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

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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, genopyle 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
Examples

# Full replications
library(agricolae)
# Example 1
data(plrv)
model<- with(plrv,AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
model$ANOVA # see help(plot.AMMI)
# biplot
plot(model)
# triplot PC 1,2,3
plot(model, type=2, number=TRUE)
# biplot PC1 vs Yield
plot(model, first=0, second=1, number=TRUE)
# Example 2
data(CIC)
data1<-CIC$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

Description

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

Usage

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

Arguments

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

Details

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

Value

Genotypes within and outside the area.

distance Distance from genotype to origin (0,0)

Note

Complement graphics AMMI

Author(s)

Felipe de Mendiburu

See Also

AMMI

Examples

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

Usage

\[ \text{audpc}(\text{evaluation, dates, type = "absolute"}) \]

Arguments

- \text{evaluation}: Table of data of the evaluations: Data frame
- \text{dates}: Vector of dates corresponding to each evaluation
- \text{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
date<-c(40,80,90) # percentages
evaluation<-data.frame(E1=40,E2=80,E3=90)
audpc(evaluation,dates)
```

```
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")
```
audps

The Area Under the Disease Progress Stairs

Description

A better estimate of disease progress is the area under the disease progress stairs (AUDPS). The AUDPS approach improves the estimation of disease progress by giving a weight closer to optimal to the first and last observations.

Usage

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

Arguments

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

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

Value

Vector with relative or absolute audps.

Author(s)

Felipe de Mendiburu

References


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)
plot(x,y,"s",ylim=c(0,100),xlim=c(10,32),axes=FALSE,col="red",ylab="",xlab="")
title(cex.main=0.8,main="Absolute or Relative AUDPS\nTotal area=(31.5-10.5)*100=2100",ylab="evaluation",xlab="dates")
points(x,y,type="h")
z<-c(14,21,28)
points(z,y[-3],col="blue",lty=2,pch=19)
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**

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

**Arguments**

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

**Details**

- `x`: data frame formed by 5 columns: name of the bars, height, level out: LSD.test, HSD, waller.test, scheffe.test, duncan.test, SNK.test, friedman, kruskal, waerden.test and Median.test.

**Value**

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

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

**Author(s)**

Felipe de Mendiburu

**See Also**

- `LSD.test`, `HSD.test`, `waller.test`, `kruskal`, `bar.group`

**Examples**

```r
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],
        angle=125,density=6,
        main="range")
```
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 differente. duncan: Duncan’s new multiple range test waller: Waller-Duncan test. snk: Student-Newman-Keuls (SNK)
Value

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

Author(s)

F. de Mendiburu

References

Linear Estimation and Design of Experiments. D.D. Joshi. WILEY EASTERN LIMITED 1987, New Delhi, India.

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

```r
library(agricolae)
run<-gl(10,3)
monovinyl<-c(16,18,32,19,46,45,26,39,61,21,35,55,19,47,48,20,33,31,13,13,34,21,30,52,24,10,50,40,31,37)
out<-BIB.test(run,psi,monovinyl,test="waller",group=FALSE)
print(out)
bar.err(out$means,variation="range",ylim=c(0,60),bar=FALSE,col=0)
out<-BIB.test(run,psi,monovinyl,test="waller",group=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=TRUE,console=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=FALSE,console=TRUE)
rm(run,psi,monovinyl,out)
# Example linear estimation and design of experiments. D.D. Joshi. 1987
# Professor of Statistics, Institute of Social Sciences Agra, India
# 6 varieties of wheat crop in a BIB whit 10 blocks of 3 plots each.
y <-c(69,77,72,63,70,54,65,65,57,59,50,45,68,75,59,38,60,60,62,55,54,65,62,65,61,39,54,67,63,56)
varieties<-gl(6,5)
block <- c(1,2,3,4,5,1,2,6,7,8,1,3,6,9,10,2,4,7,9,10,3,5,7,8,9,4,5,6,8,10)
BIB.test(block, varieties, y)
# Example Introduction to experimental statistics. Ching Chun Li. 1964
# pag. 395 table. 27.2
# 7 trt, k=3 and b=7.
y <-c(10,15,11,4,12,15,5,14,10,14,19,19,8,10,17,6,11,12,5,14,21)
block<-gl(7,3)
trt <- c(1,2,4,2,3,5,3,4,6,4,5,7,1,5,6,2,6,7,1,3,7)
out<-BIB.test(block, trt, y, test="duncan")
bar.group(out$groups,col="blue",density=4,ylim=c(0,max(y)))
rm(y,block,trt,out)
```
Description

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

Usage

carolina(model, data)

Arguments

  model        Constant
  data         Data frame

Details

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

Value

  model        model analysis (I, II or III) of caroline design
               and variance and additive variance of male, female and male.female interaction.

Author(s)

  Felipe de Mendiburu

References

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

See Also

  DC

Examples

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

  carolina2 <- DC$carolina2
  # str(carolina2)
  majes<-subset(carolina2, carolina2[,1]==1)
  majes<-majes[,c(2,5,4,3,6:8)]
  output<-carolina(model=2, majes[,c(1:4,6)])
  output[][-1]
carolina3 <- DC$carolina3
# str(carolina3)
output<-carolina(model=3,carolina3)
output[][-1]

---

### Chz2006

#### Data amendment Carhuaz 2006

**Description**

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

**Usage**

data(Chz2006)

**Format**

The format is: List of 2

- amendment  a factor
- crop    a factor
- block   a numeric vector, replications
- plant   a numeric vector, number plant
- wilt_percent a numeric vector, wilt percentage at 60 days
- health  a numeric vector, kg/8m2
- rot     a numeric vector, kg/8m2

**Details**

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

**Source**

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

**References**

International Potato Center. CIP - Lima Peru.
Examples

library(agricolae)
data(Chz2006)
str(Chz2006)
wilt<-Chz2006$wilt
yield<-Chz2006$yield
means <- tapply.stat(wilt[,5],wilt[,1:3],function(x) mean(x,na.rm=TRUE))
names(means)[4]<-"wilt_percent"
model <- aov(wilt_percent ~ block + crop, means)
anova(model)
cv.model(model)
yield<-yield[order(paste(yield[,1],yield[,2],yield[,3])),]
correlation(means[,4],yield[,4],method="spearman")

CIC

Data for late blight of potatoes

Description

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

Usage

data(CIC)

Format

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

Locality  a factor with levels Comas Oxapampa
Genotype a factor
Rep  a numeric vector, replications
E9  a numeric vector, infestans percentage 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 percentage, 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.
Examples

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

clay  Data of Ralstonia population in clay soil

Description

An evaluation over a time period.

Usage

```r
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

```r
library(agricolae)
data(clay)
str(clay)
```
Description
Fifty-three potato varieties developed by the breeding program of the International Potato Center and released in different countries around the world were evaluated for their resistance to late blight in two locations in Peru.

Usage
data(ComasOxapampa)

Format
A data frame with 168 observations on the following 4 variables.
cultivar  a factor with 56 levels
replication a factor with 3 levels
comas    a numeric vector
oxapampa a numeric vector

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

Source

References
International Potato Center. CIP - Lima Peru.

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


### 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


### See Also

- `hclust`, `hgroups`, `hcut`
### Examples

```r
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)
```

---

### corn

#### Data of corn

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

#### Usage

```r
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
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


data(corn)
str(corn)

correl Correlation Coefficient

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
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"))
```

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"))
```

cotton

**Data of cotton**

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

**Usage**

data(cotton)

**Format**

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

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

**Source**

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

**References**

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

**Examples**

```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**

`cv.model(x)`

**Arguments**

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

**Details**

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

**Value**

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

**Author(s)**

Felipe de Mendiburu

**See Also**

`LSD.test`, `HSD.test`, `waller.test`

**Examples**

```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**

`cv.similarity(A)`
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


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

**Usage**

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

**Value**

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

**Author(s)**

Felipe de Mendiburu

**References**


**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.beta(trt,k,r,serie=2)
book<-outdesign$book
plots<-book[,1]
dim(plots)<-c(k,s,r)
for (i in 1:r) print(t(plots[,,i]))
outdesign$sketch
# Example two
trt<-letters[1:12]
t <- length(trt)
rs<-3
rs<-t/k
outdesign<- design.beta(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
```

**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=12, r=3, 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")
**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**

```r
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**

```r
c(\text{"Wichmann-Hill"}, \text{"Marsaglia-Multicarry"}, \text{"Super-Duper"}, \text{"Mersenne-Twister"}, \text{"Knuth-TAOCP"}, \text{"user-supplied"}, \text{"Knuth-TAOCP-2002"}, \text{"default"})
```

**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.graeco, design.lattice, design.lsd, design.rcbd, design.strip
Examples

```r
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

```r
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

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt1</td>
<td>checks</td>
</tr>
<tr>
<td>trt2</td>
<td>new</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>
</tbody>
</table>
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

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$book
# write in hard disk
# write.table(book,"dau.txt", row.names=FALSE, sep="\t")
# file.show("dau.txt")
# Augmented designs in Completely Randomized Design
trt<-c(T1,T2)
r<-c(4,4,4,4,1,1,1,1,1,1)
outdesign <- design.crd(trt,r)
outdesign$book
**design.graeco**

**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**

```r
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)
```

**Designation**

Lattice designs

**Description**

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

**Usage**

```r
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.lsd Latin Square Design

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

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

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

Details

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

**Arguments**

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

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**

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

**Arguments**

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

**Details**

```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.graeco`, `design.lattice`, `design.lsd`, `design.rcbd`, `design.split`
Examples

```r
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**

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

**Arguments**

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

**Details**

```r
```

**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.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="",...)
**diffograph**

las parameters of the plot()
pch parameters of the plot()
bty parameters of the plot()
cex parameters of the plot()
lwd parameters of the plot()
xlab parameters of the plot()
ylab parameters of the plot()
... Other parameters of the function plot()

**Details**

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

**Value**

x list, object comparison test

**Author(s)**

Felipe de Mendiburu

**References**


**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**

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

---

**duncan.test**

*Duncan’s new multiple range test*

**Description**

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

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

Arguments

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

Details

It is necessary first makes a analysis of variance.

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(1,2,4,2,3,5,3,4,6,4,5,7,1,5,6,7,1,3,7)
preference<-c(2,3,1,2,2,1,1,3,1,2,3,3,1,2,3,1,2,3,1,2)
out<-durbin.test(person,variety,preference,group=TRUE,console=TRUE,
main="Seven varieties of ice cream manufacturer")
#startgraph
bar.group(out$groups,horiz=TRUE,xlim=c(0,10),density=4,las=1)
#endgraph
# Example 2. Myles Hollander, pag 311
# Source: W. Moore and C.I. Bliss. 1942
day<gl(7,3)
chemical<-c("A","B","D","A","C","E","C","C","F","G","B","C","F",
"B","E","F""
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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

### References
Practical Nonparametrics Statistics. W.J. Conover, 1999

### See Also
- BIB.test
- DAU.test
- duncan.test
- durbin.test
- HSD.test
- kruskal.test
- 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.

Technologies: 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.
genxenv

Usage

data(frijol)

Format

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

- technology  a factor with levels a b c d
- production  a numeric vector
- index  a numeric vector

References

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

Examples

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

genxenv  Data of potato yield in a different environment

Description

50 genotypes and 5 environments.

Usage

data(genxenv)

Format

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

- ENV  a numeric vector
- GEN  a numeric vector
- YLD  a numeric vector

Source

International Potato Center. CIP - Lima Peru.

References

International Potato Center. CIP - Lima Peru.

Examples

library(agricolae)
data(genxenv)
str(genxenv)
Glycoalkaloids  Data Glycoalkaloids

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

Usage
data(Glycoalkaloids)

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

HPLC  a numeric vector
spectrophotometer  a numeric vector

Source
International Potato Center. CIP - Lima Peru.

References
International Potato Center. CIP - Lima Peru.

Examples
library(agricolae)
data(Glycoalkaloids)
str(Glycoalkaloids)

graph.freq  Histogram

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

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

- **x**: a vector of values, 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$breaks)
axis(2, seq(0, 20, 0.1))
# To reproduce histogram.
h1 <- graph.freq(h, col="blue", frequency=2, border="red", density=8, axes=FALSE, xlab="YIELD", ylab="relative")
axis(1, h$breaks)
axis(2, seq(0, 4, 0.1))
# summary, only frequency
limits <- seq(10, 40, 5)
frequencies <- c(2, 6, 8, 7, 3, 4)
# startgraph
h <- graph.freq(limits, counts=frequencies, col="bisque", xlab="Classes")
```
polygons.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
give.freq(h,col="red",type="b",ylab="Accumulated relative frequency", xlab="Variable")
# only . frequency polygon
h<-graph.freq(limits,counts=frequencies,border=FALSE,col=NULL,xlab=" ",ylab="")
title(main="Polygon of frequency", xlab="Variable", ylab="Frecuency")
polygon.freq(h,col="blue")
grid(col="brown")
#endgraph
# Draw curve for Histogram
h<- graph.freq(yield,axes=FALSE, frequency=3, ylab="f(yield)",col="yellow")
axis(1,h$breaks)
axis(2,seq(0,0.18,0.03),las=2)
lines(density(yield), col = "red", lwd = 2)
title("Draw curve for Histogram")

---

**grass**  

*Data for Friedman test*

**Description**

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

**Usage**

data(grass)

**Format**

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

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

**Details**

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


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


Examples

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

*Data growth of trees*

**Description**

Data growth of pijuayo trees in several localities.

**Usage**

data(growth)

**Format**

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

- `place` a factor with levels L1 L2
- `slime` a numeric vector
- `height` a numeric vector

**Source**

Experimental data (Pucallpa - Peru)

**References**

ICRAF lima Peru.

**Examples**

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

---

haynes  

*Data of AUDPC for nonparametrical stability analysis*

**Description**

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

**Usage**

data(haynes)
Format

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

clon - a factor with levels A84118-3 AO80432-1 AO84275-3 AWN86514-2 B0692-4 B0718-3 B0749-2 F 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)

Hco2006

Data amendment Huanuco 2006

Description

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

Usage

data(Hco2006)

Format

The format is: List of 2

amendment - a factor
crop - a factor
block - a numeric vector, replications
plant - a numeric vector, number plant
wilt_percent - a numeric vector, wilt percentage at 60 days
health - a numeric vector, kg/8m2, 20 plants
rot - a numeric vector, kg/8m2, 20 plants
Details

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

Source

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

References

International Potato Center. CIP - Lima Peru.

Examples

```r
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**

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

---

**Data of potato, Heterosis**

**Description**

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

**Usage**

data(heterosis)

**Format**

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

- **Place**: 1=La Molina, 2=Huancayo
- **Replication**: a numeric vector
- **Treatment**: a numeric vector
- **Factor**: a factor with levels Control progenie progenitor testigo
- **Female**: a factor with levels Achirana LT-8 MF-I MF-II Serrana TPS-2 TPS-25 TPS-7
- **Male**: a factor with levels TPS-13 TPS-67 TS-15
- **v1**: Yield (Kg/plant)
- **v2**: Reducing sugars (scale): 1 low and 5=High
- **v3**: Tuber dry matter (percentage)
- **v4**: Tuber number/plant
- **v5**: Average tuber weight (g)
Details

The study was conducted in 3 environments, La Molina-PERU to 240 masl. during autumn-winter and spring, and in Huancayo-PERU 3180 masl., during summer. The experimental material consisted of 24 families half brother in the form of tubers derived from TPS, obtained crossing between 8 female and 3 male parents. Design used was randomized complete block with three repetitions. The experimental unit was 30 plants in two rows at a distance of 30 cm 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))
test2 <- with(site1,HSD.test(v1, Treatment,DFe,CMe))
model22<-with(site2,lineXtester(Replication, Female, Male, v3))
model3<-with(site3,lineXtester(Replication, Female, Male, v4))
```

hgroups

_ groups of hclust_

Description

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

Usage

hgroups(hmerge)

Arguments

hmerge The object is components of the hclust
Value

The merge clusters is printed.

Author(s)

F. de Mendiburu

See Also

hclust, hcut, consensus

Examples

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

HSD.test Multiple comparisons: Tukey

Description

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

Usage

HSD.test(y, trt, D Fehler, MS error, alpha = 0.05, group = TRUE, main = NULL, unbalanced = FALSE, console = FALSE)

Arguments

y model(aov or lm) or answer of the experimental unit
trt Constant (only y=model) or vector treatment applied to each experimental unit
D Fehler Degree free
MS error Mean Square Error
alpha Significant level
group TRUE or FALSE
main Title
un balanced TRUE or FALSE. not equal replication
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

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

library(agricolae)
data(huasahuasi)
names(huasahuasi)
str(huasahuasi$AUDPC)
str(huasahuasi$YIELD)
index.AMMI

AMMI index and yield stability

Description

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

Usage

index.AMMI(model)

Arguments

model          object AMMI

Details

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

\[
ASV = \sqrt{SSpc1/SSpc2 \cdot (PC1i)^2 + (PC2i)^2}
\]

\[
YSI = RASV + RY
\]

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

Value

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

Author(s)

F. de Mendiburu

References


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

See Also

AMMI.plot.AMMI
Examples

```r
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**

```r
```

**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 22-05-05 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

\[ V_x = V(x)/x \]

- \( V(x) \) 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' index of soil heterogeneity.

Value

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

Author(s)

Felipe de Mendiburu

References

Examples

```r
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)

# 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  

<table>
<thead>
<tr>
<th>Class intervals</th>
</tr>
</thead>
</table>

Description

List class intervals.

Usage

```r
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.
**kruskal**

**Usage**

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

**Arguments**

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

**Details**

For equal or different repetition.
For the adjustment methods, see the function p.adjusted.
p-adj = "none" is t-student.

**Value**

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

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

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

**Examples**

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

*Finding the Kurtosis coefficient*

**Description**

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

**Usage**

```r
kurtosis(x)
```

**Arguments**

- `x` a numeric vector

**Value**

- `x` The kurtosis of `x`

**See Also**

- `skewness`

**Examples**

```r
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**

```r
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WS</td>
<td>object weather-severity</td>
</tr>
<tr>
<td>Cultivar</td>
<td>chr</td>
</tr>
<tr>
<td>ApplSys</td>
<td>chr</td>
</tr>
<tr>
<td>InocDate</td>
<td>days</td>
</tr>
<tr>
<td>LGR</td>
<td>num, see example</td>
</tr>
<tr>
<td>IniSpor</td>
<td>num</td>
</tr>
<tr>
<td>SR</td>
<td>num, see example</td>
</tr>
<tr>
<td>IE</td>
<td>num, Initialization infection</td>
</tr>
<tr>
<td>LP</td>
<td>num, latent period</td>
</tr>
<tr>
<td>InMicCol</td>
<td>num</td>
</tr>
<tr>
<td>MatTime</td>
<td>chr</td>
</tr>
<tr>
<td>...</td>
<td>plot graphics parameters</td>
</tr>
</tbody>
</table>

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).
lateblight

Value

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

Note

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

Author(s)

Jorge L. Andrade-Piedra (1) (j.andrade@cgiar.org), Gregory A. Forbes (1) (g.forbes@cgiar.org),
Robert J. Hijmans (2) (rhiijmans@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

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E. Ticknor, and P. A. Arneson. Ithaca, Cornell University, Department of Plant Pathology, Ithaca,
NY, USA.

See Also

weatherSeverity

Examples

library(agricolae)
f <- system.file("external/weather.csv", package="agricolae")
weather <- read.csv(f,header=FALSE)
f <- system.file("external/severity.csv", package="agricolae")
severity <- read.csv(f)
weather[,1]<-as.Date(weather[,1],format = "%m/%d/%Y")
# Parameters dates
dates<-as.Date(dates)
EmergDate <- as.Date("2000/01/19")
EndEpidDate <- as.Date("2000-04-22")
dates<-as.Date(dates)
NoReadingsH<- 1
RHthreshold <- 90
WS<-weatherSeverity(weather,severity,dates,EmergDate,EndEpidDate,
NoReadingsH,RHthreshold)
# Parameters Lateblight
InocDate="2000-03-18"
LGR <- 0.00410
IniSpor <- 0
SR <- 292000000
IE <- 1.0
LP <- 2.82
InMicCol < 9
Cultivar <- 'NICOLA'
ApplSys <- "NOFUNGICIDE"
main<="Cultivar: NICOLA"
#--------------------------
model<lateblight(WS, Cultivar,ApplSys, InocDate, LGR,IniSpor,SR,IE, LP,
MatTime="LATESEASON",InMicCol,main=main,type="l",x1im=c(65,95),lwd=1.5,
xlab="Time (days after emergence)", ylab="Severity (Percentage)")
# reproduce graph
x<- model$Ofile$nday
y<- model$Ofile$SimSeverity
w<- model$Gfile$nday
z<- model$Gfile$MeanSeverity
Min<-model$Gfile$MinObs
Max<-model$Gfile$MaxObs
plot(x,y,type="l",xlim=c(65,95),lwd=1.5,xlab="Time (days after emergence)",
ylab="Severity (Percentage)")
points(w,z,col="blue",cex=1,pch=19)
npoints <- length(w)
for ( i in 1:npoints){
segments(w[i],Min[i],w[i],Max[i],lwd=1.5,col="blue")
}
legend("topleft",c("Disease progress curves","Weather-Severity"),
title="Description",lty=1,pch=c(3,19),col=c("black","blue"))


lineXtester  

**Line x Tester Analysis**

**Description**

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

**Usage**

lineXtester(replications, lines, testers, y)
Arguments

replications  Replications
lines         Lines
 testers       Testers
 y            Variable, response

Details

ANOVA with parents and crosses
ANOVA for line X tester analysis
ANOVA for line X tester analysis including parents
Standard Errors for Combining Ability Effects.
Genetic Components.
...
Proportional contribution of lines, testers and their interactions to total variance

Value

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

Author(s)

Felipe de Mendiburu

References

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979. Hierarchial and
factorial mating designs for quantitative genetic analysis in tetrasomic potato. R. Orpis; 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))
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

**LxT**

**Data Line by tester**

**Description**

Data frame with yield by line x tester.

**Usage**

`data(LxT)`

**Format**

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

- `replication` a numeric vector
- `line` a numeric vector
- `tester` a numeric vector
- `yield` a numeric vector

**Source**

Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979
markers  Data of molecular markers

Description
A partial study on 27 molecular markers.

Usage
data(markers)

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

marker1  a numeric vector
marker2  a numeric vector
marker3  a numeric vector
marker4  a numeric vector
marker5  a numeric vector
marker6  a numeric vector
marker7  a numeric vector
marker8  a numeric vector
marker9  a numeric vector
marker10 a numeric vector
marker11 a numeric vector
marker12 a numeric vector
marker13 a numeric vector
marker14 a numeric vector
marker15 a numeric vector
marker16 a numeric vector
marker17 a numeric vector
marker18 a numeric vector
marker19 a numeric vector
marker20 a numeric vector
marker21 a numeric vector
marker22 a numeric vector
marker23 a numeric vector
marker24 a numeric vector
marker25 a numeric vector
marker26 a numeric vector
marker27 a numeric vector
Median.test

Source
International Potato Center Lima-Peru.

References
International Potato Center Lima-Peru.

Examples
library(agricolae)
data(markers)
str(markers)

Median.test  Median test. Multiple comparisons

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

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

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

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

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

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

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

Examples

```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 sow-
ing, SIMPLE ROW. The goal is to analyze the behavior of three hybrid melon varieties and one  
standard.

Usage

```r
data(melon)
```

Format

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

- **row**  
  a numeric vector
- **col**  
  a numeric vector
- **variety**  
  a factor with levels V1 V2 V3 V4
- **yield**  
  a numeric vector
Details

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

Source

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

References

Universidad Nacional Agraria la molina.

Examples

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

montecarlo Random generation by Montecarlo

Description

Random generation form data, use function density and parameters

Usage

montecarlo(data, k, ...)

Arguments

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

Value

Generate random numbers with empirical distribution.

Author(s)

Felipe de Mendiburu

See Also

density
Examples

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

---

Data of native potato

Description

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

Usage

`data(natives)`

Format

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

- `variety`: a numeric vector
- `number`: a numeric vector
- `weight`: a numeric vector
- `size`: a numeric vector

Source

International Potato Center. CIP - Lima Peru.

Examples

```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

```r
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

```r
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**

```r
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**

```r
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**

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

**Examples**

```r
library(agricolae)
data(growth)
#startgraph
h1<-with(growth,hist(height,col="green",xlim=c(6,14)))
ogive.freq(h1)
#endgraph
```
order.group

Arguments

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

Value

Ogive points.

Author(s)

Felipe de Mendiburu

See Also

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

Examples

library(agricolae)
data(growth)
h<-graph.freq(growth$height,plot=FALSE)
points<-ogive.freq(h,col="red",frame=FALSE,
xlab="Height", ylab="Accumulated relative frequency", main="ogive")
plot(points,type="b",pch=16,las=1,bty="l")

order.group

Ordering the treatments according to the multiple comparison

Description

This function allows us to compare the treatments averages or the adding of their ranges with the minimal significant difference which can vary from one comparison to another one.

Usage

order.group(trt, means, N, MSError, Tprob, std.err, parameter=1, snk=0,
Dferror=NULL, alpha=NULL, 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  Constant 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

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, significant 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

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

**Description**
Potato Wild

**Usage**
data(pamCIP)

**Format**
A data frame with 43 observations on the following 107 variables. Rownames: code and genotype’s name. Column data: molecular markers.

**Details**
To study the molecular markers in Wild.

**Source**
Laboratory data.

**References**
International Potato Center Lima-Peru (CIP)

**Examples**

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

---

**paracsho**  
*Data of Paracsho biodiversity*

**Description**
A locality in Peru. A biodiversity.

**Usage**
data(paracsho)
path.analysis

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 BROCONIDAE CALUPHORIDAE CECIDOMYIIDAE CHENEUMONIDAE CHRYOMELIDAE
CICADELLIDAE CUCICIDAE ERIOPHAMIDAE HEMEROBIIIDAE ICHNEUMONIDAE LOUCHAPIIDAE MIRIDAE
MUSCIDAE MUSICADAE MUSLIDAE MYCETOPHILIDAE MYCETOPHILIIDAE NENPHALIDAE NOCLUIDAE
NOCTERIDAE NOCTUIDAE PERALIDAE PIPUNCULIDAE PROCTOTRUPIDAE PSYLLIDAE PYRALIDAE
SARCOPHAGIDAE SARCOPILAGIDAE SCATOPHAGIDAE SCATOPHOGIDAE SCIARIDAE SERSIDAE SYRPHIDAE
TACHINIDAE TIPULIDAE
Number.of.specimens a numeric vector

Details

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

Source

Entomology dataset.

References

International Potato Center.

Examples

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

path.analysis  Path Analysis

Description

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

Usage

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

- **corr.x**  
  Matrix of correlations of the independent variables

- **corr.y**  
  vector of dependent correlations with each one of the independent ones

**Details**

It is necessary first to calculate the correlations.

**Value**

Direct and indirect effects and residual Effect^2.

**Author(s)**

Felipe de Mendiburu

**References**

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

**See Also**

correlation

**Examples**

```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(cor.x,cor.y)
```
Analysis of the Partially Balanced Incomplete Block Design

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

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

Arguments
- block: blocks
- trt: Treatment
- replication: Replication
- y: Response
- k: Block size
- method: Estimation method: REML, ML and VC
- test: Comparison treatments
- alpha: Significant test
- console: logical, print output
- group: logical, groups

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

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

```r
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,
        1,1,2,4,5,6,7,8,5,4,3,1,1,2,5,4,2,7,6,8,5,4,5,7,6,5,5,4)
rm(Genotype)
not run
```

plot.AMMI

```
PLOT AMMI
```

Description

Biplot AMMI.

Usage

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

- **x**: object AMMI
- **first**: position axis x, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **second**: position axis y, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **third**: position axis z, 0=Y-dependent, 1=PC1, 2=PC2, 3=PC3
- **type**: 1=biplot, 2=tripplot 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 tripplot, the components are normalized in scale 0-1.
- **type=3** produce graphs on a 2d point set that are all subgraphs of the Delaunay triangulation 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(relative neigh) package=spdep

Author(s)

Felipe de Mendiburu

See Also

AMMI

Examples

```R
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=count, 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
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$breaks)  
axis(2,seq(0,20,0.1))  
# To reproduce histogram.  
h1 <- plot(h, col="blue", frequency=2,border="red", density=8,axes=FALSE,  
lab="YIELD",ylab="relative")  
axis(1,h$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",  
lab=".frequency")  
#endgraph  
# Statistics  
measures<-stat.freq(h)  
print(measures)  
# frequency table full  
round(table.freq(h),2)  
#startgraph  
# ogive  
ogive.freq(h,col="red",type="b",ylab="Accumulated relative frequency",  
xlab="Variable")  
# only frequency polygon  
h<-graph.freq(limits,counts=frequencies,border=FALSE,col=NULL,xlab=" ",ylab="")  
title( main="Polygon of frequency",  
xlab="Variable", ylab="Frecuency")  
polygon.freq(h,col="blue")  
grid(col="brown")  
#endgraph  
# Draw curve for Histogram  
h<- graph.freq(yield,axes=FALSE, frequency=3, ylab="f(yield)",col="yellow")  
axis(1,h$breaks)  
axis(2,seq(0,0.18,0.03),las=2)  
lines(density(yield), col = "red", lwd = 2)  
title("Draw curve for Histogram")
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, cex=NULL, hy=0,...)

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
cex optional, group label size
hy optional, default =0, sum group label position
... Parameters of the function barplot()

Details

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

Author(s)

Felipe de Mendiburu

See Also

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

Examples

library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison<- LSD.test(model,"virus",alpha=0.01,group=TRUE)
#startgraph
par(cex=1.5)
plot(comparison,horiz=TRUE,xlim=c(0,50),las=1)
title(cex.main=0.8,main="Comparison between treatment 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.

- block  a numeric vector
- plot  a factor with levels p1 p2 p3 p4 p5 p6
- A  a factor with levels a1 a2
- B  a factor with levels b1 b2 b3
- yield  a numeric vector

Source

International Potato Center. CIP

Examples

library(agricolae)
data(plots)
str(plots)
plots[,1] <-as.factor(plots[,1])
# split-plot analysis
model <- aov(yield ~ block + A + Error(plot)+ B + A:B, data=plots)
summary(model)
b<-nlevels(plots$B)
a<-nlevels(plots$A)
r<-nlevels(plots$block)
dfa <- df.residual(model$plot)
Ea <- deviance(model$plot)/dfa
dfb <- df.residual(model$Within)
Eb <- deviance(model$Within)/dfb
Eab <- (Ea +(b-1)*Eb)/(b*r)
# Satterthwaite
dfab<-(Ea +(b-1)*Eb)^2/(Ea^2/dfa +((b-1)*Eb)^2/dfb)
# Comparison A, A(b1), A(b2), A(b3)
comparison1 <-with(plots,LSD.test(yield,A,dfa,Ea))
comparison2 <-with(plots,LSD.test(yield[B=="b1"],A[B=="b1"],dfab,Eab))
comparison3 <-with(plots,LSD.test(yield[B=="b2"],A[B=="b2"],dfab,Eab))
comparison4 <-with(plots,LSD.test(yield[B=="b3"],A[B=="b3"],dfab,Eab))
# Comparison B, B(a1), B(a2)

comparison5 <- with(plots, LSD.test(yield, B, dfb, Eb))
comparison6 <- with(plots, LSD.test(yield[A == "a1"], B[A == "a1"], dfb, Eb))
comparison7 <- with(plots, LSD.test(yield[A == "a2"], B[A == "a2"], dfb, Eb))

---

plrv

### Data clones from the PLRV population

#### Description

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

#### Usage

data(plrv)

#### Format

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

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

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

Rep a numeric vector

WeightPlant a numeric vector

WeightPlot a numeric vector

Yield a numeric vector

#### Source

International Potato Center Lima-Peru

#### References

International Potato Center Lima-Peru

#### Examples

library(agricolae)
data(plrv)
str(plrv)
The polygon of frequency on the histogram

**Description**

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

**Usage**

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

**Arguments**

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

**Author(s)**

Felipe de Mendiburu Delgado

**See Also**

`polygon.freq`, `table.freq`, `stat.freq`, `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 of cutting**

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

**Usage**

```
data(potato)```
Format
A data frame with 18 observations on the following 4 variables.

date a numeric vector
variety a factor with levels Canchan Unica
harvest a numeric vector
cutting a numeric vector

Source
Experimental data.

References
International Potato Center

Examples
library(agricolae)
data(potato)
str(potato)

ralstonia

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

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

Usage
data(ralstonia)

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

place a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2
Day2 a numeric vector
Day15 a numeric vector
Day29 a numeric vector
Day43 a numeric vector
Day58 a numeric vector
Day73 a numeric vector
Day133 a numeric vector
Details

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

Source

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

References

International Potato Center. CIP - Lima Peru.

Examples

```r
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 (homogeneity 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
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,
1.4,1.9,3.1,1.7,2.8,4.2,1.3,1.7,3.7,1.7,3.2,3.0,1.6,2.0,2.2,1.4,2.2,2.3,1.0,
2.2,3.8,1.5,2.2,2.0,1.6)
Ascorbic <-c(51,65,54,55,52,59,41,46,42,51,54,53,41,45,50,45,49,50,51,49,
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
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
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

<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

\[
\text{lm(formula = CV ~ I(1/marker))}
\]

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 Resampling for linear models

Description

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

Usage

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

Arguments

model model in R
data data for the study of the modelk number of re-samplingsconsole 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)
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)
```

---

Descrition

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.
Examples

# Analysis 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.
**similarity**

**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**


**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\nDeal with different virus")
# Old version scheffe.test()
df<-df.residual(model)
MSerror<-deviance(model)/df
Fc<-anova(model)["virus",4]
out <- with(sweetpotato,scheffe.test(yield, virus, df, MSerror, Fc))
print(out)
```

---

**similarity**

*Matrix of similarity in binary data*

**Description**

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

**Usage**

`similarity(A)`

**Arguments**

<table>
<thead>
<tr>
<th>A</th>
<th>Matrix, data binary</th>
</tr>
</thead>
</table>
Value

Distance matrix. Class = dist.

Author(s)

Felipe de Mendiburu

See Also

cv.similarity, resampling.cv

Examples

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

Description

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

Usage

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

Arguments

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

Value

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

See Also
resampling.model

Examples

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

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.
**skewness**

**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
```
Description

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

Usage

SNK.test(y, trt, 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
  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

soil

Data of soil analysis for 13 localities

Description

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

Usage

data(soil)

Format

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

- **place**: a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2
- **pH**: a numeric vector
- **EC**: a numeric vector, electrical conductivity
- **CaCO3**: a numeric vector
- **MO**: a numeric vector
- **CIC**: a numeric vector
- **P**: a numeric vector
- **K**: a numeric vector
- **sand**: a numeric vector
- **slime**: a numeric vector

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)
```
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 sp.plot

sp.plot

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)
ssp.plot

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. One 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: Splip Split plot analysis

Author(s)

Felipe de Mendiburu

References


See Also

sp.plot, strip.plot, design.split, design.strip

Examples

# Statistical procedures for agricultural research, pag 143
# Grain Yields of Three Rice Varieties Grown under
# Three Management practices and Five Nitrogen levels; in a
# split-split-plot design with nitrogen as main-plot,
# management practice as subplot, and variety as sub-subplot
# 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$gl.a; glb<-model$gl.b; glc<-model$gl.c
Ea<-model$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
```

---

### 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
stat.freq

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 create 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)

strip.plot  Strip-Plot analysis

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

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

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

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

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

Author(s)
Felipe de Mendiburu
References


See Also

ssp.plot, sp.plot, design.split, design.strip

Examples

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

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

See Also

`polygon.freq`, `table.freq`, `stat.freq`, `intervals.freq`, `graph.freq`, `join.freq`, `ogive.freq`, `normal.freq`

Examples

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

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

---

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

### Description

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

### Usage

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

### Arguments

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

### Value

Frequency table.

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


**Author(s)**

Felipe de Mendiburu

**See Also**

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

**Examples**

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

---

**sweetpotato**

*Data of sweetpotato yield*

**Description**

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

**Usage**

`data(sweetpotato)`

**Format**

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

- **virus** a factor with levels cc fc ff oo
- **yield** a numeric vector

**Source**

Experimental field.

**References**

International Potato Center. CIP - Lima Peru

**Examples**

```r
library(agricolae)
data(sweetpotato)
str(sweetpotato)
```
table.freq

frequency Table of a Histogram

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

Usage

table.freq(object)

Arguments

object Object by function graph.freq()

Value

Frequency table.

<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>

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

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

Variance K, ties, Kendall

Description
The Kendall method in order to find the K variance.

Usage
vark(x, y)

Arguments
x Vector
y vector

Details
Script in C to R.

Value
variance of K for Kendall’s tau

Author(s)
Felipe de Mendiburu

References

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

Examples
library(agricolae)
x <-c(1,1,1,4,2,2,3,1,3,2,1,1,2,3,2,1,1,2,1,2)
y <-c(1,1,2,3,4,4,2,1,2,3,1,1,3,4,2,1,1,3,1,2)
vark(x,y)
waerden.test  

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

**Description**

A nonparametric test for several independent samples.

**Usage**

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

**Arguments**

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

**Details**

The data consist of k samples of possibly unequal sample size. The post hoc test is using the criterium Fisher’s least significant difference (LSD).

**Value**

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

**Author(s)**

Felipe de Mendiburu

**References**

Practical Nonparametrics Statistics. W.J. Conover, 1999

**See Also**

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

```r
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**

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

**Arguments**

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

**Details**

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

**Value**

Waller value for the Waller and Duncan test.

**Author(s)**

Felipe de Mendiburu
References


See Also

waller.test

Examples

```r
# 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

```r
waller.test(y, trt, D Fehler, 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
- `D Fehler`: 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

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

Author(s)

Felipe de Mendiburu

References


Steel & 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
weatherSeverity

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
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.
Format

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

- **locality**: a factor with levels Cajamarca, Lima, Oxapampa in PERU
- **site**: a numeric vector
- **dose**: a factor with levels F0, F150, F80
- **entry**: a factor with levels AKW5075, AMM5136, AMM5150, AMM5163, ARB5125, CLLUNC118, P1385, SAL136
- **replication**: a numeric vector, replications
- **height**: a numeric vector, plant height, centimeters
- **stalks**: a numeric vector, number of stalks
- **wfr**: a numeric vector, weight of fresh roots, grams
- **wff**: a numeric vector, weight of fresh foliage, grams
- **wfk**: a numeric vector, weight fresh kroner, grams
- **roots**: a numeric vector, matter of dried roots, grams
- **FOS**: a numeric vector, fructo-oligosaccharides, 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)
```
zigzag  

order plot in serpentine

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

Usage
zigzag(outdesign)

Arguments
outdesign output design

Value
fieldbook Remuneration of serpentine plots.

Author(s)
Felipe de Mendiburu

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

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