Package ‘agricolae’

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Type Package

Title Statistical Procedures for Agricultural Research

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Imports klaR, MASS, nlme, cluster, spdep, AlgDesign, graphics

Suggests RANN, rgeos

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. Agrico-
lae offers extensive functionality on experimental design especially for agricultural and plant breeding experiments, which can also be useful for other purposes. It sup-
ports planning of lattice, Alpha, Cyclic, Complete Block, Latin Square, Graeco-
Latin Squares, augmented block, factorial, split and strip plot designs. There are also vari-
ous analysis facilities for experimental data, e.g. treatment comparison procedures and sev-
eral non-parametric tests comparison, biodiversity indexes and consensus cluster.

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agricolae-package

**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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Planning of field experiments: lattice, factorial, RCBD, CRD, Latin Square, Youden, Graeco, BIB, Alpha design, Cyclic, augmented block, split and strip plot Designs. Comparison of multi-location trials: AMMI, Index AMMI Stability (biplot, triplot), comparison between treatments: LSD, Bonferroni and other p-adjust, HSD, Waller, Student Newman Keuls SNK, Duncan, REGW, Scheffe; Non parametric tests: Kruskal, Friedman, Durbin, Van Der Waerden, Median. Analysis of genetic experiments: North Carolina designs, LinexTester, Balanced Incomplete Block, Strip plot, Split-Plot, Partially Balanced Incomplete Block, analysis Mother and baby trials (see data RioChillon).
AMMI


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

AMMI Analysis

Description

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

Usage

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

Arguments

ENV

Environment

GEN

Genotype

REP

Replication

Y

Response

MSE

Mean Square Error

console

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 genopyte and environment
- **analysis**: analysis of variance principal components
- **means**: average genotype and environment
- **biplot**: data to produce graphics
- **PC**: class princomp

Author(s)

F. de Mendiburu

References


See Also

- `linextester`, `plot.AMMI`

Examples

```r
# Full replications
library(agricolae)
# Example 1
data(plrv)
model<- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console=FALSE))
model$ANOVA
# see help(plot.AMMI)
# biplot
plot(model)
# triplot PC 1,2,3
plot(model, type=2, number=TRUE)
# biplot PC1 vs Yield
plot(model, first=0, second=1, number=TRUE)
# Example 2
data(CIC)
data1<-CIC$comas[,c(1,6,7,17,18)]
data2<-CIC$oxapampa[,c(1,6,7,19,20)]
cic <- rbind(data1,data2)
model<-with(cic, AMMI(Locality, Genotype, Rep, relative))
model$ANOVA
plot(model,0,1,angle=20,ecol="brown")
# Example 3
# Only means. Mean square error is well-known.
data(sinRepAmmi)
REP <- 3
MSError <- 93.24224
#startgraph
model<-with(sinRepAmmi, AMMI(ENV, GEN, REP, YLD, MSError,PC=TRUE))
```
AMMI.contour

# 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.

**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 TRIPOINT one.

**Value**

- **model**: output AMMI
- **distance**: Numeric >0 and <=1
- **shape**: Numeric
Note

Complement graphics AMMI

Author(s)

Felipe de Mendiburu

See Also

AMMI

Examples

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

---

**audpc**

*Categorizing the absolute or relative value of the AUDPC*

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

Value

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

Author(s)

Felipe de Mendiburu

References


Examples

library(agricolae)
dates<-c(14,21,28) # days
# example 1: evaluation - vector
evaluation<-c(40,80,90)
audpc(evaluation,dates)
# example 2: evaluation: data frame nrow=1
evaluation<-data.frame(E1=40,E2=80,E3=90) # percentages
plot(dates,evaluation,type="h",ylim=c(0,100),col="red",axes=FALSE)
title(cex.main=0.8,main="Absolute or Relative AUDPC\nTotal area = 100*(28-14)=1400")
lines(dates,evaluation,col="red")
text(18,20,"A = (21-14)*(80+40)/2")
text(25,60,"B = (28-21)*(90+80)/2")
text(25,40,"audpc = A+B = 1015")
text(24.5,33,"relative = audpc/area = 0.725")
abline(h=0)
axis(1,dates)
axis(2,seq(0,100,5),las=2)
lines(rbind(c(14,40),c(14,100)),lty=8,col="green")
lines(rbind(c(14,100),c(28,100)),lty=8,col="green")
lines(rbind(c(28,90),c(28,100)),lty=8,col="green")
# It calculates audpc absolute
absolute<-audpc(evaluation,dates,type="absolute")
print(absolute)
rm(evaluation, dates, absolute)
# example 3: evaluation dataframe nrow>1
data(disease)
dates<-c(1,2,3) # week
evaluation<-disease[,c(4,5,6)]
# It calculates audpc relative
index <-audpc(evaluation, dates, type = "relative")
# Correlation between the yield and audpc
correlation(disease$yield, index, method="kendall")
# example 4: days infile
data(CIC)
comas <- CIC$comas
oxapampa <- CIC$oxapampa
dcomas <- names(comas)[9:16]
days<- as.numeric(substr(dcomas,2,3))
AUDPC< - audpc(dcomas[,9:16],days)
relative< - audpc(dcomas[,9:16],days,type = "relative")
h1<-graph.freq(AUDPC,border="red",density=4,col="blue")
table.freq(h1)
h2<-graph.freq(relative,border="red",density=4,col="blue",
frequency=2, ylab="relative frequency")

---

**The Area Under the Disease Progress Stairs**

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

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

**Author(s)**

Felipe de Mendiburu
References

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

Examples

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

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

Details

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

Value

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

Author(s)

Felipe de Mendiburu

See Also

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

Examples

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

# horiz = TRUE
bar.group

bar.err(out$means,variation="SE",horiz=TRUE,xlim=c(0,45),bar=FALSE,col=0)
#startgraph
par(mfrow=c(1,1))
#endgraph

bar.group

Plotting the multiple comparison of means

Description

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

Usage

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

Arguments

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

Details

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

Value

x Data frame
horiz Logical TRUE or FALSE
...

Author(s)

Felipe de Meniburu

See Also

LSD.test, HSD.test, kruskal, friedman, durbin.test, waller.test
Examples

# Example 1
library(agricolae)
data(sweetpotato)
model<-aov(yield~virus,data=sweetpotato)
comparison<- LSD.test(model,"virus",alpha=0.01,group=TRUE)
print(comparison$groups)
=startgraph
par(cex=1.5)
bar.group(comparison$groups,horiz=TRUE,density=8,col="blue",border="red",
xlim=c(0,50),las=1)
title(cex.main=0.8,main="Comparison between treatment 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

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

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

Author(s)

F. de Mendiburu

References


See Also

durbin.test

Examples

library(agricolae)
run<-gl(10,3)
monovinyl<-c(16,18,32,19,46,45,26,39,61,21,35,55,19,47,48,20,33,31,13,13,34,21, 30,52,24,10,50,24,31,37)
out<-BIB.test(run,psi,monovinyl,test="waller",group=FALSE)
print(out)
bar.err(out$means,variation="range",ylim=c(0,60),bar=FALSE,col=0)
out<-BIB.test(run,psi,monovinyl,test="waller",group=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=TRUE,console=TRUE)
out<-BIB.test(run,psi,monovinyl,test="tukey",group=FALSE,console=TRUE)
rm(run,psi,monovinyl,out)

# Example linear estimation and design of experiments. D.D. Joshi. 1987
# Professor of Statistics, Institute of Social Sciences Agra, India
# 6 varieties of wheat crop in a BIB whit 10 blocks of 3 plots each.
y <-c(69,77,72,63,70,54,65,65,57,59,50,45,68,75,59,38,60,60,62, 55,54,65,62,65,61,39,54,67,63,56)
carolina

Varieties<-gl(6,5)
block<-c(1,2,3,4,5,1,2,6,7,8,1,3,6,9,10,2,4,7,9,10,3,5,7,8,9,4,5,6,8,10)
BIB.test(block, varieties, y)

# Example Introduction to experimental statistics. Ching Chun Li. 1964
# pag. 395 table. 27.2
# 7 trt, k=3 and b=7.
y<-c(10,15,11,4,12,15,5,14,10,14,19,19,8,10,17,6,11,12,5,14,21)
block<gl(7,3)
trt<-c(1,2,4,2,3,5,3,4,6,4,5,7,1,5,6,2,6,7,1,3,7)
out<-BIB.test(block, trt, y, test="duncan")
bar.group(out$groups,col="blue",density=4,ylim=c(0,max(y)))
rm(y,block,trt,out)

---

carolina North Carolina Designs I, II and III

Description

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

Usage

carolina(model, data)

Arguments

  model Constant
  data Data frame

Details

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

Value

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

Author(s)

Felipe de Mendiburu

References

  Biometrical Methods in Quantitative Genetic Analysis, Singh, Chaudhary. 1979
Data amendment Carhuaz 2006

Description

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

Usage

data(Chz2006)

Format

The format is: List of 2

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

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

Source

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

References

International Potato Center. CIP - Lima Peru.

Examples

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

---

CIC

Data for late blight of potatoes

Description

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

Usage

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 percentaje, xx is days. ORD1, ORD2, SBLK and row are references location of the plot in the field.

Source


References

International Potato Center. CIP - Lima Peru.

Examples

library(agricola)
data(CIC)
CIC$comas
CIC$oxapampa

clay

Data of Ralstonia population in clay soil

Description

An evaluation over a time period.

Usage

data(clay)

Format

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

per.clay a numeric vector
days a numeric vector
ralstonia a numeric vector

Source

Experimental field.

References

International Potato Center. CIP - Lima Peru.
Examples

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

ComasOxapampa  Data AUDPC Comas - Oxapampa

Description

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

Usage

data(ComasOxapampa)

Format

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

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

Details

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

Source


References

International Potato Center. CIP - Lima Peru.
**Examples**

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

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

Author(s)
F. de Mendiburu

References

See Also
hclust, hgroups, hcut

Examples
library(agricolae)
data(pamCIP)
# only code
rownames(pamCIP)<-substr(rownames(pamCIP),1,6)
# par(cex=0.8)
output<-consensus( pamCIP,distance="binary", method="complete",nboot=5)
# Order consensus
Groups<-output$table[dend[,,c(6,5)]]
Groups<-Groups[order(Groups[,2],decreasing=TRUE),]
print(Groups)
## Identification of the codes with the numbers.
cbind(output$dendrogram$labels)
## To reproduce dendrogram
dend<-output$dendrogram
data<-output$table.dend
dend
plot(dend)
text(data[,3],data[,4],data[,5])
# Other examples
# classical dendrogram
dend<-as.dendrogram(output$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)
Description
Data from a completely randomized design where four different methods of growing corn resulted in various yields per acre on various plots of ground where the four methods were tried. Ordinarily, only one statistical analysis is used, but here we will use the kuskal-wallis test so that a rough comparison may be made with the mediasn test.

Usage
data(corn)

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

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

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

Source
Book: Practical Nonparametric Statistics.

References

Examples
data(corn)
str(corn)
correl

Correlation Coefficient

Description

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

Usage

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

Arguments

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

Value

x Numeric
y Numeric
...

Author(s)

Felipe de Mendiburu

References


See Also

correlation

Examples

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

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

Description

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

Usage

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

Arguments

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

Details

Parameters equal to function cor()

Value

table Numeric

Author(s)

Felipe de Mendiburu

References


See Also

correl
Examples

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

```r
cotton
```

Data of cotton

Description

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

Usage

data(cotton)

Format

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

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

Source


References


Examples

```
library(agricolae)
data(cotton)
str(cotton)
```
**cv.model**

*Coefficient of the experiment variation*

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

- `x` object

**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

Description

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

Usage

cv.similarity(A)

Arguments

A matrix of binary data

Value

A Data frame or matrix, numerics

Author(s)

Felipe de Mendiburu

See Also

similarity, resampling.cv

Examples

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

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

Author(s)

F. de Mendiburu

References

See Also

BIB.test, LSD.test, HSD.test, PBIB.test

Examples

```r
library(agricolae)
blocks<-c(rep("I",7),rep("II",6),rep("III",7))
trt<-c("A","B","C","D","E","F","H","J","A","B","C","D","E","F","H","J")
yield<-c(83,77,78,70,75,74,79,81,81,91,79,78,92,79,87,81,89,96,82)
model<- DAU.test(blocks, trt, yield, method="1sd", group=TRUE)
print(model$groups)
```

Description

Data for the analysis of carolina 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

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
Design of experiments for a factorial

Description

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

Usage

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

Arguments

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

Details


Value

parameters list
book dataframe
design.alpha

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
```r
# 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

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

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 list
statistics dataframe
sketch list
book dataframe

Author(s)

Felipe de Mendiburu

References

designs. printed in Great Britain. Online: http://biomet.oxfordjournals.org/cgi/content/abstract/63/1/83

See Also

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

Examples

library(agricolae)
#Example one
trt<-1:30
t <- length(trt)
# size block k
k<-3
# Blocks s
s<-t/k
# replications r
design.bib

Randomized Balanced Incomplete Block Designs. BIB

Description

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

Usage

```r
design.bib(trt, k, r=NULL, serie = 2, seed = 0, kinds = "Super-Duper", maxRep=20,randomization=TRUE)
```

Arguments

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

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

Author(s)

Felipe de Mendiburu

References


See Also

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

Examples

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

**Completely Randomized Design**

**Description**

It generates completely a randomized design with equal or different repetition. "Random" uses the methods of number generation in R. The seed is by set.seed(seed, kinds).

**Usage**

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

**Arguments**

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

**Details**


**Value**

- **parameters**: list
- **book**: dataframe

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

- parameters: list
- sketch: list
- book: dataframe

### Author(s)

Felipe de Mendiburu

### References


### See Also

design.ab, design.alpha, design.bib, design.crd, design.split, design.dau, design.graeco, design.lattice, design.1sd, design.rcbd, design.strip

### Examples

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

---

**design.dau**

**Augmented block design**

### Description

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

### Usage

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

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

Details

```
```

Value

- **parameters**: list
- **book**: dataframe

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

## design.graeco

### Graeco - latin square design

#### Description
A graeco - latin square is a KxK pattern that permits the study of k treatments simultaneously with three different blocking variables, each at k levels.
The function is only for squares of the odd numbers and even numbers (4, 8, 10 and 12)

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

#### Arguments
- **trt1**: Treatments
- **trt2**: Treatments
- **serie**: number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
- **seed**: seed
- **kinds**: method for to randomize
- **randomization**: TRUE or FALSE - randomize

#### Details
```
```

#### Value
- **parameters**: list
- **book**: dataframe

#### Author(s)
Felipe de Mendiburu

#### References
See Also

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

Examples

library(agricolae)
T1<-c("a", "b", "c", "d")
T2<-c("v", "w", "x", "y")
outdesign <- design.graeco(T1, T2, serie=1)
graeco<-outdesign$book
plots <- as.numeric(graeco[,1])
print(outdesign$sketch)
print(matrix(plots, byrow=TRUE, ncol=4))  # 10 x 10
T1 <- letters[1:10]
T2 <- 1:10
outdesign <- design.graeco(T1, T2, serie=2)
print(outdesign$sketch)

design.lattice  Lattice designs

Description

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

Usage

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

Arguments

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>trt</td>
<td>treatments</td>
</tr>
<tr>
<td>r</td>
<td>r=2(simple) or r=3(triple) lattice</td>
</tr>
<tr>
<td>serie</td>
<td>number plot, 1: 11,12; 2: 101,102; 3: 1001,1002</td>
</tr>
<tr>
<td>seed</td>
<td>seed</td>
</tr>
<tr>
<td>kinds</td>
<td>method for to randomize</td>
</tr>
<tr>
<td>randomization</td>
<td>TRUE or FALSE - randomize</td>
</tr>
</tbody>
</table>

Details

**Value**

- parameters: list
- statistics: data frame
- sketch: list
- book: dataframe

**Author(s)**

Felipe de Mendiburu

**References**


**See Also**

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

**Examples**

```r
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**

```r
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  list
book  dataframe

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

Details


Value

- **parameters**: list
- **book**: dataframe

Author(s)

Felipe de Mendiburu

References

design.split

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

Examples

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

---

design.split Split Plot Design

Description

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

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trt1</td>
<td>Treatments in Plots</td>
</tr>
<tr>
<td>trt2</td>
<td>Treatments in Subplots</td>
</tr>
<tr>
<td>r</td>
<td>Replications or blocks</td>
</tr>
<tr>
<td>design</td>
<td>Experimental design</td>
</tr>
<tr>
<td>serie</td>
<td>number plot, 1: 11,12; 2: 101,102; 3: 1001,1002</td>
</tr>
<tr>
<td>seed</td>
<td>seed</td>
</tr>
<tr>
<td>kinds</td>
<td>method for to randomize</td>
</tr>
<tr>
<td>first</td>
<td>TRUE or FALSE - randomize rep 1</td>
</tr>
<tr>
<td>randomization</td>
<td>TRUE or FALSE - randomize</td>
</tr>
</tbody>
</table>
design.strip

Description

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

Usage

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

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

Details


Value

parameters list
book    dataframe

Author(s)

Felipe de Mendiburu

References


See Also

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

Examples

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

**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="", ...)

Arguments

x Object created by a test of comparison, group=FALSE

main The main title (on top)

color1 non significant color

color2 significant color

color3 center line color

cex.axis parameters of the plot()

las parameters of the plot()

pch parameters of the plot()

bty parameters of the plot()

cex parameters of the plot()

lwd parameters of the plot()

xlab parameters of the plot()

ylab parameters of the plot()

... Other parameters of the function plot()
disease

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)
diffofgraph(x,cex.axis=0.8,xlab="Yield",ylab="")

# Example 2
x<- REGW.test(model,"virus",alpha=0.01,group=FALSE)
diffofgraph(x,cex.axis=0.6,xlab="Yield",ylab="",color1="brown",color2="green")
```

disease  | Data evaluation of the disease overtime

Description

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

Usage

data(disease)
Format

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

- plots a numeric vector
- rep a numeric vector
- trt a factor with levels T0 T1 T2 T3 T4 T5 T6
- E2 a numeric vector
- E5 a numeric vector
- E7 a numeric vector
- yield a numeric vector

Source

Experimental data.

References

International Potato Center. CIP - Lima Peru.

Examples

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

---

duncan.test

*Duncan’s new multiple range test*

Description

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

Usage

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

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

Details

It is necessary first makes a analysis of variance.

Value

- **y**: class (aov or lm) or vector numeric
- **trt**: constant (only y=model) or vector alfanumeric
- **DFerror**: Numeric
- **MSError**: Numeric
- **alpha**: Numeric
- **group**: Logic
- **main**: Text

Author(s)

Felipe de Mendiburu

References


See Also

LSD.test, waller.test, HSD.test, SNK.test

Examples

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

Value

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

Author(s)
Felipe de Mendiburu
**friedman**

**Friedman test and multiple comparison of treatments**

**Description**

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

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>judge</td>
<td>Identification of the judge in the evaluation</td>
</tr>
<tr>
<td>trt</td>
<td>Treatment</td>
</tr>
<tr>
<td>evaluation</td>
<td>Variable</td>
</tr>
</tbody>
</table>
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.
**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**

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

---

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

Arguments

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

Value

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

Author(s)

Felipe de Mendiburu
See Also

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

Examples

library(agricolae)
data(genxenv)
yield <- subset(genxenv$YLD, genxenv$ENV==2)
yield <- round(yield,1)
h <- graph.freq(yield, axes=FALSE, frequency=1, ylab="frequency", col="yellow")
axis(1, h$breaks)
axis(2, seq(0, 20, 0.1))
# To reproduce histogram.
h1 <- graph.freq(h, col="blue", frequency=2, border="red", density=8, axes=FALSE,
xlabel="YIELD", ylabel="relative")
axis(1, h$breaks)
axis(2, seq(0, 400, 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", xlabel="Classes")
polygon.freq(h, col="red")
title(main="Histogram and polygon of frequency",
ylabel="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",
xlabel="Variable")
# only frequency polygon
h <- graph.freq(limits, counts=frequencies, border=FALSE, col=NULL, xlab="", ylab="")
title(main="Polygon of frequency",
xlabel="Variable", ylabel="Frequency")
polygon.freq(h, col="blue")
ggrid(col="brown")
#endgraph
# Draw curve for Histogram
h <- graph.freq(yield, axes=FALSE, frequency=3, ylab="f(yield)", col="yellow")
axis(1, h$breaks)
axis(2, seq(0, 0.18, 0.03), las=2)
lines(density(yield), col = "red", lwd = 2)
title("Draw curve for Histogram")
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)
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.

<table>
<thead>
<tr>
<th>Clone</th>
<th>FL</th>
<th>MI</th>
<th>ME</th>
<th>MN</th>
<th>ND</th>
<th>NY</th>
<th>PA</th>
<th>WI</th>
</tr>
</thead>
<tbody>
<tr>
<td>aXT11XMS</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
<td>a numeric vector</td>
</tr>
<tr>
<td>aoXPTSRM1</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>aoXTRWUMS</td>
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<tr>
<td>awnXVU1TMR</td>
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<tr>
<td>bPVYRMT</td>
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<tr>
<td>bPW1XMS</td>
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<tr>
<td>bPWTYMRf</td>
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<td>bzura</td>
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<td></td>
</tr>
<tr>
<td>cPPXSPPXM1</td>
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<tr>
<td>elba</td>
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<td>greta</td>
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<td>stobrawa</td>
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</tr>
</tbody>
</table>

References


Examples

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

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

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

Arguments

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

Value

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

Author(s)

F. de Mendiburu

See Also

hclust, consensus, hgroups

Examples

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

heterosis Data of potato, Heterosis

Description

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

data(heterosis)

Format

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

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

Details

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

Source

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

References

Examples

library(agricolae)
data(heterosis)
str(heterosis)
site1 <- subset(heterosis, heterosis[,1]==1)
site2 <- subset(heterosis, heterosis[,1]==2)
site3 <- subset(heterosis, heterosis[,1]==3)
model1 <- with(site1, lineXtester(Replication, Female, Male, v1))
DFe <- df.residual(model1)
CMe <- deviance(model1)/DFe
test1 <- with(site1, HSD.test(v1, Factor,DFe,CMe))
test2 <- with(site1, HSD.test(v1, Treatment,DFe,CMe))
model22 <- with(site2, lineXtester(Replication, Female, Male, v3))
model33 <- with(site3, lineXtester(Replication, Female, Male, v4))


hgroups

groups of hclus

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 hclus

Value

data

object merge of hclus

Author(s)

F. de Mendiburu

See Also

hclus, hcut, consensus
Examples

```r
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**

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

**Arguments**

- `y`: model(aov or lm) or answer of the experimental unit
- `trt`: Constant (only y=model) or vector treatment applied to each experimental unit
- `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**

```r
y: class (aov or lm) or vector numeric
trt: constant (only y=model) or vector alfanumeric
DFerror: Numeric
MSError: Numeric
alpha: Numeric
group: Logic
main: Text
```
Author(s)
Felipe de Mendiburu

References

See Also
LSD.test, waller.test, SNK.test, duncan.test

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

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**

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

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

Usage

index.AMMI(model)

Arguments

model object AMMI

Details

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

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

$$YSI = RASV + RY$$

$$RASV = \text{rank}(ASV) \text{ and } RY = \text{rank}(Y \text{ across by environment})$$

Value

<table>
<thead>
<tr>
<th>ASV</th>
<th>AMMI stability value</th>
</tr>
</thead>
<tbody>
<tr>
<td>YSI</td>
<td>Yield stability index</td>
</tr>
<tr>
<td>rASV</td>
<td>Rank of AMMI stability value</td>
</tr>
<tr>
<td>rYSI</td>
<td>Rank of yield stability index</td>
</tr>
<tr>
<td>means</td>
<td>average genotype by environment</td>
</tr>
</tbody>
</table>

Author(s)

F. de Mendiburu

References


**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**

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

**See Also**

`AMMI.plot.AMMI`
Author(s)
Felipe de Mendiburu

References

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

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

Usage
index.smith(data, PLOT=TRUE,...)

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

Details
\[ V_x = \frac{V(x)}{x} \]
\[ V(x) \] is the between-plot variance, \( V_x \) is the variance per unit area for plot size of \( x \) basic unit, and
\( b \) is the Smith’s index of soil heterogeneity.

Value
data Numeric
...
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$uniformity)
uniformity
# regression variance per unit area an plot size.
model <- lm(Vx - I(log(Size)),uniformity)
coeff <- coef(model)
x<-1:max(uniformity$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

### Class intervals

#### Description
List class intervals.

#### Usage
```
intervals.freq(x)
```

#### Arguments
- `x` class graph.freq, histogram or numeric

#### Value
- `classes` matrix numeric
Author(s)
Felipe de Mendiburu

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

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

join.freq

Join class for histogram

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

Usage
join.freq(histogram, join)

Arguments
join

Value

Author(s)
Felipe de Mendiburu
See Also

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

Examples

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

kendall

Correlation of Kendall

Description

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

Usage

kendall(data1, data2)

Arguments

data1 vector
data2 vector

Value

data1 Numeric
data2 Numeric

Author(s)

Felipe de Mendiburu

References

kruskal

Kruskal Wallis test and multiple comparison of treatments.

Description

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

Usage

```r
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. p.adj = "holm", "hommel", "hochberg", "bonferroni", "BH", "BY", "fdr". see p.adjust() p.adj ="none" is t-student. p.adj ="hommel" is not applied in this test.

Value

- `y`: vector numeric
- `trt`: vector alphanumeric
- `alpha`: level significant
- `p.adj`: text, see p.adjust
- `group`: Logic
- `main`: Title
**kurtosis**

**Author(s)**
Felipe de Mendiburu

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

**See Also**
`friedman`, `durbin.test`

**Examples**
```r
corn <- c(3, 4, 5, 2, 3, 4, 5, 6, 4, NA, 7)
kurtosis(corn)
```

---

**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 order.group.

Usage

lastC(x)

Arguments

x letters

Value

x character

Author(s)

Felipe de Mendiburu

See Also

order.group

Examples

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

# "a" "b" "b" "c" "d"

lateblight

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.
lateblight

Usage

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

Arguments

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

Details

LATEBLIGHT Version LB2004 was created in October 2004 (Andrade-Piedra et al., 2005a, b and c), based on the C-version written by B.E. Ticknor ('BET 21191 modification of cbm8d29.c'), reported by Doster et al. (1990) and described in detail by Fry et al. (1991) (This version is referred as LB1990 by Andrade-Piedra et al. [2005a]). The first version of LATEBLIGHT was developed by Bruhn and Fry (1981) and described in detail by Bruhn et al. (1980).

Value

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

Note

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

Author(s)

Jorge L. Andrade-Piedra (1) (j.andrade@cgar.org), Gregory A. Forbes (1) (g.forbes@cgiar.org), Robert J. Hijmans (2) (rhijmans@ucdavis.edu), William E. Fry (3) (wef1@cornell.edu) Translation from C language into SAS language: G.A. Forbes Modifications: J.L. Andrade-Piedra and R.J. Hijmans Translation from SAS into R: Felipe de Mendiburu (1) (1) International Potato Center, P.O. Box 1558, Lima 12, Peru (2) University of California, One Shields Avenue, Davis, California 95616, USA (3) Cornell University, 351 Plant Science, Ithaca, NY 14853, USA
References


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
WSC<--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'
AppSys <- "NOFUNGICIDE"
main<="Cultivar: NICOLA"

#------------------------
model<-lateblight(WS, Cultivar,AppSys, InocDate, LGR,IniSpor,SR,IE, LP,
MatTime='LATESEASON',InMicCol,main=main,type="1",xlim=c(65,95),lwd=1.5,
xlab="Time (days after emergence)", ylab="Severity (Percentage)"
)
# reproduce graph
x<- model$ofile$nday
y<- model$ofile$SimSeverity
w<- model$ofile$nday
z<- model$ofile$MeanSeverity
Min<-model$file$MinObs
Max<-model$file$MaxObs
plot(x,y,type="l",xlim=c(65,95),lwd=1.5,xlab="Time (days after emergence)",
ylab="Severity (Percentage)"
)
points(w,z,col="blue",cex=1,pch=19)
npoints <- length(w)
for ( i in 1:npoints)
{ segments(w[i],Min[i],w[i],Max[i],lwd=1.5,col="blue")
}
legend("topleft",c("Disease progress curves","Weather-Severity"),
title="Description",lty=1,pch=c(3,19),col=c("black","blue"))
Details


Value

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

Author(s)

Felipe de Mendiburu

References


See Also

AMMI

Examples

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

Multiple comparisons, "Least significant difference" and Adjust P-values

Description

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

Usage

LSD.test(y, trt, DEerror, 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
- **DError**: Degrees of freedom of the experimental error
- **MSerror**: Means square error of the experimental
- **alpha**: Level of risk for the test
- **p.adj**: Method for adjusting p values (see p.adjust)
- **group**: TRUE or FALSE
- **main**: title of the study
- **console**: logical, print output

Details

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

Value

- **y**: class (aov or lm) or vector numeric
- **trt**: constant (only y=model) or vector alfanumeric
- **DError**: Numeric
- **MSerror**: Numeric
- **alpha**: Numeric
- **p.adj**: text, see p.adjust
- **group**: Logic
- **main**: Numeric
Author(s)

Felipe de Mendiburu

References


See Also

HSD.test, waller.test, SNK.test, bar.err, bar.group, duncan.test

Examples

library(agricolae)
data(sweetpotato)
model<-aov(yield~virus, data=sweetpotato)
out <- LSD.test(model,"virus", p.adj="bonferroni")
#stargraph
bar.group(out$groups,ylim=c(0,45),density=4,border="blue")
#endgraph

# Old version LSD.test()
df<-df.residual(model)
MSError<-deviance(model)/df
out <- with(sweetpotato,LSD.test(yield,virus,df,MSError, p.adj="bonferroni", group=FALSE))
#stargraph
# Variation range: Max - Min
bar.err(out$means,variation="range",ylim=c(0,44),bar=FALSE,col=0)
#endgraph
LSD.test(model,"virus",p.adj="bon",console=TRUE)

LxT

Data Line by tester

Description

Data frame with yield by line x tester.

Usage

data(LxT)
markers

Format

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

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

Source

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

---

**markers**  
*Data of molecular markers*

Description

A partial study on 27 molecular markers.

Usage

data(markers)

Format

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

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

Source
International Potato Center Lima-Peru.

References
International Potato Center Lima-Peru.

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

| Median.test | Median test. Multiple comparisons |

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

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

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

Details

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

Value

- **statistics**: Numeric
- **parameters**: Numeric
- **Medians**: data.frame
- **comparison**: data.frame
- **data**: data.frame

Author(s)

Felipe de Mendiburu

References

Practical Nonparametrics Statistics. W.J. Conover, 1999

See Also

- `kruskal.chisq.test`

Examples

```r
library(agricolae)
# example 1
data(corn)
comparison<-with(corn,Median.test(observation,method))
comparison

# example 2
trt<-c(rep(1,9),rep(2,10),rep(3,7),rep(4,8))
y<-c(83,91,94,89,89,96,91,90,91,90,81,83,84,83,88,91,89,84,101,100,91,93,96,95,94,78,82,81,77,79,81,80,81)
comparison<-Median.test(y,trt)
```
Data of yield of melon in a Latin square experiment

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

Usage
data(melon)

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

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

Details
Varieties: Hibrindo Mission (V1); Hibrindo Mark (V2); Hibrindo Topfligth (V3); Hibrindo 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**

Generates random.

**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)
h<-graph.freq(x=breaks, counts=counts, plot=FALSE)
montecarlo(h, k=100)
```
Data of native potato

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

Usage
data(natives)

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

variety a numeric vector
number a numeric vector
weight a numeric vector
size a numeric vector

Source
International Potato Center. CIP - Lima Peru.

Examples
library(agricolae)
data(natives)
str(natives)

Nonadditivity model test

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

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

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 error

Details

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

Value

- **y**: Numeric
- **factor1**: Alphanumeric
- **factor2**: Alphanumeric
- **df**: Numeric
- **MSerror**: Numeric

Author(s)

Felipe de Mendiburu

References


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**

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

**Arguments**

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

**Value**

- `Histogram`: object
- `frequency`: numeric
- `probability`: logic `False` or `True`

**Author(s)**

Felipe de Mendiburu

**See Also**

- `polygon.freq`, `table.freq`, `stat.freq`, `intervals.freq`, `sturges.freq`, `join.freq`, `ogive.freq`, `graph.freq`

**Examples**

```
library(agricolae)
data(growth)
#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
```
**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,...)
```

**Arguments**

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

**Value**

- `table`: data.frame

**Author(s)**

Felipe de Mendiburu

**See Also**

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

**Examples**

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

Ordering the treatments according to the multiple comparison

Description

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

Usage

order.group(trt, means, N, MSerror, Tprob, std.err, parameter=1, snk=0, DError=NULL, alpha=NULL, sdtdif=NULL, vartau=NULL, console)

Arguments

- trt: Treatments
- means: Means of treatment
- N: Replications
- MSerror: Mean square error
- Tprob: minimum value for the comparison
- std.err: standard error
- parameter: Constante 1 (Sd), 0.5 (Sx)
- snk: Constante = 1 (Student Newman Keuls)
- DError: 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

Value

- trt: Factor
- means: Numeric
- N: Numeric
- MSerror: Numeric
- Tprob: value between 0 and 1
- std.err: Numeric
- parameter: Constant
- snk: Constant
- DError: Numeric
- alpha: Numeric
- sdtdif: Numeric
- vartau: Numeric, matrix
Author(s)
Felipe de Mendiburu

See Also
order.stat

Examples

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

order.stat grouping the treatments averages in a comparison with a minimum value

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

Usage
order.stat(treatment, means, minimum, console)
**Arguments**

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

**Value**

- `trt`  
  Factor
- `means`  
  Numeric
- `minimum`  
  Numeric

**Author(s)**

Felipe de Mendiburu

**See Also**

`order.group`

**Examples**

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

---

**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, significance value to comparison
- pvalue: Matrix of probabilities to comparison
- console: logical, print output

Value

- trt: Factor
- means: Numeric
- pvalue: matrix

Author(s)

Felipe de Mendiburu

See Also

- `order.group`, `order.stat`

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
groups <- orderPvalue(treatments, means, alpha, pvalue, console = TRUE)
```

Description

Potato Wild

Usage

data(pamCIP)
Format

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

Details

To study the molecular markers in Wild.

Source

Laboratory data.

References

International Potato Center Lima-Peru (CIP)

Examples

library(aigricolae)
data(pamCIP)
str(pamCIP)

paracsho

Data of Paracsho biodiversity

Description

A locality in Peru. A biodiversity.

Usage

data(paracsho)

Format

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

date  a factor with levels 15-12-05 17-11-05 18-10-05 20-09-05 22-08-05 23-07-05
plot  a factor with levels PARACSHO
Treatment a factor with levels CON SIN
Orden  a factor with levels COLEOPTERA DIPTERA HEMIPTERA HYMENOPTERA LEPIDOPTERA NEUROPTERA NEUROPTERO NOCTUIDAE
Family a factor with levels

AGROMYZIDAE ANTHOCORIDAE ANTHOMYIDAE ANTHOMYLIDAE BLEPHAROCERIDAE
BRACONIDAE BROCONIDAE CALUPHORIDAE CECIDOMYIDAE CHENEUMONIDAE CHREUMONIDAE
CICADELLIDAE CUCIDIDAE ERIOPHIDIIDAE HEMEROBIIIDAE ICHNEUMONIDAE LOUCHAPIDAE
MIRIDAE MUSCIDAE MUSICADAE MUSLIDAE MYCETOPHILIDAE MYCETOPHILIDAE NENPHALIDAE
NOCTERIDAE NOCTUIDAE PERALIDAE PIPIUNCULIDAE PROCTOTRUPIDAE PSYLIDAE PYRALIDAE
SARCOPHAGIDAE SARCOPLAGIDAE SCATOPHAGIDAE SCATOPHAGIDAE 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)

Description

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

Usage

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

Arguments

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

Details

It is necessary first to calculate the correlations.
Value

```
corr.x Numeric
corr.y Numeric
```

Author(s)

Felipe de Mendiburu

References

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

See Also

correlation

Examples

```
# Path analysis. Multivarial Analysis. Anderson. Prentice Hall, pag 616
library(agricolae)
# Example 1
corr.x<- matrix(c(1,0.5,0.5,1),c(2,2))
corr.y<- rbind(0.6,0.7)
names<-c("X1","X2")
dimnames(corr.x)<-list(names,names)
dimnames(corr.y)<-list(names,"Y")
path.analysis(corr.x,corr.y)
# Example 2
# data of the progress of the disease related bacterial wilt to the ground
# for the component CE Ca K2 Cu
data(wilt)
data(soil)
x<-soil[,c(3,12,14,20)]
y<-wilt[,14]
cor.y<-correlation(y,x)$correlation
cor.x<-correlation(x)$correlation
path.analysis(corr.x,cor.y)
```
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 differente. Estimate: specifies the estimation method for the covariance parameters. The REML is the default method. The REML specification performs residual (restricted) maximum likelihood, and The ML specification performs maximum likelihood, and the VC specifications apply only to variance component models.

Value

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

Author(s)

F. de Mendiburu
References


See Also

BIB.test, design.alpha

Examples

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

Description

Biplot AMMI.

Usage

```r
## 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,...)
```
plot.AMMI

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=triplet 3=influence genotype
- **number**: TRUE or FALSE names or number genotypes
- **gcol**: genotype color
- **ecol**: environment color
- **icol**: influence color
- **angle**: angle from the shaft of the arrow to the edge of the arrow head
- **lwd**: parameter line width in function arrow
- **length**: parameter length in function arrow
- **xlab**: x labels
- **ylab**: y labels
- **xlim**: x limites
- **ylim**: y limites
- **...**: other parameters of plot

Details

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

help(graphneigh) package=spdep

Author(s)

Felipe de Mendiburu

See Also

- AMMI

Examples

```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")
```
## S3 method for class 'graph.freq'

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

### Arguments

- `x`  
  A vector of values, a vector hist(), graphFreq()
- `counts`  
  Frequency and `x` is class intervals
- `breaks`  
  A vector giving the breakpoints between histogram cells
- `frequency`  
  1=counts, 2=relative, 3=density
- `plot`  
  Logic
- `nclass`  
  Number of classes
- `xlab`  
  X labels
- `ylab`  
  Y labels
- `axes`  
  TRUE or FALSE
- `las`  
  Numeric in 0,1,2,3; the style of axis labels. see plot()
- `...`  
  Other parameters of plot

### Value

- `breaks`  
  A vector giving the breakpoints between histogram cells
- `counts`  
  Frequency and `x` is class intervals
- `mids`  
  Center point in class
- `relative`  
  Frequency
- `density`  
  Numeric

### Description

In many situations it has intervals of class defined with its respective frequencies. By means of this function, the graph 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.
Author(s)
Felipe de Mendiburu

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

Examples

library(agricolae)
data(genxenv)
yield <- subset(genxenv$YLD, genxenv$ENV==2)
yield <- round(yield, 1)
h <- graph.freq(yield, axes=FALSE, frequency=1, ylab="frequency", col="yellow")
axis(1, h$breaks)
axis(2, seq(0, 20, 0.1))
# To reproduce histogram.
h1 <- plot(h, col="blue", frequency=2, border="red", density=8, axes=FALSE,
  xlab="YIELD", ylab="relative")
axis(1, h$breaks)
axis(2, seq(0, 40, 0.1))
# summary, only frequency
limits <- seq(0, 40, 5)
frequencies <- c(2, 6, 8, 7, 3, 4)
startgraph
h2 <- graph.freq(limits, counts=frequencies, col="bisque", xlab="Classes")
polygon.freq(h, col="red")
title(main="Histogram and polygon of frequency",
ylab="frecuency")
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
h3 <- graph.freq(limits, counts=frequencies, border=FALSE, col=NULL, xlab="",
ylab="")
title(main="Polygon of frequency",
xlab="Variable", ylab="Frecuency")
polygon.freq(h, col="blue")
ggrid(col="brown")
endgraph
# Draw curve for Histogram
h4 <- graph.freq(yield, axes=FALSE, frequency=3, ylab="f(yield)", col="yellow")
axis(1, h$breaks)
axis(2, seq(0, 0.18, 0.03), las=2)
lines(density(yield), col = "red", lwd = 2)
title("Draw curve for Histogram")

---

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

**Description**

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

**Usage**

data(plots)

**Format**

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

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

**Source**

International Potato Center. CIP

**Examples**

library(agricolae)
data(plots)
str(plots)
plots[,1] <- as.factor(plots[,1])
# split-plot analysis
model <- aov(yield ~ block + A + Error(plot)+ B + A:B, data=plots)
summary(model)
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)
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 1PRN1X 1PTNRR 1R1NS1 1T1NRX 1UWNRV 1VSNY RR1N1Y RSSN11
RSUNV RT1NR RUUNW S1TN1R S1WNV S1YNRP SRPN1V STRN1U STVNR SU1NRV SVTNR1 TPRNW
TPUNR TPVN1R TRWNW TUPNS UPVNR 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`

Value

- `histogram`: Object
- `frequency`: 1=counts, 2=relative, 3=density

Author(s)

Felipe de Mendiburu Delgado

See Also

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

Examples

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

#startgraph
h2<-with(growth,graph.freq(height,frequency=2,col="yellow",xlim=c(6,14)))
polygon.freq(h2,frequency=2,col="red")
#endgraph
```
potato

Data of cutting

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

Usage
data(potato)

Format
A data frame with 18 observations on the following 4 variables.
date a numeric vector
variety a factor with levels Canchan Unica
harvest a numeric vector
cutting a numeric vector

Source
Experimental data.

References
International Potato Center

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

ralstonia

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

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

Usage
data(ralstonia)
**Format**

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

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

**Details**

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

**Source**

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

**References**

International Potato Center. CIP - Lima Peru.

**Examples**

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

---

**reg.homog**

*Homologation of regressions*

**Description**

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

**Usage**

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

- `trt`: treatment
- `x`: independent variable
- `y`: dependent variable

**Value**

- `trt`: factor
- `x`: numeric
- `y`: numeric

**Author(s)**

Felipe de Mendiburu

**References**

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

**Examples**

```r
library(agricolae)
data(frijol)
evaluation<-with(frijol,reg.homog(technology,index,production))
# Example 2. Applied Regression Analysis a Research tools
# 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,
2.8,3.8,2.6,2.2,4.3,2.6,3.6,2.6,4.3,2.1,3.5,1.6,2.0,4.0,1.5,2.4,2.8,
1.4,1.9,3.1,1.7,2.8,4.2,1.3,1.7,3.7,1.7,3.2,3.0,1.6,2.0,2.2,1.4,2.2,2.3,1.0,
2.2,3.8,1.5,2.2,2.0,1.6)
Ascorbic <-c(51,65,54,55,52,59,45,41,66,42,51,54,53,41,45,50,49,50,51,49,
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)
```

**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
DFerror Degree free
MSerror Mean Square Error
alpha Significant level
group TRUE or FALSE
main Title
console logical, print output

Details

It is necessary first makes a analysis of variance.

Value

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

Author(s)

Felipe de Mendiburu

References

Multiple comparisons theory and methods. Departament of statistics the Ohio State University.

See Also

LSD.test, waller.test, duncan.test, HSD.test, SNK.test
Examples

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

Description

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

Usage

resampling.cv(A, size, npoints)

Arguments

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

Value

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

Author(s)

Felipe de Mendiburu

References


See Also

cv.similarity,similarity
Examples

library(agricolae)
#example table of molecular markers
data(markers)
study<-resampling.cv(markers, size=1, npoints=15)

# Results of the model
summary(study$model)
coef<-coef(study$model)
py<-predict(study$model)
Rsq<-summary(study$model)"r.squared"
table.cv<-data.frame(study$table.cv, estimate=py)
print(table.cv)

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

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

resampling.model  Resampling for linear models

Description

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

Usage

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

Arguments

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

Value

- **model**: output linear model, lm
- **solution**: anova resampling
- **acum**: cumulative frequency
- **samples**: samples number

Author(s)

Felipe de Mendiburu

References


See Also

- simulation.model

Examples

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

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

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

#example 4 Factorial in RCD
data(potato)
potato[,1]<-as.factor(potato[,1])
potato[,2]<-as.factor(potato[,2])
```
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)
```

<table>
<thead>
<tr>
<th>RioChillon</th>
<th>Data and analysis Mother and baby trials</th>
</tr>
</thead>
</table>

**Description**

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

**Usage**

```r
data(RioChillon)
```

**Format**

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

**Details**

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

References
International Potato Center. CIP - Lima Peru.

Examples

# Analisys the Mother/Baby Trial Design
library(agricolae)
data(RioChillon)
# First analysis the Mother Trial Design.
model<-aov(yield ~ block + clon, RioChillon$mother)
anova(model)
cv.model(model)
comparison<-with(RioChillon$mother,LSD.test(yield,clon, 18, 4.922, group=TRUE))
# Second analysis the babies Trial.
comparison<-with(RioChillon$babies, friedman(farmer,clon, yield, group=TRUE))
# Third
# The researcher makes use of data from both mother and baby trials and thereby obtains
# information on suitability of new technologies or cultivars
# for different agro-ecologies and acceptability to farmers.

scheffe.test Multiple comparisons, scheffe

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

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

Arguments

y model(aov or lm) or answer of the experimental unit
trt Constant( only y=model) or vector treatment applied to each experimental unit
DFerror Degrees of freedom
MSerror Mean Square Error
Fc F Value
alpha Significant level
scheffe.test


group            TRUE or FALSE
main             Title
console          logical, print output

Details

It is necessary first makes a analysis of variance.

Value

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>class (aov or lm) or vector numeric</td>
</tr>
<tr>
<td>trt</td>
<td>constant (only y=model) or vector alfanumeric</td>
</tr>
<tr>
<td>DError</td>
<td>Numeric</td>
</tr>
<tr>
<td>MSerror</td>
<td>Numeric</td>
</tr>
<tr>
<td>Fc</td>
<td>Numeric</td>
</tr>
<tr>
<td>alpha</td>
<td>Numeric</td>
</tr>
<tr>
<td>group</td>
<td>Logic</td>
</tr>
<tr>
<td>main</td>
<td>Text</td>
</tr>
</tbody>
</table>

Author(s)

Felipe de Mendiburu

References


See Also

HSD.test, LSD.test, SNK.test, bar.err, bar.group, duncan.test

Examples

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

Matrix of similarity in binary data

Description

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

Usage

similarity(A)

Arguments

A  Matrix, data binary

Value

A  Numeric (0,1)

Author(s)

Felipe de Mendiburu

See Also

cv.similarity, resampling.cv

Examples

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

Description

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

Usage

\[
simulation\text{-model}(\text{model}, \text{file}, \text{categorical} = \text{NULL}, \text{k}, \text{console} = \text{FALSE})
\]

Arguments

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

Value

- \text{model} output linear model, \text{lm}
- \text{simulation} anova simulation

Author(s)

Felipe de Mendiburu

See Also

- \text{resampling\_model}

Examples

\[
\text{library(agricolae)}
\text{#example 1}
\text{data(clay)}
\text{model}\left<\text{"ralstonia ~ days"}\right>
\text{simulation\_model(model, clay, k=15, console=TRUE)}
\text{#example 2}
\text{data(sweetpotato)}
\text{model}\left<\text{"yield~virus"}\right>
\text{simulation\_model(model, sweetpotato, categorical=1, k=15, console=TRUE)}
\]
# Example 3
```r
data(Glycoalkaloids)
model<-'HPLC - spectrophotometer'
simulation.model(model,Glycoalkaloids,k=15,console=TRUE)
```

# Example 4
```r
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
```r
data(sinRepAmmi)
```

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

- **ENV** a factor with levels A1 A2 A3 A4 A5
- **GEN** a numeric vector
- **YLD** a numeric vector

## Source
Experimental data.

## References
International Potato Center - Lima Peru.

## Examples
```r
library(agricolae)
data(sinRepAmmi)
str(sinRepAmmi)
```
skewness

Finding the skewness coefficient

Description

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

Usage

skewness(x)

Arguments

x  a numeric vector

Value

x  The skewness of x

See Also

kurtosis

Examples

library(agricolae)
x<-c(3,4,5,2,3,4,NA,5,6,4,7)
skewness(x)
# value is 0.3595431, is slightly asymmetric (positive) to the right

SNK.test  Student-Newman-Keuls (SNK)

Description

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

Usage

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

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

Details

It is necessary first makes an analysis of variance.

Value

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

Author(s)

Felipe de Mendiburu

References


See Also

- LSD.test, waller.test, HSD.test, duncan.test

Examples

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

soil Data of soil analysis for 13 localities

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

Usage
data(soil)

Format
A data frame with 13 observations on the following 23 variables.
place a factor with levels Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora SR1 SR2
pH a numeric vector
EC a numeric vector, electrical conductivity
CaCO3 a numeric vector
MO a numeric vector
CIC a numeric vector
P a numeric vector
K a numeric vector
sand a numeric vector
slime a numeric vector
clay a numeric vector
Ca a numeric vector
Mg a numeric vector
K2 a numeric vector
Na a numeric vector
Al_H a numeric vector
K_Mg  a numeric vector
Ca_Mg  a numeric vector
B  a numeric vector
Cu  a numeric vector
Fe  a numeric vector
Mn  a numeric vector
Zn  a numeric vector

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

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

References
International Potato Center - Lima, PERU.

Examples
library(agricolae)
data(soil)
str(soil)

sp.plot

Spilt-Plot analysis

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

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

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

Details

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

Value

- `block`: vector, numeric or character
- `pplot`: vector, numeric or character
- `splot`: vector, numeric or character
- `Y`: vector, numeric

Author(s)

Felipe de Mendiburu

References


See Also

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

Examples

```r
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)
```
Description

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

Usage

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

Arguments

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

Details

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

Value

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

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
# factores, with three replications.
library(agricolae)
yield<-c(3.320,3.766,4.660,3.188,3.625,5.232,5.468,5.759,6.215,
4.246,5.255,6.829,3.132,5.389,5.217,3.864,4.311,5.915,4.752,
4.809,5.170,5.788,6.130,7.106,4.842,5.742,5.869,4.375,4.315,
5.389,4.507,4.875,5.400,4.756,5.295,6.046,4.422,5.308,6.318,
4.863,5.345,6.011,4.678,5.896,7.309,6.101,5.896,6.573,5.595,
7.254,5.122,4.873,5.495,6.780,5.925,7.442,5.988,6.533,6.914,
6.768,7.856,7.626,6.894,6.974,7.812,4.815,4.166,4.225,5.390,
5.163,4.478,6.509,6.569,7.991,5.779,6.164,7.362,6.573,7.422,
8.958,5.355,7.442,7.018,6.706,8.592,8.480,8.452,8.662,9.112,
7.646,9.942,6.698,8.526,9.140,7.414,9.016,8.966,8.508,9.688,
9.896,5.244,5.584,7.642,7.092,7.212,8.714,8.656,8.514,9.320,
block<-rep(gl(3,15),3)
nitrogen<-rep(c(rep(0,3),rep(50,3),rep(100,3),rep(140,3)),9)
management<-rep(c("m1","m2","m3"),45)
variety<-gl(3,45)
model<-ssp.plot(block,nitrogen,management,variety,yield)
gla<-model$g1.a; glb<-model$g1.b; glc<-model$g1.c
Ea<-model$e1.a; Eb<-model$e1.b; Ec<-model$e1.c
LSD.test(yield,nitrogen,gla,Ea,console=TRUE)
LSD.test(yield,management,glb,Eb,console=TRUE)
LSD.test(yield,variety,glc,Ec,console=TRUE)
# with aov
A<-data.frame(block, nitrogen,management,variety,yield)
A[,2]<-as.factor(A[,2])
AOV<-aov(yield ~ block + nitrogen*management*variety + Error(block/nitrogen/management),data=A)
summary(AOV)

stability.nonpar Nonparametric stability analysis

Description

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

Usage

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

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

Value

- **ranking**: data.frame
- **statistics**: data.frame

Author(s)

Felipe de Mendiburu

References


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)
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) usign 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` : data.frame
- `statistics` : data.frame
- `stability` : data.frame
Author(s)

Felipe de Mendiburu

References


See Also

stability.nonpar

Examples

library(agricolae)
# example 1
# Experimental data,
# replication rep= 4
# Mean square error, MSErr = 1.8
# 12 environment
# 17 genotype = 1,2,3,..., 17
# yield averages of 13 genotypes in localities
v1 <- c(10.2, 8.8, 8.8, 9.3, 9.6, 7.2, 8.4, 9.6, 7.9, 10.9, 3.8, 8.0, 10.1, 9.4, 10.8, 6.3, 7.4)
V2 <- c(7.8, 7.0, 6.9, 7.8, 3.7, 4.6, 5.6, 8.7, 9.3, 6.8, 8.1, 7.1, 7.1, 6.4, 4.1)
V3 <- c(5.3, 4.4, 5.3, 4.4, 5.5, 4.6, 6.2, 6.0, 6.5, 5.3, 5.7, 4.4, 4.2, 5.6, 5.8, 3.9, 3.8)
V4 <- c(7.8, 5.9, 7.3, 5.9, 7.8, 6.3, 7.9, 7.5, 7.6, 5.4, 5.6, 7.8, 6.5, 8.1, 7.5, 5.0, 5.4)
V5 <- c(9, 9.2, 8.8, 10.6, 8.3, 9.3, 9.6, 8.8, 7.9, 7.7, 9.5, 9.4, 9.4, 10.3, 8.8, 8.7)
V6 <- c(6.9, 7.7, 7.9, 7.9, 7.9, 7.9, 6.5, 7.2, 5.4, 6.2, 7.2, 8.8, 7.3, 7.1, 6.4)
V7 <- c(4.9, 2.5, 3.4, 2.5, 3.2, 5.3, 5.6, 3.8, 3.9, 3.0, 3.0, 2.5, 2.6, 3.8, 2.8, 3.1)
V8 <- c(6.4, 6.4, 8.1, 7.2, 7.5, 6.6, 7.7, 7.6, 7.8, 7.5, 6.0, 7.2, 6.8, 7.6, 6.9, 7.2, 7.3)
V9 <- c(8.4, 6.1, 6.8, 6.1, 8.2, 6.9, 6.9, 9.1, 9.2, 7.7, 6.7, 7.8, 6.5, 5.2, 2.8, 3.6, 8.7)
V10 <- c(8.7, 9.4, 8.8, 7.9, 7.8, 11.4, 9.9, 8.6, 8.5, 8.0, 8.3, 9.1, 11.0, 8.1, 17.8, 8.0)
V11 <- c(5.4, 5.2, 5.6, 4.6, 4.8, 5.7, 6.6, 6.8, 5.2, 4.8, 4.9, 5.4, 4.5, 5.6, 7.0, 6.0, 5.6)
V12 <- c(8.6, 8.0, 9.2, 8.1, 8.3, 8.9, 8.6, 9.6, 9.5, 7.7, 7.6, 8.3, 6.6, 9.5, 9.0, 9.0, 8.5)
data<-data.frame(V1,V2,V3,V4,V5,V6,V7,V8,V9,V10,V11,V12)ownames(data)<-LETTERS[1:17]
stability.par(data, rep=4, MSErr=1.8, alpha=0.1, main="Genotype",console=TRUE)

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

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

Usage

stat.freq(histogram)

Arguments

histogram Object created by function hist()

Value

histogram Object

Author(s)

Felipe de mendiburu

See Also

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

Examples

library(agricolae)
data(growth)
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

- **BLOCK**: vector, numeric
- **COL**: vector, numeric
- **ROW**: vector, numeric
- **Y**: vector, numeric

Author(s)

Felipe de Mendiburu

References


See Also

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

Examples

```r
# 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))
comparison<-with(YIELD, LSD.test(yield,clon,model$gl.a,model$Ea))
comparison<-with(YIELD, LSD.test(yield,trt,model$gl.b,model$Eb))
# simple effects
A<-model$data
a<-nlevels(A$clon)
b<-nlevels(A$trt)
r<-nlevels(A$block)
```
Class intervals for a histogram, the rule of Sturges

Description

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

Usage

sturges.freq(x,k=0)
Arguments

x  vector
k  constant

Value

x  Numeric
k  Numeric

Author(s)

Felipe de mendiburu

References


See Also

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

Examples

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

*frequency Table of a Histogram*

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

- `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)
```
Description

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

Usage

data(sweetpotato)

Format

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

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

Source

Experimental field.

References

International Potato Center. CIP - Lima Peru

Examples

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

**frequency Table of a Histogram**

---

**Description**

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

**Usage**

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

**Arguments**

- **object**: Object by function `graph.freq()`

**Value**

- **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(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

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

Author(s)

Felipe de Mendiburu

Examples

library(agricolae)
# case of 1 single factor
data(sweetpotato)
tapply.stat(sweetpotato[,2],sweetpotato[,1],mean)
with(sweetpotato,tapply.stat(yield,virus,mean))
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)))
Description

The Kendall method in order to find the K variance.

Usage

vark(x, y)

Arguments

x Vector
y vector

Details

variance of K for Kendall’s tau

Value

x Numeric
y Numeric

Author(s)

Felipe de Mendiburu

References


See Also

cor.matrix, cor.vector, cor.mv

Examples

library(agridole)
x <-c(1,1,1,4,2,2,3,1,3,2,1,1,2,3,2,1,1,2,1,2,1,2)
y <-c(1,1,2,3,4,4,2,1,2,3,1,1,3,4,2,1,1,3,1,2)
vark(x,y)
Multiple comparisons. The van der Waerden (Normal Scores)

Description
A nonparametric test for several independent samples.

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

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

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

Value
- **y**: Numeric
- **trt**: factor
- **alpha**: Numeric
- **group**: Logic
- **main**: text

Author(s)
Felipe de Mendiburu

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

See Also
kruskal
Examples

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

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 I/Type II error seriousness ratio for the Waller-Duncan test. Reasonable values for `KRATIO` are 50, 100, and 500, which roughly correspond for the two-level case to `ALPHA` levels of 0.1, 0.05, and 0.01. By default, the procedure uses the default value of 100.

Value

- `K`: Numeric integer > 1, examples 50, 100, 500
- `q`: Numeric
- `f`: Numeric
- `Fc`: Numeric

Author(s)

Felipe de Mendiburu
References


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

waller.test(y, trt, DError, MSError, Fc, K = 100, group=TRUE, main = NULL, console=FALSE)
waller.test

Arguments

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

Details

It is necessary first makes a analysis of variance.

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

Value

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

Author(s)

Felipe de Mendiburu

References


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

Weather and Severity

Description

Weather and Severity

Usage

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

Arguments

- `weather`: object, see example
- `severity`: object, see example
- `dates`: vector dates
- `EmergDate`: date
- `EndEpidDate`: date

See Also

HSD.test, LSD.test, SNK.test, bar.err, bar.group, duncan.test

Examples

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

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)
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)
Data of Bacterial Wilt (AUDPC) and soil

**Description**

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

**Usage**

data(wilt)

**Format**

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

- `place`: a factor with levels `Chmar Chz Cnt1 Cnt2 Cnt3 Hco1 Hco2 Hco3 Hyo1 Hyo2 Namora Sr1 Sr2`  
- `Day7`: a numeric vector  
- `Day11`: a numeric vector  
- `Day15`: a numeric vector  
- `Day19`: a numeric vector  
- `Day23`: a numeric vector  
- `Day27`: a numeric vector  
- `Day31`: a numeric vector  
- `Day35`: a numeric vector  
- `Day39`: a numeric vector  
- `Day43`: a numeric vector  
- `Day47`: a numeric vector  
- `Day51`: a numeric vector  
- `AUDPC`: a numeric vector  
- `relative`: a numeric vector

**Details**

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

**Source**

Experimental field, 2004. Data Kindly provided by Dr. Sylvie Priou, Liliam Gutarra and Pedro Aley.
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 cannot be digested by the human body that have joined several beneficial properties in health, such as improve the absorption of calcium, reducing the level of triglycerides and cholesterol and stimulate better gastrointestinal function.

Usage

data(yacon)

Format

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

- **locality**: a factor with levels, Cajamarca, Lima, Oxapampa in PERU
- **site**: a numeric vector
- **dose**: a factor with levels fP f1UP fXP
- **entry**: a factor with levels akwUPWU ammU1SV ammU1UP ammU1VS arbU1RU cllunc11X p1SXU sal1SV
- **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
- **F0S**: a numeric vector, fructo-oligosaccharides, percentage

References

International Potato Center. CIP - Lima Peru.

Examples

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

Examples

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

Description

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

Usage

zigzag(outdesign)

Arguments

outdesign output design
**Value**

fieldbook  
restore field book

**Author(s)**

Felipe de Mendiburu

**See Also**

designNab, designNalpha, designNbib, designNsplit, designNcyclic, designNdau, designNgraeco,  
designNlattice, designNlsd, designNrcbd, designNstrip

**Examples**

libraryNagricolae  
trt<letters[1:5]  
r<-4  
outdesign <- designNrcbd(trt,r,seed=9)  
fieldbook <- zigzag(outdesign)
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