

# Package ‘agricolae’

September 1, 2014

**Type** Package

**Title** Statistical Procedures for Agricultural Research

**Version** 1.2-1

**Date** 2014-09-01

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**Imports** klaR, MASS, nlme, cluster, spdep

**Description** Agricolae was presented in the thesis "A statistical analysis tool for agricultural research" to obtain the degree of Master on science, mention Systems Engineering, Faculty of Industrial and Systems Engineering, National Engineering University (UNI), Lima-Peru. Original idea, support and data sets came from CIP (International Potato Center). Agricolae offers extensive functionality on experimental design especially for agricultural and plant breeding experiments, which can also be useful for other purposes. It supports planning of lattice, Alpha, Cyclic, Complete Block, Latin Square, Graeco-Latin Squares, augmented block, factorial, split and strip plot designs. There are also various analysis facilities for experimental data, e.g. treatment comparison procedures and several non-parametric tests comparison, biodiversity indexes and consensus cluster.

**License** GPL

**URL** <http://tarwi.lamolina.edu.pe/~fmendiburu>

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2014-09-01 17:45:19

**R topics documented:**

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agricolae-package      *Statistical Procedures for Agricultural Research*

---

**Description**

This package contains functionality for the Statistical Analysis of experimental designs applied specially for field experiments in agriculture and plant breeding. Original idea, support and data sets came from CIP (International Potato Center)

**Details**

Package: agricolae  
Type: Package  
Version: 1.2-1  
Date: 2014-09-01  
License: GPL

Planning of field experiments: lattice, factorial, RCBD, CRD, Latin Square, Youden, Graeco, BIB, Alpha design, Cyclic, augmented block, split and strip plot Designs. Comparison of multi-location trials: AMMI, Index AMMI Stability (biplot, triplot), comparison between treatments: LSD, Bonferroni and other p-adjust, HSD, Waller, Student Newman Keuls SNK, Duncan, Scheffe; Non parametric tests: Kruskal, Friedman, Durbin, Van Der Waerden, Median. Analysis of genetic experiments: North Carolina designs, LinexTester, Balanced Incomplete Block, Strip plot, Split-Plot, Partially Balanced Incomplete Block, analysis Mother and baby trials (see data RioChillon). Resampling and simulation: resampling.model, simulation.model, montecarlo, lateblight Simulator for potato. Ecology: Biodiversity Index, Path Analysis. Soil Uniformity: Smith's Index. Cluster Analysis: Consensus Cluster. Descriptive statistics utilities: \*.freq

### Author(s)

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Maintainer: Felipe de Mendiburu <f.mendiburu@cgiar.org>

### References

De Mendiburu, Felipe (2009). Una herramienta de analisis estadistico para la investigacion agricola. Tesis. Universidad Nacional de Ingenieria (UNI-PERU).

Universidad Nacional Agraria La Molina, Lima-PERU. Facultad de Economia y Planificacion Departamento Academico de Estadistica e Informatica

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AMMI

*AMMI Analysis*

---

### Description

Additive Main Effects and Multiplicative Interaction Models (AMMI) are widely used to analyze main effects and genotype by environment (GEN, ENV) interactions in multilocation variety trials. Furthermore, this function generates data to biplot, triplot graphs and analysis.

### Usage

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

### Arguments

ENV	Environment
GEN	Genotype
REP	Replication
Y	Response
MSE	Mean Square Error
console	ouput TRUE or FALSE
PC	Principal components ouput TRUE or FALSE

**Details**

additional graphics see `help(plot.AMMI)`.

**Value**

ANOVA	analysis of variance general
genXenv	class by, genopyte and environment
analysis	analysis of variance principal components
means	average genotype and environment
biplot	data to produce graphics
PC	class princomp

**Author(s)**

F. de Mendiburu

**References**

Crossa, J. 1990. Statistical analysis of multilocation trials. *Advances in Agronomy* 44:55-85

**See Also**

[lineXtester.plot.AMMI](#)

**Examples**

```
# Full replications
library(agricolae)
# Example 1
data(plrv)
attach(plrv)
model<- AMMI(Locality, Genotype, Rep, Yield, console=FALSE)
model$ANOVA
# see help(plot.AMMI)
detach(plrv)
# biplot
plot(model)
# triplot PC 1,2,3
plot(model, type=2, number=TRUE)
# biplot PC1 vs Yield
plot(model, first=0,second=1, number=TRUE)
# Example 2
data(CIC)
data1<-CIC$comas[,c(1,6,7,17,18)]
data2<-CIC$oxapampa[,c(1,6,7,19,20)]
cic <- rbind(data1,data2)
attach(cic)
model<-AMMI(Locality, Genotype, Rep, relative)
detach(cic)
```

```

model$ANOVA
plot(model,0,1,angle=20,ecol="brown")
# Example 3
# Only means. Mean square error is well-known.
data(sinRepAmmi)
attach(sinRepAmmi)
REP <- 3
MSerror <- 93.24224
#startgraph
model<-AMMI(ENV, GEN, REP, YLD, MSerror,PC=TRUE)
detach(sinRepAmmi)
# print anova
print(model$ANOVA,na.print = "")
# Biplot with the one restored observed.
plot(model,0,1,type=1)
# with principal components model$PC is class "princomp"
pc<- model$PC
pc$loadings
summary(pc)
biplot(pc)
# Principal components by means of the covariance similar AMMI
# It is to compare results with AMMI
cova<-cov(model$genXenv)
values<-eigen(cova)
total<-sum(values$values)
round(values$values*100/total,2)
# AMMI: 64.81 18.58 13.50 3.11 0.00

```

---

AMMI.contour

*AMMI contour*


---

## Description

Draws a polygon or a circumference around the center of the Biplot with a proportional radio at the longest distance of the genotype.

## Usage

```
AMMI.contour(model, distance, shape, ...)
```

## Arguments

model	Object
distance	Circumference radius >0 and <=1
shape	Numerical, relating to the shape of the polygon outline.
...	Parameters corresponding to the R lines function

**Details**

First, it is necessary to execute the AMMI function. It is only valid for the BIPLLOT function but not for the TRIPLLOT one.

**Value**

model	output AMMI
distance	Numeric >0 and <=1
shape	Numeric

**Note**

Complement graphics AMMI

**Author(s)**

Felipe de Mendiburu

**See Also**

[AMMI](#)

**Examples**

```
library(agricolae)
# see AMMI.
data(sinRepAmmi)
Environment <- sinRepAmmi$ENV
Genotype <- sinRepAmmi$GEN
Yield <- sinRepAmmi$YLD
REP <- 3
MSerror <- 93.24224
model<-AMMI(Environment, Genotype, REP, Yield, MSerror)
plot(model)
AMMI.contour(model,distance=0.7,shape=8,col="red",lwd=2,lty=5)
```

---

audpc

*Calculating the absolute or relative value of the AUDPC*

---

**Description**

Area Under Disease Progress Curve. The AUDPC measures the disease throughout a period. The AUDPC is the area that is determined by the sum of trapezes under the curve.

**Usage**

```
audpc(evaluation, dates, type = "absolute")
```



**Arguments**

evaluation	Table of data of the evaluations: Data frame
dates	Vector of dates corresponding to each evaluation
type	relative, absolute

**Details**

AUDPC. For the illustration one considers three evaluations (14, 21 and 28 days) and percentage of damage in the plant 40, 80 and 90 (interval between dates of evaluation 7 days).  $AUDPC = 1045$ . The evaluations can be at different interval.

**Value**

evaluation	data frame, matrix or numeric vector
dates	a numeric vector
type	text

**Author(s)**

Felipe de Mendiburu

**References**

Campbell, C. L., L. V. Madden. (1990): Introduction to Plant Disease Epidemiology. John Wiley & Sons, New York City.

**Examples**

```
library(agricolae)
dates<-c(14,21,28) # days
# example 1: evaluation - vector
evaluation<-c(40,80,90)
audpc(evaluation,dates)
# example 2: evaluation: dataframe nrow=1
evaluation<-data.frame(E1=40,E2=80,E3=90) # percentages
plot(dates,evaluation,type="h",ylim=c(0,100),col="red",axes=FALSE)
title(cex.main=0.8,main="Absolute or Relative AUDPC\nTotal area = 100*(28-14)=1400")
lines(dates,evaluation,col="red")
text(dates,evaluation+5,evaluation)
text(18,20,"A = (21-14)*(80+40)/2")
text(25,60,"B = (28-21)*(90+80)/2")
text(25,40,"audpc = A+B = 1015")
text(24.5,33,"relative = audpc/area = 0.725")
abline(h=0)
axis(1,dates)
axis(2,seq(0,100,5),las=2)
lines(rbind(c(14,40),c(14,100)),lty=8,col="green")
lines(rbind(c(14,100),c(28,100)),lty=8,col="green")
lines(rbind(c(28,90),c(28,100)),lty=8,col="green")
# It calculates audpc absolute
```

```

absolute<-audpc(evaluation,dates,type="absolute")
print(absolute)
rm(evaluation, dates, absolute)
# example 3: evaluation dataframe nrow>1
data(disease)
dates<-c(1,2,3) # week
evaluation<-disease[,c(4,5,6)]
# It calculates audpc relative
index <-audpc(evaluation, dates, type = "relative")
# Correlation between the yield and audpc
correlation(disease$yield, index, method="kendall")
# example 4: days infile
data(CIC)
comas <- CIC$comas
oxapampa <- CIC$oxapampa
dcomas <- names(comas)[9:16]
days<- as.numeric(substr(dcomas,2,3))
AUDPC<- audpc(comas[,9:16],days)
relative<-audpc(comas[,9:16],days,type = "relative")
h1<-graph.freq(AUDPC,border="red",density=4,col="blue")
table.freq(h1)
h2<-graph.freq(relative,border="red",density=4,col="blue",
frequency=2, ylab="relative frequency")

```

---

audps

*The Area Under the Disease Progress Stairs*


---

### Description

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.

### Usage

```
audps(evaluation, dates, type = "absolute")
```

### Arguments

evaluation	Table of data of the evaluations: Data frame
dates	Vector of dates corresponding to each evaluation
type	relative, absolute

### Details

AUDPS. For the illustration one considers three evaluations (14, 21 and 28 days) and percentage of damage in the plant 40, 80 and 90 (interval between dates of evaluation 7 days). AUDPS = 1470. The evaluations can be at different interval. AUDPS= sum( rectangle area by interval in times evaluation ) see example.

**Value**

evaluation	data frame, matrix or numeric vector
dates	a numeric vector
type	text

**Author(s)**

Felipe de Mendiburu

**References**

Ivan Simko and Hans-Peter Piepho (2011). The Area Under the Disease Progress Stairs: Calculation, Advantage, and Application. Analytical and Theoretical Plant Pathology

**Examples**

```
library(agricolae)
dates<-c(14,21,28) # days
# example 1: evaluation - vector
evaluation<-c(40,80,90)
audps(evaluation,dates)
audps(evaluation,dates,"relative")
x<-seq(10.5,31.5,7)
y<-c(40,80,90,90)
plot(x,y,"s",ylim=c(0,100),xlim=c(10,32),axes=FALSE,col="red",ylab="",xlab="")
title(cex.main=0.8,main="Absolute or Relative AUDPS\nTotal area=(31.5-10.5)*100=2100",
ylab="evaluation",xlab="dates" )
points(x,y,type="h")
z<-c(14,21,28)
points(z,y[-3],col="blue",lty=2,pch=19)
points(z,y[-3],col="blue",lty=2,pch=19)
axis(1,x,pos=0)
axis(2,c(0,40,80,90,100),las=2)
text(dates,evaluation+5,dates,col="blue")
text(14,20,"A = (17.5-10.5)*40",cex=0.8)
text(21,40,"B = (24.5-17.5)*80",cex=0.8)
text(28,60,"C = (31.5-24.5)*90",cex=0.8)
text(14,95,"audps = A+B+C = 1470")
text(14,90,"relative = audps/area = 0.7")
# It calculates audpc absolute
absolute<-audps(evaluation,dates,type="absolute")
print(absolute)
rm(evaluation, dates, absolute)
```

---

bar.err                      *Plotting the standard error or standard deviance of a multiple comparison of means*

---

### Description

It plots bars of the averages of treatments and standard error or standard deviance. It uses the objects generated by a procedure of comparison like LSD, HSD, Kruskal and Waller-Duncan.

### Usage

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

### Arguments

x	object means of the comparisons the LSD.test, HSD.test, ..., etc
variation	SE=standard error or range=Max-Min
horiz	Horizontal or vertical bars
bar	paint bar
...	Parameters of the function barplot()

### Details

x: data frame formed by 5 columns: name of the bars, height, level out: LSD.test, HSD, waller.test, scheffe.test, duncan.test, SNK.test, friedman, kruskal, waerden.test. x: out\$means

### Value

x	object
variation	character std, SE or range
horiz	TRUE or FALSE
bar	TRUE or FALSE
...	Parameters of the function barplot()

### Author(s)

Felipe de Mendiburu

### See Also

[LSD.test](#), [HSD.test](#), [waller.test](#), [kruskal](#), [bar.group](#)

**Examples**

```

library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
out <- waller.test(model,"virus", console=TRUE,
main="Yield of sweetpotato\ndealt with different virus")
par(mfrow=c(2,2),cex=1)
bar.err(out$means,variation="range",horiz=TRUE,xlim=c(0,45),angle=125,density=6,
main="range")
bar.err(out$means,variation="SD",ylim=c(0,45),col=colors()[30],
main="Standard deviation",density=8)
bar.err(out$means,variation="SE",horiz=TRUE,xlim=c(0,45),density=8,
col="brown",main="Standard error")
bar.err(out$means,variation="range",ylim=c(0,45),bar=FALSE,col="green",
main="range")
par(mfrow=c(1,2),cex=1)
bar.err(out$means,variation="range",ylim=c(0,45),bar=FALSE,col=0)
abline(h=0)
# horiz = TRUE
bar.err(out$means,variation="SE",horiz=TRUE,xlim=c(0,45),bar=FALSE,col=0)
#startgraph
par(mfrow=c(1,1))
#endgraph

```

bar.group

*Plotting the multiple comparison of means***Description**

It plots bars of the averages of treatments to compare. It uses the objects generated by a procedure of comparison like LSD, HSD, Kruskal, Waller-Duncan, Friedman or Durbin. It can also display the 'average' value over each bar in a bar chart.

**Usage**

```
bar.group(x, horiz = FALSE, ...)
```

**Arguments**

x	Object created by a test of comparison
horiz	Horizontal or vertical bars
...	Parameters of the function barplot()

**Details**

x: data frame formed by 5 columns: name of the bars, height and level of the bar.

**Value**

x                    Data frame  
 horiz               Logical TRUE or FALSE  
 ...

**Author(s)**

Felipe de Meniburu

**See Also**

[LSD.test](#), [HSD.test](#), [kruskal](#), [friedman](#), [durbin.test](#), [waller.test](#)

**Examples**

```
# Example 1
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison<- LSD.test(model,"virus",alpha=0.01,group=TRUE)
print(comparison$groups)
#startgraph
par(cex=1.5)
bar.group(comparison$groups,horiz=TRUE,density=8,col="blue",border="red",
xlim=c(0,50),las=1)
title(cex.main=0.8,main="Comparison between\ntreatment means",xlab="Yield",ylab="Virus")
#endgraph
# Example 2
library(agricolae)
x <- 1:4
y <- c(0.29, 0.44, 0.09, 0.49)
xy <- data.frame(x,y,y)
#startgraph
par(cex=1.5)
bar.group(xy,density=30,angle=90,col="brown",border=FALSE,ylim=c(0,0.6),lwd=2,las=1)
#endgraph
```

---

BIB.test

*Finding the Variance Analysis of the Balanced Incomplete Block Design*

---

**Description**

Analysis of variance BIB and comparison mean adjusted.

**Usage**

```
BIB.test(block, trt, y, test = c("lsd","tukey","duncan","waller","snk"),  
alpha = 0.05, group = TRUE,console=FALSE)
```

**Arguments**

block	blocks
trt	Treatment
y	Response
test	Comparison treatments
alpha	Significant test
group	logical
console	logical, print output

**Details**

Test of comparison treatment. lsd: Least significant difference. tukey: Honestly significant difference. duncan: Duncan's new multiple range test waller: Waller-Duncan test. snk: Student-Newman-Keuls (SNK)

**Value**

block	Vector
trt	Vector
y	numeric vector
test	Character
alpha	Numeric
group	TRUE or FALSE

**Author(s)**

F. de Mendiburu

**References**

Design of Experiments. Robert O. Kuehl. 2nd ed., Duxbury, 2000 Linear Estimation and Design of Experiments. D.D. Joshi. WILEY EASTERN LIMITED 1987, New Delhi, India. Introduction to experimental statistics. Ching Chun Li McGraw - Hill Book Company, Inc. New York. 1964

**See Also**

[durbin.test](#)

**Examples**

```

library(agricolae)
# Example Design of Experiments. Robert O. Kuehl. 2da. Edicion. 2001
run<-gl(10,3)
psi<-c(250,325,475,250,475,550,325,400,550,400,475,550,325,475,550,
250,400,475,250,325,400,250,400,550,250,325,550,325,400,475)
monovinyll<-c(16,18,32,19,46,45,26,39,61,21,35,55,19,47,48,20,33,31,13,13,34,21,
30,52,24,10,50,24,31,37)
out<-BIB.test(run,psi,monovinyll,test="waller",group=FALSE)
print(out)
bar.err(out$means,variation="range",ylim=c(0,60),bar=FALSE,col=0)
out<-BIB.test(run,psi,monovinyll,test="waller",group=TRUE)
out<-BIB.test(run,psi,monovinyll,test="tukey",group=TRUE,console=TRUE)
out<-BIB.test(run,psi,monovinyll,test="tukey",group=FALSE,console=TRUE)
rm(run,psi,monovinyll,out)
# Example linear estimation and design of experiments. D.D. Joshi. 1987
# Professor of Statistics, Institute of Social Sciences Agra, India
# 6 varieties of wheat crop in a BIB whit 10 blocks of 3 plots each.
y <-c(69,77,72,63,70,54,65,65,57,59,50,45,68,75,59,38,60,60,62,
55,54,65,62,65,61,39,54,67,63,56)
varieties<-gl(6,5)
block <- c(1,2,3,4,5,1,2,6,7,8,1,3,6,9,10,2,4,7,9,10,3,5,7,8,9,4,5,6,8,10)
BIB.test(block, varieties, y)
# Example Introduction to experimental statistics. Ching Chun Li. 1964
# pag. 395 table. 27.2
# 7 trt, k=3 and b=7.
y <-c(10,15,11,4,12,15,5,14,10,14,19,19,8,10,17,6,11,12,5,14,21)
block<-gl(7,3)
trt <- c(1,2,4,2,3,5,3,4,6,4,5,7,1,5,6,2,6,7,1,3,7)
out<-BIB.test(block, trt, y, test="duncan")
bar.group(out$groups,col="blue",density=4,ylim=c(0,max(y)))
rm(y,block,trt,out)

```

---

carolina

*North Carolina Designs I, II and III*


---

**Description**

Statistic analysis of the Carolina I, II and III genetic designs.

**Usage**

```
carolina(model,data)
```

**Arguments**

model	Constant
data	Data frame



**Details**

model = 1,2 and 3 is I, II and III see carolina1,2 and 3.

**Value**

model            1, 2 or 3  
data            in order  
carolina 1 :    set, male, female, progeny, replication, response ...  
carolina 2 :    set, male, female, replication, response ...  
carolina 3 :    set, male, female, replication, response ...

**Author(s)**

Felipe de Mendiburu

**References**

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979

**See Also**

[DC](#)

**Examples**

```
library(agricolae)
data(DC)
carolina1 <- DC$carolina1
# str(carolina1)
output<-carolina(model=1,carolina1)
output[[][-1]

carolina2 <- DC$carolina2
# str(carolina2)
majes<-subset(carolina2,carolina2[,1]==1)
majes<-majes[,c(2,5,4,3,6:8)]
output<-carolina(model=2,majes[,c(1:4,6)])
output[[][-1]

carolina3 <- DC$carolina3
# str(carolina3)
output<-carolina(model=3,carolina3)
output[[][-1]
```

Chz2006

*Data amendment Carhuaz 2006***Description**

Incidents and performance of healthy tubers and rotten potato field infested with naturally *Ralstonia solanacearum* Race 3/Bv 2A, after application of inorganic amendments and a rotation crop in Carhuaz Peru, 2006.

**Usage**

```
data(Chz2006)
```

**Format**

The format is: List of 2

amendment a factor

crop a factor

block a numeric vector, replications

plant a numeric vector, number plant

wilt\_percent a numeric vector, wilt percentage at 60 days

health a numeric vector, kg/8m2

rot a numeric vector, kg/8m2

**Details**

Application of inorganic amendment and crop rotation to control bacterial wilt of the potato (MBP).

**Source**

Experimental field, 2006. Data Kindly provided by Pedro Aley.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(Chz2006)
str(Chz2006)
wilt<-Chz2006$wilt
yield<-Chz2006$yield
means <- tapply.stat(wilt[,5],wilt[,1:3],function(x) mean(x,na.rm=TRUE))
names(means)[4]<-"wilt_percent"
model <- aov(wilt_percent ~ block + crop, means)
```

```
anova(model)
cv.model(model)
yield<-yield[order(paste(yield[,1],yield[,2],yield[,3])),]
correlation(means[,4],yield[,4],method="spearman")
```

CIC

*Data for late blight of potatoes***Description**

A study of *Phytophthora infestans* in the potato plant in the localities of Comas and Oxapampa in Peru, 2005.

**Usage**

```
data(CIC)
```

**Format**

The format is: List of 2 (comas, oxapampa)

Locality a factor with levels Comas Oxapampa

Genotype a factor

Rep a numeric vector, replications

E9 a numeric vector, infestans porcentaje to 9 days

AUDPC a numeric vector: the area under the disease-progress curve

Relative a numeric vector, relative area

**Details**

comas: temperature=59.9 Fahrenheit, relative humidity=83.3 oxapampa: temperature=64.8 Fahrenheit, relative humidity=86.2 AUDPC and relative see function audpc(). help(audpc) Exx: Evaluation in porcentaje, xx is days. ORD1, ORD2, SBLK and row are references location of the plot in the field.

**Source**

Experimental field, 2004-2005. Data Kindly provided by Matilde Orrillo.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(CIC)
CIC$comas
CIC$oxapampa
```

---

`clay`*Data of Ralstonia population in clay soil*

---

**Description**

An evaluation over a time period.

**Usage**

```
data(clay)
```

**Format**

A data frame with 69 observations on the following 3 variables.

`per.clay` a numeric vector

`days` a numeric vector

`ralstonia` a numeric vector

**Source**

Experimental field.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(clay)
str(clay)
```

---

`ComasOxapampa`*Data AUDPC Comas - Oxapampa*

---

**Description**

Fifty-three potato varieties developed by the breeding program of the International Potato Center and released in different countries around the world were evaluated for their resistance to late blight in two locations in Peru.

**Usage**

```
data(ComasOxapampa)
```

**Format**

A data frame with 168 observations on the following 4 variables.

`cultivar` a factor with 56 levels

`replication` a factor with 3 levels

`comas` a numeric vector

`oxapampa` a numeric vector

**Details**

The experimental design was a randomized complete block design with 3 replications of 15 apical stem cuttings in Oxapampa and 10 tubers in Mariscal Castilla. Plots were 11.9 x 18.5 m in size with 30 cm in-row and 0.9 m between-row spacings. Spreader rows around plots were used at each site. Mancozeb was applied weekly until 30 days after transplanting or planting, after which the plants were left to natural infection. Due to climatic conditions not conducive to the disease in Oxapampa, inoculum was enhanced with local isolate (POX 067, with virulence R1, 2, 3, 4, 5, 6, 7, 10, 11) at a concentration of 5000-sporangia/ ml at 49 days after planting. Percentage of foliar infection was estimated visually every 3 days for 8 times in Oxapampa and every 7 days for 12 times in Comas, then values were converted to the relative area under the diseases progress curve (rAUPDC). rAUDPC rankings were analyzed for phenotypic stability with nonparametric measures.

**Source**

Experimental field, 2002. Data Kindly provided by Wilmer Perez.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(ComasOxapampa)
# Oxapampa (10 35 31 S latitude, 75 23 0 E longitude, 1813 m.a.s.l )
# Comas, Mariscal Castilla (11 42 54 S latitude, 75 04 45 E longitude, 2800 m.a.s.l,)
# cultivars LBr-40 (resistant), Cruza 148 (moderately resistant) and Pimpernell (susceptible)
str(ComasOxapampa)
means <- tapply.stat(ComasOxapampa[,3:4],ComasOxapampa$cultivar,mean)
correlation(means$comas,means$oxapampa, method="kendall")
```

---

consensus

*consensus of clusters*

---

**Description**

The criterion of the consensus is to produce many trees by means of bootstrap and to such calculate the relative frequency with members of the clusters.

**Usage**

```
consensus(data,distance=c("binary","euclidean","maximum","manhattan",
"canberra","minkowski","gower"),method=c("complete","ward","single","average",
"mcquitty","median","centroid"),nboot=500,duplicate=TRUE,cex.text=1,
col.text="red", ...)
```

**Arguments**

data	data frame
distance	method distance, see dist()
method	method cluster, see hclust()
nboot	The number of bootstrap samples desired.
duplicate	control is TRUE other case is FALSE
cex.text	size text on percentage consensus
col.text	color text on percentage consensus
...	parameters of the plot dendrogram

**Details**

distance: "euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski", "gower".  
Method: "ward", "single", "complete", "average", "mcquitty", "median", "centroid". see functions:  
dist(), hclust() and daisy() of cluster.

**Value**

data	numerical, the rownames is necessary'
nboot	integer
duplicate	logical TRUE or FALSE
cex.text	size text on consensus
col.text	color text on consensus

**Author(s)**

F. de Mendiburu

**References**

An Introduction to the Bootstrap. Bradley Efron and Robert J. Tibshirani. 1993. Chapman and Hall/CRC

**See Also**

[hclust](#), [hgroups](#), [hcut](#)

## Examples

```

library(agricolae)
data(pamCIP)
# only code
rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
# par(cex=0.8)
output<-consensus( pamCIP,distance="binary", method="complete",nboot=5)
# Order consensus
Groups<-output$table.dend[,c(6,5)]
Groups<-Groups[order(Groups[,2],decreasing=TRUE),]
print(Groups)
## Identification of the codes with the numbers.
cbind(output$dendrogram$labels)
## To reproduce dendrogram
dend<-output$dendrogram
data<-output$table.dend
plot(dend)
text(data[,3],data[,4],data[,5])
# Other examples
# classical dendrogram
dend<-as.dendrogram(output$dendrogram)
plot(dend,type="r",edgePar = list(lty=1:2, col=2:1))
text(data[,3],data[,4],data[,5],col="blue",cex=1)
plot(dend,type="t",edgePar = list(lty=1:2, col=2:1))
text(data[,3],data[,4],data[,5],col="blue",cex=1)
## Without the control of duplicates
output<-consensus( pamCIP,duplicate=FALSE,nboot=5)
## using distance gower, require cluster package.
# output<-consensus( pamCIP,distance="gower", method="complete",nboot=5)

```

---

corn

*Data of corn*

---

## Description

Data from a completely randomized design where four different methods of growing corn resulted in various yields per acre on various plots of ground where the four methods were tried. Ordinarily, only one statistical analysis is used, but here we will use the kuskal-wallis test so that a rough comparison may be made with the medians test.

## Usage

```
data(corn)
```

## Format

A data frame with 34 observations on the following 3 variables.

method a numeric vector

observation a numeric vector

rx a numeric vector

### Details

The observations are ranked from the smallest, 77, of rank 1 to the largest 101, of rank N=34. Ties values receive the average rank.

### Source

Book: Practical Nonparametric Statistics.

### References

Practical Nonparametrics Statistics. W.J. Conover. Third Edition, 1999.

### Examples

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

---

correl	<i>Correlation Coefficient</i>
--------	--------------------------------

---

### Description

An exact correlation for ties or without ties. Methods of Kendall, Spearman and Pearson.

### Usage

```
correl(x, y, method = "pearson", alternative="two.sided")
```

### Arguments

x	Vector
y	Vector
method	"pearson", "kendall", "spearman"
alternative	"two.sided", "less", "greater"

### Value

x	Numeric
y	Numeric
...	



**Author(s)**

Felipe de Mendiburu

**References**

Numerical Recipes in C. Second Edition.

**See Also**

[correlation](#)

**Examples**

```
library(agricolae)
data(soil)
attach(soil)
correl(pH,clay,method="kendall")
correl(pH,clay,method="spearman")
correl(pH,clay,method="pearson")
detach(soil)
```

---

correlation

*Correlation analysis. Methods of Pearson, Spearman and Kendall*

---

**Description**

It obtains the coefficients of correlation and p-value between all the variables of a data table. The methods to apply are Pearson, Spearman and Kendall. In case of not specifying the method, the Pearson method will be used. The results are similar to SAS.

**Usage**

```
correlation(x,y=NULL, method = c("pearson", "kendall", "spearman")
,alternative="two.sided")
```

**Arguments**

x	table, matrix or vector
y	table, matrix or vector
method	"pearson", "kendall", "spearman"
alternative	"two.sided", "less", "greater"

**Details**

Parameters equal to function cor()

**Value**

table            Numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

[correl](#)

**Examples**

```
library(agricolae)
# example 1
data(soil)
analysis<-correlation(soil[,2:8],method="pearson")
analysis

# Example 2: correlation between pH, variable 2 and other elements from soil.
data(soil)
attach(soil)
analysis<-correlation(pH,soil[,3:8],method="pearson",alternative="less")
analysis
detach(soil)

# Example 3: correlation between pH and clay method kendall.
data(soil)
attach(soil)
correlation(pH,clay,method="kendall", alternative="two.sided")
detach(soil)
```

---

cotton

*Data of cotton*

---

**Description**

Data of cotton collected in experiments of two localities in Lima and Pisco, Peru.

**Usage**

```
data(cotton)
```

**Format**

A data frame with 96 observations on the following 5 variables.

site a factor with levels Lima Pisco  
block a factor with levels I II III IV V VI  
lineage a numeric vector  
epoca a numeric vector  
yield a numeric vector

**Source**

Book spanish: Metodos estadisticos para la investigacion. Autor: Calzada Benza Universidad Nacional Agraria - La Molina - Peru..

**References**

Book spanish: Metodos estadisticos para la investigacion. Autor: Calzada Benza Universidad Nacional Agraria - La Molina - Peru.

**Examples**

```
library(agricolae)
data(cotton)
str(cotton)
```

---

cv.model

*Coefficient of the experiment variation*

---

**Description**

It obtains the coefficient of variation of the experiment obtained by models lm() or aov()

**Usage**

```
cv.model(x)
```

**Arguments**

x object of model lm() or AOV()

**Details**

```
sqrt(MSError)*100/mean(x)
```

**Value**

x object

**Author(s)**

Felipe de Mendiburu

**See Also**[LSD.test](#), [HSD.test](#), [waller.test](#)**Examples**

```
# see examples from LSD , Waller-Duncan or HSD and complete with it:
library(agricolae)
# not run
# cv<-cv.model(model)
```

---

`cv.similarity`*Coefficient of the similarity matrix variation*

---

**Description**

This process consists of finding the coefficient of the distances of similarity of binary tables (1 and 0) as used for scoring molecular marker data for presence and absence of PCR amplification products.

**Usage**`cv.similarity(A)`**Arguments**

A                    matrix of binary data

**Value**

A                    Data frame or matrix, numerics

**Author(s)**

Felipe de Mendiburu

**See Also**[similarity](#), [resampling.cv](#)

**Examples**

```
# molecular markers.
library(agricolae)
data(markers)
cv<-cv.similarity(markers)
```

---

DAU.test

*Finding the Variance Analysis of the Augmented block Design*


---

**Description**

Analysis of variance Augmented block and comparison mean adjusted.

**Usage**

```
DAU.test(block, trt, y, method = c("lsd", "tukey"), alpha=0.05, group=TRUE, console=FALSE)
```

**Arguments**

block	blocks
trt	Treatment
y	Response
method	Comparison treatments
alpha	Significant test
group	TRUE or FALSE
console	logical, print output

**Details**

Method of comparison treatment. lsd: Least significant difference. tukey: Honestly significant difference.

**Value**

block	Vector
trt	Vector
y	numeric vector
method	Character
alpha	Numeric
group	Logic

**Author(s)**

F. de Mendiburu

**References**

Federer, W. T. (1956). Augmented (or hoonuiaku) designs. *Hawaiian Planters, Record* LV(2):191-208.

**See Also**

[BIB.test](#), [LSD.test](#), [HSD.test](#), [PBIB.test](#)

**Examples**

```
library(agricolae)
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)
model<- DAU.test(block,trt,yield,method="lsd", group=TRUE)
print(model$groups)
```

---

 DC

*Data for the analysis of carolina genetic design*

---

**Description**

Data for the analysis of carolina I, II and III genetic design

**Usage**

```
data(DC)
```

**Details**

DC is list, 3 data.frame: carolina1(72 obs, 6 var), carolina2(300 obs, 9 var) and carolina3(64 obs, 5 var).

Carolina1: Data for the analysis of Carolina I Genetic design. In this design F2 or any advanced generation maintained by random mating, produced from cross between two pure-lines, is taken as base population. From the population an individual is randomly selected and used as a male. A set of 4 randomly selected plans are used as females and are mated to the above male. Thus a set of 4 full-sib families are produced. This is denoted as a male group. Similarly, a large number of male groups are produced. No female is used for any second mating. four male groups (16 female groups) from a set.

Carolina2: Data for the analysis of Carolina II Genetic design. Both paternal and maternal half-sibs are produced in this design. From an F2 population, n1 males and n2 females are randomly selected and each male is crossed to each of the females. Thus n1 x n2 progenies are produced which are analysed in a suitably laid experiment.

Carolina3: Data for the analysis of Carolina III genetic design. The F2 population is produced by crossing two inbreds, say L1 and L2. The material for estimation of genetic parameters is produced by back crossing randomly selected F2 individuals (using as males) to each of the inbreds (used as females).

### Source

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979.

### References

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979.

### Examples

```
data(DC)
names(DC)
str(DC$carolina1)
str(DC$carolina2)
str(DC$carolina3)
```

---

delete.na	<i>Omitting the rows or columns with missing observations of a matrix (NA)</i>
-----------	--

---

### Description

In many situations it is required to omit the rows or columns less or greater with NA of the matrix.

### Usage

```
delete.na(x, alternative=c("less", "greater") )
```

### Arguments

x	matrix with NA
alternative	"less" or "greater"

### Value

x	matrix
---	--------

### Author(s)

Felipe de Mendiburu

**Examples**

```

library(agricolae)
x<-c(2,5,3,7,5,NA,8,0,4,3,NA,NA)
dim(x)<-c(4,3)
x
#      [,1] [,2] [,3]
#[1,]  2   5   4
#[2,]  5  NA   3
#[3,]  3   8  NA
#[4,]  7   0  NA

delete.na(x,"less")
#      [,1]
#[1,]  2
#[2,]  5
#[3,]  3
#[4,]  7

delete.na(x,"greater")
#      [,1] [,2] [,3]
#[1,]  2   5   4

```

---

design.ab

*Design of experiments for a factorial*


---

**Description**

It generates a design of blocks, randomize and latin square for combined n. factors uses the methods of number generation in R. The seed is by set.seed(seed, kinds).

**Usage**

```

design.ab(trt, r, serie = 2, design=c("rcbd","crd","lsd"),
seed = 0, kinds = "Super-Duper",first=TRUE)

```

**Arguments**

trt	n levels factors
r	Replications or Blocks
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
design	type
seed	Seed
kinds	Method for to randomize
first	TRUE or FALSE - randomize rep 1



**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-
TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

```
parameters    list
book          dataframe
```

**Author(s)**

Felipe de Mendiburu

**References**

Introduction to Experimental Statistics. Ching Chun Li. McGraw-Hill Book Company, INC, New York, 1964

**See Also**

[design.split](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
# factorial 3 x 2 with 3 blocks
library(agricolae)
trt<-c(3,2) # factorial 3x2
outdesign <-design.ab(trt, r=3, serie=2)
book<-outdesign$book
head(book,10) # print of the field book
# factorial 2 x 2 x 2 with 5 replications in completely randomized design.
trt<-c(2,2,2)
outdesign<-design.ab(trt, r=5, serie=2,design="crd")
book<-outdesign$book
print(book)
# factorial 3 x 3 in latin square design.
trt <-c(3,3)
outdesign<-design.ab(trt, serie=2, design="lsd")
book<-outdesign$book
print(book)
```

---

design.alpha	<i>Alpha design type (0,1)</i>
--------------	--------------------------------

---

**Description**

Creates alpha designs starting from the alpha design fixing under the 4 series formulated by Patterson and Williams.

**Usage**

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

**Arguments**

trt	Treatments
k	size block
r	Replications
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize

**Details**

Parameters for the alpha design: I.  $r=2$ ,  $k \leq s$ ; II.  $r=3$ ,  $s$  odd,  $k \leq s$ ; III.  $r=3$ ,  $s$  even,  $k \leq s-1$ ; IV.  $r=4$ ,  $s$  odd but not a multiple of 3,  $k \leq s$

$r$ = replications  $s$ =number of blocks  $k$ =size of block Number of treatment is equal to  $k*s$

**Value**

parameters	list
statistics	dataframe
sketch	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

H.D. Patterson and E.R. Williams. Biometrika (1976) A new class of resolvable incomplete block designs. printed in Great Britain. Online: <http://biomet.oxfordjournals.org/cgi/content/abstract/63/1/83>

**See Also**

[design.ab](#), [design.split](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
#Example one
trt<-1:30
t <- length(trt)
# size block k
k<-3
# Blocks s
s<-t/k
# replications r
r <- 2
outdesign<- design.alpha(trt,k,r,serie=2)
book<-outdesign$book
plots<-book[,1]
dim(plots)<-c(k,s,r)
for (i in 1:r) print(t(plots[,i]))
outdesign$sketch
# Example two
trt<-letters[1:12]
t <- length(trt)
k<-3
r<-3
s<-t/k
outdesign<- design.alpha(trt,k,r,serie=2)
book<-outdesign$book
plots<-book[,1]
dim(plots)<-c(k,s,r)
for (i in 1:r) print(t(plots[,i]))
outdesign$sketch
```

---

design.bib

*Randomized Balanced Incomplete Block Designs. BIB*

---

**Description**

Creates Randomized Balanced Incomplete Block Design. "Random" uses the methods of number generation in R. The seed is by `set.seed(seed, kinds)`.

**Usage**

```
design.bib(trt, k, serie = 2, seed = 0, kinds = "Super-Duper")
```

**Arguments**

trt	Treatments
k	size block
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize

**Details**

kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )

**Value**

parameters	list
statistics	dataframe
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Design of Experiments. Robert O. Kuehl. 2nd ed., Duxbury, 2000

**See Also**

[design.ab](#), [design.alpha](#), [design.split](#), [design.crd](#), [design.cyclic](#), [design.dau](#), [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
# 4 treatments and k=3 size block
trt<-c("A","B","C","D")
k<-3
outdesign<-design.bib(trt,k,serie=2,seed =41,kinds ="Super-Duper") # seed = 41
print(outdesign$parameters)
book<-outdesign$book
plots <-as.numeric(book[,1])
field <-as.character(book[,3])
t(matrix(plots,c(3,4)))
t(matrix(field,c(3,4)))
# write in hard disk
# write.csv(book,"book.csv", row.names=FALSE)
# file.show("book.csv")
```

---

`design.crd`*Completely Randomized Design*

---

### Description

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)`.

### Usage

```
design.crd(trt, r, serie = 2, seed = 0, kinds = "Super-Duper")
```

### Arguments

<code>trt</code>	Treatments
<code>r</code>	Replications
<code>serie</code>	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
<code>seed</code>	seed
<code>kinds</code>	method for to randomize

### Details

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

### Value

<code>parameters</code>	list
<code>book</code>	dataframe

### Author(s)

Felipe de Mendiburu

### References

Introduction to Experimental Statistics. Ching Chun Li. McGraw-Hill Book Company, INC, New York, 1964

### See Also

[design.ab](#), [design.alpha](#), [design.bib](#), [design.split](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```

library(agricolae)
trt <-c("CIP-101", "CIP-201", "CIP-301", "CIP-401", "CIP-501")
r <-c(4,3,5,4,3)
# seed = 12543
outdesign1 <-design.crd(trt,r,serie=2,2543,"Mersenne-Twister")
book1<-outdesign1
# no seed
outdesign2 <-design.crd(trt,r,serie=3)
print(outdesign2$parameters)
book2<-outdesign2
# write to hard disk
# write.table(book1,"crd.txt", row.names=FALSE, sep="\t")
# file.show("crd.txt")

```

---

design.cyclic

*Cyclic designs*


---

**Description**

The cyclic design is a incomplete blocks designs, it is generated from a incomplete block initial of the size k, the plan is generated and randomized. The efficient and robust cyclic designs for 6 to 30 treatments, replications  $\leq 10$ .

**Usage**

```
design.cyclic(trt, k, r, serie = 2, rowcol = FALSE, seed = 0, kinds = "Super-Duper")
```

**Arguments**

trt	vector treatments
k	block size
r	Replications
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
rowcol	TRUE: row-column design
seed	init seed random
kinds	random method

**Details**

Number o treatment 6 to 30. (r) Replication 2 to 10. (k) size of block 2 to 10. replication =  $i*k$ , "i" is value integer.

**Value**

parameters	list
sketch	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Kuehl, Robert(2000), Design of Experiments. 2nd ed., Duxbury. John, J.A. (1981) Efficient Cyclic Design. J. R. Statist. Soc. B, 43, No. 1, pp, 76-80.

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.split](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
trt<-letters[1:8]
# block size = 2, replication = 6
outdesign1 <- design.cyclic(trt,k=2, r=6,serie=2)
names(outdesign1)
# groups 1,2,3
outdesign1$sketch[[1]]
outdesign1$sketch[[2]]
outdesign1$sketch[[3]]
outdesign1$book
# row-column design
outdesign2<- design.cyclic(trt,k=2, r=6, serie=2, rowcol=TRUE)
outdesign2$sketch
```

---

design.dau

*Augmented block design*

---

**Description**

In these designs, some treatments (checks) are replicate r times and other treatments (new) are replicated once.

**Usage**

```
design.dau(trt1, trt2, r, serie = 2, seed = 0, kinds = "Super-Duper", name="trt")
```

**Arguments**

trt1	checks
trt2	new
r	Replications or blocks
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize
name	name of treatments

**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

parameters	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

1. Augmented (or Hoonuiaku) Design. Federer, W.T. (1956), Hawaii Plr. rec., 55: 191-208. 2. In Augmented Designs. Federer, W.T and Raghavarao, D. (1975). Biometrics, vol. 31, No. 1 (mar., 1975), pp. 29-35

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.split](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
# 4 treatments and 5 blocks
T1<-c("A","B","C","D")
T2<-letters[20:26]
outdesign <-design.dau(T1,T2, r=5,serie=2)
# field book
book<-outdesign$book
by(book,book[2],function(x) paste(x[,1],"-",as.character(x[,3])))
# write in hard disk
# write.table(book,"dau.txt", row.names=FALSE, sep="\t")
# file.show("dau.txt")
# Augmented designs in Completely Randomized Design
```



```
trt<-c(T1,T2)
r<-c(4,4,4,4,1,1,1,1,1,1)
outdesign <- design.crd(trt,r)
outdesign$book
```

---

design.graeco	<i>Graeco - latin square design</i>
---------------	-------------------------------------

---

### Description

A graeco - latin square is a  $K \times K$  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)

### Usage

```
design.graeco(trt1, trt2, serie = 2, seed = 0, kinds = "Super-Duper")
```

### Arguments

trt1	Treatments
trt2	Treatments
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize

### Details

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

### Value

parameters	list
book	dataframe

### Author(s)

Felipe de Mendiburu

### References

1. Statistics for Experimenters Design, Innovation, and Discovery Second Edition. George E. P. Box. Wiley-Interscience. 2005.
2. Experimental design. Cochran and Cox. Second edition. Wiley Classics Library Edition published 1992.

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#), [design.cyclic](#), [design.dau](#), [design.split](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
T1<-c("a","b","c","d")
T2<-c("v","w","x","y")
outdesign <- design.graeco(T1,T2,serie=1)
graeco<-outdesign$book
plots <-as.numeric(graeco[,1])
trt <- paste(graeco[,4],graeco[,5])
dim(plots)<-c(4,4)
dim(trt) <-c(4,4)
print(t(plots))
print(t(trt))
# 10 x 10
T1 <- letters[1:10]
T2 <- 1:10
outdesign <- design.graeco(T1,T2,serie=2)
graeco<-outdesign$book
trt <- paste(graeco[,4],graeco[,5])
dim(trt) <-c(10,10)
print(t(trt))
```

---

design.lattice

*Lattice designs*

---

**Description**

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

**Usage**

```
design.lattice(trt, r=3, serie = 2, seed = 0, kinds = "Super-Duper")
```

**Arguments**

trt	treatments
r	r=2(simple) or r=3(triple) lattice
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize

**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

parameters	list
statistics	data frame
sketch	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

FIELD PLOT TECHNIQUE. Erwin L. LeCLERG. 2nd ed., 1962, Burgess Publishing Company, Minnesota

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.split](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
# triple lattice
trt<-LETTERS[1:9]
outdesign<-design.lattice(trt,r=3,serie=2) # triple lattice design ( 9 trt)
# simple lattice
trt<-1:100
outdesign<-design.lattice(trt,r=2,serie=3) # simple lattice design, 10x10
```

---

design.lsd

*Latin Square Design*

---

**Description**

It generates Latin Square Design. "Random" uses the methods of number generation in R. The seed is by `set.seed(seed, kinds)`.

**Usage**

```
design.lsd(trt, serie = 2, seed = 0, kinds = "Super-Duper",first=TRUE)
```

**Arguments**

trt	Treatments
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize
first	TRUE or FALSE - randomize rep 1

**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-
TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

parameters	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Introduction to Experimental Statistics. Ching Chun Li. McGraw-Hill Book Company, INC, New York, 1969

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.split](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
varieties<-c("perricholi", "yungay", "maria bonita", "tomasa")
outdesign <- design.lsd(varieties, serie=2, seed=23)
lsd <- outdesign$book
print(lsd) # field book.
plots <- as.numeric(lsd[,1])
trt <- as.character(lsd[,4])
dim(plots)<-c(4,4)
dim(trt) <-c(4,4)
print(t(plots))
print(t(trt))
# Write on hard disk.
# write.table(lsd, "lsd.txt", row.names=FALSE, sep="\t")
# file.show("lsd.txt")
```

---

design.rcbd	<i>Randomized Complete Block Design</i>
-------------	---

---

**Description**

It generates Randomized Complete Block Design. "Random" uses the methods of number generation in R. The seed is by `set.seed(seed, kinds)`.

**Usage**

```
design.rcbd(trt, r, serie = 2, seed = 0, kinds = "Super-Duper", first=TRUE,
continue=FALSE )
```

**Arguments**

trt	Treatments
r	Replications or blocks
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize
first	TRUE or FALSE - randomize rep 1
continue	TRUE or FALSE, continuous numbering of plot

**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-
TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

parameters	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Introduction to Experimental Statistics. Ching Chun Li. McGraw-Hill Book Company, INC, New York, 1964

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.split](#), [design.strip](#)

**Examples**

```

library(agricolae)
# 5 treatments and 6 blocks
trt<-c("A","B","C","D","E")
outdesign <-design.rcbd(trt,6,serie=2,986,"Wichmann-Hill") # seed = 986
book <-outdesign$book # field book
# write in hard disk
# write.table(book,"rcbd.txt", row.names=FALSE, sep="\t")
# file.show("rcbd.txt")
# Plots in field model ZIGZAG
fieldbook <- zigzag(outdesign)
print(t(matrix(fieldbook[,1],5,6)))
print(t(matrix(fieldbook[,3],5,6)))
# continuous numbering of plot
outdesign <-design.rcbd(trt,6,serie=0,continue=TRUE)
head(outdesign$book)

```

---

design.split

*Split Plot Design*


---

**Description**

It generates split plot design. "Random" uses the methods of number generation in R. The seed is by set.seed(seed, kinds).

**Usage**

```

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

```

**Arguments**

trt1	Treatments in Plots
trt2	Treatments in Subplots
r	Replications or blocks
design	Experimental design
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize
first	TRUE or FALSE - randomize rep 1

**Details**

```

kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-
TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )

```

**Value**

parameters	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Statistical Procedures for Agricultural Research. Kwanchai A. Gomez, Arturo A. Gomez. John Wiley & Sons, new York, 1984

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#), [design.cyclic](#), [design.dau](#), [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
# 4 treatments and 5 blocks in split-plot
t1<-c("A","B","C","D")
t2<-c(1,2,3)
outdesign <-design.split(t1,t2,r=3,serie=2,seed=45,kinds ="Super-Duper")#seed=45
book<-outdesign$book# field book
# write in hard disk
# write.table(book,"book.txt", row.names=FALSE, sep="\t")
# file.show("book.txt")
```

---

design.strip

*Strip Plot Design*

---

**Description**

It generates strip plot design. "Random" uses the methods of number generation in R. The seed is by set.seed(seed, kinds).

**Usage**

```
design.strip(trt1, trt2,r, serie = 2, seed = 0, kinds = "Super-Duper")
```

**Arguments**

trt1	Row treatments
trt2	column treatments
r	Replications
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize

**Details**

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

**Value**

parameters	list
book	dataframe

**Author(s)**

Felipe de Mendiburu

**References**

Statistical Procedures for Agricultural Research. Kwanchai A. Gomez, Arturo A. Gomez. John Wiley & Sons, new York, 1984

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.split](#)

**Examples**

```
library(agricolae)
# 4 and 3 treatments and 3 blocks in strip-plot
t1<-c("A","B","C","D")
t2<-c(1,2,3)
r<-3
outdesign <- design.strip(t1,t2,r, serie=2,seed=45,kinds ="Super-Duper") # seed = 45
book <- outdesign$book # field book
# write in hard disk
# write.table(book,"book.txt", row.names=FALSE, sep="\t")
# file.show("book.txt")
```



---

design.youden	<i>Incomplete Latin Square Design</i>
---------------	---------------------------------------

---

### Description

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)`.

### Usage

```
design.youden(trt, r, serie = 2, seed = 0, kinds = "Super-Duper", first=TRUE)
```

### Arguments

trt	Treatments
r	Replications or number of columns
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
seed	seed
kinds	method for to randomize
first	TRUE or FALSE - randomize rep 1

### Details

```
kinds <- c("Wichmann-Hill", "Marsaglia-Multicarry", "Super-Duper", "Mersenne-Twister", "Knuth-TAOCP", "user-supplied", "Knuth-TAOCP-2002", "default" )
```

### Value

parameters	list
book	dataframe

### Author(s)

Felipe de Mendiburu

### References

Design and Analysis of experiment. Hinkelmann, Klaus and Kempthorne, Oscar. Wiley-Interscience. Copyright (2008) by John Wiley and Sons. Inc., Hoboken, new Yersey

### See Also

[design.ab](#), [design.alpha](#), [design.bib](#), [design.crd](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#), [design.lattice](#), [design.split](#), [design.rcbd](#), [design.strip](#), [design.lsd](#)

**Examples**

```

library(agricolae)
varieties<-c("perricholi","yungay","maria bonita","tomasa")
outdesign <-design.youden(varieties,r=3,serie=2,seed=23)
youden <- outdesign$book
print(youden) # field book.
plots <-as.numeric(youden[,1])
trt <-as.character(youden[,4])
dim(plots)<-c(3,4)
dim(trt) <-c(3,4)
print(t(plots))
print(t(trt))
# Write on hard disk.
# write.table(youden,"youden.txt", row.names=FALSE, sep="\t")
# file.show("youden.txt")

```

---

disease

*Data evaluation of the disease overtime*


---

**Description**

Three evaluations over time and the potato yield when applying several treatments.

**Usage**

```
data(disease)
```

**Format**

A data frame with 21 observations on the following 7 variables.

plots a numeric vector

rep a numeric vector

trt a factor with levels T0 T1 T2 T3 T4 T5 T6

E2 a numeric vector

E5 a numeric vector

E7 a numeric vector

yield a numeric vector

**Source**

Experimental data.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(disease)
str(disease)
```

---

duncan.test	<i>Duncan's new multiple range test</i>
-------------	---

---

**Description**

This test is adapted from the Newman-Keuls method. Duncan's test does not control family wise error rate at the specified alpha level. It has more power than the other post tests, but only because it doesn't control the error rate properly. The Experimentwise Error Rate at:  $1-(1-\alpha)^{(a-1)}$ ; where "a" is the number of means and is the Per-Comparison Error Rate. Duncan's procedure is only very slightly more conservative than LSD. The level by alpha default is 0.05.

**Usage**

```
duncan.test(y, trt, DFerror, MSerror, alpha = 0.05, group=TRUE, main = NULL, console=FALSE)
```

**Arguments**

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each experimental unit
DFerror	Degree free
MSerror	Mean Square Error
alpha	Significant level
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

It is necessary first makes a analysis of variance.

**Value**

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
alpha	Numeric
group	Logic
main	Text

**Author(s)**

Felipe de Mendiburu

**References**

Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997

**See Also**

[LSD.test](#), [waller.test](#) , [HSD.test](#) , [SNK.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison <- duncan.test(model,"virus",
main="Yield of sweetpotato. Dealt with different virus")
duncan.test(model,"virus",alpha=0.01,console=TRUE)
# version old duncan.test()
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
comparison <- duncan.test(yield,virus,df,MSerror, group=TRUE)
print(comparison$groups)
detach(sweetpotato)
```

---

durbin.test

---

*Durbin test and multiple comparison of treatments*


---

**Description**

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.

**Usage**

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

**Arguments**

judge	Identification of the judge in the evaluation
trt	Treatments
evaluation	variable

alpha	level of significant
group	TRUE or FALSE
main	Title
console	logical, print output

**Value**

juege	Vector, numeric
trt	Vector, numeric
evaluation	Vector, numeric
alpha	Vector, numeric, default is 0.05
group	Logic
main	text

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999 Nonparametric Statistical Methods. Myles Hollander and Douglas A. Wolfe, 1999

**See Also**

[kruskal](#), [friedman](#), [BIB.test](#)

**Examples**

```
library(agricolae)
# Example 1. Conover, pag 391
person<-gl(7,3)
variety<-c(1,2,4,2,3,5,3,4,6,4,5,7,1,5,6,2,6,7,1,3,7)
preference<-c(2,3,1,3,1,2,2,1,3,1,2,3,3,1,2,3,1,2,3,1,2)
out<-durbin.test(person,variety,preference,group=TRUE,console=TRUE,
main="Seven varieties of ice cream manufacturer")
#startgraph
bar.group(out$groups,horiz=TRUE,xlim=c(0,10),density=4,las=1)
#endgraph
# Example 2. Myles Hollander, pag 311
# Source: W. Moore and C.I. Bliss. 1942
day<-gl(7,3)
chemical<-c("A","B","D","A","C","E","C","D","G","A","F","G","B","C","F",
"B","E","G","D","E","F")
toxic<-c(0.465,0.343,0.396,0.602,0.873,0.634,0.875,0.325,0.330,0.423,0.987,
0.426,0.652,1.142,0.989,0.536,0.409,0.309,0.609,0.417,0.931)
out<-durbin.test(day,chemical,toxic,group=TRUE,console=TRUE,
main="Logarithm of Toxic Dosages")
```

---

`friedman`*Friedman test and multiple comparison of treatments*

---

**Description**

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.

**Usage**

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

**Arguments**

<code>judge</code>	Identification of the judge in the evaluation
<code>trt</code>	Treatment
<code>evaluation</code>	Variable
<code>alpha</code>	Significant test
<code>group</code>	TRUE or FALSE
<code>main</code>	Title
<code>console</code>	logical, print output

**Value**

<code>judge</code>	Vector
<code>trt</code>	Vector
<code>evaluation</code>	Vector
<code>alpha</code>	Numeric
<code>group</code>	Logic
<code>main</code>	Text

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

[kruskal](#), [durbin.test](#)

**Examples**

```
library(agricolae)
data(grass)
attach(grass)
out<-friedman(judge,trt, evaluation,alpha=0.05, group=TRUE,console=TRUE,
main="Data of the book of Conover")
detach(grass)
#startgraph
bar.group(out$groups,density=3,border="red",col="blue",ylim=c(0,45))
#endgraph
```

---

frijol

*Data of frijol*

---

**Description**

Data of frijol under 4 technologies for the homogeneity of regression study. Yield of Frijol in kg/ha in clean and dry grain.

Tecnologies: 20-40-20 kg/ha. N. P2O5 and K2O + 2 t/ha of gallinaza. 40-80-40 kg/ha. N. P2O5 and K2O + 2 t/ha of gallinaza. 60-120-60 kg/ha. N. P2O5 and K2O + 2 t/ha of gallinaza. 40-80-40 kg/ha. N. P2O5 and K2O + 4 t/ha of gallinaza.

**Usage**

```
data(frijol)
```

**Format**

A data frame with 84 observations on the following 3 variables.

technology a factor with levels a b c d

production a numeric vector

index a numeric vector

**References**

Oriente antioqueno (1972) (ICA.- Orlando Martinez W.) Colombia.

**Examples**

```
library(agricolae)
data(frijol)
str(frijol)
```

---

genxenv

*Data of potato yield in a different environment*

---

**Description**

50 genotypes and 5 environments.

**Usage**

```
data(genxenv)
```

**Format**

A data frame with 250 observations on the following 3 variables.

ENV a numeric vector

GEN a numeric vector

YLD a numeric vector

**Source**

International Potato Center. CIP - Lima Peru.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(genxenv)
str(genxenv)
```

---

Glycoalkaloids

*Data Glycoalkaloids*

---

**Description**

A measurement of the Glycoalkaloids by two methods: HPLC and spectrophotometer.

**Usage**

```
data(Glycoalkaloids)
```



**Format**

A data frame with 25 observations on the following 2 variables.

HPLC a numeric vector

spectrophotometer a numeric vector

**Source**

International Potato Center. CIP - Lima Peru.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(Glycoalkaloids)
str(Glycoalkaloids)
```

---

graph.freq

*Histogram*


---

**Description**

In many situations it has intervals of class defined with its respective frequencies. By means of this function, the graphic of frequency is obtained and it is possible to superpose the normal distribution, polygon of frequency, Ojiva and to construct the table of complete frequency.

**Usage**

```
graph.freq(x, breaks=NULL, counts=NULL, frequency=1, plot=TRUE, nclass=NULL,
xlab="", ylab="", axes = "", las=1, ...)
```

**Arguments**

x	a vector of values, a object hist(), graph.freq()
counts	frequency and x is class intervals
breaks	a vector giving the breakpoints between histogram cells
frequency	1=counts, 2=relative, 3=density
plot	logic
nclass	number of classes
xlab	x labels
ylab	y labels
las	numeric in 0,1,2,3; the style of axis labels. see plot()
axes	TRUE or FALSE
...	other parameters of plot

**Value**

breaks	a vector giving the breakpoints between histogram cells
counts	frequency and x is class intervals
mids	center point in class
relative	frequency
density	Numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(genxenv)
yield <- subset(genxenv$YLD, genxenv$ENV==2)
yield <- round(yield,1)
h<- graph.freq(yield,axes=FALSE, frequency=1, ylab="frequency",col="yellow")
axis(1,h$breaks)
axis(2,seq(0,20,0.1))
# To reproduce histogram.
h1 <- graph.freq(h, col="blue", frequency=2,border="red", density=8,axes=FALSE,
xlab="YIELD",ylab="relative")
axis(1,h$breaks)
axis(2,seq(0,.4,0.1))
# summary, only frequency
limits <-seq(10,40,5)
frequencies <-c(2,6,8,7,3,4)
#startgraph
h<-graph.freq(limits,counts=frequencies,col="bisque",xlab="Classes")
polygon.freq(h,col="red")
title( main="Histogram and polygon of frequency",
ylab="frequency")
#endgraph
# Statistics
measures<-stat.freq(h)
print(measures)
# frequency table full
round(table.freq(h),2)
#startgraph
# ogive
ogive.freq(h,col="red",type="b",ylab="Accumulated relative frequency",
xlab="Variable")
# only .frequency polygon
```

```

h<-graph.freq(limits,counts=frequencies,border=FALSE,col=NULL,xlab=" ",ylab="")
title( main="Polygon of frequency",
xlab="Variable", ylab="Frecuency")
polygon.freq(h,col="blue")
grid(col="brown")
#endgraph
# Draw curve for Histogram
h<- graph.freq(yield,axes=FALSE, frequency=3, ylab="f(yield)",col="yellow")
axis(1,h$breaks)
axis(2,seq(0,0.18,0.03),las=2)
lines(density(yield), col = "red", lwd = 2)
title("Draw curve for Histogram")

```

---

grass

*Data for Friedman test*


---

### Description

Twelve homeowners are selected randomly to participate in an experiment with a plant nursery. Each homeowner is asked to select four fairly identical areas in his yard and to plant four different types of grasses, one in each area.

### Usage

```
data(grass)
```

### Format

A data frame with 48 observations on the following 3 variables.

judge a numeric vector

trt a factor with levels t1 t2 t3 t4

evaluation a numeric vector

### Details

Each of the 12 blocks consists of four fairly identical plots of land, each receiving care of approximately the same degree of skill because the four plots are presumably cared for by the same homeowner.

### Source

Book: Practical Nonparametrics Statistics, pag 372.

### References

Practical Nonparametrics Statistics. W.J. Conover, 1999

**Examples**

```
data(grass)
str(grass)
```

---

greenhouse

*Data in greenhouse*

---

**Description**

Potato minituber production in greenhouse, three sets of data in potato varieties with different methods: hydroponics, Aeroponic, Pots and Plant beds, the unit is in grams and the number of tubers in units,

**Usage**

```
data(greenhouse)
```

**Details**

greenhouse is list, three tables: greenhouse1(480 obs, 5 var), yield for plant, unit is grams. greenhouse2(48 obs, 5 var), Yields of 10 plants by experimental unit(grams). planting date(April 24, 2004) and harvest date(July 16, 2004) and greenhouse3(480 obs, 5 var), Tubers by plants.

**Source**

International Potato Center(CIP). Lima-Peru. Data Kindly provided by Carlos Chuquillanqui.

**References**

- Produccion de semila de papa por hidroponia tecnica de flujo continuo de una pelicula de solucion nutritiva (nft) Carlos Chuquillanqui(CIP), Jorge Tenorio(CIP) and L. F. Salazar(Agdia Inc). AGROENFOQUE Lima-Peru (2004) - Potato Minituber Production Using Aeroponics: Effect of Plant Density and Harvesting Intervals American Journal of Potato Research, Jan/Feb 2006 by Faran, Imma, Mingo-Castel, Angel M

**Examples**

```
library(agricolae)
data(greenhouse)
greenhouse1 <- greenhouse$greenhouse1
greenhouse2 <- greenhouse$greenhouse2
greenhouse3 <- greenhouse$greenhouse3
```

---

growth

*Data growth of trees*

---

**Description**

Data growth of pijuayo trees in several localities.

**Usage**

```
data(growth)
```

**Format**

A data frame with 30 observations on the following 3 variables.

place a factor with levels L1 L2

slime a numeric vector

height a numeric vector

**Source**

Experimental data (Pucallpa - Peru)

**References**

ICRAF lima Peru.

**Examples**

```
library(agricolae)
data(growth)
str(growth)
```

---

haynes

*Data of AUDPC for nonparametrical stability analysis*

---

**Description**

Published data. Haynes. Mean area under the disease progress curve (AUDPC) for each of 16 potato clones evaluated at eight sites across the United States in 1996

**Usage**

```
data(haynes)
```

**Format**

A data frame with 16 observations on the following 9 variables.

clone a factor with levels A84118-3 A080432-1 A084275-3 AWN86514-2 B0692-4 B0718-3 B0749-2F  
B0767-2 Bertita Bzura C0083008-1 Elba Greta Krantz Libertas Stobrawa

FL a numeric vector

MI a numeric vector

ME a numeric vector

MN a numeric vector

ND a numeric vector

NY a numeric vector

PA a numeric vector

WI a numeric vector

**References**

Haynes K G, Lambert D H, Christ B J, Weingartner D P, Douches D S, Backlund J E, Fry W and Stevenson W. 1998. Phenotypic stability of resistance to late blight in potato clones evaluated at eight sites in the United States American Journal Potato Research 75, pag 211-217.

**Examples**

```
library(agricolae)
data(haynes)
str(haynes)
```

---

Hco2006

*Data amendment Huanuco 2006*

---

**Description**

Incidents and performance of healthy tubers and rotten potato field infested with naturally *Ralstonia solanacearum* Race 3/Bv 2A, after application of inorganic amendments and a rotation crop in Huanuco Peru, 2006.

**Usage**

```
data(Hco2006)
```

**Format**

The format is: List of 2

amendment a factor

crop a factor

block a numeric vector, replications

plant a numeric vector, number plant

wilt\_percent a numeric vector, wilt percentage at 60 days

health a numeric vector, kg/8m2, 20 plants

rot a numeric vector, kg/8m2, 20 plants

**Details**

Application of inorganic amendment and crop rotation to control bacterial wilt of the potato (MBP).

**Source**

Experimental field, 2006. Data Kindly provided by Pedro Aley.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(Hco2006)
str(Hco2006)
wilt<-Hco2006$wilt
yield<-Hco2006$yield
means <- tapply.stat(wilt[,5],wilt[,1:3],function(x) mean(x,na.rm=TRUE))
names(means)[4]<-"wilt_percent"
model <- aov(wilt_percent ~ block + crop, means)
anova(model)
cv.model(model)
yield<-yield[order(paste(yield[,1],yield[,2],yield[,3])),]
correlation(means[,4],yield[,4],method="spearman")
```

---

hcut

*Cut tree of consensus*

---

**Description**

It shows dendrogram of a consensus of a tree generated by hclust.

**Usage**

```
hcut(consensus,h,group,col.text="blue",cex.text=1,...)
```

**Arguments**

consensus	object consensus
h	numeric scalar or vector with heights where the tree should be cut.
group	an integer scalar with the desired number of group
col.text	color of number consensus
cex.text	size of number consensus
...	Other parameters of the function plot() in cut()

**Value**

hcut returns a data.frame with group memberships and consensus tree.

**Author(s)**

F. de Mendiburu

**See Also**

[hclust](#), [consensus](#), [hgroups](#)

**Examples**

```
library(agricolae)
data(pamCIP)
# only code
rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
# groups of clusters
# output<-consensus(pamCIP,nboot=100)
# hcut(output,h=0.4,group=5,main="Group 5")
#
# hcut(output,h=0.4,group=8,type="t",edgePar=list(lty=1:2,col=2:1),main="group 8"
# ,col.text="blue",cex.text=1)
```

---

heterosis

*Data of potato, Heterosis*

---

**Description**

Determination of heterosis, general combining ability (GCA) and specific combining ability in tuber dry matter, reducing sugars and agronomic characteristics in TPS families.



**Usage**

```
data(heterosis)
```

**Format**

A data frame with 216 observations on the following 11 variables.

Place 1: La Molina, 2=Huancayo

Replication a numeric vector

Treatment a numeric vector

Factor a factor with levels Control progenie progenitor testigo

Female a factor with levels Achirana LT-8 MF-I MF-II Serrana TPS-2 TPS-25 TPS-7

Male a factor with levels TPS-13 TPS-67 TS-15

v1 Yield (Kg/plant)

v2 Reducing sugars (scale):1 low and 5=High

v3 Tuber dry matter (percentage)

v4 Tuber number/plant

v5 Average tuber weight (g)

**Details**

The study was conducted in 3 environments, La Molina-PERU to 240 masl. during autumn-winter and spring, and in Huancayo-PERU 3180 masl., during summer. The experimental material consisted of 24 families half brother in the form of tubers derived from TPS, obtained crossing between 8 female and 3 male parents. Design used was randomized complete block with three repetitions. The experimental unit was 30 plants in two rows at a distance of 30cm between plants and 90 cm between rows. Variables evaluated were Yield, Tubers number, Dry matter and content and reducing sugars. The analysis was conducted line x tester. The control variety was Desiree.

**Source**

International Potato Center(CIP). Lima-Peru. Data Kindly provided by of Rolando Cabello.

**References**

Tesis "Heterosis, habilidad combinatoria general y especifica para materia seca, azucares reductores y caracteres agronomicos en familias de tuberculos provenientes de semilla sexual de papa. Magister Scientiae Rodolfo Valdivia Lorente. Universidad Nacional Agraria La molina-Lima Peru, Escuela de Post Grado, Mejoramiento genetico de plantas, 2004". Poster: Congreso de la Sociedad Peruana de Genetica - Peru, 2008.

**Examples**

```
library(agricolae)
data(heterosis)
str(heterosis)
site1<-subset(heterosis,heterosis[,1]==1)
site2<-subset(heterosis,heterosis[,1]==2)
site3<-subset(heterosis,heterosis[,1]==3)
attach(site1)
model1<-lineXtester(Replication, Female, Male, v1)
DFe <- df.residual(model1)
CMe <- deviance(model1)/DFe
test1 <- HSD.test(v1, Factor,DFe,CMe)
test2 <- HSD.test(v1, Treatment,DFe,CMe)
detach(site1)
attach(site2)
model2<-lineXtester(Replication, Female, Male, v3)
detach(site2)
attach(site3)
model3<-lineXtester(Replication, Female, Male, v4)
detach(site3)
```

---

hgroups

*groups of hclust*

---

**Description**

Returns a vector with group memberships. This function is used by the function `consensus` of `clusters`.

**Usage**

```
hgroups(hmerge)
```

**Arguments**

`hmerge`            The object is components of the `hclust`

**Value**

`data`            object merge of `hcluster`'

**Author(s)**

F. de Mendiburu

**See Also**

[hclust](#), [hcut](#), [consensus](#)

**Examples**

```
library(agricolae)
data(pamCIP)
# only code
rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
distance <- dist(pamCIP,method="binary")
clusters<- hclust( distance, method="complete")
# groups of clusters
hgroups(clusters$merge)
```

---

HSD.test

*Multiple comparisons: Tukey*


---

**Description**

It makes multiple comparisons of treatments by means of Tukey. The level by alpha default is 0.05.

**Usage**

```
HSD.test(y, trt, DFerror, MSerror, alpha = 0.05, group=TRUE, main = NULL,console=FALSE)
```

**Arguments**

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each experimental unit
DFerror	Degree free
MSerror	Mean Square Error
alpha	Significant level
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

It is necessary first makes a analysis of variance.

**Value**

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
alpha	Numeric
group	Logic
main	Text

**Author(s)**

Felipe de Mendiburu

**References**

Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997

**See Also**

[LSD.test](#), [waller.test](#) , [SNK.test](#) , [duncan.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- HSD.test(model,"virus", group=TRUE,console=TRUE,
main="Yield of sweetpotato\nDealt with different virus")
#stargraph
bar.group(out$groups,ylim=c(0,45),density=4,border="blue")
#endgraph
out<-HSD.test(model,"virus", group=FALSE)
means<-out$means

# Old version HSD.test()
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
HSD.test(yield,virus,df,MSerror, group=TRUE,console=TRUE,
main="Yield of sweetpotato. Dealt with different virus")
detach(sweetpotato)
```

---

huasahuasi

*Data: Rainfall thresholds as support for timing fungicide applications  
in the control of potato late blight in Peru*

---

**Description**

Timing fungicide sprays based on accumulated rainfall thresholds can be a successful component of integrated management packages that include cultivars with moderate or high levels of resistance to late blight. The simplicity of measuring accumulated rainfall means that the technology can potentially be used by resource-poor farmers in developing countries.

**Usage**

```
data(huasahuasi)
```

**Format**

The format is: List of 2 ( AUDPC, YIELD )

block a factor with levels I II III

trt a factor with levels 40mm 7-days Non-application

clon a factor with levels C386209.10 C387164.4 Cruza148 Musuq Yungay

y1da a numeric vector, Kgr./plot

y2da a numeric vector, Kgr./plot

y3ra a numeric vector, Kgr./plot

d44 a numeric vector, 44 days

d51 a numeric vector, 51 days

d100 a numeric vector, 100 days

**Details**

The experimental unit was formed by 4 furrows of 1.8 m of length, with distance between furrows from 0.90 m and between plants of 0.30 m. In each furrow was installed 5 plants. The experiment had 3 repetitions. From the beginning of the experiment were fulfilled the following treatments  
Thresholds 40 mm: Apply the fungicide when 40 precipitation mm accumulates. The minimum interval between applications will be of 7 days. Schedule 7 days: The applications should be carried out every 7 days calendar. Without application: No fungicide application will be made. The evaluation of the severity of the late blight in each treatment started to emergency 80 percentage and then evaluations were made every 7 days until being observed a physiological maturation of the crop.

**Source**

Experimental field, 2003. Data Kindly provided by Wilmer Perez.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(huasahuasi)
names(huasahuasi)
str(huasahuasi$AUDPC)
str(huasahuasi$YIELD)
```

index.AMMI

*AMMI index and yield stability***Description**

calculate AMMI stability value (ASV) and Yield stability index (YSI).

**Usage**

```
index.AMMI(model)
```

**Arguments**

model            object AMMI

**Details**

AMMI stability value (ASV) was calculated using the following formula, as suggested by Purchase (1997)

$$ASV = \sqrt{SSpc1/SSpc2 * (PC1i)^2 + (PC2i)^2}$$

$$YSI = RASV + RY$$

RASV = rank(ASV) and RY = rank(Y across by environment)

**Value**

ASV	AMMI stability value
YSI	Yield stability index
rASV	Rank of AMMI stability value
rYSI	Rank of yield stability index
means	average genotype by environment

**Author(s)**

F. de Mendiburu

**References**

The use of an AMMI model and its parameters to analyse yield stability in multienvironment trials. N. SABAGHNIA, S.H. SABAGHPOUR AND H. DEGHANI. Journal of Agricultural Science (2008), 146, 571-581. f 2008 Cambridge University Press 571 doi:10.1017/S0021859608007831 Printed in the United Kingdom

Parametric analysis to describe genotyperenvironment interaction and yield stability in winter wheat. PURCHASE, J. L. (1997). Ph.D. Thesis, Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa.

**See Also**

[AMMI,plot.AMMI](#)

**Examples**

```
library(agricolae)
# Index AMMI
data(plrv)
attach(plrv)
model<- AMMI(Locality, Genotype, Rep, Yield, console=FALSE)
detach(plrv)
Idx<-index.AMMI(model)
names(Idx)
# Crops with improved stability according AMMI.
print(Idx[order(Idx[,3]),])
# Crops with better response and improved stability according AMMI.
print(Idx[order(Idx[,4]),])
```

---

index.bio

*Biodiversity Index*

---

**Description**

Scientists use a formula called the biodiversity index to describe the amount of species diversity in a given area.

**Usage**

```
index.bio(data, method = c("Margalef", "Simpson.Dom", "Simpson.Div",
"Berger.Parker", "McIntosh", "Shannon"), level=95, nboot=100, console=TRUE)
```

**Arguments**

data	number of specimens
method	Describe method bio-diversity
level	Significant level
nboot	size bootstrap
console	output console TRUE

**Details**

method bio-diversity. "Margalef" "Simpson.Dom" "Simpson.Div" "Berger.Parker" "McIntosh" "Shannon"

**Value**

data	vector
method	method bio-diversity
level	value 0-100 percentage
nboot	size 100, 500,...

**Author(s)**

Felipe de Mendiburu

**References**

Magurran, A.E. (1988) Ecological diversity and its measurement. Princeton University Press  
 Efron, B., Tibshirani, R. (1993) An Introduction to the Bootstrap. Chapman and Hall/CRC

**Examples**

```
library(agricolae)
data(paracsho)
# date 22-06-05 and treatment CON = application with insecticide
specimens <- paracsho[1:10,6]
output1 <- index.bio(specimens,method="Simpson.Div",level=95,nboot=100)
output2 <- index.bio(specimens,method="Shannon",level=95,nboot=100)
rbind(output1, output2)
```

---

index.smith

*Uniformity soil. Smith's Index of Soil Heterogeneity*

---

**Description**

Smith's index of soil heterogeneity is used primarily to derive optimum plot size. The index gives a single value as a quantitative measure of soil heterogeneity in an area. Graph CV for plot size and shape.

**Usage**

```
index.smith(data, ...)
```

**Arguments**

data	dataframe or matrix
...	Parameters of the plot()

**Details**

$$V_x = V(x)/x \cdot b$$

$V(x)$  is the between-plot variance,  $V_x$  is the variance per unit area for plot size of  $x$  basic unit, and  $b$  is the Smith' index of soil heterogeneity.





**Value**

classes            matrix numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [graph.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
# example 1
data(growth)
h<-hist(growth$height,plot=FALSE)
intervals.freq(h)
# example 2
x<-seq(10,40,5)
y<-c(2,6,8,7,3,4)
intervals.freq(x)
histogram <- graph.freq(x,counts=y)
```

---

join.freq

*Join class for histogram*

---

**Description**

In many situations it is required to join classes because of the low .frequency in the intervals. In this process, it is required to join the intervals and add the .frequencies of them.

**Usage**

```
join.freq(histogram, join)
```

**Arguments**

histogram        Class graph.freq  
 join             vector

**Value**

histogram        Class graph.freq

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [graph.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(natives)
# histogram
h1<-graph.freq(natives$size,plot=FALSE)
round(table.freq(h1),4)
# Join classes 9, 10,11 and 12 with little frequency.
h2<-join.freq(h1,9:12)
# new table
plot(h2,col="bisque",xlab="Size")
round(summary(h2),4)
```

---

kendall

*Correlation of Kendall*

---

**Description**

Correlation of Kendall two set. Compute exact p-value with ties.

**Usage**

```
kendall(data1, data2)
```

**Arguments**

data1	vector
data2	vector

**Value**

data1	Numeric
data2	Numeric

**Author(s)**

Felipe de Mendiburu

**References**

Numerical Recipes in C. Second Edition. Pag 634

**See Also**[correlation](#)**Examples**

```
library(agricolae)
x <-c(1,1,1,4,2,2,3,1,3,2,1,1,2,3,2,1,1,2,1,2)
y <-c(1,1,2,3,4,4,2,1,2,3,1,1,3,4,2,1,1,3,1,2)
kendall(x,y)
```

kruskal

*Kruskal Wallis test and multiple comparison of treatments.***Description**

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

**Usage**

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

**Arguments**

y	response
trt	treatment
alpha	level signification
p.adj	Method for adjusting p values (see p.adjust)
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

For equal or different repetition. p.adj = "holm", "hochberg", "bonferroni", "BH", "BY", "fdr". see p.adjust() p.adj = "none" is t-student. p.adj = "hommel" is not applied in this test.

**Value**

y	vector numeric
trt	vector alphanumeric
alpha	level significant
p.adj	text, see p.adjust
group	Logic
main	Title

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

[friedman, durbin.test](#)

**Examples**

```
library(agricolae)
data(corn)
attach(corn)
str(corn)
comparison<-kruskal(observation,method,group=TRUE, main="corn")
comparison<-kruskal(observation,method,p.adj="bon",group=FALSE, main="corn")
detach(corn)
```

---

kurtosis

*Finding the Kurtosis coefficient*

---

**Description**

It obtains the value of the kurtosis for a normally distributed variable. The result is similar to SAS.

**Usage**

```
kurtosis(x)
```

**Arguments**

x                    a numeric vector

**Value**

x                    The kurtosis of x

**See Also**

[skewness](#)

**Examples**

```
library(agricolae)
x<-c(3,4,5,2,3,4,5,6,4,NA,7)
kurtosis(x)
# value is -0.1517996
```

---

lastC	<i>Setting the last character of a chain</i>
-------	--

---

**Description**

A special function for the group of treatments in the multiple comparison tests. Use `order.group`.

**Usage**

```
lastC(x)
```

**Arguments**

x	letters
---	---------

**Value**

x	character
---	-----------

**Author(s)**

Felipe de Mendiburu

**See Also**

[order.group](#)

**Examples**

```
library(agricolae)
x<-c("a", "ab", "b", "c", "cd")
lastC(x)
# "a" "b" "b" "c" "d"
```

---

lateblight	<i>LATEBLIGHT - Simulator for potato late blight Version LB2004</i>
------------	---

---

**Description**

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.

**Usage**

```
lateblight(WS, Cultivar, ApplSys, InocDate, LGR, IniSpor, SR, IE, LP, InMicCol,
MatTime=c('EARLYSEASON', 'MIDSEASON', 'LATESEASON'), ...)
```

**Arguments**

WS	object weather-severity
Cultivar	chr
ApplSys	chr
InocDate	days
LGR	num, see example
IniSpor	num
SR	num, see example
IE	num, Initialization infection
LP	num, latent period
InMicCol	num
MatTime	chr
...	plot graphics parameters

**Details**

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).

**Value**

Ofile	"Date", "nday", "MicCol", "SimSeverity", ...
Gfile	"dates", "nday", "MeanSeverity", "StDevSeverity"

**Note**

All format data for date is yyyy-mm,dd, for example "2000-04-22". change with function as.Date()

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## References

Andrade-Piedra, J. L., Hijmans, R. J., Forbes, G. A., Fry, W. E., and Nelson, R. J. 2005a. Simulation of potato late blight in the Andes. I: Modification and parameterization of the LATEBLIGHT model. *Phytopathology* 95:1191-1199. Andrade-Piedra, J. L., Hijmans, R. J., Juarez, H. S., Forbes, G. A., Shtienberg, D., and Fry, W. E. 2005b. Simulation of potato late blight in the Andes. II: Validation of the LATEBLIGHT model. *Phytopathology* 95:1200-1208. Andrade-Piedra, J. L., Forbes, G. A., Shtienberg, D., Grunwald, N. J., Chacon, M. G., Taibe, M. V., Hijmans, R. J., and Fry, W. E. 2005c. Qualification of a plant disease simulation model: Performance of the LATEBLIGHT model across a broad range of environments. *Phytopathology* 95:1412-1422. Bruhn, J.A., Bruck, R.I., Fry, W.E., Arneson, P.A., and Keokosky, E.V. 1980. User's manual for LATEBLIGHT: a plant disease management game. Cornell University, Department of Plant Pathology, Ithaca, NY, USA. Mimeo 80-1. Bruhn, J.A., and Fry, W.E. 1981. Analysis of potato late blight epidemiology by simulation modeling. *Phytopathology* 71:612-616. Doster, M. A., Milgroom, M. G., and Fry, W. E. 1990. Quantification of factors influencing potato late blight suppression and selection for metalaxyl resistance in *Phytophthora infestans* - A simulation approach. *Phytopathology* 80:1190-1198. Fry, W.E., Milgroom, M.G., Doster, M.A., Bruhn, J.A., and Bruck, R.I. 1991. LATEBLIGHT: a plant disease management game - User Manual. Version 3.1. Microsoft Windows Adaptation by B. E. Ticknor, and P. A. Arneson. Ithaca, Cornell University, Department of Plant Pathology, Ithaca, NY, USA.

## See Also

[weatherSeverity](#)

## Examples

```
library(agricolae)
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 Lateblight
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"
#-----
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)")
# reproduce graph
x<- model$file$nday
y<- model$file$SimSeverity
w<- model$file$nday
z<- model$file$MeanSeverity
Min<-model$file$MinObs
Max<-model$file$MaxObs
plot(x,y,type="l",xlim=c(65,95),lwd=1.5,xlab="Time (days after emergence)",
ylab="Severity (Percentage)")
points(w,z,col="blue",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="blue")
}
legend("topleft",c("Disease progress curves","Weather-Severity"),
title="Description",lty=1,pch=c(3,19),col=c("black","blue"))

```

---

lineXtester

*Line x Tester Analysis*


---

### Description

It makes the Line x Tester Genetic Analysis. It also estimates the general and specific combinatory ability effects and the line and tester genetic contribution.

### Usage

```
lineXtester(replications, lines, testers, y)
```

### Arguments

replications	Replications
lines	Lines
testers	Testers
y	Variable, response

**Details**

output: Standard Errors for combining ability effects. Componentes geneticos. Variancias. Contribucion proporcional. ANOVA with parents and crosses. ANOVA for line X tester analysis. ANOVA for line X tester analysis including parents. GCA Effects. Lines Effects. Testers Effects. Standard Errors for Combining Ability Effects. Genetic Components. Proportional contribution of lines, testers and their interactions. to total variance.

**Value**

replications	vector, numeric
lines	vector, numeric
testers	vector, numeric
y	vector, numeric

**Author(s)**

Felipe de Mendiburu

**References**

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979. Hierarchical and factorial mating designs for quantitative genetic analysis in tetrasomic potato. R. Ortiz; A.Golmirzaie. Theor Appl Genet (2002) 104:675-679

**See Also**

[AMMI](#)

**Examples**

```
# see structure line by testers
library(agricolae)
# example 1
data(heterosis)
site1<-subset(heterosis,heterosis[,1]==1)
attach(site1)
output1<-lineXtester(Replication, Female, Male, v2)
detach(site1)
# example 2
data(LxT)
str(LxT)
attach(LxT)
output2<-lineXtester(replication, line, tester, yield)
detach(LxT)
```

---

LSD.test	<i>Multiple comparisons, "Least significant difference" and Adjust P-values</i>
----------	---

---

### Description

Multiple comparisons of treatments by means of LSD and a grouping of treatments. The level by alpha default is 0.05. Returns p-values adjusted using one of several methods

### Usage

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

### Arguments

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each experimental unit
DFerror	Degrees of freedom of the experimental error
MSerror	Means square error of the experimental
alpha	Level of risk for the test
p.adj	Method for adjusting p values (see p.adjust)
group	TRUE or FALSE
main	title of the study
console	logical, print output

### Details

For equal or different repetition. p.adj = "holm", "hochberg", "bonferroni", "BH", "BY", "fdr". see p.adjust() p.adj = "none" is t-student. p.adj = "hommel" is not applied in this test.

### Value

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
alpha	Numeric
p.adj	text, see p.adjust
group	Logic
main	Numeric

**Author(s)**

Felipe de Mendiburu

**References**

Steel, R.; Torri, J.; Dickey, D. (1997) Principles and Procedures of Statistics A Biometrical Approach. pp178.

**See Also**

[HSD.test](#), [waller.test](#), [SNK.test](#), [bar.err](#), [bar.group](#), [duncan.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- LSD.test(model,"virus", p.adj="bonferroni")
#stargraph
bar.group(out$groups,ylim=c(0,45),density=4,border="blue")
#endgraph
# Old version LSD.test()
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
out <- LSD.test(yield,virus,df,MSerror, p.adj="bonferroni", group=FALSE)
detach(sweetpotato)
#stargraph
# Variation range: Max - Min
bar.err(out$means,variation="range",ylim=c(0,44),bar=FALSE,col=0)

#endgraph
LSD.test(model,"virus",p.adj="bon",console=TRUE)
```

---

LxT

*Data Line by tester*

---

**Description**

Data frame with yield by line x tester.

**Usage**

data(LxT)

**Format**

A data frame with 92 observations on the following 4 variables.

**replication** a numeric vector

**line** a numeric vector

**tester** a numeric vector

**yield** a numeric vector

**Source**

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979

---

markers

*Data of molecular markers*

---

**Description**

A partial study on 27 molecular markers.

**Usage**

data(markers)

**Format**

A data frame with 23 observations on the following 27 variables.

marker1 a numeric vector

marker2 a numeric vector

marker3 a numeric vector

marker4 a numeric vector

marker5 a numeric vector

marker6 a numeric vector

marker7 a numeric vector

marker8 a numeric vector

marker9 a numeric vector

marker10 a numeric vector

marker11 a numeric vector

marker12 a numeric vector

marker13 a numeric vector

marker14 a numeric vector

marker15 a numeric vector

marker16 a numeric vector  
marker17 a numeric vector  
marker18 a numeric vector  
marker19 a numeric vector  
marker20 a numeric vector  
marker21 a numeric vector  
marker22 a numeric vector  
marker23 a numeric vector  
marker24 a numeric vector  
marker25 a numeric vector  
marker26 a numeric vector  
marker27 a numeric vector

**Source**

International Potato Center Lima-Peru.

**References**

International Potato Center Lima-Peru.

**Examples**

```
library(agricolae)
data(markers)
str(markers)
```

---

Median.test

*Median test. Multiple comparisons*

---

**Description**

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

**Usage**

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

**Arguments**

y	Variable response
trt	Treatments
correct	a logical indicating whether to apply continuity correction when computing the test statistic for 2 groups. The correction will not be bigger than the differences themselves. No correction is done if simulate.p.value = TRUE.
simulate.p.value	a logical indicating whether to compute p-values by Monte Carlo simulation
console	logical, print output

**Details**

The data consist of k samples of possibly unequal sample size.

**Value**

statistics	Numeric
parameters	Numeric
Medians	data.frame
comparison	data.frame
data	data.frame

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

[kruskal,chisq.test](#)

**Examples**

```
library(agricolae)
# example 1
data(corn)
attach(corn)
comparison<-Median.test(observation,method)
comparison
detach(corn)
# example 2
trt<-c(rep(1,9),rep(2,10),rep(3,7),rep(4,8))
y<-c(83,91,94,89,96,91,92,90,91,90,81,83,84,83,88,91,89,84,101,100,91,93,
96,95,94,78,82,81,77,79,81,80,81)
comparison<-Median.test(y,trt)
```

---

melon

*Data of yield of melon in a Latin square experiment*

---

### Description

An irrigation system evaluation by exudation using four varieties of melon, under modality of sowing, SIMPLE ROW. The goal is to analyze the behavior of three hybrid melon varieties and one standard.

### Usage

```
data(melon)
```

### Format

A data frame with 16 observations on the following 4 variables.

row a numeric vector

col a numeric vector

variety a factor with levels V1 V2 V3 V4

yield a numeric vector

### Details

Varieties: Hibrido Mission (V1); Hibrido Mark (V2); Hibrido Topfligth (V3); Hibrido Hales Best Jumbo (V4).

### Source

Tesis. "Evaluacion del sistema de riego por exudacion utilizando cuatro variedades de melon, bajo modalidad de siembra, SIMPLE HILERA". Alberto Angeles L. Universidad Agraria la Molina - Lima Peru.

### References

Universidad Nacional Agraria la molina.

### Examples

```
library(agricolae)
data(melon)
str(melon)
```



---

`montecarlo`*Random generation by Montecarlo*

---

**Description**

Random generation form data, use function density and parameters

**Usage**

```
montecarlo(data, k, ...)
```

**Arguments**

<code>data</code>	vector or object(hist, graph.freq)
<code>k</code>	number of simulations
<code>...</code>	Other parameters of the function density, only if data is vector

**Value**

Generates random.

**Author(s)**

Felipe de Mendiburu

**See Also**

[density](#)

**Examples**

```
library(agricolae)
r<-rnorm(50, 10,2)
montecarlo(r, k=100, kernel="epanechnikov")
# other example
h<-hist(r,plot=FALSE)
montecarlo(h, k=100)
# other example
breaks<-c(0, 150, 200, 250, 300)
counts<-c(10, 20, 40, 30)
h<-graph.freq(x=breaks,counts=counts,plot=FALSE)
montecarlo(h, k=100)
```

---

natives	<i>Data of native potato</i>
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---

**Description**

An evaluation of the number, weight and size of 24 native potatoes varieties.

**Usage**

```
data(natives)
```

**Format**

A data frame with 876 observations on the following 4 variables.

variety a numeric vector

number a numeric vector

weight a numeric vector

size a numeric vector

**Source**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(natives)
str(natives)
```

---

nonadditivity	<i>Nonadditivity model test</i>
---------------	---------------------------------

---

**Description**

The resistance for the transformable nonadditivity, due to J. W. Tukey, is based on the detection of a curvilinear relation between  $y$ -est( $y$ ) and est( $y$ ). A freedom degree for the transformable nonadditivity.

**Usage**

```
nonadditivity(y, factor1, factor2, df, MSError)
```

**Arguments**

y	Answer of the experimental unit
factor1	Firts treatment applied to each experimental unit
factor2	Second treatment applied to each experimental unit
df	Degrees of freedom of the experimental error
MSerror	Means square error of the experimental

**Details**

Only two factor: Block and treatment or factor 1 and factor 2.

**Value**

y	Numeric
factor1	alphanumeric
factor2	alphanumeric
df	Numeric
MSerror	Numeric

**Author(s)**

Felipe de Mendiburu

**References**

1. Steel, R.; Torri,J; Dickey, D.(1997) Principles and Procedures of Statistics A Biometrical Approach
2. George E.P. Box; J. Stuart Hunter and William G. Hunter. Statistics for experimenters. Wile Series in probability and statistics

**Examples**

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

---

normal.freq	<i>Normal curve on the histogram</i>
-------------	--------------------------------------

---

**Description**

A normal distribution graph elaborated from the histogram previously constructed. The average and variance are obtained from the data grouped in the histogram.

**Usage**

```
normal.freq(histogram, frequency=1, ...)
```

**Arguments**

histogram	object constructed by the function hist
frequency	1=counts, 2=relative, 3=density
...	Other parameters of the function hist

**Value**

Histogram	object
frequency	numeric
probability	logic False or True

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [graph.freq](#)

**Examples**

```
library(agricolae)
data(growth)
attach(growth)
#startgraph
h1<-hist(height,col="green",xlim=c(6,14))
normal.freq(h1,col="blue")
#endgraph
#startgraph
h2<-graph.freq(height,col="yellow",xlim=c(6,14),frequency=2)
normal.freq(h2,.frequency=2)
#endgraph
detach(growth)
```

ogive.freq

*Plotting the ogive from a histogram***Description**

It plots the cumulative relative .frequencies with the intervals of classes defined in the histogram.

**Usage**

```
ogive.freq(histogram, type="", xlab="", ylab="", axes="", las=1, ...)
```

**Arguments**

histogram	object created by the function hist() or graph.freq()
type	what type of plot should be drawn. See plot()
xlab	x labels
ylab	y labels
axes	TRUE or FALSE
las	numeric in 0,1,2,3; the style of axis labels. see plot()
...	Parameters of the plot()

**Value**

table	data.frame
-------	------------

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [graph.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(growth)
h<-graph.freq(growth$height, plot=FALSE)
points<-ogive.freq(h, col="red", frame=FALSE,
xlab="Height", ylab="Accumulated relative frequency", main="ogive")
print(points)
```

---

 order.group

*Ordering the treatments according to the multiple comparison*


---

### Description

This function allows us to compare the treatments averages or the adding of their ranges with the minimal significant difference which can vary from one comparison to another one. This function is used by the HSD, LSD, Kruskal-Wallis, Friedman or Durbin procedures.

### Usage

```
order.group(trt, means, N, MSerror, Tprob, std.err, parameter=1, snk=0,
DFerror=NULL, alpha=NULL, sdt dif=NULL, vartau=NULL, console)
```

### Arguments

trt	Treatments
means	Means of treatment
N	Replications
MSerror	Mean square error
Tprob	minimum value for the comparison
std.err	standard error
parameter	Constante 1 (Sd), 0.5 (Sx)
snk	Constante = 1 (Student Newman Keuls)
DFerror	Degrees of freedom of the experimental error
alpha	Level of risk for the test
sdt dif	standard deviation of difference in BIB
vartau	matrix var-cov in PBIB
console	logical, print output

### Value

trt	Factor
means	Numeric
N	Numeric
MSerror	Numeric
Tprob	value between 0 and 1
std.err	Numeric
parameter	Constant
snk	Constant
DFerror	Numeric
alpha	Numeric
sdt dif	Numeric
vartau	Numeric, matrix

**Author(s)**

Felipe de Mendiburu

**See Also**[order.stat](#)**Examples**

```

library(agricolae)
treatments <- c("A", "B", "C", "D", "E", "F")
means<-c(20,40,35,72,49,58)
std.err<-c(1.2, 2, 1.5, 2.4, 1, 3.1)
minimun<-c(15,38,30,68,43,54)
maximun<-c(23,45,39,76,53,61)
replications <- c(4,4,3,4,3,3)
MSerror <- 55.8
value.t <- 2.1314
groups<-order.group(treatments,means,replications,MSerror,value.t,std.err,console=TRUE)
Means<-data.frame(treatments,means,std.err,r=replications,Min = minimun,
Max = maximun)
rownames(Means)<-Means[,1]
Means<-Means[,-1]
par(mfrow=c(2,2))
bar.group(groups,ylim=c(0,80))
bar.err(Means,variation="SD", bar=FALSE,col="green",ylim=c(0,80),
main="Standard deviation")
bar.err(Means,variation="SE", bar=FALSE,col=colors()[15],ylim=c(0,80),
main="Standard error",)
out<-bar.err(Means,variation="range", bar=FALSE,col=colors()[25],ylim=c(0,80),
space=2,main="Range")
points(out$index,out$means,pch=17,col="orange",cex=2)

```

order.stat

---

*Grouping the treatments averages in a comparison with a minimum value*

---

**Description**

When there are treatments and their respective values, these can be compared with a minimal difference of meaning.

**Usage**

```
order.stat(treatment, means, minimum,console)
```

**Arguments**

treatment	treatment
means	means of treatment
minimum	minimum value for the comparison
console	logical, print output

**Value**

trt	Factor
means	Numeric
minimum	Numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

[order.group](#)

**Examples**

```
library(agricolae)
treatments <- c("A","B","C","D","E","F")
means<-c(2,5,3,7,9,5)
minimum.diff <- 2
groups<-order.stat(treatments,means,minimum.diff,console=TRUE)
```

---

pamCIP

*Data Potato Wild*

---

**Description**

Potato Wild

**Usage**

```
data(pamCIP)
```

**Format**

A data frame with 43 observations on the following 107 variables. Rownames: code and genotype's name. column data: molecular markers.



**Details**

To study the molecular markers in Wild.

**Source**

Laboratory data.

**References**

International Potato Center Lima-Peru (CIP)

**Examples**

```
library(agricolae)
data(pamCIP)
str(pamCIP)
```

---

paracsho

*Data of Paracsho biodiversity*

---

**Description**

A locality in Peru. A biodiversity.

**Usage**

```
data(paracsho)
```

**Format**

A data frame with 110 observations on the following 6 variables.

`date` a factor with levels 15-12-05 17-11-05 18-10-05 20-09-05 22-06-05 23-08-05 28-07-05

`plot` a factor with levels PARACSHO

`Treatment` a factor with levels CON SIN

`Orden` a factor with levels COLEOPTERA DIPTERA HEMIPTERA HYMENOPTERA LEPIDOPTERA NEUROPTERA  
NEUROPTERO NOCTUIDAE

`Family` a factor with levels AGROMYZIDAE ANTHOCORIDAE ANTHOMYIIDAE ANTHOMYLIDAE BLEPHAROCERIDAE  
BRACONIDAE BROCONIDAE CALUPHORIDAE CECIDOMYIDAE CHENEUMONIDAE CHNEUMONIDAE CHRYSOMELIDAE  
CICADELLIDAE CULICIDAE ERIOCPAMIDAE HEMEROBIIDAE ICHNEUMONIDAE LOUCHAPIDAE MIRIDAE  
MUSCIDAE MUSICADAE MUSLIDAE MYCETOPHILIDAE MYCETOPHILIIDAE NENPHALIDAE NOCLUIDAE  
NOCTERIDAE NOCTUIDAE PERALIDAE PIPUNCULIDAE PROCTOTRUPIDAE PSYLLIDAE PYRALIDAE  
SARCOPHAGIDAE SARCOPILAGIDAE SCATOPHAGIDAE SCATOPHOGIDAE SCIARIDAE SERSIDAE SYRPHIDAE  
TACHINIDAE TIPULIDAE

`Number.of.specimens` a numeric vector

**Details**

Country Peru, Department Junin, province Tarma, locality Huasahuasi.

**Source**

Entomology dataset.

**References**

International Potato Center.

**Examples**

```
library(agricolae)
data(paracsho)
str(paracsho)
```

---

path.analysis

*Path Analysis*

---

**Description**

If the cause and effect relationship is well defined, it is possible to represent the whole system of variables in a diagram form known as path-analysis. The function calculates the direct and indirect effects and uses the variables correlation or covariance.

**Usage**

```
path.analysis(corr.x, corr.y)
```

**Arguments**

corr.x	Matrix of correlations of the independent variables
corr.y	vector of dependent correlations with each one of the independent ones

**Details**

It is necessary first to calculate the correlations.

**Value**

corr.x	Numeric
corr.y	Numeric

**Author(s)**

Felipe de Mendiburu

**References**

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979

**See Also**

[correlation](#)

**Examples**

```
# Path analysis. Multivarial Analysis. Anderson. Prentice Hall, pag 616
library(agricolae)
# Example 1
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")
path.analysis(corr.x, corr.y)
# Example 2
# data of the progress of the disease related bacterial wilt to the ground
# for the component CE Ca K2 Cu
data(wilt)
data(soil)
x<-soil[,c(3,12,14,20)]
y<-wilt[,14]
cor.y<-correlation(y,x)$correlation
cor.x<-correlation(x)$correlation
path.analysis(cor.x, cor.y)
```

---

PBIB.test

*Analysis of the Partially Balanced Incomplete Block Design*

---

**Description**

Analysis of variance PBIB and comparison mean adjusted. Applied to resolvable designs: Lattices and alpha design.

**Usage**

```
PBIB.test(block, trt, replication, y, k, method=c("REML", "ML", "VC"),
test = c("lsd", "tukey"), alpha=0.05, console=FALSE, group=TRUE)
```

**Arguments**

block	blocks
trt	Treatment
replication	Replication

y	Response
k	Block size
method	Estimation method: REML, ML and VC
test	Comparison treatments
alpha	Significant test
console	logical, print output
group	logical, groups

### Details

Method of comparison treatment. lsd: least significant difference. tukey: Honestly significant difference. Estimate: specifies the estimation method for the covariance parameters. The REML is the default method. The REML specification performs residual (restricted) maximum likelihood, and The ML specification performs maximum likelihood, and the VC specifications apply only to variance component models.

### Value

block	Vector, consecutive numbers by replication
trt	Vector numeric or character
replication	Vector
y	numeric vector
k	numeric constant
method	Character: REML, ML and VC
test	Character: comparison methods lsd and tukey
alpha	Numeric
group	Logic

### Author(s)

F. de Mendiburu

### References

1. Iterative Analysis of Generalized Lattice Designs. E.R. Williams (1977) Austral J. Statistics 19(1) 39-42.
2. Experimental design. Cochran and Cox. Second edition. Wiley Classics Library Edition published 1992

### See Also

[BIB.test](#), [design.alpha](#)

**Examples**

```

require(agricolae)
# alpha design
Genotype<-paste("geno",1:30,sep="")
ntr<-length(Genotype)
r<-2
k<-3
s<-10
obs<-ntr*r
b <- s*r
book<-design.alpha(Genotype,k,r,seed=5)
book$book[,3]<- gl(20,3)
# dataset
y<-c(5,2,7,6,4,9,7,6,7,9,6,2,1,1,3,2,4,6,7,9,8,7,6,4,3,2,2,1,1,2,
     1,1,2,4,5,6,7,8,6,5,4,3,1,1,2,5,4,2,7,6,6,5,6,4,5,7,6,5,5,4)
dbook<-data.frame(book$book,yield=y)
rm(y,Genotype)
# NOT RUN
# analysis
# require(nlme) # method = REML or LM in PBIB.test and require(MASS) method=VC
attach(dbook)
model <- PBIB.test(block, Genotype, replication, yield, k=3, method="VC")
detach(dbook)
# model$ANOVA
# bar.group(model$groups,ylim=c(0,9), density=20, las=2)

```

---

plot.AMMI

*PLOT AMMI*


---

**Description**

Biplot AMMI.

**Usage**

```

## S3 method for class 'AMMI'
plot(x,first=1,second=2,third=3,type=1,number=FALSE,gcol=NULL,ecol=NULL,
     icol=NULL,angle=25,lwd=1.8,length=0.1,xlab=NULL,ylab=NULL,xlim=NULL,ylim=NULL,...)

```

**Arguments**

x	object AMMI
first	position axis x, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
second	position axis y,0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
third	position axis z,0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
type	1=biplot, 2= triplot 3=influence genotype
number	TRUE or FALSE names or number genotypes

gcol	genotype color
ecol	environment color
icol	influence color
angle	angle from the shaft of the arrow to the edge of the arrow head
lwd	parameter line width in function arrow
length	parameter length in function arrow
xlab	x labels
ylab	y labels
xlim	x limites
ylim	y limites
...	other parameters of plot

### Details

type=1 produce graphs biplot. type=2 produce graphs triplot, the components are normalized in scale 0-1. type=3 produce graphs on a 2d point set that are all subgraphs of the Delaunay triangulation. The Gabriel graph is a subgraph of the delaunay triangulation and has the relative neighbor graph as a sub-graph.

help(graphneigh) package=spdep

### Author(s)

Felipe de Mendiburu

### See Also

[AMMI](#)

### Examples

```
library(agricolae)
data(plrv)
attach(plrv)
model<- AMMI(Locality, Genotype, Rep, Yield)
detach(plrv)
# biplot PC2 vs PC1
plot(model)
## plot PC1 vs Yield
plot(model,0,1,gcol="blue",ecol="green")
## triplot PC 2,3,4
plot(model,first=2,second=3,third=4, type=2,number=TRUE)
# biplot with influence genotype in pc3 vs pc2
plot(model,first=2,second=3, type=3,number=TRUE,icol="green")
```

---

plot.graph.freq	<i>Histogram</i>
-----------------	------------------

---

**Description**

In many situations it has intervals of class defined with its respective frequencies. By means of this function, the graphic of frequency is obtained and it is possible to superpose the normal distribution, polygon of frequency, Ojiva and to construct the table of complete frequency.

**Usage**

```
## S3 method for class 'graph.freq'
plot(x, breaks=NULL, counts=NULL, frequency=1, plot=TRUE,
     nclass=NULL, xlab="", ylab="", axes = "", las=1, ...)
```

**Arguments**

x	a vector of values, a object hist(), graphFreq()
counts	frequency and x is class intervals
breaks	a vector giving the breakpoints between histogram cells
frequency	1=counts, 2=relative, 3=density
plot	logic
nclass	number of classes
xlab	x labels
ylab	y labels
axes	TRUE or FALSE
las	numeric in 0,1,2,3; the style of axis labels. see plot()
...	other parameters of plot

**Value**

breaks	a vector giving the breakpoints between histogram cells
counts	frequency and x is class intervals
mids	center point in class
relative	frequency
density	Numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```

library(agricolae)
data(genxenv)
yield <- subset(genxenv$YLD,genxenv$ENV==2)
yield <- round(yield,1)
h<- graph.freq(yield,axes=FALSE, frequency=1, ylab="frequency",col="yellow")
axis(1,h$breaks)
axis(2,seq(0,20,0.1))
# To reproduce histogram.
h1 <- plot(h, col="blue", frequency=2,border="red", density=8,axes=FALSE,
xlab="YIELD",ylab="relative")
axis(1,h$breaks)
axis(2,seq(0,.4,0.1))
# summary, only frequency
limits <-seq(10,40,5)
frequencies <-c(2,6,8,7,3,4)
#startgraph
h<-graph.freq(limits,counts=frequencies,col="bisque",xlab="Classes")
polygon.freq(h,col="red")
title( main="Histogram and polygon of frequency",
ylab=".frequency")
#endgraph
# Statistics
measures<-stat.freq(h)
print(measures)
# frequency table full
round(table.freq(h),2)
#startgraph
# ogive
ogive.freq(h,col="red",type="b",ylab="Accumulated relative frequency",
xlab="Variable")
# only frequency polygon
h<-graph.freq(limits,counts=frequencies,border=FALSE,col=NULL,xlab=" ",ylab="")
title( main="Polygon of frequency",
xlab="Variable", ylab="Frecuency")
polygon.freq(h,col="blue")
grid(col="brown")
#endgraph
# Draw curve for Histogram
h<- graph.freq(yield,axes=FALSE, frequency=3, ylab="f(yield)",col="yellow")
axis(1,h$breaks)
axis(2,seq(0,0.18,0.03),las=2)
lines(density(yield), col = "red", lwd = 2)
title("Draw curve for Histogram")

```



plots

*Data for an analysis in split-plot***Description**

Experimental data in blocks, factor A in plots and factor B in sub-plots.

**Usage**

```
data(plots)
```

**Format**

A data frame with 18 observations on the following 5 variables.

block a numeric vector

plot a factor with levels p1 p2 p3 p4 p5 p6

A a factor with levels a1 a2

B a factor with levels b1 b2 b3

yield a numeric vector

**Source**

International Potato Center. CIP

**Examples**

```
library(agricolae)
data(plots)
str(plots)
plots[,1] <- as.factor(plots[,1])
# split-plot analysis
model <- aov(yield ~ block + A + Error(plot)+ B + A:B, data=plots)
summary(model)
attach(plots)
b<-nlevels(B)
a<-nlevels(A)
r<-nlevels(block)
dfa <- df.residual(model$plot)
Ea <- deviance(model$plot)/dfa
dfb <- df.residual(model$Within)
Eb <- deviance(model$Within)/dfb
Eab <- (Ea +(b-1)*Eb)/(b*r)
# Satterthwaite
dfab<-(Ea +(b-1)*Eb)^2/(Ea^2/dfa +((b-1)*Eb)^2/dfb)
# Comparison A, A(b1), A(b2), A(b3)
comparison1 <-LSD.test(yield,A,dfa,Ea)
comparison2 <-LSD.test(yield[B=="b1"],A[B=="b1"],dfab,Eab)
```

```

comparison3 <-LSD.test(yield[B=="b2"],A[B=="b2"],dfab,Eab)
comparison4 <-LSD.test(yield[B=="b3"],A[B=="b3"],dfab,Eab)
# Comparison B, B(a1), B(a2)
comparison5 <-LSD.test(yield,B,dfb,Eb)
comparison6 <-LSD.test(yield[A=="a1"],B[A=="a1"],dfb,Eb)
comparison7 <-LSD.test(yield[A=="a2"],B[A=="a2"],dfb,Eb)
detach(plots)

```

---

plrv

*Data clones from the PLRV population*

---

### Description

Six environments: Ayacucho, La Molina 02, San Ramon 02, Huancayo, La Molina 03, San Ramon 03.

### Usage

```
data(plrv)
```

### Format

A data frame with 504 observations on the following 6 variables.

Genotype a factor with levels 102.18 104.22 121.31 141.28 157.26 163.9 221.19 233.11  
235.6 241.2 255.7 314.12 317.6 319.20 320.16 342.15 346.2 351.26 364.21 402.7  
405.2 406.12 427.7 450.3 506.2 Canchan Desiree Unica

Locality a factor with levels Ayac Hyo-02 LM-02 LM-03 SR-02 SR-03

Rep a numeric vector

WeightPlant a numeric vector

WeightPlot a numeric vector

Yield a numeric vector

### Source

International Potato Center Lima-Peru

### References

International Potato Center Lima-Peru

### Examples

```

library(agricolae)
data(plrv)
str(plrv)

```

---

polygon.freq	<i>The polygon of frequency on the histogram</i>
--------------	--

---

### Description

The polygon is constructed single or on a histogram. It is necessary to execute the function previously hist.

### Usage

```
polygon.freq(histogram, frequency=1, ...)
```

### Arguments

histogram	Object constructed by the function hist
frequency	numeric, counts(1), relative(2) and density(3)
...	Other parameters of the function hist

### Value

histogram	Object
frequency	1=counts, 2=relative, 3=density

### Author(s)

Felipe de Mendiburu Delgado

### See Also

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [graph.freq](#), [normal.freq](#)

### Examples

```
library(agricolae)
data(growth)
attach(growth)
#startgraph
h1<-hist(height,border=FALSE,xlim=c(6,14))
polygon.freq(h1,frequency=1,col="red")
#endgraph
#startgraph
h2<-graph.freq(height,frequency=2,col="yellow",xlim=c(6,14))
polygon.freq(h2,frequency=2,col="red")
#endgraph
detach(growth)
```

---

potato	<i>Data of cutting</i>
--------	------------------------

---

**Description**

A study on the yield of two potato varieties performed at the CIP experimental station.

**Usage**

```
data(potato)
```

**Format**

A data frame with 18 observations on the following 4 variables.

date a numeric vector

variety a factor with levels Canchan Unica

harvest a numeric vector

cutting a numeric vector

**Source**

Experimental data.

**References**

International Potato Center

**Examples**

```
library(agricolae)
data(potato)
str(potato)
```

---

ralstonia	<i>Data of assessment of the population in the soil R.solanacearum</i>
-----------	--

---

**Description**

The assessment of the population of *R.solanacearum* on the floor took place after 48 hours of infestation, during days 15, 29, 43, 58, and 133 days after the infestation soil. More information on soil data(soil).

**Usage**

```
data(ralstonia)
```

**Format**

A data frame with 13 observations on the following 8 variables.

place a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2

Day2 a numeric vector

Day15 a numeric vector

Day29 a numeric vector

Day43 a numeric vector

Day58 a numeric vector

Day73 a numeric vector

Day133 a numeric vector

**Details**

Logarithm average counts of colonies on plates containing half of M-SMSA 3 repetitions (3 plates by repetition) incubated at 30 degrees centigrade for 48 hours.  $\log(1+UFC/g \text{ soil})$

**Source**

Experimental field, 2004. Data Kindly provided by Dr. Sylvie Priou, Liliam Gutarra and Pedro Aley.

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

```
library(agricolae)
data(ralstonia)
str(ralstonia)
```

---

reg.homog

*Homologation of regressions*

---

**Description**

It makes the regressions homogeneity test for a group of treatments where each observation presents a linearly dependent reply from another one. There is a linear function in every treatment. The objective is to find out if the linear models of each treatment come from the same population.

**Usage**

```
reg.homog(trt, x, y)
```

**Arguments**

trt	treatment
x	independent variable
y	dependent variable

**Value**

trt	factor
x	numeric
y	numeric

**Author(s)**

Felipe de Mendiburu

**References**

Book in Spanish: Metodos estadisticos para la investigacion. Calzada Benza 1960

**Examples**

```
library(agricolae)
data(frijol)
attach(frijol)
evaluation<-reg.homog(technology,index,production)
detach(frijol)
# Example 2. Applied Regression Analysis a Research tools
# 1988. John O.Rawlings. Wadsworth & brooks/cole Advanced Books
# & Software. Pacific Grove. California.
# Statistics/probability. Series
LineNumber<-c(rep("39","30"),rep("52","30"))
PlantingDate<-rep(c("16","20","21"),20)
HeadWt <- c(2.5,3.0,2.2,2.2,2.8,1.8,3.1,2.8,1.6,4.3,2.7,2.1,2.5,2.6,3.3,4.3,
2.8,3.8,3.8,2.6,3.2,4.3,2.6,3.6,1.7,2.6,4.2,3.1,3.5,1.6,2.0,4.0,1.5,2.4,2.8,
1.4,1.9,3.1,1.7,2.8,4.2,1.3,1.7,3.7,1.7,3.2,3.0,1.6,2.0,2.2,1.4,2.2,2.3,1.0,
2.2,3.8,1.5,2.2,2.0,1.6)
Ascorbic <-c(51,65,54,55,52,59,45,41,66,42,51,54,53,41,45,50,45,49,50,51,49,
52,45,55,56,61,49,49,42,68,58,52,78,55,70,75,67,57,70,61,58,84,67,47,71,68,
56,72,58,72,62,63,63,68,56,54,66,72,60,72)
trt<-paste(LineNumber,PlantingDate,sep="-")
output<-reg.homog(trt,HeadWt,Ascorbic)
```

---

`resampling.cv`*Resampling to find the optimal number of markers*

---

**Description**

This process finds the curve of CV for a different number of markers which allows us to determine the number of optimal markers for a given relative variability. A method of the curvature.

**Usage**

```
resampling.cv(A, size, npoints)
```

**Arguments**

A	data frame or matrix of binary data
size	number of re-samplings
npoints	Number of points to consider the model

**Value**

A	Matrix of numerical values of (1,0)
size	constant numeric
npoints	numeric

**Author(s)**

Felipe de Mendiburu

**References**

Efron, B., Tibshirani, R. (1993) An Introduction to the Bootstrap. Chapman and Hall/CRC

**See Also**

[cv.similarity](#), [similarity](#)

**Examples**

```
library(agricolae)
#example table of molecular markers
data(markers)
study<-resampling.cv(markers,size=1,npoints=15)
#
# Results of the model
summary(study$model)
coef<-coef(study$model)
py<-predict(study$model)
Rsqr<-summary(study$model)$"r.squared"
```

```

table.cv <- data.frame(study$table.cv,estimate=py)
print(table.cv)

# Plot CV
#startgraph
limy<-max(table.cv[,2])+10
plot(table.cv[,c(1,2)],col="red",frame=FALSE,xlab="number of markers",
ylim=c(10,limy), ylab="CV",cex.main=0.8,main="Estimation of the number of markers")
ty<-quantile(table.cv[,2],1)
tx<-median(table.cv[,1])
tz<-quantile(table.cv[,2],0.95)
text(tx,ty, cex=0.8,as.expression(substitute(CV == a + frac(b,markers),
list(a=round(coef[1],2),b=round(coef[2],2)))) )
text(tx,tz,cex=0.8,as.expression(substitute(R^2==r,list(r=round(Rsq,3)))))

# Plot CV = a + b/n.markers
fy<-function(x,a,b) a+b/x
x<-seq(2,max(table.cv[,1]),length=50)
y <- coef[1] + coef[2]/x
lines(x,y,col="blue")
#grid(col="brown")
rug(table.cv[,1])
#endgraph

```

---

resampling.model

*Resampling for linear models*


---

### Description

This process consists of finding the values of P-value by means of a re-sampling (permutation) process along with the values obtained by variance analysis.

### Usage

```
resampling.model(model, data, k, console=FALSE)
```

### Arguments

model	model in R
data	data for the study of the model
k	number of re-samplings
console	logical, print output

### Value

model	ouput linear model, lm
solution	anova resampling
acum	cumulative frequency
samples	samples number



**Author(s)**

Felipe de Mendiburu

**References**

Efron, B., Tibshirani, R. (1993) An Introduction to the Bootstrap. Chapman and Hall/CRC Phillip I. Good, (2001) Resampling Methods. Birkhauser. Boston . Basel . Berlin

**See Also**

[simulation.model](#)

**Examples**

```
#example 1 Simple linear regression
library(agricolae)
data(clay)
model<-"ralstonia ~ days"
analysis<-resampling.model(model,clay,k=2,console=TRUE)

#example 2 Analysis of variance: RCD
data(sweetpotato)
model<-"yield~virus"
analysis<-resampling.model(model,sweetpotato,k=2,console=TRUE)

#example 3 Simple linear regression
data(Glycoalkaloids)
model<-"HPLC ~ spectrophotometer"
analysis<-resampling.model(model,Glycoalkaloids,k=2,console=TRUE)

#example 4 Factorial in RCD

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=2,console=TRUE)
```

---

rice

*Data of Grain yield of rice variety IR8*

---

**Description**

The data correspond to the yield of rice variety IR8 (g/m<sup>2</sup>) for land uniformity studies. The growing area is 18x36 meters.

**Usage**

```
data(rice)
```

**Format**

A data frame with 36 observations on the following 18 variables.

V1 a numeric vector  
V2 a numeric vector  
V3 a numeric vector  
V4 a numeric vector  
V5 a numeric vector  
V6 a numeric vector  
V7 a numeric vector  
V8 a numeric vector  
V9 a numeric vector  
V10 a numeric vector  
V11 a numeric vector  
V12 a numeric vector  
V13 a numeric vector  
V14 a numeric vector  
V15 a numeric vector  
V16 a numeric vector  
V17 a numeric vector  
V18 a numeric vector

**Details**

Table 12.1 Measuring Soil Heterogeneity

**Source**

Statistical Procedures for Agriculture Research. Second Edition. Kwanchai A. Gomez and Arturo A. Gomez. 1976. USA Pag. 481.

**References**

Statistical Procedures for Agriculture Research. Second Edition. Kwanchai A. Gomez and Arturo A. Gomez. 1976. USA

**Examples**

```
library(agricolae)  
data(rice)  
str(rice)
```

---

RioChillon

*Data and analysis Mother and baby trials*

---

## Description

Mother/Baby Trials allow farmers and researchers to test best-bet technologies or new cultivars. Evaluation of advanced Clones of potato in the Valley of Rio Chillon - PERU (2004)

## Usage

```
data(RioChillon)
```

## Format

The format is list of 2:

1. mother: data.frame: 30 obs. of 3 variables:
  - block (3 levels)
  - clon (10 levels)
  - yield (kg.)
2. babies: data.frame: 90 obs. of 3 variables:
  - farmer (9 levels)
  - clon (10 levels)
  - yield (kg.)

## Details

1. Replicated researcher-managed "mother trials" with typically 10 treatments evaluated in small plots.
2. Unreplicated "baby trials" with 10 treatments evaluated in large plots.
3. The "baby trials" with a subset of the treatments in the mother trial.

## Source

Experimental field.

## References

International Potato Center. CIP - Lima Peru.

## Examples

```
# Analisis the Mother/Baby Trial Design
library(agricolae)
data(RioChillon)
# First analysis the Mother Trial Design.
model<-aov(yield ~ block + clon, RioChillon$mother)
anova(model)
cv.model(model)
```

```

attach(RioChillon$mother)
comparison<-LSD.test(yield,clon, 18, 4.922, group=TRUE)
detach(RioChillon$mother)
# Second analysis the babies Trial.
attach(RioChillon$babies)
comparison<-friedman(farmer,clon, yield, group=TRUE)
detach(RioChillon$babies)
# Third
# The researcher makes use of data from both mother and baby trials and thereby obtains
# information on suitability of new technologies or cultivars
# for different agro-ecologies and acceptability to farmers.

```

---

scheffe.test

*Multiple comparisons, scheffe*

---

### Description

Scheffe 1959, method is very general in that all possible contrasts can be tested for significance and confidence intervals can be constructed for the corresponding linear. The test is conservative.

### Usage

```

scheffe.test(y, trt, DFerror, MSerror, Fc, alpha = 0.05, group=TRUE, main = NULL,
console=FALSE )

```

### Arguments

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each experimental unit
DFerror	Degrees of freedom
MSerror	Mean Square Error
Fc	F Value
alpha	Significant level
group	TRUE or FALSE
main	Title
console	logical, print output

### Details

It is necessary first makes a analysis of variance.

**Value**

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
Fc	Numeric
alpha	Numeric
group	Logic
main	Text

**Author(s)**

Felipe de Mendiburu

**References**

Robert O. Kuehl. 2nd ed. Design of experiments. Duxbury, copyright 2000. Steel, R.; Torri, J.; Dickey, D. (1997) Principles and Procedures of Statistics A Biometrical Approach. pp189

**See Also**

[HSD.test](#), [LSD.test](#), [SNK.test](#) , [bar.err](#), [bar.group](#), [duncan.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
comparison <- scheffe.test(model,"virus", group=TRUE,console=TRUE,
main="Yield of sweetpotato\nDealt with different virus")
# Old version scheffe.test()
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
Fc<-anova(model)["virus",4]
comparison <- scheffe.test(yield, virus, df, MSerror, Fc, group=TRUE,
main="Yield of sweetpotato. Dealt with different virus")
detach(sweetpotato)
```

---

similarity	<i>Matrix of similarity in binary data</i>
------------	--

---

**Description**

It finds the similarity matrix of binary tables (1 and 0).

**Usage**

```
similarity(A)
```

**Arguments**

A	Matrix, data binary
---	---------------------

**Value**

A	Numeric (0,1)
---	---------------

**Author(s)**

Felipe de Mendiburu

**See Also**

[cv.similarity](#), [resampling.cv](#)

**Examples**

```
#example table of molecular markers
library(agricolae)
data(markers)
distance<-similarity(markers)
#startgraph
tree<-hclust(distance,method="mcquitty")
plot(tree,col="blue")
#endgraph
```

---

simulation.model	<i>Simulation of the linear model under normality</i>
------------------	---

---

### Description

This process consists of validating the variance analysis results using a simulation process of the experiment. The validation consists of comparing the calculated values of each source of variation of the simulated data with respect to the calculated values of the original data. If in more than 50 percent of the cases they are higher than the real one, then it is considered favorable and the probability reported by the ANOVA is accepted, since the P-Value is the probability of ( $F > F.value$ ).

### Usage

```
simulation.model(model,file, categorical = NULL,k,console=FALSE)
```

### Arguments

model	Model in R
file	Data for the study of the model
categorical	position of the columns of the data that correspond to categorical variables
k	Number of simulations
console	logical, print output

### Value

model	output linear model, lm
simulation	anova simulation

### Author(s)

Felipe de Mendiburu

### See Also

[resampling.model](#)

### Examples

```
library(agricolae)
#example 1
data(clay)
model<-"ralstonia ~ days"
simulation.model(model,clay,k=15,console=TRUE)
#example 2
data(sweetpotato)
model<-"yield~virus"
simulation.model(model,sweetpotato,categorical=1,k=15,console=TRUE)
```

```
#example 3
data(Glycoalkaloids)
model<-"HPLC ~ spectrophotometer"
simulation.model(model,Glycoalkaloids,k=15,console=TRUE)
#example 4
data(potato)
model<-"cutting~date+variety"
simulation.model(model,potato,categorical=c(1,2,3),k=15,console=TRUE)
```

---

sinRepAmmi

*Data for AMMI without repetition*

---

## Description

Data frame for AMMI analysis with 50 genotypes in 5 environments.

## Usage

```
data(sinRepAmmi)
```

## Format

A data frame with 250 observations on the following 3 variables.

ENV a factor with levels A1 A2 A3 A4 A5

GEN a numeric vector

YLD a numeric vector

## Source

Experimental data.

## References

International Potato Center - Lima Peru.

## Examples

```
library(agricolae)
data(sinRepAmmi)
str(sinRepAmmi)
```



---

skewness	<i>Finding the skewness coefficient</i>
----------	---

---

**Description**

It returns the skewness of a distribution. It is similar to SAS.

**Usage**

```
skewness(x)
```

**Arguments**

x                    a numeric vector

**Value**

x                    The skewness of x

**See Also**

[kurtosis](#)

**Examples**

```
library(agricolae)
x<-c(3,4,5,2,3,4,NA,5,6,4,7)
skewness(x)
# value is 0,3595431, is slightly asimetrica (positive) to the right
```

---

SNK.test	<i>Student-Newman-Keuls (SNK)</i>
----------	-----------------------------------

---

**Description**

SNK is derived from Tukey, but it is less conservative (finds more differences). Tukey controls the error for all comparisons, where SNK only controls for comparisons under consideration. The level by alpha default is 0.05.

**Usage**

```
SNK.test(y, trt, DFerror, MSerror, alpha = 0.05, group=TRUE, main = NULL, console=FALSE)
```

**Arguments**

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each experimental unit
DFerror	Degree free
MSerror	Mean Square Error
alpha	Significant level
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

It is necessary first makes a analysis of variance.

**Value**

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
alpha	Numeric
group	Logic
main	Text

**Author(s)**

Felipe de Mendiburu

**References**

Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997

**See Also**

[LSD.test](#), [waller.test](#) , [HSD.test](#) , [duncan.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison <- SNK.test(model,"virus",
main="Yield of sweetpotato. Dealt with different virus")
SNK.test(model,"virus", group=FALSE)
# version old SNK.test()
```

```
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
comparison <- SNK.test(yield,virus,df,MSerror, group=TRUE)
print(comparison$groups)
detach(sweetpotato)
```

---

soil

*Data of soil analysis for 13 localities*

---

### **Description**

We analyzed the physical and chemical properties of different soils, as full characterization of soil and special analysis of micro-elements. These analyses were conducted in the laboratory analysis of soils, plants, water and fertilizers in the La Molina National Agrarian University (UNALM). To which the different soil samples were dried to the environment, screened (mesh 0.5x0, 5 mm) and sterilized by steam 4 to 5 hours with a Lindinger Steam aerator SA150 and SA700, with the possible aim of eliminating bacteria saprophytic or antagonists to prevent the growth of bacteria (*R.solanacearum*).

### **Usage**

```
data(soil)
```

### **Format**

A data frame with 13 observations on the following 23 variables.

place a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2

pH a numeric vector

EC a numeric vector, electrical conductivity

CaCO3 a numeric vector

MO a numeric vector

CIC a numeric vector

P a numeric vector

K a numeric vector

sand a numeric vector

slime a numeric vector

clay a numeric vector

Ca a numeric vector

Mg a numeric vector

K2 a numeric vector

Na a numeric vector

Al\_H a numeric vector  
K\_Mg a numeric vector  
Ca\_Mg a numeric vector  
B a numeric vector  
Cu a numeric vector  
Fe a numeric vector  
Mn a numeric vector  
Zn a numeric vector

### Details

Cnt1= Canete, Cnt2=Valle Dulce(Canete), Cnt3=Valle Grande(Canete), Chz=Obraje-Carhuaz(Ancash), Chmar=Chucmar-Chota(Huanuco), Hco1= Mayobamba-Chinchao(Huanuco), Hco2=Nueva Independencia-Chinchao(Huanuco), Hco3=San Marcos-Umari(Huanuco), Hyo1=La Victoria-Huancayo(Junin), Hyo1=El Tambo-Huancayo(Junin), Namora=Namora(Cajamarca), SR1= El Milagro-San Ramon(Junin), Sr2=La Chinchana-San Ramon(Junin).

### Source

Experimental field, 2004. Data Kindly provided by Dr. Sylvie Priou, Liliam Gutarra and Pedro Aley.

### References

International Potato Center - Lima, PERU.

### Examples

```
library(agricolae)
data(soil)
str(soil)
```

---

sp.plot

*Spilip-Plot analysis*

---

### Description

The variance analysis of a split plot design is divided into two parts: the plot-factor analysis and the sub-plot factor analysis.

### Usage

```
sp.plot(block, pplot, splot, Y)
```

**Arguments**

block	replications
pplot	main-plot Factor
splot	sub-plot Factor
Y	Variable, response

**Details**

The split-plot design is specifically suited for a two-factor experiment on of the factors is assigned to main plot (main-plot factor), the second factor, called the subplot factor, is assigned into subplots.

**Value**

block	vector, numeric or character
pplot	vector, numeric or character
splot	vector, numeric or character
Y	vector, numeric

**Author(s)**

Felipe de Mendiburu

**References**

Statistical procedures for agricultural research. Kwanchai A. Gomez, Arturo A. Gomez. Second Edition. 1984.

**See Also**

[ssp.plot](#), [strip.plot](#), [design.split](#), [design.strip](#)

**Examples**

```
library(agricolae)
data(plots)
attach(plots)
model<-sp.plot(block,A,B,yield)
detach(plots)
# with aov
plots[,1]<-as.factor(plots[,1])
AOV <- aov(yield ~ block + A*B + Error(block/A),data=plots)
summary(AOV)
```

---

`ssp.plot`*Split-split-Plot analysis*

---

**Description**

The variance analysis of a split-split plot design is divided into three parts: the main-plot, subplot and sub-subplot analysis.

**Usage**

```
ssp.plot(block, pplot, splot, ssplot, Y)
```

**Arguments**

<code>block</code>	replications
<code>pplot</code>	Factor main plot
<code>splot</code>	Factor subplot
<code>ssplot</code>	Factor sub-subplot
<code>Y</code>	Variable, response

**Details**

The split-split-plot design is an extension of the split-plot design to accommodate a third factor: one factor in main-plot, other in subplot and the third factor in sub-subplot

**Value**

<code>block</code>	vector, numeric or character
<code>pplot</code>	vector, numeric or character
<code>splot</code>	vector, numeric or character
<code>ssplot</code>	vector, nnumeric or character
<code>Y</code>	vector, numeric

**Author(s)**

Felipe de Mendiburu

**References**

Statistical procedures for agricultural research. Kwanchai A. Gomez, Arturo A. Gomez. Second Edition. 1984.

**See Also**

[sp.plot](#), [strip.plot](#), [design.split](#), [design.strip](#)

**Examples**

```

# Statistical procedures for agricultural research, pag 143
# Grain Yields of Three Rice Varieties Grown under
#Three Management practices and Five Nitrogen levels; in a
#split-split-plot design with nitrogen as main-plot,
#management practice as subplot, and variety as sub-subplot
#factores, with three replications.
library(agricolae)
yield<-c(3.320,3.766,4.660,3.188,3.625,5.232,5.468,5.759,6.215,
4.246,5.255,6.829,3.132,5.389,5.217,3.864,4.311,5.915,4.752,
4.809,5.170,5.788,6.130,7.106,4.842,5.742,5.869,4.375,4.315,
5.389,4.507,4.875,5.400,4.756,5.295,6.046,4.422,5.308,6.318,
4.863,5.345,6.011,4.678,5.896,7.309,6.101,5.096,6.573,5.595,
6.357,7.016,5.442,6.398,6.953,6.209,6.992,7.565,6.860,6.857,
7.254,5.122,4.873,5.495,6.780,5.925,7.442,5.988,6.533,6.914,
6.768,7.856,7.626,6.894,6.974,7.812,4.815,4.166,4.225,5.390,
5.163,4.478,6.509,6.569,7.991,5.779,6.164,7.362,6.573,7.422,
8.950,5.355,7.442,7.018,6.706,8.592,8.480,8.452,8.662,9.112,
8.042,9.080,9.660,9.314,9.224,10.360,5.536,6.462,8.020,6.546,
7.646,9.942,6.698,8.526,9.140,7.414,9.016,8.966,8.508,9.680,
9.896,5.244,5.584,7.642,7.092,7.212,8.714,8.650,8.514,9.320,
6.902,7.778,9.128,8.032,9.294,9.712)
block<-rep(gl(3,15),3)
nitrogen<-rep(c(rep(0,3),rep(50,3),rep(80,3),rep(110,3),rep(140,3)),9)
management<-rep(c("m1","m2","m3"),45)
variety<-gl(3,45)
model<-ssp.plot(block,nitrogen,management,variety,yield)
gla<-model$gl.a; glb<-model$gl.b; glc<-model$gl.c
Ea<-model$Ea; Eb<-model$Eb; Ec<-model$Ec
LSD.test(yield,nitrogen,gla,Ea,console=TRUE)
LSD.test(yield,management,glb,Eb,console=TRUE)
LSD.test(yield,variety,glc,Ec,console=TRUE)
# with aov
A<-data.frame(block, nitrogen,management,variety,yield)
A[,2]<-as.factor(A[,2])
AOV<-aov(yield ~ block + nitrogen*management*variety + Error(block/nitrogen/management),data=A)
summary(AOV)

```

---

stability.nonpar

*Nonparametric stability analysis*


---

**Description**

A method based on the statistical ranges of the study variable per environment for the stability analysis.

**Usage**

```
stability.nonpar(data, variable = NULL, ranking = FALSE, console=FALSE)
```

**Arguments**

data	First column the genotypes following environment
variable	Name of variable
ranking	logical, print ranking
console	logical, print output

**Value**

ranking	data.frame
statistics	data.frame

**Author(s)**

Felipe de Mendiburu

**References**

Haynes K G, Lambert D H, Christ B J, Weingartner D P, Douches D S, Backlund J E, Fry W and Stevenson W. 1998. Phenotypic stability of resistance to late blight in potato clones evaluated at eight sites in the United States American Journal Potato Research 75, pag 211-217.

**See Also**

[stability.par](#)

**Examples**

```
library(agricolae)
data(haynes)
stability.nonpar(haynes,"AUDPC",ranking=TRUE,console=TRUE)
# Example 2
data(CIC)
data1<-CIC$comas[,c(1,6,7,17,18)]
data2<-CIC$oxapampa[,c(1,6,7,19,20)]
cic <- rbind(data1,data2)

means <- by(cic[,5], cic[,c(2,1)], function(x) mean(x,na.rm=TRUE))
means <-as.data.frame(means[,])
cic.mean<-data.frame(genotype=row.names(means),means)
cic.mean<-delete.na(cic.mean,"greater")
out<-stability.nonpar(cic.mean)
out$ranking
out$statistics
```



---

 stability.par

*Stability analysis. SHUKLA'S STABILITY VARIANCE AND KANG'S*


---

### Description

This procedure calculates the stability variations as well as the statistics of selection for the yield and the stability. The averages of the genotype through the different environment repetitions are required for the calculations. The mean square error must be calculated from the joint variance analysis.

### Usage

```
stability.par(data,rep,MSerror,alpha=0.1,main=NULL,cova = FALSE,name.cov=NULL,
file.cov=0,console=FALSE)
```

### Arguments

data	matrix of averages, by rows the genotypes and columns the environment
rep	Number of repetitions
MSerror	Mean Square Error
alpha	Label significant
main	Title
cova	Covariable
name.cov	Name covariable
file.cov	Data covariable
console	logical, print output

### Details

Stable (i) determines the contribution of each genotype to GE interaction by calculating  $\text{var}(i)$ ; (ii) assigns ranks to genotypes from highest to lowest yield receiving the rank of 1; (iii) calculates protected LSD for mean yield comparisons; (iv) adjusts yield rank according to LSD (the adjusted rank labeled Y); (v) determines significance of  $\text{var}(i)$  using an approximate F-test; (vi) assigns stability rating (S) as follows: -8, -4 and -2 for  $\text{var}(i)$  significant at the 0.01, 0.05 and 0.10 probability levels, and 0 for nonsignificant  $\text{var}(i)$  (the higher the  $\text{var}(i)$ , the less stable the genotype); (vii) sums adjusted yield rank, Y, and stability rating, S, for each genotype to determine YS(i) statistic; and (viii) calculates mean YS(i) and identifies genotypes (selection) with  $\text{YS}(i) > \text{mean YS}(i)$ .

### Value

analysis	data.frame
statistics	data.frame
stability	data.frame

**Author(s)**

Felipe de Mendiburu

**References**

Kang, M. S. 1993. Simultaneous selection for yield and stability: Consequences for growers. *Agron. J.* 85:754-757. Manjit S. Kang and Robert Mangari. 1995. Stable: A basic program for calculating stability and yield-stability statistics. *Agron. J.* 87:276-277

**See Also**[stability.nonpar](#)**Examples**

```
library(agricolae)
# example 1
# Experimental data,
# replication rep= 4
# Mean square error, MSerror = 1.8
# 12 environment
# 17 genotype = 1,2,3,..., 17
# yield averages of 13 genotypes in localities
V1 <- c(10.2,8.8,8.8,9.3,9.6,7.2,8.4,9.6,7.9,10,9.3,8.0,10.1,9.4,10.8,6.3,7.4)
V2 <- c(7,7.8,7.0,6.9,7,8.3,7.4,6.5,6.8,7.9,7.3,6.8,8.1,7.1,7.1,6.4,4.1)
V3 <- c(5.3, 4.4, 5.3, 4.4, 5.5, 4.6, 6.2, 6.0, 6.5, 5.3, 5.7, 4.4, 4.2,5.6,5.8,3.9,3.8)
V4 <- c(7.8, 5.9, 7.3, 5.9, 7.8, 6.3, 7.9, 7.5, 7.6, 5.4, 5.6, 7.8, 6.5,8.1,7.5,5.0,5.4)
V5 <- c(9, 9.2, 8.8, 10.6, 8.3, 9.3, 9.6, 8.8, 7.9, 9.1, 7.7, 9.5, 9.4,9.4,10.3,8.8,8.7)
V6 <- c(6.9, 7.7, 7.9, 7.9, 7, 8.9,9.4, 7.9, 6.5, 7.2, 5.4, 6.2, 7.2,8.8,7.3,7.1,6.4)
V7 <- c(4.9, 2.5, 3.4, 2.5, 3,2.5, 3.6, 5.6,3.8, 3.9, 3.0, 3.0, 2.5,2.6,3.8,2.8,1.6)
V8 <- c(6.4, 6.4, 8.1, 7.2, 7.5, 6.6, 7.7, 7.6, 7.8, 7.5, 6.0, 7.2, 6.8,7.6,6.9,7.2,7.3)
V9 <- c(8.4, 6.1, 6.8, 6.1, 8.2, 6.9, 6.9, 9.1, 9.2, 7.7, 6.7, 7.8, 6.5,5.2,8.3,6.8,7.1)
V10 <-c(8.7, 9.4, 8.8, 7.9, 7.8, 7.8, 11.4, 9.9, 8.6, 8.5, 8.0, 8.3, 9.1,11.0,8.1,7.8,8.0)
V11 <-c(5.4, 5.2, 5.6, 4.6, 4.8, 5.7, 6.6, 6.8, 5.2, 4.8, 4.9, 5.4, 4.5,5.6,7.0,6.0,5.6)
V12 <-c(8.6, 8.0, 9.2, 8.1, 8.3, 8.9, 8.6, 9.6, 9.5, 7.7, 7.6, 8.3, 6.6,9.5,9.0,9.0,8.5)
data<-data.frame(V1,V2,V3,V4,V5,V6,V7,V8,V9,V10,V11,V12)
rownames(data)<-LETTERS[1:17]
stability.par(data, rep=4, MSerror=1.8, alpha=0.1, main="Genotype",console=TRUE)

#example 2 covariable. precipitation
precipitation<- c(1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100)
stability.par(data, rep=4, MSerror=1.8, alpha=0.1, main="Genotype",
  cov=TRUE, name.cov="Precipitation", file.cov=precipitation,console=TRUE)
```

**Description**

By this process the variance and central measures are found: average, medium and mode of grouped data.

**Usage**

```
stat.freq(histogram)
```

**Arguments**

histogram      Object create by function hist()

**Value**

histogram      Object

**Author(s)**

Felipe de mendiburu

**See Also**

[polygon.freq](#), [table.freq](#), [graph.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(growth)
attach(growth)
grouped<-hist(height,plot=FALSE)
detach(growth)
measures<-stat.freq(grouped)
print(measures)
```

---

strip.plot

*Strip-Plot analysis*

---

**Description**

The variance analysis of a strip-plot design is divided into three parts: the horizontal-factor analysis, the vertical-factor analysis, and the interaction analysis.

**Usage**

```
strip.plot(BLOCK, COL, ROW, Y)
```

**Arguments**

BLOCK	replications
COL	Factor column
ROW	Factor row
Y	Variable, response

**Details**

The strip-plot design is specifically suited for a two-factor experiment in which the desired precision for measuring the interaction effects between the two factors is higher than that for measuring the main effect two factors

**Value**

BLOCK	vector, numeric
COL	vector, numeric
ROW	vector, numeric
Y	vector, numeric

**Author(s)**

Felipe de Mendiburu

**References**

Statistical procedures for agricultural research. Kwanchai A. Gomez, Arturo A. Gomez. Second Edition. 1984.

**See Also**

[ssp.plot](#), [sp.plot](#), [design.split](#), [design.strip](#)

**Examples**

```
# Yield
library(agricolae)
data(huasahuasi)
YIELD<-huasahuasi$YIELD
attach(YIELD)
market <- y1da + y2da
non_market <- y3da
yield <- market + non_market
model<-strip.plot(block, clon, trt, yield)
comparison<-LSD.test(yield,clon,model$gl.a,model$Ea)
comparison<-LSD.test(yield,trt,model$gl.b,model$Eb)
detach(YIELD)
# simple effects
A<-model$data
a<-nlevels(A$clon)
```

```

b<-nlevels(A$strtr)
r<-nlevels(A$block)
Ea<-model$Ea; Eb<-model$Ec; Ec<-model$Ec;
gla<-model$gl.a; glb<-model$gl.b; glc<-model$gl.c;
B <-tapply.stat(A[,4],A[,2:3],mean)
std<-tapply.stat(A[,4],A[,2:3],function(x) sd(x)/sqrt(length(x)))
B<-data.frame(B[,1:2],yield=B[,3],std=std[,3])
cmab<-(b-1)*Ec + Ea
cmba<-(a-1)*Ec + Eb
# order.group
# Tukey
ta <- qtkey(0.95,a,gla)
tb <- qtkey(0.95,b,glb)
tc <- qtkey(0.95,a*b,glc)
tab<- ((b-1)*Ec*tc + Ea*ta)/cmab
tba<- ((a-1)*Ec*tc + Eb*tb)/cmba
# Comparison of clones by treatment
groups<-by(B,B[,2], function(x) order.group(x$clon,x$yield,N=b*r, cmab,tab,
std.err=x$std,parameter=0.5,console=FALSE))
groups
# Comparison of treatments by clon
groups<-by(B,B[,1], function(x) order.group(x$strtr,x$yield,N=a*r, cmba,tba,
std.err=x$std,parameter=0.5,console=FALSE))
groups
# LSD t-student
ta <- qt(0.975,gla)
tb <- qt(0.975,glb)
tc <- qt(0.975,glc)
tab<- ((b-1)*Ec*tc + Ea*ta)/cmab
tba<- ((a-1)*Ec*tc + Eb*tb)/cmba
# Comparison of clones by treatment
groups<-by(B,B[,2], function(x) order.group(x$clon,x$yield,N=b*r, cmab, tab,
std.err=x$std,console=FALSE))
groups
# Comparison of treatments by clon
groups<-by(B,B[,1], function(x) order.group(x$strtr,x$yield,N=a*r, cmba,tba,
std.err=x$std,console=FALSE))
groups

```

---

sturges.freq

*Class intervals for a histogram, the rule of Sturges*


---

### Description

if  $k=0$  then classes:  $k = 1 + \log(n,2)$ . if  $k > 0$ , fixed nclass.

### Usage

```
sturges.freq(x,k=0)
```

**Arguments**

x	vector
k	constant

**Value**

x	Numeric
k	Numeric

**Author(s)**

Felipe de mendiburu

**References**

Reza A. Hoshmand. 1988. Statistical Methods for Agricultural Sciences, Timber Press, Incorporated, pag 18-21.

**See Also**

[polygon.freq](#), [table.freq](#), [stat.freq](#), [intervals.freq](#), [graph.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(natives)
attach(natives)
classes<-sturges.freq(size)
# information of the classes
breaks <- classes$breaks
breaks
#startgraph
# Histogram with the established classes
h<-graph.freq(size,breaks,frequency=1, col="yellow",axes=FALSE,
  xlim=c(0,0.12),main="",xlab="",ylab="")
axis(1,breaks,las=2)
axis(2,seq(0,400,50),las=2)
title(main="Histogram of frequency\nSize of the tubercule of the Oca",
xlab="Size of the oca", ylab="Frequency")
#endgraph
detach(natives)
```

---

summary.graph.freq      *frequency Table of a Histogram*

---

### Description

It finds the absolute, relative and accumulated frequencies with the class intervals defined from a previously calculated histogram by the "hist" of R function.

### Usage

```
## S3 method for class 'graph.freq'  
summary(object,...)
```

### Arguments

object	Object by function graph.freq()
...	other parameters of graphic

### Value

object	Object by graph.freq()
--------	------------------------

### Author(s)

Felipe de Mendiburu

### See Also

[polygon.freq](#), [stat.freq](#), [graph.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

### Examples

```
library(agricolae)  
data(growth)  
attach(growth)  
h2<-graph.freq(height,plot=FALSE)  
summary(h2)  
detach(growth)
```

---

`sweetpotato`*Data of sweetpotato yield*

---

**Description**

The data correspond to an experiment with costanero sweetpotato made at the locality of the Tacna department, southern Peru. The effect of two viruses (Spmv and Spsv) was studied. The treatments were the following: CC (Spsv) = Sweetpotato chlorotic dwarf, FF (Spmv) = Feathery mottle, FC (Spmv y Spsv) = Viral complex and OO (witness) healthy plants. In each plot, 50 sweetpotato plants were sown and 12 plots were employed. Each treatment was made with 3 repetitions and at the end of the experiment the total weight in kilograms was evaluated. The virus transmission was made in the cuttings and these were sown in the field.

**Usage**

```
data(sweetpotato)
```

**Format**

A data frame with 12 observations on the following 2 variables.

`virus` a factor with levels cc fc ff oo

`yield` a numeric vector

**Source**

Experimental field.

**References**

International Potato Center. CIP - Lima Peru

**Examples**

```
library(agricolae)
data(sweetpotato)
str(sweetpotato)
```



---

table.freq	<i>frequency Table of a Histogram</i>
------------	---------------------------------------

---

**Description**

It finds the absolute, relative and accumulated frequencies with the class intervals defined from a previously calculated histogram by the "hist" of R function.

**Usage**

```
table.freq(object)
```

**Arguments**

object            Object by function graph.freq()

**Value**

object            Object by graph.freq()

**Author(s)**

Felipe de Mendiburu

**See Also**

[polygon.freq](#), [stat.freq](#), [graph.freq](#), [intervals.freq](#), [sturges.freq](#), [join.freq](#), [ogive.freq](#), [normal.freq](#)

**Examples**

```
library(agricolae)
data(growth)
attach(growth)
h2<-graph.freq(height,plot=FALSE)
detach(growth)
table.freq(h2)
```

---

tapply.stat

*Statistics of data grouped by factors*


---

**Description**

This process lies in finding statistics which consist of more than one variable, grouped or crossed by factors. The table must be organized by columns between variables and factors.

**Usage**

```
tapply.stat(y, x, stat = "mean")
```

**Arguments**

y	data.frame variables
x	data.frame factors
stat	Method

**Value**

y	Numeric
x	Numeric
stat	method = "mean", ...

**Author(s)**

Felipe de Mendiburu

**Examples**

```
library(agricolae)
# case of 1 single factor
data(sweetpotato)
tapply.stat(sweetpotato[,2],sweetpotato[,1],mean)
attach(sweetpotato)
tapply.stat(yield,virus,sd)
tapply.stat(yield,virus,function(x) max(x)-min(x))
tapply.stat(yield,virus,function(x) quantile(x,0.75,6)-quantile(x,0.25,6))
detach(sweetpotato)
# other case
data(cotton)
attach(cotton)
tapply.stat(yield,cotton[,c(1,3,4)],mean)
tapply.stat(yield,cotton[,c(1,4)],max)
detach(cotton)
# Height of pijuayo
data(growth)
attach(growth)
```

```
tapply.stat(height, growth[,2:1], function(x) mean(x,na.rm=TRUE))
detach(growth)
```

---

vark *Variance K, ties, Kendall*

---

### Description

The Kendall method in order to find the K variance.

### Usage

```
vark(x, y)
```

### Arguments

x	Vector
y	vector

### Details

variance of K for Kendall's tau

### Value

x	Numeric
y	Numeric

### Author(s)

Felipe de Mendiburu

### References

Numerical Recipes in C. Second Edition.

### See Also

cor.matrix, cor.vector, cor.mv

### Examples

```
library(agricolae)
x <-c(1,1,1,4,2,2,3,1,3,2,1,1,2,3,2,1,1,2,1,2)
y <-c(1,1,2,3,4,4,2,1,2,3,1,1,3,4,2,1,1,3,1,2)
vark(x,y)
```

waarden.test

*Multiple comparisons. The van der Waerden (Normal Scores)*

---

**Description**

A nonparametric test for several independent samples.

**Usage**

```
waarden.test(y, trt, alpha=0.05, group=TRUE, main=NULL, console=FALSE)
```

**Arguments**

y	Variable response
trt	Treatments
alpha	Significant level
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

The data consist of k samples of possibly unequal sample size.

**Value**

y	Numeric
trt	factor
alpha	Numeric
group	Logic
main	text

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

[kruskal](#)

**Examples**

```

library(agricolae)
# example 1
data(corn)
attach(corn)
comparison<-waerden.test(observation,method,group=TRUE)
comparison<-waerden.test(observation,method,group=FALSE)
detach(corn)
# example 2
data(sweetpotato)
attach(sweetpotato)
comparison<-waerden.test(yield,virus,alpha=0.01,group=TRUE)
detach(sweetpotato)

```

waller

*Computations of Bayesian t-values for multiple comparisons***Description**

A Bayes rule for the symmetric multiple comparisons problem.

**Usage**

```
waller(K, q, f, Fc)
```

**Arguments**

K	Is the loss ratio between type I and type II error
q	Numerator Degrees of freedom
f	Denominator Degrees of freedom
Fc	F ratio from an analysis of variance

**Details**

K-RATIO (K): value specifies the Type 1/Type 2 error seriousness ratio for the Waller-Duncan test. Reasonable values for KRATIO are 50, 100, and 500, which roughly correspond for the two-level case to ALPHA levels of 0.1, 0.05, and 0.01. By default, the procedure uses the default value of 100.

**Value**

K	Numeric integer > 1, examples 50, 100, 500
q	Numeric
f	Numeric
Fc	Numeric
...	

**Author(s)**

Felipe de Mendiburu

**References**

Waller, R. A. and Duncan, D. B. (1969). A Bayes Rule for the Symmetric Multiple Comparison Problem, *Journal of the American Statistical Association* 64, pages 1484-1504.

Waller, R. A. and Kemp, K. E. (1976) Computations of Bayesian t-Values for Multiple Comparisons, *Journal of Statistical Computation and Simulation*, 75, pages 169-172.

Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997.

**See Also**

[waller.test](#)

**Examples**

```
# Table Duncan-Waller K=100, F=1.2 pag 649 Steel & Torry
library(agricolae)
K<-100
Fc<-1.2
q<-c(8,10,12,14,16,20,40,100)
f<-c(seq(4,20,2),24,30,40,60,120)
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)
print(W.D)
```

---

waller.test

---

*Multiple comparisons, Waller-Duncan*


---

**Description**

The Waller-Duncan k-ratio t test is performed on all main effect means in the MEANS statement. See the K-RATIO option for information on controlling details of the test.

**Usage**

```
waller.test(y, trt, DFerror, MSerror, Fc, K = 100, group=TRUE, main = NULL,
  console=FALSE)
```

**Arguments**

y	model(aov or lm) or answer of the experimental unit
trt	Constant( only y=model) or vector treatment applied to each unit
DFerror	Degrees of freedom
MSerror	Mean Square Error
Fc	F Value
K	K-RATIO
group	TRUE or FALSE
main	Title
console	logical, print output

**Details**

It is necessary first makes a analysis of variance.

K-RATIO (K): value specifies the Type 1/Type 2 error seriousness ratio for the Waller-Duncan test. Reasonable values for KRATIO are 50, 100, and 500, which roughly correspond for the two-level case to ALPHA levels of 0.1, 0.05, and 0.01. By default, the procedure uses the default value of 100.

**Value**

y	class (aov or lm) or vector numeric
trt	constant (only y=model) or vector alphanumeric
DFerror	Numeric
MSerror	Numeric
Fc	Numeric
K	Numeric
group	Logic
main	Text

**Author(s)**

Felipe de Mendiburu

**References**

Waller, R. A. and Duncan, D. B. (1969). A Bayes Rule for the Symmetric Multiple Comparison Problem, *Journal of the American Statistical Association* 64, pages 1484-1504.

Waller, R. A. and Kemp, K. E. (1976) Computations of Bayesian t-Values for Multiple Comparisons, *Journal of Statistical Computation and Simulation*, 75, pages 169-172.

Steel & Torry & Dickey. Third Edition 1997 Principles and procedures of statistics a biometrical approach

**See Also**

[HSD.test](#), [LSD.test](#), [SNK.test](#) , [bar.err](#), [bar.group](#), [duncan.test](#)

**Examples**

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- waller.test(model,"virus", group=TRUE)
#startgraph
par(mfrow=c(2,2))
# variation: SE is error standard
# variation: range is Max - Min
bar.err(out$means,variation="SD",horiz=TRUE,xlim=c(0,45),bar=FALSE,
col=colors()[25],space=2, main="Standard deviation",las=1)
bar.err(out$means,variation="SE",horiz=FALSE,ylim=c(0,45),bar=FALSE,
col=colors()[15],space=2,main="SE",las=1)
bar.err(out$means,variation="range",ylim=c(0,45),bar=FALSE,col="green",
space=3,main="Range = Max - Min",las=1)
bar.group(out$groups,horiz=FALSE,ylim=c(0,45),density=8,col="red",
main="Groups",las=1)
#endgraph
# Old version HSD.test()
attach(sweetpotato)
df<-df.residual(model)
MSerror<-deviance(model)/df
Fc<-anova(model)["virus",4]
out <- waller.test(yield, virus, df, MSerror, Fc, group=TRUE)
print(out$mean)
detach(sweetpotato)
```

---

weatherSeverity

*Weather and Severity*

---

**Description**

Weather and Severity

**Usage**

```
weatherSeverity(weather, severity, dates, EmergDate, EndEpidDate, NoReadingsH,
RHthreshold)
```

**Arguments**

weather	object, see example
severity	object, see example
dates	vector dates



EmergDate	date
EndEpidDate	date
NoReadingsH	num, 1
RHthreshold	num, percentage

## Details

Weather and severity

## Value

Wfile	"Date", "Rainfall", "Tmp", "HumidHrs", "humidtmp"
Sfile	"Cultivar", "ApplSys", "dates", "nday", "MeanSeverity", "StDevSeverity"
EmergDate	date
EndEpidDate	date

## Note

All format data for date is yyyy-mm,dd, for example "2000-04-22". change with function as.Date()

## See Also

[lateblight](#)

## Examples

```
library(agricolae)
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 and threshold
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)
```

---

wilt

*Data of Bacterial Wilt (AUDPC) and soil*

---

### Description

Percentage of bacterial wilt and area under the curve of disease progression (AUDPC) relative tomato plants transplanted in different soil types artificially infested with *R.solanacearum* 133 days before.

### Usage

```
data(wilt)
```

### Format

A data frame with 13 observations on the following 15 variables.

place a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2

Day7 a numeric vector

Day11 a numeric vector

Day15 a numeric vector

Day19 a numeric vector

Day23 a numeric vector

Day27 a numeric vector

Day31 a numeric vector

Day35 a numeric vector

Day39 a numeric vector

Day43 a numeric vector

Day47 a numeric vector

Day51 a numeric vector

AUDPC a numeric vector

relative a numeric vector

### Details

Percentajes bacterial wilt. Day7 = evaluated to 7 days, Days11 = evaluated to 11 days. see `data(soil)` and `data(ralstonia)`

### Source

Experimental field, 2004. Data Kindly provided by Dr. Sylvie Priou, Liliam Gutarra and Pedro Aley.

## References

International Potato Center. CIP - Lima Peru.

## Examples

```
library(agricolae)
data(wilt)
days<-c(7,11,15,19,23,27,31,35,39,43,47,51)
AUDPC<-audpc(wilt[, -1], days)
relative<-audpc(wilt[, -1], days, type="relative")
```

---

yacon

*Data Yacon*

---

## Description

The yacon (*Smallanthus sonchifolius*) is a plant native to the Andes, considered a traditional crop in Peru and natural source of FOS, which is a type of carbohydrate that can not be digested by the and the human body that have joined several beneficial properties in health, such as improve the absorption of calcium, reducing the level of triglycerides and cholesterol and stimulate better gastrointestinal function.

## Usage

```
data(yacon)
```

## Format

A data frame with 432 observations on the following 19 variables.

locality a factor with levels, Cajamarca, Lima, Oxapampa in PERU

site a numeric vector

dose a factor with levels F0 F150 F80

entry a factor with levels AKW5075 AMM5136 AMM5150 AMM5163 ARB5125 CLLUNC118 P1385 SAL136

replication a numeric vector, replications

height a numeric vector, plant height, centimeters

stalks a numeric vector, number of stalks

wfr a numeric vector, weight of fresh roots, grams

wff a numeric vector, weight of fresh foliage, grams

wfk a numeric vector, weight fresh kroner, grams

roots a numeric vector, matter of dried roots, grams

FOS a numeric vector, fructo-oligosaccharides, porcentaje

glucose a numeric vector, porcentaje  
 fructose a numeric vector, porcentaje  
 sucrose a numeric vector, porcentaje  
 brix a numeric vector, degrees Brix  
 foliage a numeric vector, matter dry foliage, grams  
 dry a numeric vector, dry matter kroner, grams  
 IH a numeric vector, Index harvest, 0 to 1

### Details

Proportion or fraction of the plant that is used (seeds, fruit, root) on dry basis. Part usable in a proportion of total mass dissected. Plant of frijol, weight = 100g and frijol = 50g then, IH = 50/100 = 0.5 or 50 porcentaje. Degrees Brix is a measurement of the mass ratio of dissolved sugar to water in a liquid.

### Source

CIP. Experimental field, 2003, Data Kindly provided by Ivan Manrique and Carolina Tasso.

### References

International Potato Center. CIP - Lima Peru.

### Examples

```
library(agricolae)
data(yacon)
str(yacon)
```

---

zigzag

*order plot in serpentine*

---

### Description

applied to designs: complete block, latin square, graeco, split plot, strip plot, lattice, alpha lattice, Augmented block, cyclic, Balanced Incomplete Block and factorial.

### Usage

```
zigzag(outdesign)
```

### Arguments

outdesign      output design

**Value**

fieldbook      restore field book

**Author(s)**

Felipe de Mendiburu

**See Also**

[design.ab](#), [design.alpha](#), [design.bib](#), [design.split](#) , [design.cyclic](#) , [design.dau](#) , [design.graeco](#),  
[design.lattice](#), [design.lsd](#), [design.rcbd](#), [design.strip](#)

**Examples**

```
library(agricolae)
trt<-letters[1:5]
r<-4
outdesign <- design.rcbd(trt,r,seed=9)
fieldbook <- zigzag(outdesign)
```

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