Package ‘agricolae’

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Type Package

Title Statistical Procedures for Agricultural Research

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Imports MASS, nlme, cluster, AlgDesign, graphics

Description Original idea was presented in the thesis ``A statistical analysis tool for agricultural research'' to obtain the degree of Master on science, National Engineering University (UNI), Lima-Peru. Some experimental data for the examples come from the CIP and others research. 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

NeedsCompilation no

Depends R (>= 2.10)

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R topics documented:

`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.

Details

Package:	agricolae
Type:	Package
Version:	1.3-7
Date:	2023-10-22
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, REGW, 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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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)
model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
model$ANOVA
# see help(plot.AMMI)
# biplot
plot(model)
# biplot PC1 vs Yield
plot(model, first=0,second=1, number=TRUE)
# Example 2
data(CIC)
data1<-CIC$comas[,c(1,6,7,17,18)]
data2<-CIC$oxapampa[,c(1,6,7,19,20)]
cic <- rbind(data1,data2)
model<-with(cic,AMMI(Locality, Genotype, Rep, relative))
model$ANOVA
plot(model,0,1,angle=20,ecol="brown")
# Example 3
# Only means. Mean square error is well-known.
data(sinRepAmmi)
REP <- 3
MSerror <- 93.24224
#startgraph
model<-with(sinRepAmmi,AMMI(ENV, GEN, REP, YLD, MSerror,PC=TRUE))
# print anova
print(model$ANOVA,na.print = "")
```

```
# Biplot with the one restored observed.
plot(model,0,1)
# 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 BIPLOT function but not for the TRIPLOT one.

Value

Genotypes within and outside the area.

`distance`	Distance from genotype to origin (0,0)

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

Vector with relative or absolute audpc.

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

Vector with relative or absolute audps.

Author(s)

Felipe de Mendiburu

References

Ivan Simko, and Hans-Peter Piepho, (2012). The area under the disease progress stairs: Calculation, advantage, and application. Phytopathology 102:381- 389.

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

Arguments

`x`	object means of the comparisons the LSD.test, HSD.test,...,etc
`variation`	SE=standard error, range=Max-Min or IQR=interquartil range
`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 and Median.test.

Value

A list with numeric vectors giving the coordinates of all the bar midpoints drawn.

`x`	eje-1 coordinate
`height`	eje-2 coordinate by group

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")
oldpar<-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(oldpar)
oldpar<-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(oldpar)
#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, Kruskall, 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, decreasing=TRUE, ...)
```

Arguments

`x`	Object created by a test of comparison
`horiz`	Horizontal or vertical bars
`decreasing`	Logical, decreasing order of the mean
`...`	Parameters of the function barplot()

Details

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

Value

A list with numeric vectors giving the coordinates of all the bar midpoints drawn.

`x`	eje-1 coordinate
`height`	eje-2 coordinate by group

Author(s)

Felipe de Meniburu

See Also

`LSD.test`, `HSD.test`, `kruskal` , `friedman`, `durbin.test`, `waller.test` , `plot.group`

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)
oldpar<-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")
# Example 2
library(agricolae)
x <- 1:4
y <- c(0.29, 0.44, 0.09, 0.49)
xy <- data.frame(x,y,y)
par(oldpar)
oldpar<-par(cex=1.5)
bar.group(xy,density=30,angle=90,col="brown",border=FALSE,ylim=c(0,0.6),lwd=2,las=1)
par(oldpar)
```

`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 differente. duncan: Duncan's new multiple range test waller: Waller-Duncan test. snk: Student-Newman-Keuls (SNK)

Value

parameters	Design parameters
statistics	Statistics of the model
comparison	Comparison between treatments
means	Adjusted mean and statistics summary
groups	Grouping of treatments

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

DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

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)
monovinyl<-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,monovinyl,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,monovinyl,test="waller",group=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=TRUE,console=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=FALSE,console=TRUE)
rm(run,psi,monovinyl,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`	model analysis (I, II or III) of caroline design

and variance and additive variance of male, female and male.female interaction.

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 percentaje 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 percentaje, 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 conductive 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 boostrap and to such calculate the relative frequency with members of the clusters.

Usage

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

Value

`table.dend`	The groups and consensus percentage
`dendrogram`	The class object is hclust, dendrogram plot
`duplicate`	Homonymous elements

Author(s)

F. de Mendiburu

References

An Introduction to the Boostrap. 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)
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 mediasn 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 averarge rank.

Source

Book: Practical Nonparametric Statistics.

References

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

Examples

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

`correl` *Correlation Coefficient*

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

The correlation of x,y vector with the statistical value and its probability

Author(s)

Felipe de Mendiburu

References

Numerical Recipes in C. Second Edition.

See Also

correlation

Examples

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

---

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

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 , Kendall and lin's concordance index. 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", "lin")
,alternative="two.sided")
```

Arguments

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

Details

Parameters equal to function cor()

Value

The correlation matrix with its probability

Author(s)

Felipe de Mendiburu

References

Lin LI. A concordance correlation coefficient to evaluate reproducibility. Biometrics. 1989; 45, 255-268.

See Also

`correl`

Examples

```
library(agricolae)
data(soil)
# example 1
analysis<-correlation(soil[,2:8],method="pearson")
analysis
# Example 2: correlation between pH, variable 2 and other elements from soil.
analysis<-with(soil,correlation(pH,soil[,3:8],method="pearson",alternative="less"))
analysis
# Example 3: correlation between pH and clay method kendall.
with(soil,correlation(pH,clay,method="kendall", alternative="two.sided"))
```

`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

Returns the coefficient of variation of the experiment according to the applied statistical model

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

Returns the coefficient of variation of the similarity model

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 differente. The controls can have different repetitions, at least two, do not use missing data.

Value

`means`	Statistical summary of the study variable
`parameters`	Design parameters
`statistics`	Statistics of the model
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups
`SE.difference`	Standard error of: Two Control Treatments Two Augmented Treatments Two Augmented Treatments(Different Blocks) A Augmented Treatment and A Control Treatment
`vartau`	Variance-covariance matrix of the difference in treatments

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, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

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

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 whitch 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` *Omitting the rows or columns with missing observations of a matrix (NA)*

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,randomization=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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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` *Alpha design type (0,1)*

Description

Generates an alpha designs starting from the alpha design fixing under the series formulated by Patterson and Williams. These designs are generated by the alpha arrangements. They are similar to the lattice designs, but the tables are rectangular s by k (with s blocks and k<s columns. The number of treatments should be equal to s*k and all the experimental units r*s*k (r replications).

Usage

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

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
`randomization`	TRUE or FALSE - randomize

Details

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

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

Value

`parameters`	Design parameters
`statistics`	Design statistics
`sketch`	Design sketch
`book`	Fieldbook

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, r=NULL, serie = 2, seed = 0, kinds = "Super-Duper",
maxRep=20,randomization=TRUE)
```

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
`maxRep`	repetition maximum
`randomization`	TRUE or FALSE - randomize

Details

The package AlgDesign is necessary.

if r = NULL, then it calculates the value of r smaller for k defined. In the case of r = value, then the possible values for "r" is calculated

K is the smallest integer number of treatments and both values are consistent in design.

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

Value

`parameters`	Design parameters
`statistics`	Design statistics
`sketch`	Design sketch
`book`	Fieldbook

Author(s)

Felipe de Mendiburu

References

1. Experimental design. Cochran and Cox. Second edition. Wiley Classics Library Edition published 1992

2. Optimal Experimental Design with R. Dieter Rasch, Jurgen Pilz, Rob Verdooren and Albrecht Gebhardt. 2011 by Taylor and Francis Group, LLC CRC Press is an imprint of Taylor and Francis Group, an Informa business.

3. 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])
matrix(plots,byrow=TRUE,ncol=k)
print(outdesign$sketch)
# 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",randomization=TRUE)
```

Arguments

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

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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 <= 10.

Usage

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

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
`randomization`	TRUE or FALSE - randomize

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`	Design parameters
`sketch`	Design sketch
`book`	Fieldbook

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

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

Usage

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

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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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). Bometrics, 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$book
by(book,book[2],function(x) paste(x[,1],"-",as.character(x[,3])))
# write in hard disk
# write.table(book,"dau.txt", row.names=FALSE, sep="\t")
# file.show("dau.txt")
# Augmented designs in Completely Randomized Design
trt<-c(T1,T2)
r<-c(4,4,4,4,1,1,1,1,1,1,1)
outdesign <- design.crd(trt,r)
outdesign$book
```

---

design.graeco *Graeco - latin square design*

Description

A graeco - latin square is a KxK pattern that permits the study of k treatments simultaneously with three different blocking variables, each at k levels.

The function is only for squares of the odd numbers and even numbers (4, 8, 10 and 12)

Usage

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

Arguments

trt1	Treatments
trt2	Treatments
serie	number plot, 1: 11,12; 2: 101,102; 3: 1001,1002

seed	seed
kinds	method for to randomize
randomization	TRUE or FALSE - randomize

Details

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

Value

parameters	Design parameters
book	Fieldbook

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$book
plots <-as.numeric(graeco[,1])
print(outdesign$sketch)
print(matrix(plots,byrow=TRUE,ncol=4))
# 10 x 10
T1 <- letters[1:10]
T2 <- 1:10
outdesign <-  design.graeco(T1,T2,serie=2)
print(outdesign$sketch)
```

`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",randomization=TRUE)
```

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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`statistics`	Design statistics
`sketch`	Design sketch
`book`	Fieldbook

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,randomization=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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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$book
print(outdesign$sketch)
print(lsd) # field book.
plots <-as.numeric(lsd[,1])
print(matrix(plots,byrow = TRUE, ncol = 4))
# Write on hard disk.
# write.table(lsd,"lsd.txt", row.names=FALSE, sep="\t")
# file.show("lsd.txt")
```

`design.mat` *Experimental design matrix*

Description

Generate the design matrix from the fieldbook generated by an experimental plan or a dataframe for analysis.

Usage

```
design.mat(book, locations)
```

Arguments

book	data frame or matrix, field book
locations	numeric, column position of the field book

Value

X is matrix design.

Author(s)

Felipe de Mendiburu

See Also

design.ab, design.alpha,design.bib, design.crd , design.cyclic , design.split , design.graeco, design.lattice, design.lsd, design.rcbd, design.strip, design.dau

Examples

```
# dataframe: data analysis
library(agricolae)
data(sweetpotato)
X<-design.mat(sweetpotato,1)
print(X)
# fieldbook: RCBD design
trt <- LETTERS[1:4]
r<-3
plan<-design.rcbd(trt,r,seed=11)
X<-design.mat(plan$book,2:3)
print(X)
```

---

design.rcbd *Randomized Complete Block Design*

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,randomization=TRUE )
```

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
randomization	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`sketch`	Design sketch
`book`	Fieldbook

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$book # field book
# write in hard disk
# write.table(book,"rcbd.txt", row.names=FALSE, sep="\t")
# file.show("rcbd.txt")
# Plots in field model ZIGZAG
fieldbook <- zigzag(outdesign)
print(outdesign$sketch)
print(matrix(fieldbook[,1],byrow=TRUE,ncol=5))
# 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,randomization=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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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",randomization=TRUE)
```

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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`book`	Fieldbook

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 *Incomplete Latin Square Design*

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
,randomization=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
`randomization`	TRUE or FALSE - randomize

Details

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

Value

`parameters`	Design parameters
`sketch`	Design sketch
`book`	Fieldbook

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 Yersy

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")
r<-3
outdesign <-design.youden(varieties,r,serie=2,seed=23)
youden <- outdesign$book
print(outdesign$sketch)
plots <-as.numeric(youden[,1])
print(matrix(plots,byrow=TRUE,ncol=r))
print(youden) # field book.
# Write on hard disk.
# write.table(youden,"youden.txt", row.names=FALSE, sep="\t")
# file.show("youden.txt")
```

---

diffograph *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 (Fisher), duncan, Tukey (HSD), Student Newman Keul (SNK), Scheffe, Ryan, Einot and Gabriel and Welsch (REGW), Kruskal Wallis, Friedman and Waerden.

Usage

```
diffograph(x, main=NULL,color1="red",color2="blue",color3="black",
cex.axis=0.8,las=1,pch=20,bty="l",cex=0.8,lwd=1,xlab="",ylab="",...)
```

Arguments

x	Object created by a test of comparison, group=FALSE
main	The main title (on top)
color1	non significant color

color2	significant color
color3	center line color
cex.axis	parameters of the plot()
las	parameters of the plot()
pch	parameters of the plot()
bty	parameters of the plot()
cex	parameters of the plot()
lwd	parameters of the plot()
xlab	parameters of the plot()
ylab	parameters of the plot()
...	Other parameters of the function plot()

Details

The graph.diff function should be used for functions: LSD, duncan, SNK, scheffe, REGW, HSD, kruskal, friedman and waerden test.

Value

x	list, object comparison test

Author(s)

Felipe de Mendiburu

References

Multiple comparisons theory and methods. Departament of statistics the Ohio State University. USA, 1996. Jason C. Hsu. Chapman Hall/CRC

See Also

LSD.test, HSD.test, duncan.test, SNK.test, scheffe.test, REGW.test, kruskal,friedman, waerden.test

Examples

```
# Example 1
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
x<- LSD.test(model,"virus",alpha=0.01,group=FALSE)
diffograph(x,cex.axis=0.8,xlab="Yield",ylab="")
# Example 2
x<- REGW.test(model,"virus",alpha=0.01,group=FALSE)
diffograph(x,cex.axis=0.6,xlab="Yield",ylab="",color1="brown",color2="green")
```

`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` *Duncan's new multiple range test*

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.

if y = model, then to apply the instruction:
duncan.test(model, "trt", alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
where the model class is aov or lm.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`duncan`	Critical Range Table
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

1. Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997
2. Multiple comparisons theory and methods. Departament of statistics the Ohio State University. USA, 1996. Jason C. Hsu. Chapman Hall/CRC.

See Also

BIB.test, DAU.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

Examples

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
out <- duncan.test(model,"virus",
main="Yield of sweetpotato. Dealt with different virus")
plot(out,variation="IQR")
duncan.test(model,"virus",alpha=0.01,console=TRUE)
# version old duncan.test()
df<-df.residual(model)
MSerror<-deviance(model)/df
out <- with(sweetpotato,duncan.test(yield,virus,df,MSerror, group=TRUE))
plot(out,horiz=TRUE,las=1)
print(out$groups)
```

---

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

Details

The post hoc test is using the criterium Fisher's least significant difference.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`means`	Statistical summary of the study variable
`rank`	rank table of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

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

See Also

`BIB.test`, `DAU.test`, `duncan.test`, `friedman`, `HSD.test`, `kruskal`, `LSD.test`, `Median.test`, `PBIB.test`, `REGW.test`, `scheffe.test`, `SNK.test`, `waerden.test`, `waller.test`, `plot.group`

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")
plot(out)
```

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

Description

The data consist of b-blocks mutually independent k-variate random variables Xij, i=1,..,b; j=1,..k. The random variable X is in block i and is associated with treatment j. 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

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

Details

The post hoc friedman test is using the criterium Fisher's least significant difference (LSD)

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

BIB.test, DAU.test, duncan.test, durbin.test, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

Examples

```
library(agricolae)
data(grass)
out<-with(grass,friedman(judge,trt, evaluation,alpha=0.05, group=TRUE,console=TRUE,
main="Data of the book of Conover"))
#startgraph
plot(out,variation="IQR")
#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.

Tecnnologies: 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`	values 0,1,2 and 3 are the axis styles. 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`	Relative frequency, height
`density`	Density frequency, height

Author(s)

Felipe de Mendiburu

See Also

`polygon.freq`, `table.freq`, `stat.freq`,`inter.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 frecuency
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 homeowern.

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 Farran, 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` `AO80432-1` `AO84275-3` `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)
model1<-with(site1,lineXtester(Replication, Female, Male, v1))
DFe <- df.residual(model1)
CMe <- deviance(model1)/DFe
test1 <- with(site1,HSD.test(v1, Factor,DFe,CMe))
test2 <- with(site1,HSD.test(v1, Treatment,DFe,CMe))
model22<-with(site2,lineXtester(Replication, Female, Male, v3))
model3<-with(site3,lineXtester(Replication, Female, Male, v4))
```

---

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

The merge clusters is printed.

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,
unbalanced=FALSE,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
unbalanced	TRUE or FALSE. not equal replication
console	logical, print output

Details

It is necessary first makes a analysis of variance.

if y = model, then to apply the instruction:
HSD.test (model, "trt", alpha = 0.05, group = TRUE, main = NULL, unbalanced=FALSE, console=FALSE)
where the model class is aov or lm.

Value

statistics	Statistics of the model
parameters	Design parameters
means	Statistical summary of the study variable
comparison	Comparison between treatments
groups	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

1. Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997
2. Multiple comparisons theory and methods. Departament of statistics the Ohio State University. USA, 1996. Jason C. Hsu. Chapman Hall/CRC.

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

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
# Variation range: max and min
plot(out)
#endgraph
out<-HSD.test(model,"virus", group=FALSE)
print(out$comparison)
# Old version HSD.test()
df<-df.residual(model)
MSerror<-deviance(model)/df
with(sweetpotato,HSD.test(yield,virus,df,MSerror, group=TRUE,console=TRUE,
main="Yield of sweetpotato. Dealt with different virus"))
```

`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. DEHGHANI. 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 genotype x environment 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)
model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
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

Index and confidence intervals.

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 Boostrap. 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, PLOT=TRUE,...)
```

Arguments

`data`	dataframe or matrix
`PLOT`	graphics, TRUE or FALSE
`...`	Parameters of the plot()

Details

Vx=V(x)/x b

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

Value

`model`	function pattern of uniformity
`uniformity`	Table of the soil uniformity

Author(s)

Felipe de Mendiburu

References

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

Examples

```
library(agricolae)
data(rice)
#startgraph
table<-index.smith(rice,
 main="Relationship between CV per unit area and plot size",col="red")
#endgraph
uniformity <- data.frame(table$uniformity)
uniformity
# regression variance per unit area an plot size.
model <- lm(Vx ~ I(log(Size)),uniformity)
coeff <- coef(model)
x<-1:max(uniformity$Size)
Vx<- coeff[1]+coeff[2]*log(x)
#startgraph
plot(x,Vx, type="l", col="blue",
 main="Relationship between variance per unit area and plot size")
points(uniformity$Size,uniformity$Vx)
#endgraph
```

`inter.freq` *Class intervals*

Description

List class intervals.

Usage

```
inter.freq(x)
```

Arguments

x	class graph.freq, histogram or numeric

Value

It show interval classes.

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)
inter.freq(h)
# example 2
x<-seq(10,40,5)
y<-c(2,6,8,7,3,4)
inter.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 ad the .frequencies of them.

Usage

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

Arguments

histogram	Class graph.freq
join	vector

Value

New histogram with union of classes.

Author(s)

Felipe de Mendiburu

See Also

polygon.freq, table.freq, stat.freq, inter.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

The correlation of data1, data2 vector with the statistical value and its probability

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 alpha parameter by default is 0.05. Post hoc test is using the criterium Fisher's least significant difference. The adjustment methods include the Bonferroni correction and others.

Usage

```
kruskal(y, trt, alpha = 0.05, p.adj=c("none","holm","hommel",
"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.
For the adjustment methods, see the function p.adjusted.
p-adj = "none" is t-student.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

`BIB.test`, `DAU.test`, `duncan.test`, `durbin.test`, `friedman`, `HSD.test`, `LSD.test`, `Median.test`, `PBIB.test`, `REGW.test`, `scheffe.test`, `SNK.test`, `waerden.test`, `waller.test`, `plot.group`

Examples

```
library(agricolae)
data(corn)
str(corn)
comparison<-with(corn,kruskal(observation,method,group=TRUE, main="corn"))
comparison<-with(corn,kruskal(observation,method,p.adj="bon",group=FALSE, main="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 *Setting the last character of a chain*

Description

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

Usage

```
lastC(x)
```

Arguments

x	letters

Value

x	Returns the last character of a string

Author(s)

Felipe de Mendiburu

See Also

plot.group

Examples

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

`lateblight` *LATEBLIGHT - Simulator for potato late blight Version LB2004*

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()

Author(s)

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References

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

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 and SCA Effects.
Standard Errors for Combining Ability Effects.
Genetic Components.
...
Proportional contribution of lines, testers and their interactions to total variance

Value

return anova(formula = Y ~ Replications + Treatments).
where the Treatments contains parents, crosses and crosses vs Parents.
The crosses contains Lines, Testers and its interaction .

Author(s)

Felipe de Mendiburu

References

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979. Hierarchial and factorial mating designs for quantitative genetic analysis in tetrasomic potato. R. Ortis; 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)
output1<-with(site1,lineXtester(Replication, Female, Male, v2))
# example 2
data(LxT)
str(LxT)
output2<-with(LxT,lineXtester(replication, line, tester, yield))
```

`LSD.test` *Multiple comparisons, "Least significant difference" and Adjust P-values*

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","hommel",
"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.
For the adjustment methods, see the function p.adjusted.
p-adj ="none" is t-student.

It is necessary first makes a analysis of variance.
if model=y, then to apply the instruction:
LSD.test(model, "trt", alpha = 0.05, p.adj=c("none","holm","hommel", "hochberg", "bonferroni", "BH", "BY", "fdr"), group=TRUE, main = NULL,console=FALSE)
where the model class is aov or lm.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

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

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

Examples

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- LSD.test(model,"virus", p.adj="bonferroni")
#stargraph
# Variation range: max and min
plot(out)
#endgraph
# Old version LSD.test()
df<-df.residual(model)
MSerror<-deviance(model)/df
out <- with(sweetpotato,LSD.test(yield,virus,df,MSerror))
#stargraph
# Variation interquartil range: Q75 and Q25
plot(out,variation="IQR")
#endgraph
out<-LSD.test(model,"virus",p.adj="hommel",console=TRUE)
plot(out,variation="SD") # variation standard deviation
```

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

Arguments

y	Variable response
trt	Treatments
alpha	error type I
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
group	TRUE or FALSE
main	Title
console	logical, print output

Details

The data consist of k samples of possibly unequal sample size.
Greater: is the number of values that exceed the median of all data and
LessEqual: is the number less than or equal to the median of all data.

Value

statistics	Statistics of the model
parameters	Design parameters
medians	Statistical summary of the study variable
comparison	Comparison between treatments
groups	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

Examples

```
library(agricolae)
# example 1
data(corn)
out<-with(corn,Median.test(observation,method,console=FALSE))
z<-bar.err(out$medians,variation = "range",ylim=c(0,120),
           space=2,border=4,col=3,density=10,angle=45)
# example 2
out<-with(corn,Median.test(observation,method,console=FALSE,group=FALSE))
print(out$comparison)
```

---

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

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

Value

Generate random numbers with empirical distribution.

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)
op<-par(mfrow=c(1,2),cex=0.8,mar=c(2,3,0,0))
h1<-graph.freq(x=breaks,counts=counts,plot=FALSE)
r<-montecarlo(h, k=1000)
```

```
plot(h1,frequency = 3,ylim=c(0,0.008))
text(90,0.006,"Population\n100 obs.")
h2<-graph.freq(r,breaks,frequency = 3,ylim=c(0,0.008))
lines(density(r),col="blue")
text(90,0.006,"Montecarlo\n1000 obs.")
par(op)
```

`natives` *Data of native potato*

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` *Nonadditivity model test*

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

P, Q and non-additivity analysis of variance

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
analysis<-with(potato,nonadditivity(cutting, date, variety, df, MSerror))
```

`normal.freq` *Normal curve on the histogram*

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

Author(s)

Felipe de Mendiburu

See Also

`polygon.freq`, `table.freq`, `stat.freq`, `inter.freq`, `sturges.freq`, `join.freq`, `ogive.freq`, `graph.freq`

Examples

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

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`	values 0,1,2 and 3 are the axis styles. see plot()
`...`	Parameters of the plot()

Value

Ogive points.

Author(s)

Felipe de Mendiburu

See Also

`polygon.freq`, `table.freq`, `stat.freq`, `inter.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")
plot(points,type="b",pch=16,las=1,bty="l")
```

`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.

Usage

```
order.group(trt, means, N, MSerror, Tprob, std.err, parameter=1, snk=0,
DFerror=NULL,alpha=NULL,sdtdif=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
`sdtdif`	standard deviation of difference in BIB
`vartau`	matrix var-cov in PBIB
`console`	logical, print output

Details

This function was changed by orderPvalue function that use agricolae. Now the grouping in agricolae is with the probability of the treatments differences and alpha level.

Value

The output is data frame.

`trt`	Treatment Levels, Factor
`means`	height, Numeric
`M`	groups levels, Factor
`N`	replications, Numeric
`std.err`	Standard error, Numeric

Note

It is considered 81 labels as maximum for the formation of groups, greater number will not have label.

Author(s)

Felipe de Mendiburu

See Also

orderPvalue

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)
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=FALSE)
print(groups)
```

`orderPvalue` *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

```
orderPvalue(treatment, means, alpha, pvalue, console)
```

Arguments

`treatment`	treatment
`means`	means of treatment
`alpha`	Alpha value, significante value to comparison
`pvalue`	Matrix of probabilities to comparison
`console`	logical, print output

Value

The means and groups for treatments.

Note

It is considered 81 labels as maximum for the formation of groups, greater number will not have label.

Author(s)

Felipe de Mendiburu

Examples

```
library(agricolae)
treatments <- c("A","B","C")
means<-c(2,5,3)
alpha <- 0.05
pvalue<-matrix(1,nrow=3,ncol=3)
pvalue[1,2]<-pvalue[2,1]<-0.03
pvalue[1,3]<-pvalue[3,1]<-0.10
pvalue[2,3]<-pvalue[3,2]<-0.06
out<-orderPvalue(treatments,means,alpha,pvalue,console=TRUE)
barplot(out[,1],names.arg = row.names(out),col=colors()[84:87])
legend("topright",as.character(out$groups),pch=15,col=colors()[84:87],box.col=0)
```

---

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` `CHRYOMELIDAE` `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, Deparment 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

Direct and indirect effects and residual Effect^2.

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 resoluble 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.
The PBIB.test() function can be called inside a function (improvement by Nelson Nazzicari, Ph.D. Bioinformatician)

Value

`ANOVA`	Analysis of variance
`method`	Estimation method: REML, ML and VC
`parameters`	Design parameters
`statistics`	Statistics of the model
`model`	Object: estimation model
`Fstat`	Criterion AIC and BIC
`comparison`	Comparison between treatments
`means`	Statistical summary of the study variable
`groups`	Formation of treatment groups
`vartau`	Variance-Covariance Matrix

Author(s)

F. de Mendiburu

References

1. Iterative Analysis of Generalizad 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`, `DAU.test`, `duncan.test`, `durbin.test`, `friedman`, `HSD.test`, `kruskal`, `LSD.test`, `Median.test`, `REGW.test`, `scheffe.test`, `SNK.test`, `waerden.test`, `waller.test`, `plot.group`

Examples

```
require(agricolae)
# alpha design
Genotype<-c(paste("gen0",1:9,sep=""),paste("gen",10:30,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$book[,3]<- gl(20,3)
dbook<-book$book
# dataset
yield<-c(5,2,7,6,4,9,7,6,7,9,6,2,1,1,3,2,4,6,7,9,8,7,6,4,3,2,2,1,1,2,
     1,1,2,4,5,6,7,8,6,5,4,3,1,1,2,5,4,2,7,6,6,5,6,4,5,7,6,5,5,4)
rm(Genotype)
# not run
# analysis
# require(nlme) # method = REML or LM in PBIB.test and require(MASS) method=VC
model <- with(dbook,PBIB.test(block, Genotype, replication, yield, k=3, method="VC"))
# model$ANOVA
# plot(model,las=2)
```

---

plot.AMMI *PLOT AMMI*

Description

Biplot AMMI.

Usage

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

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
number	TRUE or FALSE names or number genotypes
gcol	genotype color
ecol	environment 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

Produce graphs biplot.

Author(s)

Felipe de Mendiburu

See Also

AMMI

Examples

```
library(agricolae)
data(plrv)
model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield))
# biplot PC2 vs PC1
plot(model)
## plot PC1 vs Yield
plot(model,0,1,gcol="blue",ecol="green")
```

---

plot.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

```
## 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	values 0,1,2 and 3 are the axis styles. 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	Relative frequency, height
density	Density frequency, height

Author(s)

Felipe de Mendiburu

See Also

polygon.freq, table.freq, stat.freq,inter.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 frecuency
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")
```

---

plot.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, Kruskall, Waller-Duncan, Friedman or Durbin. It can also display the 'average' value over each bar in a bar chart.

Usage

```
## S3 method for class 'group'
plot(x,variation=c("range","IQR","SE","SD"), decreasing = TRUE,
        horiz=FALSE,col=NULL,xlim=NULL,ylim=NULL,main=NULL,cex=NULL,hy=0,...)
```

Arguments

x	Object created by a test of comparison
variation	in lines by range, IQR, standard deviation or error
decreasing	Logical, decreasing order of the mean
horiz	Horizontal or vertical image
col	line colors
xlim	optional, axis x limits
ylim	optional, axis y limits
main	optional, main title
cex	optional, group label size
hy	optional, default =0, sum group label position
...	Parameters of the function barplot()

Details

The output is a vector that indicates the position of the treatments on the coordinate axes.

Author(s)

Felipe de Mendiburu

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, waller.test

Examples

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison<- LSD.test(model,"virus",alpha=0.01,group=TRUE)
#startgraph
op<-par(cex=1.5)
plot(comparison,horiz=TRUE,xlim=c(0,50),las=1)
title(cex.main=0.8,main="Comparison between\ntreatment means",xlab="Yield",ylab="Virus")
#endgraph
par(op)
```

---

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)
b<-nlevels(plots$B)
a<-nlevels(plots$A)
r<-nlevels(plots$block)
dfa <- df.residual(model$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 <-with(plots,LSD.test(yield,A,dfa,Ea))
comparison2 <-with(plots,LSD.test(yield[B=="b1"],A[B=="b1"],dfab,Eab))
comparison3 <-with(plots,LSD.test(yield[B=="b2"],A[B=="b2"],dfab,Eab))
comparison4 <-with(plots,LSD.test(yield[B=="b3"],A[B=="b3"],dfab,Eab))
# Comparison B, B(a1), B(a2)
comparison5 <-with(plots,LSD.test(yield,B,dfb,Eb))
comparison6 <-with(plots,LSD.test(yield[A=="a1"],B[A=="a1"],dfb,Eb))
comparison7 <-with(plots,LSD.test(yield[A=="a2"],B[A=="a2"],dfb,Eb))
```

---

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` *The polygon of frequency on the histogram*

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

Author(s)

Felipe de Mendiburu Delgado

See Also

polygon.freq, table.freq, stat.freq, inter.freq, sturges.freq, join.freq, graph.freq, normal.freq

Examples

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

---

potato *Data of cutting*

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` *Data of assessment of the population in the soil R.solanacearum*

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 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

list objects:
Number regressions.
Residual.
Difference of regression.
DF.homgeneity (homogenity degree free).
DF.Residual (degree free error).
F.value. Test statitics.
P.value. P Value (Significant
Criterion. conclusion

Author(s)

Felipe de Mendiburu

References

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

Examples

```
library(agricolae)
data(frijol)
evaluation<-with(frijol,reg.homog(technology,index,production))
# Example 2. Applied Regression Analysis a Research tools
# 1988. John O.Rawlings. Wadsworth & brooks/cole Advanced Books
# & Software. Pacific Grove. Califonia.
```

```
# 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)
```

`REGW.test` *Ryan, Einot and Gabriel and Welsch multiple range test*

Description

Multiple range tests for all pairwise comparisons, to obtain a confident inequalities multiple range tests.

Usage

```
REGW.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.

if y = model, then to apply the instruction:
REGW.test (model, "trt", alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
where the model class is aov or lm.

Value

statistics	Statistics of the model
parameters	Design parameters
regw	Critical Range Table
means	Statistical summary of the study variable
comparison	Comparison between treatments
groups	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

Multiple comparisons theory and methods. Departament of statistics the Ohio State University. USA, 1996. Jason C. Hsu. Chapman Hall/CRC

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, scheffe.test, SNK.test, waerden.test, waller.test, plot.group

Examples

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
out<- REGW.test(model,"virus",
main="Yield of sweetpotato. Dealt with different virus")
print(out)
REGW.test(model,"virus",alpha=0.05,console=TRUE,group=FALSE)
```

---

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

lm(formula = CV ~ I(1/marker))
Table with variation coefficient by number of markers

Author(s)

Felipe de Mendiburu

References

Efron, B., Tibshirani, R. (1993) An Introduction to the Boostrap. 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$model)
Rsq<-summary(study$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 solution with resampling.

Author(s)

Felipe de Mendiburu

References

Efron, B., Tibshirani, R. (1993) An Introduction to the Boostrap. 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/m2) 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

```
# Analisys the Mother/Baby Trial Design
library(agricolae)
data(RioChillon)
# First analysis the Mother Trial Design.
model<-aov(yield ~ block + clon, RioChillon$mother)
anova(model)
cv.model(model)
comparison<-with(RioChillon$mother,LSD.test(yield,clon, 18, 4.922, group=TRUE))
# Second analysis the babies Trial.
comparison<-with(RioChillon$babies,friedman(farmer,clon, yield, group=TRUE))
# 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.

if y = model, then to apply the instruction:
scheffe.test (model, "trt", alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
where the model class is aov or lm.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

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

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, SNK.test, waerden.test, waller.test, plot.group

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()
df<-df.residual(model)
MSerror<-deviance(model)/df
Fc<-anova(model)["virus",4]
out <- with(sweetpotato,scheffe.test(yield, virus, df, MSerror, Fc))
print(out)
```

---

similarity *Matrix of similarity in binary data*

Description

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

Usage

```
similarity(A)
```

Arguments

A	Matrix, data binary

Value

Distance matrix. Class = dist.

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 *Simulation of the linear model under normality*

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	ouput 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 *Finding the skewness coefficient*

Description

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

Usage

```
skewness(x)
```

Arguments

x	a numeric vector

Value

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 — *Student-Newman-Keuls (SNK)*

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.

if y = model, then to apply the instruction:
SNK.test (model, "trt", alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
where the model class is aov or lm.

Value

`statistics`	Statistics of the model
`parameters`	Design parameters
`snk`	Critical Range Table
`means`	Statistical summary of the study variable
`comparison`	Comparison between treatments
`groups`	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

1. Principles and procedures of statistics a biometrical approach Steel & Torry & Dickey. Third Edition 1997
2. Multiple comparisons theory and methods. Departament of statistics the Ohio State University. USA, 1996. Jason C. Hsu. Chapman Hall/CRC.

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, waerden.test, waller.test, plot.group

Examples

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

---

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 0.5xo, 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` *Splip-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. The model is mixed, the blocks are random and the study factors are fixed applied according to the design.

Value

ANOVA: Splip plot analysis

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)
model<-with(plots,sp.plot(block,A,B,yield))
# 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

`block`	replications
`pplot`	Factor main plot
`splot`	Factor subplot
`ssplot`	Factor sub-subplot
`Y`	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. The model is mixed, the blocks are random and the study factors are fixed applied according to the design.

Value

ANOVA: Splip Split plot analysis

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)
f <- system.file("external/ssp.csv", package="agricolae")
ssp<-read.csv(f)
model<-with(ssp,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
op<-par(mfrow=c(1,3),cex=0.6)
out1<-with(ssp,LSD.test(yield,nitrogen,gla,Ea,console=TRUE))
out2<-with(ssp,LSD.test(yield,management,glb,Eb,console=TRUE))
out3<-with(ssp,LSD.test(yield,variety,glc,Ec,console=TRUE))
plot(out1,xlab="Nitrogen",las=1,variation="IQR")
plot(out2,xlab="Management",variation="IQR")
plot(out3,xlab="Variety",variation="IQR")
# with aov
ssp$block<-factor(ssp$block)
ssp$nitrogen<-factor(ssp$nitrogen)
ssp$management<-factor(ssp$management)
ssp$variety<-factor(ssp$variety)
AOV<-aov(yield ~ block + nitrogen*management*variety + Error(block/nitrogen/management),data=ssp)
summary(AOV)
par(op)
```

---

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`	Statistical analysis chi square test

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 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 var(i) usign an aproximate F-test; (vi) assigns stability rating (S) as follows: -8, -4 and -2 for var(i) significant at the 0.01, 0.05 and 0.10 probability levels, and 0 for nonsignificant var(i) (the higher the 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 YS(i) > mean YS(i).

Value

analysis	Analysis of variance
statistics	Statistics of the model
stability	summary stability analysis

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

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

---

stat.freq *Descriptive measures of grouped data*

Description

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

Usage

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

Arguments

histogram	Object create by function hist()

Value

Statistics of grouped data.

Author(s)

Felipe de mendiburu

See Also

polygon.freq, table.freq, graph.freq, inter.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

```
library(agricolae)
data(growth)
grouped<-with(growth,hist(height,plot=FALSE))
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 efect two factors

Value

Data and analysis of the variance of the strip plot design.

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$YIELD
market <- YIELD$y1da + YIELD$y2da
non_market <- YIELD$y3da
yield <- market + non_market
model<-with(YIELD,strip.plot(block, clon, trt, yield))
out1<-with(YIELD,LSD.test(yield,clon,model$gl.a,model$Ea))
oldpar<-par(mar=c(3,8,1,1),cex=0.8)
plot(out1,xlim=c(0,80),horiz=TRUE,las=1)
out2<-with(YIELD,LSD.test(yield,trt,model$gl.b,model$Eb))
plot(out2,xlim=c(0,80),horiz=TRUE,las=1)
par(oldpar)
```

---

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

Statistics of sturges for a histogram.

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, inter.freq, graph.freq, join.freq, ogive.freq, normal.freq

Examples

```
library(agricolae)
data(natives)
classes<-with(natives,sturges.freq(size))
# information of the classes
breaks <- classes$breaks
breaks
#startgraph
# Histogram with the established classes
h<-with(natives,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
```

---

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

Frequency table.

`Lower`	Lower limit class
`Upper`	Upper limit class
`Main`	class point
`Frequency`	Frequency
`Percentage`	Percentage frequency
`CF`	Cumulative frequency
`CPF`	Cumulative Percentage frequency

Author(s)

Felipe de Mendiburu

See Also

`polygon.freq`, `stat.freq`, `graph.freq`, `inter.freq`, `sturges.freq`, `join.freq`, `ogive.freq`, `normal.freq`

Examples

```
library(agricolae)
data(growth)
h2<-with(growth,graph.freq(height,plot=FALSE))
print(summary(h2),row.names=FALSE)
```

`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 (Spfmv and Spcsv) was studied. The treatments were the following: CC (Spcsv) = Sweetpotato chlorotic dwarf, FF (Spfmv) = Feathery mottle, FC (Spfmv y Spcsv) = 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` *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

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

Arguments

`object` Object by function graph.freq()

Value

Frequency table.

`Lower`	Lower limit class
`Upper`	Upper limit class
`Main`	class point
`Frequency`	Frequency
`Percentage`	Percentage frequency
`CF`	Cumulative frequency
`CPF`	Cumulative Percentage frequency

Author(s)

Felipe de Mendiburu

See Also

`polygon.freq`, `stat.freq`, `graph.freq`, `inter.freq`, `sturges.freq`, `join.freq`, `ogive.freq`, `normal.freq`

Examples

```
library(agricolae)
data(growth)
h2<-with(growth,graph.freq(height,plot=FALSE))
print(table.freq(h2),row.names=FALSE)
```

`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

Statistics of quantitative variables by categorical variables.

Author(s)

Felipe de Mendiburu

Examples

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

---

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

Script in C to R.

Value

variance of K for Kendall's tau

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)
```

---

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

Description

A nonparametric test for several independent samples.

Usage

```
waerden.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.
The post hoc test is using the criterium Fisher's least
significant difference (LSD).

Value

statistics	Statistics of the model
parameters	Design parameters
means	Statistical summary of the study variable
comparison	Comparison between treatments
groups	Formation of treatment groups

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waller.test, plot.group

Examples

```
library(agricolae)
# example 1
data(corn)
out1<-with(corn,waerden.test(observation,method,group=TRUE))
print(out1$groups)
plot(out1)
out2<-with(corn,waerden.test(observation,method,group=FALSE))
print(out2$comparison)
# example 2
data(sweetpotato)
out<-with(sweetpotato,waerden.test(yield,virus,alpha=0.01,group=TRUE))
print(out)
```

---

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

Waller value for the Waller and Duncan test.

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.

if y = model, then to apply the instruction:
waller.test (model, "trt", alpha = 0.05, group = TRUE, main = NULL, console = FALSE)
where the model class is aov or lm.

Value

statistics	Statistics of the model
parameters	Design parameters
means	Statistical summary of the study variable
comparison	Comparison between treatments
groups	Formation of treatment groups

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

BIB.test, DAU.test, duncan.test, durbin.test, friedman, HSD.test, kruskal, LSD.test, Median.test, PBIB.test, REGW.test, scheffe.test, SNK.test, waerden.test, plot.group

Examples

```
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- waller.test(model,"virus", group=TRUE)
#startgraph
oldpar<-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()
df<-df.residual(model)
MSerror<-deviance(model)/df
```

```
Fc<-anova(model)["virus",4]
out <- with(sweetpotato,waller.test(yield, virus, df, MSerror, Fc, group=TRUE))
print(out)
par(oldpar)
```

`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, percentaje

`glucose` a numeric vector, percentaje

`fructose` a numeric vector, percentaje

`sucrose` a numeric vector, percentaje

`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 percentaje. 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	Remuneration of serpentine plots.

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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