Package ‘agricolae’

Type Package
Title Statistical Procedures for Agricultural Research
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Imports klaR, MASS, nlme, cluster, spdep, 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
URL http://tarwi.lamolina.edu.pe/~fmendiburu

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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:** 1.2-8
- **Date:** 2017-09-12
- **License:** GPL


Author(s)

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References


Universidad Nacional Agraria La Molina, Lima-PERU. Facultad de Economia y Planificacion Departamento Academico de Estadistica e Informatica
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: output TRUE or FALSE
- PC: Principal components output TRUE or FALSE

Details

Additional graphics see help(plot.AMMI).

Value

- ANOVA: analysis of variance general
- genXenv: class by, genotype 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


See Also

lineXtester, plot.AMMI
AMMI.contour

**Examples**

```r
# Full replications
library(agricolae)
# Example 1
data(plrv)
model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
model$ANOVA
# see help(plot.AMMI)
# biplot
plot(model)
# triplot PC 1,2,3
plot(model, type=2, number=TRUE)
# biplot PC1 vs Yield
plot(model, first=0, second=1, number=TRUE)
# Example 2
data(CIC)
data1<-CIC$comas[,c(1,6,7,17,18)]
data2<-CIC$oxapampa[,c(1,6,7,19,20)]
cic <- rbind(data1,data2)
model<-with(cic,AMMI(Locality, Genotype, Rep, relative))
model$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$ANOVA,na.print = "")
# Biplot with the one restored observed.
plot(model,0,1,type=1)
# with principal components model$PC is class "princomp"
pc<- model$PC
pc$loadings
summary(pc)
biplot(pc)
# Principal components by means of the covariance similar AMMI
# It is to compare results with AMMI
cova<-cov(model$genXenv)
values<-eigen(cova)
total<-sum(values$values)
round(values$values*100/total,2)
# AMMI: 64.81 18.58 13.50 3.11 0.00
```

---

**AMMI contour**

**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**

```r
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**

```r
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)
```
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

Examples
```r
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
Total 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")
```
**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**

```r
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


Examples

```r
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
Total 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)
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.

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 dealt with different virus")
par(mfrow=c(2,2), cex=1)
bar.err(out$means, variation="range", horiz=TRUE, xlim=c(0,45), angle=125, density=6,
main="range")
bar.err(out$means, variation="SD", ylim=c(0,45), col=colors()[30],
main="Standard deviation",density=8)
bar.err(out$means,variation="SE",horiz=TRUE,xlim=c(0,45),density=8,
col="brown",main="Standard error")
bar.err(out$means,variation="range",yylim=c(0,45),bar=FALSE,col="green",
main="range")
par(mfrow=c(1,2),cex=1)
bar.err(out$means,variation="range",ylim=c(0,45),bar=FALSE,col=0)
abline(h=0)
# horiz = TRUE
bar.err(out$means,variation="SE",horiz=TRUE,xlim=c(0,45),bar=FALSE,col=0)
#startgraph
par(mfrow=c(1,1))
#endgraph

bar.group  Plotting the multiple comparison of means

Description
It plots bars of the averages of treatments to compare. It uses the objects generated by a procedure of comparison like LSD, HSD, 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, ...)

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

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

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

BIB.test Finding the Variance Analysis of the Balanced Incomplete Block Design

Description

Analysis of variance BIB and comparison mean adjusted.

Usage

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

Arguments

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

Details

Test of comparison treatment. lsd: Least significant difference. tukey: Honestly significant different. 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

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)
run<-gl(10,3)
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)))
rn(y,block, trt, out)
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

```r
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

```r
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


References

International Potato Center. CIP - Lima Peru.
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)
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

```r
data(ComasOxapampa)
```

Format

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

- **cultivar**: a factor with 56 levels
- **replication**: a factor with 3 levels
- **comas**: a numeric vector
- **oxapampa**: a numeric vector

Details

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

Source


References

International Potato Center. CIP - Lima Peru.

Examples

```r
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")
```
Description

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

Usage

```r
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

Hall/CRC

See Also

hclust, hgroups, hcut
Examples

library(agricolae)
data(pamCIP)
# only code
rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
# par(cex=0.8)
output<-consensus( pamCIP,distance="binary", method="complete",nboot=5)
# Order consensus
Groups<-output$table.dend[,c(6,5)]
Groups<-Groups[order(Groups[,2],decreasing=TRUE),]
print(Groups)
## Identification of the codes with the numbers.
cbind(output$table.dend$labels)
## To reproduce dendrogram
dend<-output$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)

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 mediansn test.

Usage

data(corn)

Format

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

- method a numeric vector
- observation a numeric vector
- rx a numeric vector
Details

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

Source

Book: Practical Nonparametric Statistics.

References


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


See Also

correlation
Examples

```r
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**

```r
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**


**See Also**

`correl`
Examples

```r
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"))
```

data(cotton)

Description

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

Usage

```r
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

```r
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**

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

**Arguments**

- `x` object of model `lm()` or `AOV()`

**Details**

$$\sqrt{\text{MSerror}} \times 100 / \text{mean}(x)$$

**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**

```r
# 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**

```r
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.
### 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

### 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
```r
library(agricolae)
block<-c(rep("I",7),rep("II",6),rep("III",7))
trt<-c("A","B","C","D","g","k","i","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$groups)
plot(out)$groups
```

### DC

*Data for the analysis of carolina genetic design*

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

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

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

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

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

Source

References

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**

```r
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**

```r
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

Value
parameters  Design parameters
book  Fieldbook

Author(s)
Felipe de Mendiburu

References

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 $s \times k$ (with $s$ blocks and $k<s$ columns). The number of treatments should be equal to $s \times k$ and all the experimental units $r \times s \times k$ ($r$ replications).

**Usage**

```r
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, $k<=s$

$r= \text{replications } s=\text{number of blocks } k=\text{size of block }$ 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**


**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

```r
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
```

```r
# 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**

```r
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.


Value

| parameters | Design parameters |
| statistics | Design statistics |
| sketch     | Design sketch     |
| book       | Fieldbook         |

Author(s)

Felipe de Mendiburu

References


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


Value

parameters | Design parameters  
book | Fieldbook

Author(s)

Felipe de Mendiburu

References


See Also

design.ab, design.alpha, design.bib, design.split, design.cyclic, design.dau, design.graeeco, 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 of 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
**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**

```r
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

**Author(s)**

Felipe de Mendiburu

**References**


**See Also**

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

```
seed     seed
kinds    method for to randomize
name     name of treatments
randomization  TRUE or FALSE - randomize
```

**Details**


**Value**

- parameters: Design parameters
- book: Fieldbook

**Author(s)**

Felipe de Mendiburu

**References**


**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**

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

**Value**
- `parameters`: Design parameters
- `book`: Fieldbook

**Author(s)**
Felipe de Mendiburu

**References**

**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**

```
```

**Value**

- `parameters`: Design parameters
- `statistics`: Design statistics
- `sketch`: Design sketch
- `book`: Fieldbook

**Author(s)**

Felipe de Mendiburu
References

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.lsdLatin 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

Value
parameters Design parameters
book Fieldbook
**design.rcbd**

**Author(s)**
Felipe de Mendiburu

**References**


**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**

```r
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.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**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt</td>
<td>Treatments</td>
</tr>
<tr>
<td>r</td>
<td>Replications or blocks</td>
</tr>
<tr>
<td>serie</td>
<td>number plot, 1: 11,12; 2: 101,102; 3: 1001,1002</td>
</tr>
<tr>
<td>seed</td>
<td>seed</td>
</tr>
<tr>
<td>kinds</td>
<td>method for to randomize</td>
</tr>
<tr>
<td>first</td>
<td>TRUE or FALSE - randomize rep 1</td>
</tr>
<tr>
<td>continue</td>
<td>TRUE or FALSE, continuous numbering of plot</td>
</tr>
<tr>
<td>randomization</td>
<td>TRUE or FALSE - randomize</td>
</tr>
</tbody>
</table>
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).


Value

parameters Design parameters
sketch Design sketch
book Fieldbook

Author(s)

Felipe de Mendiburu

References


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)
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


Value

parameters Design parameters
book Fieldbook

Author(s)

Felipe de Mendiburu

References


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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt1</td>
<td>Row treatments</td>
</tr>
<tr>
<td>trt2</td>
<td>Column treatments</td>
</tr>
<tr>
<td>r</td>
<td>Replications</td>
</tr>
<tr>
<td>serie</td>
<td>Number plot, 1: 11,12; 2: 101,102; 3: 1001,1002</td>
</tr>
<tr>
<td>seed</td>
<td>Seed</td>
</tr>
<tr>
<td>kinds</td>
<td>Method for to randomize</td>
</tr>
<tr>
<td>randomization</td>
<td>TRUE or FALSE - randomize</td>
</tr>
</tbody>
</table>

Details


Value

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameters</td>
<td>Design parameters</td>
</tr>
<tr>
<td>book</td>
<td>Fieldbook</td>
</tr>
</tbody>
</table>

Author(s)

Felipe de Mendiburu

References


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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt</td>
<td>Treatments</td>
</tr>
<tr>
<td>r</td>
<td>Replications or number of columns</td>
</tr>
<tr>
<td>serie</td>
<td>number plot, 1: 11,12; 2: 101,102; 3: 1001,1002</td>
</tr>
<tr>
<td>seed</td>
<td>seed</td>
</tr>
<tr>
<td>kinds</td>
<td>method for to randomize</td>
</tr>
<tr>
<td>first</td>
<td>TRUE or FALSE - randomize rep 1</td>
</tr>
<tr>
<td>randomization</td>
<td>TRUE or FALSE - randomize</td>
</tr>
</tbody>
</table>

Details


Value

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameters</td>
<td>Design parameters</td>
</tr>
<tr>
<td>sketch</td>
<td>Design sketch</td>
</tr>
<tr>
<td>book</td>
<td>Fieldbook</td>
</tr>
</tbody>
</table>
Author(s)
Felipe de Mendiburu

References

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="",...)
Details

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

Value

x list, object comparison test

Author(s)

Felipe de Mendiburu

References


See Also

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

Examples

```r
# 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**

```r
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.
duncan.test

Usage

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

Arguments

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

Details

It is necessary first makes a analysis of variance.

Value

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


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
friedman  

References

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(1,2,4,2,3,1,2,3,2,1,3,2,1,2,3,1,2,3,1,2,3,1,2)
prefence<-c(2,3,1,2,3,1,2,3,1,2,3,1,2,3,1,2,3,1,2,3,1,2,3)
out<-durbin.test(person,variety,prefence,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","A","C","E","C","D","G","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,totoxic,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
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

```r
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
```

Description

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

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

```r
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**

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

---

**Description**

Data of potato yield in a different environment

50 genotypes and 5 environments.

**Usage**

```r
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**

```r
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,...)
graph.freq

Arguments

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

Value

- **breaks**: a vector giving the breakpoints between histogram cells
- **counts**: frequency and x is class intervals
- **mids**: center point in class
- **relative**: Relative frequency, height
- **density**: Density frequency, height

Author(s)

Felipe de Mendiburu

See Also

- polygon.freq, table.freq, stat.freq, intervals.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

```r
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$h$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$h$breaks)
axis(2,seq(0,4,0.1))
# summary, only frequency
limits <- seq(10,40,5)
frequencies <- c(2,6,8,7,3,4)
#startgraph
h<-graph.freq(limits,counts=frequencies,col="bisque",xlab="Classes")
```
grass

Data for Friedman test

Description

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

Usage

data(grass)

Format

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

judge a numeric vector
trt a factor with levels t1 t2 t3 t4
evaluation a numeric vector

Details

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

Source


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 Far ran, 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)
Hco2006

Format

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

clone a factor with levels A84118-3 A080432-1 A084275-3 AWN86514-2 B0692-4 B0718-3 B0749-2F B0767-2 Bertita Bzura C0083008-1 Elba Greta Krantz Libertas Stobrawa FL a numeric vector MI a numeric vector ME a numeric vector MN a numeric vector ND a numeric vector NY a numeric vector PA a numeric vector WI a numeric vector

References


Examples

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

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.
**heterosis**

**Author(s)**
F. de Mendiburu

**See Also**
- hclust
- consensus
- hgroups

**Examples**
```r
library(agricolae)
data(heterosis)
# only code
rownames(heterosis)<-substr(rownames(heterosis),1,6)
# groups of clusters
# output<-consensus(heterosis,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)
```

---

**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**
```r
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


Examples

```r
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))
model22<-with(site2,lineXtester(Replication, Female, Male, v3))
model3<-with(site3,lineXtester(Replication, Female, Male, v4))
```

hgroups

```r
groups of hclust
```

Description

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

Usage

```r
hgroups(hmerge)
```

Arguments

```r
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, DError, 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
DError  Degree free
MSError  Mean Square Error
alpha  Significant level
group  TRUE or FALSE
main  Title
console  logical, print output

Details

It is necessary first makes a analysis of variance.
Value

- 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


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

```r
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- HSD.test(model,"virus", group=TRUE,console=TRUE, main="Yield of sweetpotato Dealt 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

\[ \text{data(huasahuasi)} \]

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


References

International Potato Center. CIP - Lima Peru.

Examples

\[ \text{library(agricolae)} \]
\[ \text{data(huasahuasi)} \]
\[ \text{names(huasahuasi)} \]
\[ \text{str(huasahuasi$AUDPC)} \]
\[ \text{str(huasahuasi$YIELD)} \]
**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)  
\[
\text{ASV} = \sqrt{\text{SSpc1}/\text{SSpc2} \times (\text{PC1i})^2 + (\text{PC2i})^2}
\]
\[
\text{YSI} = \text{RASV} + \text{RY}
\]
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**

**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


Arguments

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

Details


Value

Index and confidence intervals.

Author(s)

Felipe de Mendiburu

References

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

\[ V_x = \frac{V(x)}{x} \]

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

Value

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

Author(s)

Felipe de Mendiburu

References

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

intervals.freq

Description
List class intervals.

Usage
intervals.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

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

join.freq

Join class for histogram

Description

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

Usage

```r
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`
- `intervals.freq`
- `sturges.freq`
- `graph.freq`
- `ogive.freq`
- `normal.freq`

Examples

```r
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**  

**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 significiation
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

0file  "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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Robert J. Hijmans (2) (rhijmans@ucdavis.edu), William E. Fry (3) (wef1@cornell.edu) Translation
Hijmans Translation from SAS into R: Felipe de Mendiburu (1) (1) International Potato Center,
P.O. Box 1558, Lima 12, Peru (2) University of California, One Shields Avenue, Davis, California
95616, USA (3) Cornell University, 351 Plant Science, Ithaca, NY 14853, USA

References

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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)
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
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. Hierarchical and
factorial mating designs for quantitative genetic analysis in tetrasomic potato. R. Orús; A.Golmirzaie.

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.adjust.
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

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
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
**Median.test**

**Source**

International Potato Center Lima-Peru.

**References**

International Potato Center Lima-Peru.

**Examples**

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

---

**Median.test**  \hspace{1cm} *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**

```r
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.
melon

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 Nonparametric 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

```r
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 Topflight (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)

\begin{verbatim}
library(agricolae)
data(melon)
str(melon)
\end{verbatim}

\textbf{Description}

Random generation form data, use function density and parameters

\textbf{Usage}

\texttt{montecarlo(data, k, \ldots)}

\textbf{Arguments}

\begin{verbatim}
data \quad \text{vector or object(hist, graph.freq)}
k \quad \text{number of simulations}
\ldots \quad \text{Other parameters of the function density, only if data is vector}
\end{verbatim}

\textbf{Value}

Generate random numbers with empirical distribution.

\textbf{Author(s)}

Felipe de Mendiburu

\textbf{See Also}

density
Examples

```r
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)
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
100 obs.")
h2 <- graph.freq(r, breaks, frequency = 3, ylim=c(0, 0.008))
lines(density(r), col="blue")
text(90, 0.006, "Montecarlo
1000 obs.")
```

---

**natives**

*Data of native potato*

Description

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

Usage

```r
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

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

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 First 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

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, intervals.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,...)
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, DFeorror=NULL, alpha=NULL, stddif=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

Author(s)

Felipe de Mendiburu

See Also

- `orderPvalue`

Examples

```r
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

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**

```r
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**

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

paracsho  
*Data of Paracsho biodiversity*

**Description**

A locality in Peru. A biodiversity.

**Usage**

```r
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 LEPIDOPTERA NEUROPTERA NEUROPTERO NOCTUIDAE
Family a factor with levels AGROMYZIDAE ANTHOCORIDAE ANTHOMYIIDAE ANTHOMYLIDAE BLEPHAROCERIDAE BRCANIDAE BROCONIDAE CALUPHORIDAE CECIDOMYIIDAE CHNEUMONIDAE CHREOMELIDAE CICADELLIDAE CULICIDAE ERICOPAMIDAE HEMEROBIIIDAE ICHNEUMONIDAE LOUCHAPIDAE MIRIDAE MUSICIDAE MUSCICIDAE MUSULIDA MUSCIDAE MYCETOPHILIDAE MYCETOPHILIIDAE NENPHALIDAE NOCTERIDAE NOCTUIDAE PERALIDAE PIPUNCULIDAE PSYLLIDAE PYRALIDAE SARCOPHAGIDAE SARCOPILAGIDAE SCATOPHAGIDAE SCATOPHOGIDAE SCARIDA SERSIDAE SYRPHIDAE TACHINIDAE TIPULIDAE
Number.of.specimens a numeric vector

Details

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

Source

Entomology dataset.

References

International Potato Center.

Examples

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

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

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**

```r
# 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(corr.x,cor.y)
```
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.

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

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)
dbook<-book$book
# dataset
yield<-c(5,2,7,6,4,9,7,6,7,9,6,2,1,1,3,2,4,6,7,9,8,7,6,4,3,2,2,1,1,2,
1,2,4,5,6,7,8,5,4,3,1,1,2,5,4,2,7,6,5,6,4,5,7,6,5,4)
rm(Genotype)
# not run
# analysis
# require(nlme) # method = REML or LM in PBIB.test and require(MASS) method=VC
model <- with(dbook,PBIB.test(block, Genotype, replication, yield, k=3, method="VC"))
# model$ANOVA
# plot(model,las=2)

Description
Biplot AMMI.

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

- **x**: object AMMI
- **first**
  - position axis x, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **second**
  - position axis y, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **third**
  - position axis z, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **type**
  - 1=biplot, 2= triplot, 3=influence genotype
- **number**
  - TRUE or FALSE names or number genotypes
- **gcol**: genotype color
- **ecol**: environment color
- **icol**: influence color
- **angle**: angle from the shaft of the arrow to the edge of the arrow head
- **lwd**: parameter line width in function arrow
- **length**: parameter length in function arrow
- **xlab**: x labels
- **ylab**: y labels
- **xlim**: x limits
- **ylim**: y limits
- **...**: other parameters of plot

Details

type=1 produce graphs biplot. type=2 produce graphs triplot, the components are normalizad in scale 0-1. type=3 produce graphs on a 2d point set that are all subgraphs of the Delaunay triangulation with relative neighbor graph.

The relative neighbor graph is defined by the relation, x and y are neighbors if

\[ d(x, y) \leq \min(\max(d(x, z), d(y, z))) | z \in S \]

where \(d()\) is the distance, \(S\) is the set of BIPOINT points and \(z\) is an arbitrary point in \(S\).

help(relativeneigh) package=spdep

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")
## triplot PC 2,3,4
if (requireNamespace("klaR", quietly = TRUE)) {
  plot(model,first=2,second=3,third=4, type=2,number=TRUE)
}
# biplot with influence genotype in pc3 vs pc2
if (requireNamespace("spdep", quietly = TRUE)) {
  plot(model,first=2,second=3, type=3,number=TRUE,icol="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**

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

**Arguments**

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

**Value**

- `breaks` a vector giving the breakpoints between histogram cells
- `counts` frequency and x is class intervals
- `mids` center point in class
- `relative` Relative frequency, height
- `density` Density frequency, height
Author(s)
Felipe de Mendiburu

See Also
polygon.freq, table.freq, stat.freq, intervals.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

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

Arguments

x Object created by a test of comparison
variation in lines by range, IQR, standard deviation or error
horiz Horizontal or vertical image
col line colors
xlim optional, axis x limits
ylim optional, axis y limits
main optional, main title
... 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
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
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.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>block</td>
<td>a numeric vector</td>
</tr>
<tr>
<td>plot</td>
<td>a factor with levels p1 p2 p3 p4 p5 p6</td>
</tr>
<tr>
<td>A</td>
<td>a factor with levels a1 a2</td>
</tr>
<tr>
<td>B</td>
<td>a factor with levels b1 b2 b3</td>
</tr>
<tr>
<td>yield</td>
<td>a numeric vector</td>
</tr>
</tbody>
</table>

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[planner=="b1"],A[planner=="b1"],dfab,Eab))
comparison3 <- with(plots, LSD.test(yield[planner=="b2"],A[planner=="b2"],dfab,Eab))
comparison4 <- with(plots, LSD.test(yield[planner=="b3"],A[planner=="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"],dfab, Eb))
comparison7 <- with(plots, LSD.test(yield[A=="a2"],B[A=="a2"],dfab, Eb))
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)
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

polygone.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

polygone.freq, table.freq, stat.freq, intervals.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

data(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**

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

---

<table>
<thead>
<tr>
<th>ralstonia</th>
<th>Data of assessment of the population in the soil R. solanacearum</th>
</tr>
</thead>
</table>

**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**

```r
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.homogeneity (homogenity degree free).
DF.Residual (degree free error).
F.value. Test statistics.
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
```r
library(agricolae)
data(frijol)
evaluation<-with(frijol,reg.homog(technology,index,production))
# Example 2. Applied Regression Analysis a Research tools
# & Software. Pacific Grove. California.
# Statistics/probability. Series
LineNumber<-c(rep("39","30"),rep("52","30"))
PlantingDate<-rep(c("16","20","21"),20)
HeadWt <- c(2.5,3.0,2.2,2.2,2.8,1.8,3.1,2.8,1.6,4.3,2.7,2.1,2.5,2.6,3.3,4.3,
   2.8,3.8,3.8,2.6,3.2,4.3,2.6,3.6,1.7,2.6,4.2,3.1,3.5,1.6,2.0,4.0,1.5,2.4,2.8,
   1.4,1.9,3.1,1.2,8.1,4.2,1.3,1.3,7.3,7.3,2.3,3.0,1.6,2.0,2.2,1.4,2.2,2.3,1.0,
   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,
   56,72,58,72,63,63,68,56,54,66,72,60,72)
trt<-paste(LineNumber,PlantingDate,sep="-")
output<-reg.homog(trt,HeadWt,Ascorbic)
```

REGW.test

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

**Usage**
```r
REGW.test(y, trt, DError, MSerror, alpha = 0.05, group=TRUE, main = NULL,console=FALSE)
```

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

It is necessary first makes a analysis of variance.

Value

<table>
<thead>
<tr>
<th>statistics</th>
<th>Statistics of the model</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameters</td>
<td>Design parameters</td>
</tr>
<tr>
<td>regw</td>
<td>Critical Range Table</td>
</tr>
<tr>
<td>means</td>
<td>Statistical summary of the study variable</td>
</tr>
<tr>
<td>comparison</td>
<td>Comparison between treatments</td>
</tr>
<tr>
<td>groups</td>
<td>Formation of treatment groups</td>
</tr>
</tbody>
</table>

Author(s)

Felipe de Mendiburu

References


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

\text{lm(formula = CV \sim I(1/marker))}
Table with variation coefficient by number of markers

Author(s)

Felipe de Mendiburu

References


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)
predict<-predict(study$model)
Rsq<-summary(study$model)$"r.squared"
table.cv <- data.frame(study$table.cv,estimate=predict)
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")
resampling.model

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


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)
```

---

**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


References


Examples

```r
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

```r
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, DError, MSError, Fc, alpha = 0.05, group=TRUE, main = NULL, console=FALSE )

Arguments

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

Details

It is necessary first makes a analysis of variance.
**Value**

- **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**


**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**

```r
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**

```r
similarity(A)
```

**Arguments**

- **A**: Matrix, data binary
# simulation.model

## Value

Distance matrix. Class = dist.

## Author(s)

Felipe de Mendiburu

## See Also

cv.similarity, resampling.cv

## Examples

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

---

## 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 \( F > F_{\text{value}} \).

## Usage

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

## Arguments

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

## Value

- **model**: output linear model, lm
- **simulation**: anova simulation
Author(s)
Felipe de Mendiburu

See Also
resampling.model

Examples

library(agricolae)
# example 1
data(clay)
model<="ralstonia ~ days"
simulation.model(model, clay, k=15, console=TRUE)
# example 2
data(sweetpotato)
model<="yield~virus"
simulation.model(model, sweetpotato, categorical=1, k=15, console=TRUE)
# example 3
data(Glycoalkaloids)
model<="HPLC ~ spectrophotometer"
simulation.model(model, Glycoalkaloids, k=15, console=TRUE)
# example 4
data(potato)
model<="cutting~date+variety"
simulation.model(model, potato, categorical=c(1, 2, 3), k=15, console=TRUE)

Table 1: AMMI without repetition

<table>
<thead>
<tr>
<th>ENV</th>
<th>GEN</th>
<th>YLD</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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

```r
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**

```r
skewness(x)
```

**Arguments**

- `x` a numeric vector

**Value**

The skewness of `x`.

**See Also**

`kurtosis`

**Examples**

```r
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

```r
SNK.test(y, trt, DError, MSError, alpha = 0.05, group=TRUE, main = NULL, console=FALSE)
```

Arguments

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

Details

It is necessary first makes a analysis of variance.

Value

- `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

### Examples

```r
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)
```

### Data of soil analysis for 13 localities

**Description**

We analyzed the physical and chemical properties of different soils, as full characterization of soil and special analysis of micro-elements. These analyses were conducted in the laboratory analysis of soils, plants, water and fertilizers in the La Molina National Agrarian University (UNALM).

To which the different soil samples were dried to the environment, screened (mesh 0.5x0, 5 mm) and sterilized by steam 4 to 5 hours with a Lindinger Steam aerator SA150 and SA700, with the possible aim of eliminating bacteria saprophytic or antagonists to prevent the growth of bacteria (R.solanacearum).

**Usage**

```r
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
sp.plot

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  S ppl-Plot analysis

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

Usage
sp.plot(block, pplot, splot, Y)
Arguments

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

Details

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

Value

ANOVA: Split plot analysis

Author(s)

Felipe de Mendiburu

References


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)
**ssp.plot**

### 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.

### Value

ANOVA: Split plot analysis

### Author(s)

Felipe de Mendiburu

### References


### See Also

- `sp.plot`, `strip.plot`, `design.split`, `design.strip`

### Examples

```r
# 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
# factors, 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$g1.a; glb=model$g1.b; glc=model$g1.c
Ea=model$Ea; Eb=model$Eb; Ec=model$Ec
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
AOV<-aov(yield ~ block + nitrogen*management*variety + Error(block/nitrogen/management),data=ssp)
summary(AOV)
```
**stability.nonpar**

**Nonparametric stability analysis**

**Description**

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

**Usage**

```r
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**


**See Also**

`stability.par`

**Examples**

```r
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)
```
stability.par

```r
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**

```r
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) using an approximate 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
Descriptive measures of grouped data

Description

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

Usage

stat.freq(histogram)

Arguments

histogram Object created by function hist()

Value

Statistics of grouped data.
strip.plot

Author(s)
Felipe de Mendiburu

See Also
polygon.freq, table.freq, graph.freq, intervals.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

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

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

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

Arguments

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

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

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

Author(s)
Felipe de Mendiburu
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

summary.graph.freq

See Also

polygon.freq, table.freq, stat.freq, intervals.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
Size 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.

<table>
<thead>
<tr>
<th>Lower</th>
<th>Lower limit class</th>
</tr>
</thead>
<tbody>
<tr>
<td>Upper</td>
<td>Upper limit class</td>
</tr>
<tr>
<td>Main</td>
<td>class point</td>
</tr>
<tr>
<td>Frequency</td>
<td>Frequency</td>
</tr>
<tr>
<td>Percentage</td>
<td>Percentage frequency</td>
</tr>
<tr>
<td>CF</td>
<td>Cumulative frequency</td>
</tr>
<tr>
<td>CPF</td>
<td>Cumulative Percentage frequency</td>
</tr>
</tbody>
</table>
sweetpotato

Author(s)
Felipe de Mendiburu

See Also
polygon.freq, stat.freq, graph.freq, intervals.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

library(agricolae)
data(growth)
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 (Spcs) = 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)
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.

<table>
<thead>
<tr>
<th>Lower</th>
<th>Upper</th>
<th>Main</th>
<th>Frequency</th>
<th>Percentage</th>
<th>CF</th>
<th>CPF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lower limit class</td>
<td>Upper limit class</td>
<td>class point</td>
<td>Frequency</td>
<td>Percentage frequency</td>
<td>Cumulative frequency</td>
<td>Cumulative Percentage frequency</td>
</tr>
</tbody>
</table>

Author(s)

Felipe de Mendiburu

See Also

polygon.freq, stat.freq, graph.freq, intervals.freq, sturges.freq, join.freq, ogive.freq, normal.freq

Examples

library(agricolae)
data(growth)
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(!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

See Also
cor.matrix, cor.vector, cor.mv

Examples
library(agricolae)
x <-c(1,1,1,4,2,2,3,1,3,2,1,1,2,3,2,1,2,1,2,1,2)
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)
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
waller

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

daller(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


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
Details

It is necessary first makes a analysis of variance.

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

Value

<table>
<thead>
<tr>
<th>statistics</th>
<th>Statistics of the model</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameters</td>
<td>Design parameters</td>
</tr>
<tr>
<td>means</td>
<td>Statistical summary of the study variable</td>
</tr>
<tr>
<td>comparison</td>
<td>Comparison between treatments</td>
</tr>
<tr>
<td>groups</td>
<td>Formation of treatment groups</td>
</tr>
</tbody>
</table>

Author(s)

Felipe de Mendiburu

References


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
par(mfrow=c(2,2))
# variation: SE is error standard
# variation: range is Max - Min
bar.err(out$means, variation="SD", horiz=TRUE, ylim=c(0,45), bar=FALSE, col=colors()[25], space=2, main="Standard deviation", las=1)
bar.err(out$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)

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<-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")

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, ARB5125, CLLUNC118, P1385, S136
- **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, percentage
- **glucose**: a numeric vector, percentage
- **fructose**: a numeric vector, percentage
- **sucrose**: a numeric vector, percentage
- **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 percentage. 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

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