58          -2  16   +
H   7.9   17        2       19     2.72           0  19   +
I   7.3   12        1       13     4.25          -4   9   +
J   7.1   10        1       11     2.27           0  11   +
K   6.4    3       -2        1     2.56           0   1
L   6.9    7       -1        6     1.56           0   6
M   6.8    6       -1        5     3.48          -2   3
N   7.5   14        1       15     5.16          -8   7
O   7.7   15        2       17     2.38           0  17   +
P   6.4    2       -2        0     3.45          -2  -2
Q   6.2    1       -2       -1     3.53          -2  -3
```

The selected genotypes are: A, C, E, G, H, I, J 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 In the first five locations. For this case, the altitude of the localities is included.

```
> data5<-dataStb[,1:5]
> altitude<-c(1200, 1300, 800, 1600, 2400)
> stability <- stability.par(data5,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, Haynes and Lambert and Christ and Weingartner and Douches and Backlund and Secor and Fry and Stevenson (1998).

Analysis

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

[1] "ranking"    "statistics"

> output$statistics

  MEAN es1 es2  vs1 vs2 chi.ind chi.sum
1  7.1 5.6  24 0.72  47     8.8      28
```

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, Crossa (1990).

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 Figure 8.

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, number = FALSE,
    gcol = NULL, ecol = NULL, angle = 25, lwd = 1.8,
    length = 0.1, xlab = NULL, ylab = NULL, xlim = NULL,
    ylim = NULL, ...)

> data(plrv)
> model<-with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
> names(model)

[1] "ANOVA"    "genXenv"  "analysis" "means"    "biplot"
[6] "PC"

> model$ANOVA

Analysis of Variance Table

Response: Y
           Df Sum Sq Mean Sq F value  Pr(>F)
ENV         5 122284   24457  257.04 9.1e-12 ***
REP(ENV)   12   1142      95    2.57  0.0029 **
GEN        27  17533     649   17.54 < 2e-16 ***
ENV:GEN   135  23762     176    4.75 < 2e-16 ***
Residuals 324  11998      37
---
Signif. codes:
0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> model$analysis
```

```
> oldpar<-par(cex=0.4,mar=c(4,4,1,2))
> plot(model,las=1,xlim=c(-5,6))
> par(oldpar)
```

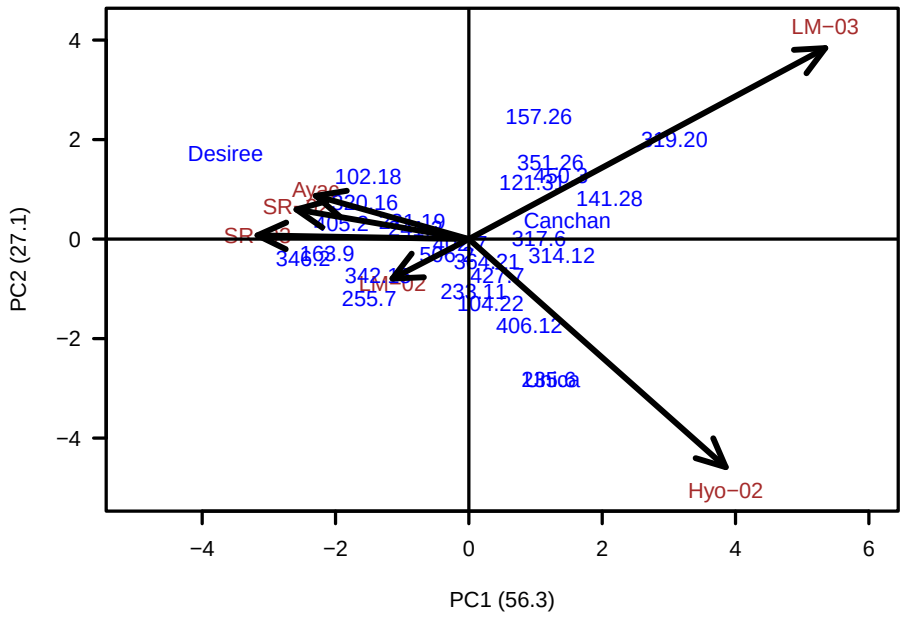

Figure 8: Biplot

```
    percent acum Df Sum.Sq Mean.Sq F.value   Pr.F
PC1    56.3   56 31  13369     431   11.65 0.0000
PC2    27.1   83 29   6428     222    5.99 0.0000
PC3     9.4   93 27   2242      83    2.24 0.0005
PC4     4.3   97 25   1028      41    1.11 0.3286
PC5     2.9  100 23    696      30    0.82 0.7059
```

```
> pc <- model$analysis[, 1]
> pc12<-sum(pc[1:2])
> pc123<-sum(pc[1:3])
```

In this case, the interaction is significant. The first two components explain 83.4 %; then the biplot can provide information about the interaction genotype-environment. With the triplot, 92.8% would be explained.

7.4 AMMI index and yield stability

Calculate AMMI stability value (ASV) and Yield stability index (YSI), Sabaghnia and Sabaghpour and Dehghani (2008); Purchase (1997).

```
> data(plrv)
> model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
```

```
> index<-index.AMMI(model)
> # Crops with improved stability according AMMI.
> print(index[order(index[,3]),])

         ASV YSI rASV rYSI means
402.7   0.28  20    1   19    27
364.21  0.72  12    2   10    34
506.2   0.75  14    3   11    33
233.11  1.06  21    4   17    29
427.7   1.15  12    5    7    36
104.22  1.46  19    6   13    31
241.2   1.68  29    7   22    26
221.19  1.80  34    8   26    23
317.6   2.19  18    9    9    35
121.31  2.29  25   10   15    30
406.12  2.56  23   11   12    33
314.12  2.92  30   12   18    28
342.15  2.92  37   13   24    26
351.26  2.98  22   14    8    36
Canchan 3.10  35   15   20    27
450.3   3.14  22   16    6    36
157.26  3.29  22   17    5    37
320.16  3.32  39   18   21    26
255.7   3.33  33   19   14    31
102.18  3.38  43   20   23    26
235.6   3.76  25   21    4    39
Unica   3.84  24   22    2    39
405.2   3.98  39   23   16    29
163.9   4.43  51   24   27    21
141.28  4.47  26   25    1    40
346.2   5.18  51   26   25    24
319.20  6.72  30   27    3    39
Desiree 7.78  56   28   28    16

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

         ASV YSI rASV rYSI means
141.28  4.47  26   25    1    40
Unica   3.84  24   22    2    39
319.20  6.72  30   27    3    39
235.6   3.76  25   21    4    39
157.26  3.29  22   17    5    37
450.3   3.14  22   16    6    36
427.7   1.15  12    5    7    36
351.26  2.98  22   14    8    36
317.6   2.19  18    9    9    35
364.21  0.72  12    2   10    34
506.2   0.75  14    3   11    33
406.12  2.56  23   11   12    33
104.22  1.46  19    6   13    31
```

```
255.7   3.33  33   19   14    31
121.31  2.29  25   10   15    30
405.2   3.98  39   23   16    29
233.11  1.06  21    4   17    29
314.12  2.92  30   12   18    28
402.7   0.28  20    1   19    27
Canchan 3.10  35   15   20    27
320.16  3.32  39   18   21    26
241.2   1.68  29    7   22    26
102.18  3.38  43   20   23    26
342.15  2.92  37   13   24    26
346.2   5.18  51   26   25    24
221.19  1.80  34    8   26    23
163.9   4.43  51   24   27    21
Desiree 7.78  56   28   28    16
```

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 9.

When the dendrogram is complex, it is convenient to extract part of it with the function hcut(), see Figure 10.

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 xaxis height percentage groups
1  -6 -24   7.5  0.029         60   6-24
2  -3  -4  19.5  0.036         80    3-4
3  -2  -8  22.5  0.038         80    2-8
4  -7 -10  10.5  0.038         60   7-10
5 -21   2  18.8  0.071        100 3-4-21
6 -16   3  21.8  0.074         80 2-8-16
```

```
> oldpar<-par(cex=0.6,mar=c(3,3,2,1))
> 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       : 0.69 secs

> par(oldpar)
```

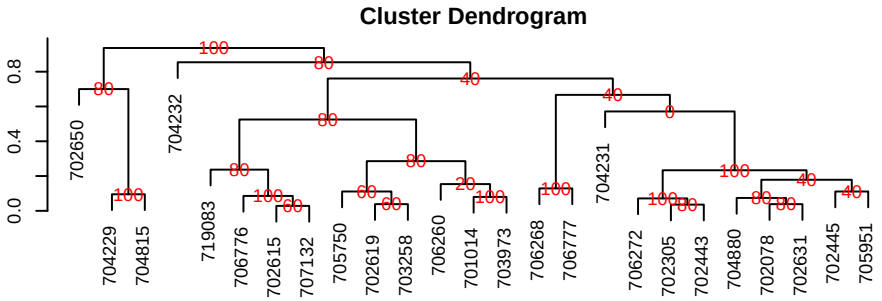

Figure 9: Dendrogram, production by consensus

```
> oldpar<-par(cex=0.6,mar=c(3,3,1.5,1))
> 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)
> par(oldpar)
```

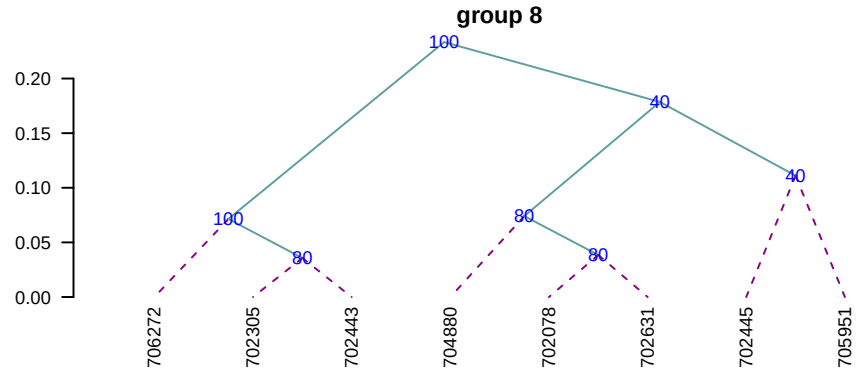

Figure 10: Dendrogram, production by hcut()

```
> oldpar<-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(oldpar)
```

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 11.

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

1000 data was simulated, being the frequency table:

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

	Lower	Upper	Main	Frequency	Percentage	CF	CPF
1	1.5	2.8	2.1	19	1.9	19	1.9
2	2.8	4.1	3.5	120	12.0	139	13.9
3	4.1	5.4	4.8	234	23.4	373	37.3
4	5.4	6.7	6.0	233	23.3	606	60.6
5	6.7	8.0	7.3	182	18.2	788	78.8
6	8.0	9.3	8.7	176	17.6	964	96.4
7	9.3	10.6	9.9	36	3.6	1000	100.0

```
> oldpar<-par(mar=c(2,0,2,1),cex=0.6)
> plot(density(soil$pH),axes=FALSE,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)
> par(oldpar)
```

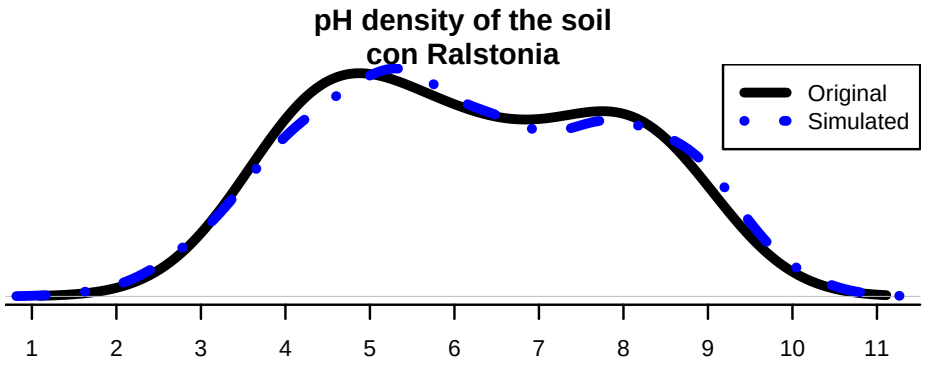

Figure 11: Distribution of the simulated and the original data

Some statistics, original data:

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

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   3.80    4.70    6.10    6.15    7.60    8.40
```

Some statistics, montecarlo simulate data:

```
> summary(simulated)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.60    4.79    6.08    6.22    7.78   10.56
```

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 permutated 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   25.1    25.1     7.3   0.02       0.02
date          2   13.9     7.0     2.0   0.18       0.19
variety:date  2    4.8     2.4     0.7   0.51       0.50
Residuals    12   41.5     3.5
```

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   25.1   25.09    7.26   0.02 *
date          2   13.9    6.95    2.01   0.18
variety:date  2    4.9    2.43    0.70   0.51
Residuals    12   41.5    3.46
---
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  Criterion
variety       1     7.3           60          40 acceptable
date          2     2.0           66          34 acceptable
variety:date  2     0.7           70          30 acceptable
---
```

The validation is referred to the percentage of decision results equal to the result of the ANOVA decision. Thus, 70% 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 0.33 0.27
X2 0.17 0.53

Residual Effect^2 =  0.43

> output

$Coeff
     X1   X2
X1 0.33 0.27
X2 0.17 0.53

$Residual
[1] 0.43
```

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, Singh and Chaudhary (1979).

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())
> options(digits = 2)
> data(heterosis)
> str(heterosis)

'data.frame':        324 obs. of  11 variables:
 $ Place      : num  1 1 1 1 1 1 1 1 1 1 ...
 $ Replication: num  1 1 1 1 1 1 1 1 1 1 ...
 $ Treatment  : num  1 2 3 4 5 6 7 8 9 10 ...
 $ Factor     : Factor w/ 3 levels "Control","progenie",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ Female     : Factor w/ 8 levels "Achirana","LT-8",..: 2 2 2 6 6 6 7 7 7 8 ...
 $ Male       : Factor w/ 3 levels "TPS-13","TPS-67",..: 3 1 2 3 1 2 3 1 2 3 ...
 $ v1         : num  0.948 1.052 1.05 1.058 1.123 ...
 $ v2         : num  1.65 2.2 1.88 2 2.45 2.63 2.75 3 2.51 1.93 ...
 $ v3         : num  17.2 17.8 15.6 16 16.5 ...
 $ v4         : num  9.93 12.45 9.3 12.77 14.13 ...
 $ v5         : num  102.6 107.4 120.5 83.8 90.4 ...

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

ANALYSIS LINE x TESTER:  v2

ANOVA with parents and crosses
==============================
                     Df  Sum Sq Mean Sq F value Pr(>F)
Replications          2  0.5192  0.2596    9.80 0.0002
Treatments           34 16.1016  0.4736   17.88 0.0000
Parents              10  7.7315  0.7731   29.19 0.0000
Parents vs. Crosses   1  0.0051  0.0051    0.19 0.6626
Crosses              23  8.3650  0.3637   13.73 0.0000
Error                68  1.8011  0.0265
Total               104 18.4219

ANOVA for line X tester analysis
```

```
================================
                Df Sum Sq Mean Sq F value Pr(>F)
Lines            7   4.98   0.711     3.6  0.019
Testers          2   0.65   0.325     1.7  0.226
Lines X Testers 14   2.74   0.196     7.4  0.000
Error           68   1.80   0.026
```

ANOVA for line X tester analysis including parents

```
==================================================
                     Df  Sum Sq Mean Sq F value Pr(>F)
Replications          2  0.5192  0.2596    9.80 0.0002
Treatments           34 16.1016  0.4736   17.88 0.0000
Parents              10  7.7315  0.7731   29.19 0.0000
Parents vs. Crosses   1  0.0051  0.0051    0.19 0.6626
Crosses              23  8.3650  0.3637   13.73 0.0000
Lines                 7  4.9755  0.7108    3.63 0.0191
Testers               2  0.6494  0.3247    1.66 0.2256
Lines X Testers      14  2.7401  0.1957    7.39 0.0000
Error                68  1.8011  0.0265
Total               104 18.4219
```

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:

```
===========
          Testers
Lines      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)   : 0.054
S.E. (gca for tester) : 0.033
S.E. (sca effect)     : 0.094
```

```
S.E. (gi - gj)line    : 0.077
S.E. (gi - gj)tester  : 0.047
S.E. (sij - skl)tester: 0.13

Genetic Components:
==================
Cov H.S. (line)   : 0.057
Cov H.S. (tester) : 0.0054
Cov H.S. (average): 0.0039
Cov F.S. (average): 0.13
F = 0, Adittive genetic variance: 0.015
F = 1, Adittive genetic variance: 0.0077
F = 0, Variance due to Dominance: 0.11
F = 1, Variance due to Dominance: 0.056

Proportional contribution of lines, testers
 and their interactions to total variance
==========================================
Contributions of lines  : 59
Contributions of testers: 7.8
Contributions of lxt    : 33

> options(digits = 7)
```

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 x m columns, and a total of n*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 12.

```
> 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

```
> oldpar<-par(mar=c(3,3,4,1),cex=0.7)
> data(rice)
> table<-index.smith(rice, col="blue",
+  main="Interaction between the CV and the plot size",type="l",xlab="Size")
> par(oldpar)
```

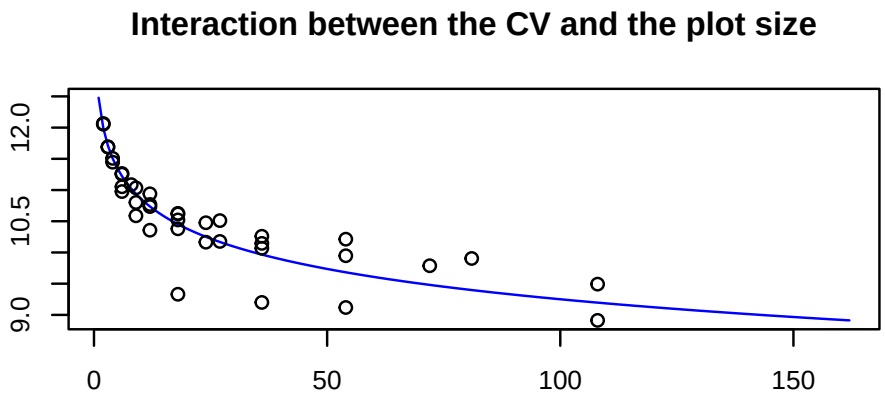

Figure 12: Adjustment curve for the optimal size of plot

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: 2.541336

95 percent confidence interval:
 2.22808 ; 3.07635
```

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

> with(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
```

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)
> with(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
```

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 <- 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.

```
> oldpar<-par(mar=c(3,3,4,1),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")
> par(oldpar)
```

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 3.26 3.28 3.31
18  2.85 2.98 3.07 3.13 3.17 3.20 3.23 3.25 3.27 3.30 3.33
19  2.85 2.98 3.07 3.13 3.18 3.22 3.24 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 13 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)
```

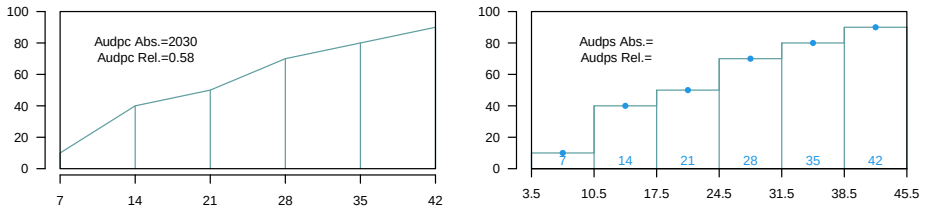

Figure 13: Area under the curve (AUDPC) and Area under the Stairs (AUDPS)

8.15 AUDPS

The Area Under the Disease Progress Stairs (AUDPS), see Figure 13. 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)
```

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
> analysis<-with(potato,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
```

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 14

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).

```
> options(digits=2)
> 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"
```

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

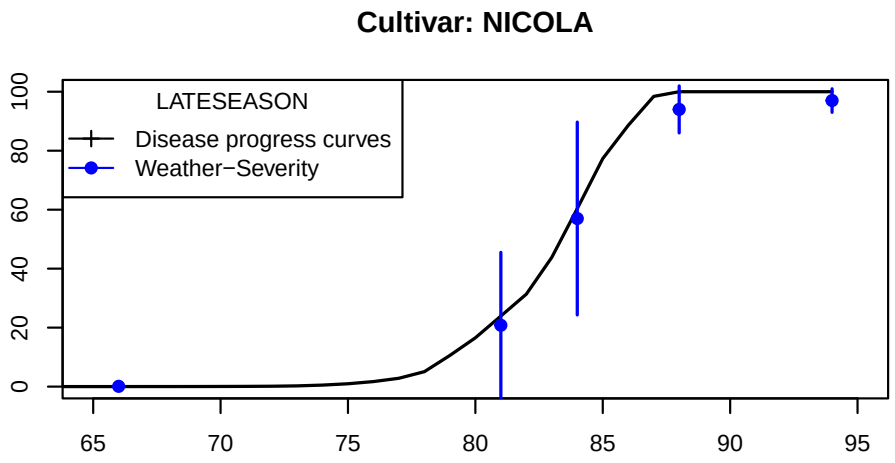

Figure 14: lateblight: LATESEASON

```
> head(model$Gfile)

           dates nday MeanSeverity StDevSeverity MinObs
Eval1 2000-03-25   66          0.1             0    0.1
Eval2 2000-04-09   81         20.8            25   -3.9
Eval3 2000-04-12   84         57.0            33   24.3
Eval4 2000-04-16   88         94.0             8   86.0
Eval5 2000-04-22   94         97.0             4   93.0
      MaxObs
Eval1    0.1
Eval2   45.5
Eval3   89.7
Eval4  102.0
Eval5  101.0

> 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 0.010      0        0
2 2000-01-21    2      0           0 0.028      2        0
3 2000-01-22    3      0           0 0.038      2        0
4 2000-01-23    4      0           0 0.049      2        0
5 2000-01-24    5      0           0 0.060      2        0
6 2000-01-25    6      0           0 0.086      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
```

```
> oldpar<-par(mar=c(3,2.5,1,1),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"))
> par(oldpar)
```

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