Package ‘AgroR’

July 21, 2025

Type Package

Title Experimental Statistics and Graphics for Agricultural Sciences

Version 1.3.7

Date 2025-06-10

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Description Performs the analysis of completely randomized experimental designs (CRD), randomized blocks (RBD) and Latin square (LSD), experiments in double and triple factorial scheme (in CRD and RBD), experiments in subdivided plot scheme (in CRD and RBD), subdivided and joint analysis of experiments in CRD and RBD, linear regression analysis, test for two samples. The package performs analysis of variance, ANOVA assumptions and multiple comparison test of means or regression, according to Pimentel-Gomes (2009, ISBN: 978-85-7133-055-9), nonparametric test (Conover, 1999, ISBN: 0471160687), test for two samples, joint analysis of experiments according to Ferreira (2018, ISBN: 978-85-7269-566-4) and generalized linear model (glm) for binomial and Poisson family in CRD and RBD (Carvalho, FJ (2019), <doi:10.14393/ufu.te.2019.1244>). It can also be used to obtain descriptive measures and graphics, in addition to correlations and creative graphics used in agricultural sciences (Agronomy, Zootechnics, Food Science and related areas). Shimizu, G. D., Marubayashi, R. Y. P., Goncalves, L. S. A. (2025) <doi:10.4025/actasciagron.v47i1.73889>.

Encoding UTF-8

RoxygenNote 7.3.2

Imports knitr, ggplot2, nortest, lme4, crayon, lmtest, emmeans, multcomp, ggrepel, MASS, cowplot, multcompView, RColorBrewer, drc, dunn.test, gtools, gridExtra

Suggests rmarkdown, roxygen2

Depends R (>= 3.6.0)

License GPL (>= 2)

URL `https://agronomiar.github.io/AgroR_package/index.html`, `https://fisher.uel.br/AgroR_shiny`, `https://fisher.uel.br/AgroR_shiny.pt`

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-07-02 08:50:05 UTC

Contents

`aacp` *Utils: Area under the curve*

Description

Performs the calculation of the area under the progress curve. Initially created for the plant disease area, whose name is "area under the disease progress curve", it can be adapted to various areas of agrarian science.

Usage

```
aacp(data)
```

Arguments

`data`	Data.frame containing evaluations in columns. Column names must be numeric and not dates or characters

Value

Returns a vector with the area values under the curve

Note

Just enter the data. Exclude treatment columns. See example.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

References

Campbell, C. L., and Madden, L. V. (1990). Introduction to plant disease epidemiology. John Wiley and Sons.

See Also

transf, sketch

Examples

```
#=======================================
# Using the simulate1 dataset
#=======================================
data("simulate1")

# Converting to readable format for function
dados=cbind(simulate1[simulate1$tempo==1,3],
            simulate1[simulate1$tempo==2,3],
            simulate1[simulate1$tempo==3,3],
            simulate1[simulate1$tempo==4,3],
            simulate1[simulate1$tempo==5,3],
            simulate1[simulate1$tempo==6,3])
colnames(dados)=c(1,2,3,4,5,6)
dados

# Creating the treatment vector
resp=aacp(dados)
trat=simulate1$trat[simulate1$tempo==1]

# Analyzing by DIC function
DIC(trat,resp)
```

`aristolochia` *Dataset: Germination of seeds of* Aristolochia *sp. as a function of temperature.*

Description

The data come from an experiment conducted at the Seed Analysis Laboratory of the Agricultural Sciences Center of the State University of Londrina, in which five temperatures (15, 20, 25, 30 and 35C) were evaluated in the germination of *Aristolochia elegans*. The experiment was conducted in a completely randomized design with four replications of 25 seeds each.

Usage

```
data("aristolochia")
```

Format

data.frame containing data set

`trat`	numeric vector with factor 1
`resp`	Numeric vector with response

See Also

cloro, laranja, enxofre, laranja, mirtilo, passiflora, phao, porco, pomegranate, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(aristolochia)
```

`barfacet` *Graph: Bar graph for one factor with facets*

Description

This is a function of the bar graph for one factor with facets

Usage

```
barfacet(
  model,
  facet = NULL,
  theme = theme_bw(),
  horiz = FALSE,
  geom = "bar",
  fill = "lightblue",
  pointsize = 4.5,
  facet.background = "gray80"
)
```

Arguments

`model`	DIC, DBC or DQL object
`facet`	vector with facets
`theme`	ggplot2 theme
`horiz`	horizontal bar or point (*default* is FALSE)
`geom`	graph type (columns or segments)
`fill`	fill bars
`pointsize`	Point size
`facet.background`	Color background in facet

Value

Returns a bar chart for one factor

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
library(AgroR)
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
     mcomp = "sk",angle=45,sup = 10,family = "serif",
     ylab = "Number of fruits/plants"))
barfacet(a,c("S1","S1","S1","S1","S1",
             "S2","S2","S3","S3"))
```

`bargraph_onefactor` *Graph: Group DIC, DBC and DQL functions column charts*

Description

Groups two or more column charts exported from DIC, DBC or DQL function

Usage

```
bargraph_onefactor(
  analysis,
  labels = NULL,
  ocult.facet = FALSE,
  ocult.box = FALSE,
  facet.size = 14,
  ylab = NULL,
  width.bar = 0.3,
  sup = NULL
)
```

Arguments

`analysis`	List with DIC, DBC or DQL object
`labels`	Vector with the name of the facets
`ocult.facet`	Hide facets
`ocult.box`	Hide box
`facet.size`	Font size facets
`ylab`	Y-axis name
`width.bar`	Width error bar
`sup`	Number of units above the standard deviation or average bar on the graph

Value

Returns a column chart grouped by facets

Examples

```
library(AgroR)
data("laranja")
a=with(laranja, DBC(trat, bloco, resp, ylab = "Number of fruits/plants"))
b=with(laranja, DBC(trat, bloco, resp,  ylab = "Number of fruits/plants"))
c=with(laranja, DBC(trat, bloco, resp, ylab = "Number of fruits/plants"))
bargraph_onefactor(analysis = list(a,b,c), labels = c("One","Two","Three"),ocult.box = TRUE)
```

`bargraph_twofactor` *Graph: Group FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC functions column charts*

Description

Groups two or more column charts exported from FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC function

Usage

```
bargraph_twofactor(
  analysis,
  labels = NULL,
  ocult.facet = FALSE,
  ocult.box = FALSE,
  facet.size = 14,
  ylab = NULL,
  width.bar = 0.3,
  sup = NULL
)
```

Arguments

`analysis`	List with DIC, DBC or DQL object
`labels`	Vector with the name of the facets
`ocult.facet`	Hide facets
`ocult.box`	Hide box
`facet.size`	Font size facets
`ylab`	Y-axis name
`width.bar`	Width bar
`sup`	Number of units above the standard deviation or average bar on the graph

Value

Returns a column chart grouped by facets

Examples

```
library(AgroR)
data(corn)
a=with(corn, FAT2DIC(A, B, Resp, quali=c(TRUE, TRUE),ylab="Heigth (cm)"))
b=with(corn, FAT2DIC(A, B, Resp, mcomp="sk", quali=c(TRUE, TRUE),ylab="Heigth (cm)"))
bargraph_twofactor(analysis = list(a,b), labels = c("One","Two"),ocult.box = TRUE)
```

`barplot_positive` *Graph: Positive barplot*

Description

Column chart with two variables that assume a positive response and represented by opposite sides, such as dry mass of the area and dry mass of the root

Usage

```
barplot_positive(
  a,
  b,
  ylab = "Response",
  var_name = c("Var1", "Var2"),
  legend.title = "Variable",
  fill_color = c("darkgreen", "brown"),
  width.col = 0.9,
  width.bar = 0.2
)
```

Arguments

`a`	Object of DIC, DBC or DQL functions
`b`	Object of DIC, DBC or DQL functions
`ylab`	Y axis names (this argument uses the *parse* function)
`var_name`	Name of the variable
`legend.title`	Legend title
`fill_color`	Bar fill color
`width.col`	Width Column
`width.bar`	Width error bar

Value

The function returns a column chart with two positive sides

Note

When there is only an effect of the isolated factor in the case of factorial or subdivided plots, it is possible to use the barplot_positive function.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

See Also

sk_graph, plot_TH, corgraph, spider_graph, line_plot

Examples

```
data("passiflora")
attach(passiflora)
a=with(passiflora, DBC(trat, bloco, MSPA))
b=with(passiflora, DBC(trat, bloco, MSR))
barplot_positive(a, b, var_name = c("DMAP","DRM"), ylab = "Dry root (g)")

a=with(passiflora, DIC(trat, MSPA,test = "noparametric"))
b=with(passiflora, DIC(trat, MSR))
barplot_positive(a, b, var_name = c("DMAP","DRM"), ylab = "Dry root (g)")
```

`bar_dunnett` *Graph: Barplot for Dunnett test*

Description

The function performs the construction of a column chart of Dunnett's test.

Usage

```
bar_dunnett(
  output.dunnett,
  ylab = "Response",
  xlab = "",
  fill = c("white", "#F8766D", "#00BFC4"),
  sup = NA,
  add.mean = TRUE,
  round = 2
)
```

Arguments

`output.dunnett`	Numerical or complex vector with treatments
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`fill`	Fill column. Use vector with two elements c(control, different treatment, no difference treatment)
`sup`	Number of units above the standard deviation or average bar on the graph
`add.mean`	Plot the average value on the graph (*default* is TRUE)
`round`	Number of cells

Value

Returns a column chart of Dunnett's test. The colors indicate difference from the control.

Examples

```
#=====================================================
# randomized block design in factorial double
#=====================================================
library(AgroR)
data(cloro)
attach(cloro)
respAd=c(268, 322, 275, 350, 320)
a=FAT2DBC.ad(f1, f2, bloco, resp, respAd,
             ylab=”Number of nodules”,mcomp=”sk”)
data=rbind(data.frame(trat=paste(f1,f2,sep = ””),bloco=bloco,resp=resp),
           data.frame(trat=c(”Test”,”Test”,”Test”,”Test”,”Test”),
                      bloco=unique(bloco),resp=respAd))
a= with(data,dunnett(trat = trat,
                  resp = resp,
                  control = ”Test”,
                  block=bloco,model = ”DBC”))
 bar_dunnett(a)
```

`bar_graph` *Graph: Bar graph for one factor*

Description

This is a function of the bar graph for one factor

Usage

```
bar_graph(model, fill = ”lightblue”, horiz = TRUE, axis.0 = FALSE)
```

Arguments

`model`	DIC, DBC or DQL object
`fill`	fill bars
`horiz`	Horizontal Column (*default* is TRUE)
`axis.0`	If TRUE causes the columns or bars to start just above the axis line.

Value

Returns a bar chart for one factor

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

barplot_positive, plot_TH, plot_TH1, corgraph, spider_graph, line_plot, plot_cor, plot_interaction, plot_jitter, seg_graph, TBARPLOT.reverse

Examples

```
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
     mcomp = "sk",angle=45,
     ylab = "Number of fruits/plants"))
bar_graph(a,horiz = FALSE)
```

`bar_graph2` *Graph: Bar graph for one factor model 2*

Description

This is a function of the bar graph for one factor

Usage

```
bar_graph2(
  model,
  point.color = "black",
  point.size = 2,
  point.shape = 16,
  text.color = "black",
  label.color = "black",
  bar.color = "black",
```

```
  title.size = 14,
  y.text = 0,
  add.info = NA,
  y.info = 0,
  width.bar = 0,
  color.info = "black",
  fill = "lightblue"
)
```

Arguments

`model`	DIC, DBC or DQL object
`point.color`	Point color
`point.size`	Point size
`point.shape`	Format point
`text.color`	Text color
`label.color`	Label color
`bar.color`	Errorbar color
`title.size`	Title size
`y.text`	Y-axis height for x-axis legend
`add.info`	Add other information
`y.info`	Y-axis height for other information
`width.bar`	Width error bar
`color.info`	Color text information
`fill`	Fill bars

Value

Returns a bar chart for one factor

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

barplot_positive, plot_TH, plot_TH1, corgraph, spider_graph, line_plot, plot_cor, plot_interaction, plot_jitter, seg_graph, TBARPLOT.reverse

Examples

```
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
     mcomp = "sk",angle=45,sup = 10,
     family = "serif",
     ylab = "Number of fruits/plants"))
bar_graph2(a)
bar_graph2(a,fill="darkblue",point.color="orange",text.color='white')
```

`bean` *Dataset: Bean*

Description

An experiment to evaluate the effect of different strains of Azospirillum on common bean cultivar IPR Sabia was carried out in a greenhouse. A completely randomized design with five strains was used. of Azospirillum (treatments) and five repetitions. The response variable analyzed was grain production per plant (g plant-1).

Usage

```
data("bean")
```

Format

data.frame containing data set

`trat` numeric vector with treatment

`prod` Numeric vector with grain production per plant

See Also

aristolochia, cloro, laranja, enxofre, laranja, mirtilo, passiflora, phao, porco, pomegranate, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(bean)
```

`cloro` *Dataset: Sodium dichloroisocyanurate in soybean*

Description

An experiment was conducted in a greenhouse in pots at the State University of Londrina. The work has the objective of evaluating the application of sodium dichloroisocyanurate (DUP) in soybean in 4 periods of application in soybean inoculated or not with Rhizobium and its influence on the number of nodules. The experiment was conducted in a completely randomized design with five replications.

Usage

```
data(cloro)
```

Format

data.frame containing data set

`f1` Categorical vector with factor 1

`f2` Categorical vector with factor 2

`bloco` Categorical vector with block

`resp` Numeric vector with number nodules

References

Rony Kauling Tonelli. Efeito do uso de dicloroisocianurato de sodio sobre a nodulacao em raizes de soja. 2016. Trabalho de Conclusao de Curso. (Graduacao em Agronomia) - Universidade Estadual de Londrina.

See Also

enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(cloro)
```

`confinterval` *Utils: Interval of confidence for groups*

Description

Calculates confidence interval for groups

Usage

```
confinterval(resp, group, alpha = 0.95, type = "upper")
```

Arguments

`resp`	numeric vector with responses
`group`	vector with groups or list with two factors
`alpha`	confidence level of the interval
`type`	lower or upper range

Value

returns a numeric vector with confidence interval grouped by treatment.

Examples

```
#===================================
# One factor
#===================================

dados=rnorm(100,10,1)
trat=rep(paste("T",1:10),10)
confinterval(dados,trat)

#===================================
# Two factor
#===================================
f1=rep(c("A","B"),e=50)
f2=rep(paste("T",1:5),e=10,2)
confinterval(dados,list(f1,f2))
```

---

conjdbc *Analysis: Joint analysis of experiments in randomized block design*

Description

Function of the AgroR package for joint analysis of experiments conducted in a randomized qualitative or quantitative single-block design with balanced data.

Usage

```
conjdbc(
  trat,
  block,
  local,
  response,
  transf = 1,
  constant = 0,
  norm = "sw",
  homog = "bt",
  homog.value = 7,
  theme = theme_classic(),
  mcomp = "tukey",
  quali = TRUE,
  alpha.f = 0.05,
  alpha.t = 0.05,
  grau = NA,
  ylab = "response",
  title = "",
  xlab = "",
  fill = "lightblue",
  angulo = 0,
  textsize = 12,
  dec = 3,
  family = "sans",
  errorbar = TRUE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`block`	Numerical or complex vector with blocks
`local`	Numeric or complex vector with locations or times
`response`	Numerical vector containing the response of the experiment.
`transf`	Applies data transformation (default is 1; for log consider 0)
`constant`	Add a constant for transformation (enter value)

`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`homog.value`	Reference value for homogeneity of experiments. By default, this ratio should not be greater than 7
`theme`	ggplot2 theme (*default* is theme_classic())
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`ylab`	Variable response name (this argument uses the *parse* function)
`title`	Graph title
`xlab`	Treatments name (this argument uses the *parse* function)
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angulo`	x-axis scale text rotation
`textsize`	Font size
`dec`	Number of cells
`family`	Font family
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE

Value

Returns the assumptions of the analysis of variance, the assumption of the joint analysis by means of a QMres ratio matrix, the analysis of variance, the multiple comparison test or regression.

Note

In this function there are three possible outcomes. When the ratio between the experiments is greater than 7, the separate analyzes are returned, without however using the square of the joint residue. When the ratio is less than 7, but with significant interaction, the effects are tested using the square of the joint residual. When there is no significant interaction and the ratio is less than 7, the joint analysis between the experiments is returned.

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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References

Ferreira, P. V. Estatistica experimental aplicada a agronomia. Edufal, 2018.

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Examples

```
library(AgroR)
data(mirtilo)

#===================================
# No significant interaction
#===================================
with(mirtilo, conjdbc(trat, bloco, exp, resp))

#===================================
# Significant interaction
#===================================
data(eucalyptus)
with(eucalyptus, conjdbc(trati, bloc, exp, resp))
```

`conjdic` *Analysis: Joint analysis of experiments in completely randomized design*

Description

Function of the AgroR package for joint analysis of experiments conducted in a completely randomized design with a qualitative or quantitative factor with balanced data.

Usage

```
conjdic(
  trat,
  repet,
  local,
  response,
  transf = 1,
  constant = 0,
```

```
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  homog.value = 7,
  quali = TRUE,
  alpha.f = 0.05,
  alpha.t = 0.05,
  grau = NA,
  theme = theme_classic(),
  ylab = "response",
  title = "",
  xlab = "",
  color = "rainbow",
  fill = "lightblue",
  angulo = 0,
  textsize = 12,
  dec = 3,
  family = "sans",
  errorbar = TRUE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`repet`	Numerical or complex vector with repetitions
`local`	Numeric or complex vector with locations or times
`response`	Numerical vector containing the response of the experiment.
`transf`	Applies data transformation (default is 1; for log consider 0)
`constant`	Add a constant for transformation (enter value)
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`homog.value`	Reference value for homogeneity of experiments. By default, this ratio should not be greater than 7
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`title`	Graph title
`xlab`	Treatments name (this argument uses the *parse* function)
`color`	When the columns are different colors (Set fill-in argument as "trat")

`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angulo`	x-axis scale text rotation
`textsize`	Font size
`dec`	Number of cells
`family`	Font family
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE

Value

Returns the assumptions of the analysis of variance, the assumption of the joint analysis by means of a QMres ratio matrix, the analysis of variance, the multiple comparison test or regression.

Note

In this function there are three possible outcomes. When the ratio between the experiments is greater than 7, the separate analyzes are returned, without however using the square of the joint residue. When the ratio is less than 7, but with significant interaction, the effects are tested using the square of the joint residual. When there is no significant interaction and the ratio is less than 7, the joint analysis between the experiments is returned.

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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References

Ferreira, P. V. Estatistica experimental aplicada a agronomia. Edufal, 2018.

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

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

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Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Examples

```
library(AgroR)
data(mirtilo)
with(mirtilo, conjdic(trat, bloco, exp, resp))
```

`conjfat2dbc` *Analysis: Joint analysis of experiments in randomized block design in scheme factorial double*

Description

Function of the AgroR package for joint analysis of experiments conducted in a randomized factorial double in block design with balanced data. The function generates the joint analysis through two models. Model 1: F-test of the effects of Factor 1, Factor 2 and F1 x F2 interaction are used in reference to the mean square of the interaction with the year. Model 2: F-test of the Factor 1, Factor 2 and F1 x F2 interaction effects are used in reference to the mean square of the residual.

Usage

```
conjfat2dbc(
  f1,
  f2,
  block,
  experiment,
  response,
  transf = 1,
  constant = 0,
  model = 1,
  norm = "sw",
  homog = "bt",
  homog.value = 7,
  alpha.f = 0.05,
  alpha.t = 0.05
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`block`	Numerical or complex vector with blocks
`experiment`	Numeric or complex vector with locations or times
`response`	Numerical vector containing the response of the experiment.
`transf`	Applies data transformation (default is 1; for log consider 0)
`constant`	Add a constant for transformation (enter value)
`model`	Define model of the analysis of variance

`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`homog.value`	Reference value for homogeneity of experiments. By default, this ratio should not be greater than 7
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)

Value

Returns the assumptions of the analysis of variance, the assumption of the joint analysis by means of a QMres ratio matrix and analysis of variance

Note

The function is still limited to analysis of variance and assumptions only.

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

References

Ferreira, P. V. Estatistica experimental aplicada a agronomia. Edufal, 2018.

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Examples

```
library(AgroR)
ano=factor(rep(c(2018,2019,2020),e=48))
f1=rep(rep(c("A","B","C"),e=16),3)
f2=rep(rep(rep(c("a1","a2","a3","a4"),e=4),3),3)
resp=rnorm(48*3,10,1)
bloco=rep(c("b1","b2","b3","b4"),36)
dados=data.frame(ano,f1,f2,resp,bloco)
with(dados,conjfat2dbc(f1,f2,bloco,ano,resp, model=1))
```

`corgraph` *Graph: Correlogram*

Description

Correlation analysis function (Pearson or Spearman)

Usage

```
corgraph(
  data,
  axissize = 12,
  legendsize = 12,
  legendposition = c(0.9, 0.2),
  legendtitle = "Correlation",
  method = "pearson",
  pallete = "RdBu",
  color.marginal = "gray50",
  size.tile.lty = 1,
  size.label.cor = 1,
  fill.label.cor = "lightyellow",
  font.family = "sans"
)
```

Arguments

`data`	data.frame with responses
`axissize`	Axes font size (*default* is 12)
`legendsize`	Legend font size (*default* is 12)
`legendposition`	Legend position (*default* is c(0.9,0.2))
`legendtitle`	Legend title (*default* is "Correlation")
`method`	Method correlation (*default* is Pearson)
`pallete`	If a string, will use that named palette. See scale_fill_distiller in the ggplot2.
`color.marginal`	Box border color
`size.tile.lty`	Box margin line thickness
`size.label.cor`	Label font size
`fill.label.cor`	Label fill color
`font.family`	Font family (*default* is sans)

Value

The function returns a correlation matrix

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("pomegranate")
corgraph(pomegranate[,-1])
```

`corn` *Dataset: Corn*

Description

A 3 x 2 factorial experiment was carried out to compare three new corn hybrids considering the change in sowing density, being 55 thousand or 65 thousand seeds per hectare. For this case, the researcher is not interested in estimating values for other densities, but only in verifying if one density differs from the other. The experiment was carried out according to a completely randomized design with 4 repetitions of each treatment.

Usage

```
data(corn)
```

Format

data.frame containing data set

`A` Categorical vector with hybrids

`B` Categorical vector with density

`resp` Numeric vector with response

See Also

enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(corn)
```

`cor_ic` *Graph: Plot Pearson correlation with interval of confidence*

Description

Plot Pearson correlation with interval of confidence

Usage

```
cor_ic(
  data,
  background = TRUE,
  axis.size = 12,
  ylab = "",
  xlab = "Correlation (r)",
  theme = theme_classic()
)
```

Arguments

`data`	data.frame with responses
`background`	background fill (*default* is TRUE)
`axis.size`	Axes font size (*default* is 12)
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	Treatments name (Accepts the *expression*() function)
`theme`	ggplot theme (*default* is theme_classic())

Value

The function returns a new graphical approach to correlation.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("pomegranate")
cor_ic(pomegranate[,-1])
```

`covercrops` *Dataset: Covercrops*

Description

Consider a 3 ×3 factorial experiment in randomized blocks, with 4 replications, on the influence of three new soybean cultivars (A1, A2 and A3) and the use of three types of green manure (B1, B2 and B3) on yield in 100 m2 plots.

Usage

```
data(covercrops)
```

Format

data.frame containing data set

`A`	Categorical vector with cultivars
`B`	Categorical vector with green manure
`Bloco`	Categorical vector with block
`Resp`	Numeric vector with yield

See Also

enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(covercrops)
```

`DBC` *Analysis: Randomized block design*

Description

This is a function of the AgroR package for statistical analysis of experiments conducted in a randomized block and balanced design with a factor considering the fixed model. The function presents the option to use non-parametric method or transform the dataset.

Usage

```
DBC(
  trat,
  block,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = TRUE,
  mcomp = "tukey",
  grau = 1,
  transf = 1,
  constant = 0,
  test = "parametric",
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  CV = TRUE,
  ylab = "response",
  xlab = "",
  textsize = 12,
  labelsize = 4,
  fill = "lightblue",
  angle = 0,
  family = "sans",
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  pointsize = 5,
  angle.label = 0,
  ylim = NA,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)

`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`test`	"parametric" - Parametric test or "noparametric" - non-parametric test
`geom`	graph type (columns, boxes or segments)
`theme`	ggplot2 theme (*default* is theme_classic())
`sup`	Number of units above the standard deviation or average bar on the graph
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`textsize`	Font size
`labelsize`	Label size
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`posi`	Legend position
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error ("mean_se"). For parametric test it is possible to plot the square root of QMres (mean_qmres).
`pointsize`	Point size
`angle.label`	label angle
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk ("sw"), Lilliefors ("li"), Anderson-Darling ("ad"), Cramer-von Mises ("cvm"), Pearson ("pearson") and Shapiro-Francia ("sf")), the test of homogeneity of variances (Bartlett ("bt") or Levene ("levene")), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey ("tukey"), LSD ("lsd"), Scott-Knott ("sk") or Duncan ("duncan")) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. Non-parametric analysis can be used by the Friedman test. The column, segment or box chart for qualitative treatments is also returned. The function also returns a standardized residual plot.

Note

Enable ggplot2 package to change theme argument.

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

CV and p-value of the graph indicate coefficient of variation and p-value of the F test of the analysis of variance.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

See Also

DIC, DQL

Examples

```
library(AgroR)

#=============================
# Example laranja
#=============================
data(laranja)
attach(laranja)
DBC(trat, bloco, resp, mcomp = "sk", angle=45, ylab = "Number of fruits/plants")

#=============================
# Friedman test
#=============================
DBC(trat, bloco, resp, test="noparametric", ylab = "Number of fruits/plants")

#=============================
# Example soybean
#=============================
data(soybean)
with(soybean, DBC(cult, bloc, prod,ylab="Grain yield (kg ha^-1)"))
```

`dbc.ad` *Analysis: Randomized block design with an additional treatment for quantitative factor*

Description

Statistical analysis of experiments conducted in a randomized block design with an additional treatment and balanced design with a factor considering the fixed model.

Usage

```
dbc.ad(
  trat,
  block,
  response,
  responsead,
  grau = 1,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  theme = theme_classic(),
  ylab = "response",
  xlab = "independent",
  family = "sans",
  posi = "top",
  pointsize = 4.5,
  linesize = 0.8,
```

```
  width.bar = NA,
  point = "mean_sd"
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`responsead`	Numerical vector with additional treatment responses
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`family`	Font family
`posi`	Legend position
`pointsize`	Point size
`linesize`	line size (Trendline and Error Bar)
`width.bar`	width of the error bars of a regression graph.
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error (*default* - "mean_se"). For quali=FALSE or quali=TRUE.

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk ("sw"), Lilliefors ("li"), Anderson-Darling ("ad"), Cramer-von Mises ("cvm"), Pearson ("pearson") and Shapiro-Francia ("sf")), the test of homogeneity of variances (Bartlett ("bt") or Levene ("levene")), the test of independence of Durbin-Watson errors, adjustment of regression models up to grade 3 polynomial. The function also returns a standardized residual plot.

Note

In some experiments, the researcher may study a quantitative factor, such as fertilizer doses, and present a control, such as a reference fertilizer, treated as a qualitative control. In these cases, there is a difference between considering only the residue in the unfolding of the polynomial, removing or not the qualitative treatment, or since a treatment is excluded from the analysis. In this approach, the residue used is also considering the qualitative treatment, a method similar to the factorial scheme with additional control.

Author(s)

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Examples

```
doses = c(rep(c(1:5),e=3))
resp = c(3, 4, 3, 5, 5, 6, 7, 7, 8, 4, 4, 5, 2, 2, 3)
bloco = rep(c("B1","B2","B3","B4","B5"),3)
dbc.ad(doses, bloco, resp, responsead=rnorm(3,6,0.1),grau=2)
```

`DBC.glm` *Analysis: Randomized block design by glm*

Description

Statistical analysis of experiments conducted in a randomized block design using a generalized linear model. It performs the deviance analysis and the effect is tested by a chi-square test. Multiple comparisons are adjusted by Tukey.

Usage

```
DBC.glm(
  trat,
  block,
  response,
  glm.family = "binomial",
  quali = TRUE,
  alpha.f = 0.05,
  alpha.t = 0.05,
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  ylab = "Response",
  xlab = "",
  fill = "lightblue",
  angle = 0,
  family = "sans",
  textsize = 12,
  labelsize = 5,
  dec = 3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  angle.label = 0
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment. Use cbind(resp, n-resp) for binomial or quasibinomial family.
`glm.family`	distribution family considered (*default* is binomial)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`geom`	Graph type (columns, boxes or segments)
`theme`	ggplot2 theme (*default* is theme_classic())
`sup`	Number of units above the standard deviation or average bar on the graph
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family
`textsize`	Font size
`labelsize`	Label size
`dec`	Number of cells
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`posi`	Legend position
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error (*default* - "mean_se").
`angle.label`	label angle

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("aristolochia")
attach(aristolochia)
# Assuming the same aristolochia data set, but considering randomized blocks
bloco=rep(paste("B",1:16),5)
resp=resp/2
DBC.glm(trat,bloco, cbind(resp,50-resp), glm.family="binomial")
```

`DBCT` *Analysis: Randomized block design evaluated over time*

Description

Function of the AgroR package for analysis of experiments conducted in a balanced qualitative, single-factorial randomized block design with multiple assessments over time, however without considering time as a factor.

Usage

```
DBCT(
  trat,
  block,
  time,
  response,
  alpha.f = 0.05,
  alpha.t = 0.05,
  mcomp = "tukey",
  geom = "bar",
  theme = theme_classic(),
  fill = "gray",
  ylab = "Response",
  xlab = "Independent",
  textsize = 12,
  labelsize = 5,
  pointsize = 4.5,
  error = TRUE,
  family = "sans",
  sup = 0,
  addmean = FALSE,
  posi = c(0.1, 0.8),
  legend = "Legend",
  ylim = NA,
  width.bar = 0.2,
  size.bar = 0.8,
  dec = 3,
  xnumeric = FALSE,
  all.letters = FALSE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`block`	Numerical or complex vector with blocks
`time`	Numerical or complex vector with times

`response`	Numerical vector containing the response of the experiment.
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD ("lsd"), Scott-Knott ("sk"), Duncan ("duncan") and Friedman ("fd"))
`geom`	Graph type (columns - "bar" or segments "point")
`theme`	ggplot2 theme (*default* is theme_classic())
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`textsize`	Font size of the texts and titles of the axes
`labelsize`	Font size of the labels
`pointsize`	Point size
`error`	Add error bar (SD)
`family`	Font family
`sup`	Number of units above the standard deviation or average bar on the graph
`addmean`	Plot the average value on the graph (*default* is TRUE)
`posi`	Legend position
`legend`	Legend title
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`width.bar`	width error bar
`size.bar`	size error bar
`dec`	Number of cells
`xnumeric`	Declare x as numeric (*default* is FALSE)
`all.letters`	Adds all label letters regardless of whether it is significant or not.

Details

The p-value of the analysis of variance, the normality test for Shapiro-Wilk errors, the Bartlett homogeneity test of variances, the independence of Durbin-Watson errors and the multiple comparison test (Tukey, Scott-Knott, LSD or Duncan).

Value

The function returns the p-value of Anova, the assumptions of normality of errors, homogeneity of variances and independence of errors, multiple comparison test, as well as a line graph

Note

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

Author(s)

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References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

See Also

DBC, DICT, DQLT

Examples

```
rm(list=ls())
data(simulate2)
attach(simulate2)

#===================================
# default
#===================================
DBCT(trat, bloco, tempo, resp)
DBCT(trat, bloco, tempo, resp,fill="rainbow")

#===================================
# segment chart
#===================================
DBCT(trat, bloco, tempo, resp, geom="point")
```

`desc` *Descriptive: Descriptive analysis*

Description

Performs the descriptive analysis of an experiment with a factor of interest.

Usage

```
desc(trat, response, ylab = "Response", xlab = "Treatment", ylim = NA)
```

Arguments

`trat`	Numerical or complex vector with treatments
`response`	Numerical vector containing the response of the experiment.
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	x name (this argument uses the *parse* function)
`ylim`	y-axis scale

Value

The function returns exploratory measures of position and dispersion, such as mean, median, maximum, minimum, coefficient of variation, etc ...

Author(s)

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See Also

desc2fat, tabledesc,dispvar

Examples

```
library(AgroR)
data("pomegranate")
with(pomegranate, desc(trat,WL))
```

`desc2fat` *Descriptive: Descriptive analysis (Two factors)*

Description

It performs the descriptive analysis of an experiment with two factors of interest.

Usage

```
desc2fat(
  f1,
  f2,
  response,
  ylab = "Response",
  xlab = c("F1", "F2"),
  theme = theme_classic()
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`response`	Numerical vector containing the response of the experiment.
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	x name (this argument uses the *parse* function)
`theme`	ggplot2 theme (*default* is theme_classic())

Value

The function returns exploratory measures of position and dispersion, such as mean, median, maximum, minimum, coefficient of variation, etc ...

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
library(AgroR)
data(cloro)
output=with(cloro, desc2fat(f1,f2,resp))
output$plot_single
output$plot_interaction
```

`desc3fat` *Descriptive: Descriptive analysis (Three factors)*

Description

Performs the descriptive graphical analysis of an experiment with three factors of interest.

Usage

```
desc3fat(
  f1,
  f2,
  f3,
  response,
  legend.title = "Legend",
  xlab = c("F1", "F2", "F3"),
  ylab = "Response",
  theme = theme_classic(),
  plot = "interaction"
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`response`	Numerical vector containing the response of the experiment.
`legend.title`	Legend title
`xlab`	x name (this argument uses the *parse* function)
`ylab`	Variable response name (this argument uses the *parse* function)
`theme`	ggplot theme
`plot`	"interaction" or "box"

Value

The function returns a triple interaction graph.

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
library(AgroR)
data(enxofre)
with(enxofre, desc3fat(f1, f2, f3, resp))
```

`desd_fat2_quant_ad` *Analysis: Regression analysis by orthogonal polynomials for double factorial scheme with additional control*

Description

Regression analysis by orthogonal polynomials for double factorial scheme with additional control. Cases in which the additional belongs to the regression curve, being common to the qualitative levels. In these cases, the additional (usually dose 0/control treatment) is not part of the factor arrangement. One option addressed by this function is to analyze a priori as a double factorial scheme with an additional one and correct the information a posteriore using information from the initial analysis, such as the degree of freedom and the sum of squares of the residue.

Usage

```
desd_fat2_quant_ad(output, ad.value = 0, design = "FAT2DIC.ad", grau = 1)
```

Arguments

`output`	Output from a FAT2DIC.ad or FAT2DBC.ad function (Use quantity factor as f2).
`ad.value`	Additional treatment quantitative factor level
`design`	Type of experimental project (FAT2DIC.ad or FAT2DBC.ad)
`grau`	Degree of the polynomial (only for the isolated effect of the quantitative factor)

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
#================================================
# Data set
trat=rep(c("A","B","C"),e=12)
dose=rep(rep(c(200,400,600,800),e=3),3)
d0=c(40,45,48)
respo=c(60,55,56, 60,65,66, 70,75,76,
        80,85,86, 50,55,56, 70,75,76,
        60,65,66, 50,45,46, 50,45,46,
```

```
        50,55,66, 70,75,76, 80,85,86)
repe=rep(c("R1","R2","R3"),12)
#===================================================
# Analysis FAT2DIC.ad
resu=FAT2DIC.ad(trat,dose,repe = repe,respo,responseAd = d0,quali = c(TRUE,FALSE),grau21 = c(1,2,1))

#===================================================
# Regression analysis
desd_fat2_quant_ad(resu,ad.value=0,design="FAT2DIC.ad")


# Data set
trat=rep(c("A","B"),e=12)
dose=rep(rep(c(200,400,600,800),e=3),2)
d0=c(40,45,48)
respo=c(60,55,56,60,65,66,70,75,76,80,85,86,50,45,46,50,55,66,70,75,76,80,85,86)
repe=rep(c("R1","R2","R3"),8)
#===================================================
# Analysis FAT2DIC.ad
resu=FAT2DIC.ad(trat,dose,repe = repe,respo,responseAd = d0,quali = c(TRUE,FALSE))
#===================================================
# Regression analysis
desd_fat2_quant_ad(resu,ad.value=0,design="FAT2DIC.ad",grau=1)
```

`DIC` *Analysis: Completely randomized design*

Description

Statistical analysis of experiments conducted in a completely randomized and balanced design with a factor considering the fixed model. The function presents the option to use non-parametric method or transform the dataset.

Usage

```
DIC(
  trat,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = TRUE,
  mcomp = "tukey",
  grau = 1,
  transf = 1,
  constant = 0,
  test = "parametric",
  mcompNP = "LSD",
```

```
  p.adj = "holm",
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  sup = NA,
  CV = TRUE,
  xlab = "",
  fill = "lightblue",
  angle = 0,
  family = "sans",
  textsize = 12,
  labelsize = 4,
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  pointsize = 5,
  angle.label = 0,
  ylim = NA,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`transf`	Applies data transformation (*default* is 1; for log consider 0, ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`test`	"parametric" - Parametric test or "noparametric" - non-parametric test
`mcompNP`	Multiple comparison test (LSD (*default*) or dunn)
`p.adj`	Method for adjusting p values for Kruskal-Wallis ("none","holm","hommel", "hochberg", "bonferroni", "BH", "BY", "fdr")
`geom`	Graph type (columns, boxes or segments)

`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`sup`	Number of units above the standard deviation or average bar on the graph
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`xlab`	Treatments name (this argument uses the *parse* function)
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family
`textsize`	Font size
`labelsize`	Label size
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`posi`	Legend position
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error ("mean_se"). For quali=FALSE or quali=TRUE. For parametric test it is possible to plot the square root of QMres (mean_qmres)
`pointsize`	Point size
`angle.label`	label angle
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk ("sw"), Lilliefors ("li"), Anderson-Darling ("ad"), Cramer-von Mises ("cvm"), Pearson ("pearson") and Shapiro-Francia ("sf")), the test of homogeneity of variances (Bartlett ("bt") or Levene ("levene")), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey ("tukey"), LSD ("lsd"), Scott-Knott ("sk") or Duncan ("duncan")) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. Non-parametric analysis can be used by the Kruskal-Wallis test. The column, segment or box chart for qualitative treatments is also returned. The function also returns a standardized residual plot.

Note

Enable ggplot2 package to change theme argument.

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

Post hoc test in nonparametric is using the criterium Fisher's least significant difference (p-adj="holm").

CV and p-value of the graph indicate coefficient of variation and p-value of the F test of the analysis of variance.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

W.J. Conover, Practical Nonparametrics Statistics. 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package 'agricolae'. R Package, Version, 1-2.

Hothorn, T. et al. Package 'lmtest'. Testing linear regression models. https://cran. r-project. org/web/packages/lmtest/lmtest. pdf. Accessed, v. 6, 2015.

See Also

DBC DQL

Examples

```
library(AgroR)
data(pomegranate)

with(pomegranate, DIC(trat, WL, ylab = "Weight loss ('%')")) # tukey
with(pomegranate, DIC(trat, WL, mcomp = "sk", ylab = "Weight loss ('%')"))
with(pomegranate, DIC(trat, WL, mcomp = "duncan", ylab = "Weight loss ('%')"))

#=============================
# Kruskal-Wallis
```

```
#=============================
with(pomegranate, DIC(trat, WL, test = "noparametric", ylab = "Weight loss ('%')"))


#=============================
# chart type
#=============================
with(pomegranate, DIC(trat, WL, geom="point", ylab = "Weight loss ('%')"))
with(pomegranate, DIC(trat, WL, ylab = "Weight loss ('%')", xlab="Treatments"))

#=============================
# quantitative factor
#=============================
data("phao")
with(phao, DIC(dose,comp,quali=FALSE,grau=2,xlab = "Dose (g vase^-1)",ylab="Leaf length (cm)"))

#=============================
# data transformation
#=============================
data("pepper")
with(pepper, DIC(Acesso, VitC, transf = 0,ylab="Vitamin C"))
```

`dic.ad` *Analysis: Completely randomized design with an additional treatment for quantitative factor*

Description

Statistical analysis of experiments conducted in a completely randomized with an additional treatment and balanced design with a factor considering the fixed model.

Usage

```
dic.ad(
  trat,
  response,
  responsead,
  grau = 1,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  theme = theme_classic(),
  ylab = "response",
  xlab = "independent",
  family = "sans",
  posi = "top",
  pointsize = 4.5,
  linesize = 0.8,
  width.bar = NA,
```

```
  point = "mean_sd"
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`response`	Numerical vector containing the response of the experiment.
`responsead`	Numerical vector with additional treatment responses
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`family`	Font family
`posi`	Legend position
`pointsize`	Point size
`linesize`	line size (Trendline and Error Bar)
`width.bar`	width of the error bars of a regression graph.
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error (*default* - "mean_se"). For quali=FALSE or quali=TRUE.

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk ("sw"), Lilliefors ("li"), Anderson-Darling ("ad"), Cramer-von Mises ("cvm"), Pearson ("pearson") and Shapiro-Francia ("sf")), the test of homogeneity of variances (Bartlett ("bt") or Levene ("levene")), the test of independence of Durbin-Watson errors, adjustment of regression models up to grade 3 polynomial. The function also returns a standardized residual plot.

Note

In some experiments, the researcher may study a quantitative factor, such as fertilizer doses, and present a control, such as a reference fertilizer, treated as a qualitative control. In these cases, there is a difference between considering only the residue in the unfolding of the polynomial, removing or not the qualitative treatment, or since a treatment is excluded from the analysis. In this approach, the residue used is also considering the qualitative treatment, a method similar to the factorial scheme with additional control.

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
datadicad=data.frame(doses = c(rep(c(1:5),e=3)),
                     resp = c(3,4,3,5,5,6,7,7,8,4,4,5,2,2,3))
with(datadicad,dic.ad(doses, resp, rnorm(3,6,0.1),grau=2))
```

`DIC.glm` *Analysis: Completely randomized design by glm*

Description

Statistical analysis of experiments conducted in a completely randomized design using a generalized linear model. It performs the deviance analysis and the effect is tested by a chi-square test. Multiple comparisons are adjusted by Tukey.

Usage

```
DIC.glm(
  trat,
  response,
  glm.family = "binomial",
  quali = TRUE,
  alpha.f = 0.05,
  alpha.t = 0.05,
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  ylab = "Response",
  xlab = "",
  fill = "lightblue",
  angle = 0,
  family = "sans",
  textsize = 12,
  labelsize = 5,
  dec = 3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  angle.label = 0
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`response`	Numerical vector containing the response of the experiment. Use cbind(resp, n-resp) for binomial or quasibinomial family.

`glm.family`	distribution family considered (*default* is binomial)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`geom`	Graph type (columns, boxes or segments)
`theme`	ggplot2 theme (*default* is theme_classic())
`sup`	Number of units above the standard deviation or average bar on the graph
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family
`textsize`	Font size
`labelsize`	Label size
`dec`	Number of cells
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`posi`	Legend position
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error (*default* - "mean_se").
`angle.label`	label angle

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data(”aristolochia”)
attach(aristolochia)
#=============================
# Use the DIC function
#=============================
DIC(trat, resp)

#=============================
# Use the DIC function noparametric
#=============================
DIC(trat, resp, test=”noparametric”)
```

```
#=============================
# Use the DIC.glm function
#=============================

resp=resp/4 # total germinated seeds

# the value 25 is the total of seeds in the repetition
DIC.glm(trat, cbind(resp,25-resp), glm.family="binomial")
```

`DICT` *Analysis: Completely randomized design evaluated over time*

Description

Function of the AgroR package for the analysis of experiments conducted in a completely randomized, qualitative, uniform qualitative design with multiple assessments over time, however without considering time as a factor.

Usage

```
DICT(
  trat,
  time,
  response,
  alpha.f = 0.05,
  alpha.t = 0.05,
  mcomp = "tukey",
  theme = theme_classic(),
  geom = "bar",
  xlab = "Independent",
  ylab = "Response",
  p.adj = "holm",
  dec = 3,
  fill = "gray",
  error = TRUE,
  textsize = 12,
  labelsize = 5,
  pointsize = 4.5,
  family = "sans",
  sup = 0,
  addmean = FALSE,
  legend = "Legend",
  ylim = NA,
  width.bar = 0.2,
  size.bar = 0.8,
  posi = c(0.1, 0.8),
  xnumeric = FALSE,
```

```
  all.letters = FALSE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`time`	Numerical or complex vector with times
`response`	Numerical vector containing the response of the experiment.
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD ("lsd"), Scott-Knott ("sk"), Duncan ("duncan") and Kruskal-Wallis ("kw"))
`theme`	ggplot2 theme (*default* is theme_classic())
`geom`	Graph type (columns - "bar" or segments "point")
`xlab`	treatments name (this argument uses the *parse* function)
`ylab`	Variable response name (this argument uses the *parse* function)
`p.adj`	Method for adjusting p values for Kruskal-Wallis ("none","holm","hommel", "hochberg", "bonferroni", "BH", "BY", "fdr")
`dec`	Number of cells
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`error`	Add error bar
`textsize`	Font size of the texts and titles of the axes
`labelsize`	Font size of the labels
`pointsize`	Point size
`family`	Font family
`sup`	Number of units above the standard deviation or average bar on the graph
`addmean`	Plot the average value on the graph (*default* is TRUE)
`legend`	Legend title
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`width.bar`	width error bar
`size.bar`	size error bar
`posi`	Legend position
`xnumeric`	Declare x as numeric (*default* is FALSE)
`all.letters`	Adds all label letters regardless of whether it is significant or not.

Value

The function returns the p-value of Anova, the assumptions of normality of errors, homogeneity of variances and independence of errors, multiple comparison test, as well as a line graph

Note

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

Author(s)

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Leandro Simoes Azeredo Goncalves

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References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

See Also

DIC, DBCT, DQLT

Examples

```
rm(list=ls())
data(simulate1)
attach(simulate1)
with(simulate1, DICT(trat, tempo, resp))
with(simulate1, DICT(trat, tempo, resp, fill="rainbow",family="serif"))
with(simulate1, DICT(trat, tempo, resp,geom="bar",sup=40))
with(simulate1, DICT(trat, tempo, resp,geom="point",sup=40))
```

`dispvar` *Descriptive: Boxplot with standardized data*

Description

It makes a graph with the variables and/or treatments with the standardized data.

Usage

```
dispvar(
  data,
  trat = NULL,
  theme = theme_bw(),
  ylab = "Standard mean",
  xlab = "Variable",
  family = "serif",
  textsize = 12,
  fill = "lightblue"
)
```

Arguments

`data`	data.frame containing the response of the experiment.
`trat`	Numerical or complex vector with treatments
`theme`	ggplot2 theme (*default* is theme_bw())
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	Treatments name (Accepts the *expression*() function)
`family`	Font family
`textsize`	Font size
`fill`	Defines chart color

Value

Returns a chart of boxes with standardized data

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

Examples

```
library(AgroR)
data("pomegranate")
dispvar(pomegranate[,-1])
trat=pomegranate$trat
dispvar(pomegranate[,-1], trat)
```

DQL *Analysis: Latin square design*

Description

This is a function of the AgroR package for statistical analysis of experiments conducted in Latin Square and balanced design with a factor considering the fixed model.

Usage

```
DQL(
  trat,
  line,
  column,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = TRUE,
  mcomp = "tukey",
  grau = 1,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  CV = TRUE,
  ylab = "Response",
  xlab = "",
  textsize = 12,
  labelsize = 4,
  fill = "lightblue",
  angle = 0,
  family = "sans",
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  pointsize = 5,
  angle.label = 0,
  ylim = NA,
  print.on = TRUE,
  plot.on = TRUE
```

```
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`line`	Numerical or complex vector with lines
`column`	Numerical or complex vector with columns
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*default* is qualitative)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Degree of polynomial in case of quantitative factor (*default* is 1)
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns, boxes or segments)
`theme`	ggplot2 theme (*default* is theme_classic())
`sup`	Number of units above the standard deviation or average bar on the graph
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	Treatments name (Accepts the *expression*() function)
`textsize`	Font size
`labelsize`	Label size
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`posi`	Legend position
`point`	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - *default*) or mean with standard error ("mean_se"). For parametric test it is possible to plot the square root of QMres (mean_qmres).

`pointsize`	Point size
`angle.label`	label angle
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk ("sw"), Lilliefors ("li"), Anderson-Darling ("ad"), Cramer-von Mises ("cvm"), Pearson ("pearson") and Shapiro-Francia ("sf")), the test of homogeneity of variances (Bartlett ("bt") or Levene ("levene")), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey ("tukey"), LSD ("lsd"), Scott-Knott ("sk") or Duncan ("duncan")) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column, segment or box chart for qualitative treatments is also returned. The function also returns a standardized residual plot.

Note

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

CV and p-value of the graph indicate coefficient of variation and p-value of the F test of the analysis of variance.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

References

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

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

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

See Also

DIC, DBC

Examples

```
library(AgroR)
data(porco)
with(porco, DQL(trat, linhas, colunas, resp, ylab="Weigth (kg)"))
```

DQLT *Analysis: Latin square design evaluated over time*

Description

Function of the AgroR package for the analysis of experiments conducted in a balanced qualitative single-square Latin design with multiple assessments over time, however without considering time as a factor.

Usage

```
DQLT(
  trat,
  line,
  column,
  time,
  response,
  alpha.f = 0.05,
  alpha.t = 0.05,
  mcomp = "tukey",
  error = TRUE,
  xlab = "Independent",
  ylab = "Response",
  textsize = 12,
  labelsize = 5,
  pointsize = 4.5,
  family = "sans",
  sup = 0,
  addmean = FALSE,
  posi = c(0.1, 0.8),
  geom = "bar",
  fill = "gray",
  legend = "Legend",
  ylim = NA,
  width.bar = 0.2,
  size.bar = 0.8,
  dec = 3,
  theme = theme_classic(),
```

```
  xnumeric = FALSE,
  all.letters = FALSE
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`line`	Numerical or complex vector with line
`column`	Numerical or complex vector with column
`time`	Numerical or complex vector with times
`response`	Numerical vector containing the response of the experiment.
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`error`	Add error bar (SD)
`xlab`	Treatments name (this argument uses the *parse* function)
`ylab`	Variable response name (this argument uses the *parse* function)
`textsize`	Font size of the texts and titles of the axes
`labelsize`	Font size of the labels
`pointsize`	Point size
`family`	Font family
`sup`	Number of units above the standard deviation or average bar on the graph
`addmean`	Plot the average value on the graph (*default* is TRUE)
`posi`	Legend position
`geom`	Graph type (columns - "bar" or segments "point")
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`legend`	Legend title
`ylim`	Define a numerical sequence referring to the y scale. You can use a vector or the ‘seq‘ command.
`width.bar`	width error bar
`size.bar`	size error bar
`dec`	Number of cells
`theme`	ggplot2 theme (*default* is theme_classic())
`xnumeric`	Declare x as numeric (*default* is FALSE)
`all.letters`	Adds all label letters regardless of whether it is significant or not.

Details

The p-value of the analysis of variance, the normality test for Shapiro-Wilk errors, the Bartlett homogeneity test of variances, the independence of Durbin-Watson errors and the multiple comparison test (Tukey, Scott-Knott, LSD or Duncan).

Value

The function returns the p-value of Anova, the assumptions of normality of errors, homogeneity of variances and independence of errors, multiple comparison test, as well as a line graph

Note

The ordering of the graph is according to the sequence in which the factor levels are arranged in the data sheet. The bars of the column and segment graphs are standard deviation.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

See Also

DQL, DICT, DBCT

Examples

```
rm(list=ls())
data(simulate3)
attach(simulate3)
DQLT(trat, linhas, colunas, tempo, resp)
```

`dunn` *Analysis: Post-hoc Dunn*

Description

Perform Kruskal wallis and dunn post-hoc test

Usage

```
dunn(trat, resp, method = "holm", alpha = 0.05, decreasing = TRUE)
```

Arguments

`trat`	Numerical or complex vector with treatments
`resp`	Vector with response
`method`	the p-value for multiple comparisons ("none", "bonferroni", "sidak", "holm", "hs", "hochberg", "bh", "by"). The default is no adjustment for multiple comparisons
`alpha`	Significance level of the post-hoc (*default* is 0.05)
`decreasing`	Should the order of the letters be increasing or decreasing.

Value

Kruskal-wallis and dunn's post-hoc test returns

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Examples

```
library(AgroR)
data(pomegranate)

with(pomegranate, dunn(trat, WL))
```

`dunnett` *Analysis: Dunnett test*

Description

The function performs the Dunnett test

Usage

```
dunnett(
  trat,
  resp,
  control,
  model = "DIC",
  block = NA,
  column = NA,
  line = NA,
  alpha.t = 0.05,
  pointsize = 5,
  pointshape = 21,
  linesize = 1,
  labelsize = 4,
  textsize = 12,
  errorsize = 1,
  widthsize = 0.2,
  label = "Response",
  family = "sans"
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`resp`	Numerical vector containing the response of the experiment.
`control`	Treatment considered control (write identical to the name in the vector)
`model`	Experimental design (DIC, DBC or DQL)
`block`	Numerical or complex vector with blocks
`column`	Numerical or complex vector with columns
`line`	Numerical or complex vector with lines
`alpha.t`	Significance level (*default* is 0.05)
`pointsize`	Point size
`pointshape`	Shape
`linesize`	Line size
`labelsize`	Label size

`textsize`	Font size
`errorsize`	Errorbar size
`widthsize`	Width errorbar
`label`	Variable label
`family`	font family

Value

I return the Dunnett test for experiments in a completely randomized design, randomized blocks or Latin square.

Note

Do not use the "-" symbol or space in treatment names

Examples

```
#=====================================================
# complete randomized design
#=====================================================
data("pomegranate")
with(pomegranate,dunnett(trat=trat,resp=WL,control="T1"))

#=====================================================
# randomized block design in factorial double
#=====================================================
library(AgroR)
data(cloro)
attach(cloro)
respAd=c(268, 322, 275, 350, 320)
a=FAT2DBC.ad(f1, f2, bloco, resp, respAd,
             ylab="Number of nodules", mcomp="sk")
data=rbind(data.frame(trat=paste(f1,f2,sep = ""),bloco=bloco,resp=resp),
           data.frame(trat=c("Test","Test","Test","Test","Test"),
                      bloco=unique(bloco),resp=respAd))
with(data,dunnett(trat = trat,
                  resp = resp,
                  control = "Test",
                  block=bloco,model = "DBC"))
```

`emerg` *Dataset: Emergence of passion fruit seeds over time .*

Description

The data come from an experiment conducted at the State University of Londrina, aiming to study the emergence of yellow passion fruit seeds over time. Data are partial from one of the treatments studied. Four replicates with eight seeds each were used.

Usage

```
data("emerg")
```

Format

data.frame containing data set

`time` numeric vector with time

`resp` Numeric vector with emergence

See Also

aristolochia, cloro, laranja, enxofre, laranja, mirtilo, passiflora, phao, porco, pomegranate, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(emerg)
```

`enxofre` *Dataset: Sulfur data*

Description

The experiment was carried out in a randomized block design in a 3 x 3 x 3 triple factorial scheme: syrup volume (75, 225 and 675 L), sulfur doses (150, 450, 1350) and time of application (vegetative, complete cycle and reproductive system) with four repetitions. Yield in kg / ha of soybean was evaluated.

Usage

```
data(enxofre)
```

Format

data.frame containing data set

`f1` Categorical vector with factor 1

`f2` Categorical vector with factor 2

`f2` Categorical vector with factor 3

`bloco` Categorical vector with block

`resp` Numeric vector

See Also

cloro, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(enxofre)
```

`eucalyptus` *Dataset: Eucaliptus grandis Barbin (2013)*

Description

The data refer to the height in meters of *Eucalyptus grandis* plants, with 7 years of age, from three trials (Araraquara - Exp 1; Bento Quintino - Exp 2; Mogi-Guacu - Exp 3) in randomized blocks, under 6 progenies. The data were taken from the book by Decio Barbin (2013) and are from the Instituto Florestal de Tupi/SP.

Usage

```
data("eucalyptus")
```

Format

data.frame containing data set

`trati` Categorical vector with treatments

`bloc` Categorical vector with block

`exp` Categorical vector with experiment

`resp` Numeric vector

References

Planejamento e Analise Estatistica de Experimentos Agronomicos (2013) - Decio Barbin - pg. 177

See Also

cloro, enxofre, laranja, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(eucalyptus)
```

`FAT2DBC` *Analysis: DBC experiments in double factorial*

Description

Analysis of an experiment conducted in a randomized block design in a double factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT2DBC(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  legend = "Legend",
  fill = "lightblue",
  angle = 0,
  textsize = 12,
  labelsize = 4,
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  family = "sans",
  point = "mean_sd",
  addmean = TRUE,
  errorbar = TRUE,
  CV = TRUE,
  sup = NA,
  color = "rainbow",
  posi = "right",
  ylim = NA,
```

```
  angle.label = 0,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with two elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`legend`	Legend title name
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`textsize`	font size
`labelsize`	label size
`dec`	number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar

`family`	font family
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`sup`	Number of units above the standard deviation or average bar on the graph
`color`	Column chart color (*default* is "rainbow")
`posi`	Legend position
`ylim`	y-axis scale
`angle.label`	label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett or Levene), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two quantitative factors.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

See Also

FAT2DBC.ad

Examples

```
#===============================================
# Example cloro
#===============================================
library(AgroR)
data(cloro)
with(cloro,FAT2DBC(f1, f2, bloco, resp, ylab="Number of nodules"))
with(cloro,FAT2DBC(f1, f2, bloco, resp, mcomp="sk", ylab="Number of nodules"))
#===============================================
# Example covercrops
#===============================================
library(AgroR)
data(covercrops)
with(covercrops,FAT2DBC(A, B, Bloco, Resp, ylab="Yield (Kg 100 m^2)"))
with(covercrops,FAT2DBC(A, B, Bloco, Resp, mcomp="sk", ylab="Yield (Kg 100 m^2)"))
```

`FAT2DBC.ad` *Analysis: DBC experiment in double factorial design with an additional treatment*

Description

Analysis of an experiment conducted in a randomized block design in a double factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT2DBC.ad(
  f1,
  f2,
  block,
  response,
  responseAd,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  ad.label = "Additional",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  labelsize = 4,
  addmean = TRUE,
  errorbar = TRUE,
  CV = TRUE,
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  angle = 0,
  posi = "right",
  family = "sans",
  point = "mean_sd",
  sup = NA,
  ylim = NA,
  angle.label = 0,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels

`block`	Numeric or complex vector with repetitions
`response`	Numerical vector containing the response of the experiment.
`responseAd`	Numerical vector with additional treatment responses
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with two elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`ad.label`	Aditional label
`color`	Column chart color (*default* is "rainbow")
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`textsize`	Font size
`labelsize`	Label Size
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`angle`	x-axis scale text rotation
`posi`	legend position

`family`	Font family
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, 'mean_sd' and 'mean_se' change which information will be displayed in the error bar.
`sup`	Number of units above the standard deviation or average bar on the graph
`ylim`	y-axis scale
`angle.label`	label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett or Levene), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.

Note

The order of the chart follows the alphabetical pattern. Please use 'scale_x_discrete' from package ggplot2, 'limits' argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two quantitative factors.

The assumptions of variance analysis disregard additional treatment

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Rodrigo Yudi Palhaci Marubayashi

References

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Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

See Also

FAT2DBC

dunnett

Examples

```
library(AgroR)
data(cloro)
respAd=c(268, 322, 275, 350, 320)
with(cloro, FAT2DBC.ad(f1, f2, bloco, resp, respAd, ylab="Number of nodules"))
```

`FAT2DIC` *Analysis: DIC experiments in double factorial*

Description

Analysis of an experiment conducted in a completely randomized design in a double factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT2DIC(
  f1,
  f2,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  lab.factor = c("F1", "F2"),
  color = "rainbow",
```

```
  fill = "lightblue",
  textsize = 12,
  labelsize = 4,
  addmean = TRUE,
  errorbar = TRUE,
  CV = TRUE,
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  angle = 0,
  posi = "right",
  family = "sans",
  point = "mean_sd",
  sup = NA,
  ylim = NA,
  angle.label = 0,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with two elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))

`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`lab.factor`	Provide a vector with two observations referring to the x-axis name of factors 1 and 2, respectively, when there is an isolated effect of the factors. This argument uses ‘parse‘.
`color`	Column chart color (*default* is "rainbow")
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`textsize`	Font size
`labelsize`	Label Size
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`angle`	x-axis scale text rotation
`posi`	Legend position
`family`	Font family
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`sup`	Number of units above the standard deviation or average bar on the graph
`ylim`	y-axis scale
`angle.label`	Label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett or Levene), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two quantitative factors.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., & de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

See Also

FAT2DIC.ad

Examples

```
#====================================
# Example cloro
#====================================
library(AgroR)
data(cloro)
with(cloro, FAT2DIC(f1, f2, resp, ylab="Number of nodules", names.fat = c("Inoculation","Stages")))

#====================================
# Example corn
#====================================
library(AgroR)
data(corn)
with(corn, FAT2DIC(A, B, Resp, quali=c(TRUE, TRUE),ylab="Heigth (cm)"))
with(corn, FAT2DIC(A, B, Resp, mcomp="sk", quali=c(TRUE, TRUE),ylab="Heigth (cm)"))
```

`FAT2DIC.ad` *Analysis: DIC experiment in double factorial design with an additional treatment*

Description

Analysis of an experiment conducted in a completely randomized design in a double factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT2DIC.ad(
  f1,
  f2,
  repe,
  response,
  responseAd,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  ad.label = "Additional",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  labelsize = 4,
  addmean = TRUE,
  errorbar = TRUE,
  CV = TRUE,
  dec = 3,
  width.column = 0.9,
  width.bar = 0.3,
  angle = 0,
  posi = "right",
  family = "sans",
  point = "mean_sd",
```

```
    sup = NA,
    ylim = NA,
    angle.label = 0,
    print.on = TRUE,
    plot.on = TRUE
  )
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`repe`	Numeric or complex vector with repetitions
`response`	Numerical vector containing the response of the experiment.
`responseAd`	Numerical vector with additional treatment responses
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with two elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`ad.label`	Aditional label
`color`	Column chart color (*default* is "rainbow")
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`textsize`	Font size
`labelsize`	Label Size

`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`CV`	Plotting the coefficient of variation and p-value of Anova (*default* is TRUE)
`dec`	Number of cells
`width.column`	Width column if geom="bar"
`width.bar`	Width errorbar
`angle`	x-axis scale text rotation
`posi`	legend position
`family`	Font family
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`sup`	Number of units above the standard deviation or average bar on the graph
`ylim`	y-axis scale
`angle.label`	label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett or Levene), the test of independence of Durbin-Watson errors, the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two quantitative factors.

The assumptions of variance analysis disregard additional treatment

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

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Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Mendiburu, F., & de Mendiburu, M. F. (2019). Package 'agricolae'. R Package, Version, 1-2.

See Also

FAT2DIC

dunnett

Examples

```
library(AgroR)
data(cloro)
respAd=c(268, 322, 275, 350, 320)
with(cloro, FAT2DIC.ad(f1, f2, bloco, resp, respAd, ylab="Number of nodules"))
```

`fat2_table` *Utils: Summary of the analysis for factor arrangement with two qualitative factors.*

Description

Summarizes the output returned in the summarise_anova function in list form. The advantage is that the table, in the case of significant interaction, is returned in a format that facilitates assembly in terms of scientific publication.

Usage

```
fat2_table(output, nf1, nf2, column = 1)
```

Arguments

`output`	Output of summarise_anova function for FAT2DIC, FAT2DIC.ad, FAT2DBC, FAT2DBC.ad, PSUBDIC and PSUBDBC design.
`nf1`	Number of levels of factor 1
`nf2`	Number of levels of factor 2
`column`	Variable column

Value

returns a list containing analysis output for experiments in FAT2DIC, FAT2DIC.ad, FAT2DBC, FAT2DBC.ad, PSUBDIC and PSUBDBC design.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Examples

```
#===============================================================
data(corn)
attach(corn)
a=FAT2DIC(A, B, Resp, quali=c(TRUE, TRUE))
output_1=summarise_anova(list(a),design="FAT2DIC",divisor = FALSE)
fat2_table(output_1,nf1=3,nf2=2,column=1)

#===============================================================
data(cloro)
respAd=c(268, 322, 275, 350, 320)
resu=with(cloro, FAT2DIC.ad(f1, f2, bloco, resp, respAd))
output_2=summarise_anova(list(resu),design="FAT2DIC.ad",divisor = FALSE)
fat2_table(output_2,nf1=2,nf2=4,column=1)
```

`FAT3DBC` *Analysis: DBC experiments in triple factorial*

Description

Analysis of an experiment conducted in a randomized block design in a triple factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT3DBC(
  f1,
  f2,
  f3,
  block,
  response,
  norm = "sw",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE, TRUE),
  mcomp = "tukey",
  transf = 1,
  constant = 0,
  names.fat = c("F1", "F2", "F3"),
```

```
  ylab = "Response",
  sup = NA,
  grau = c(NA, NA, NA),
  grau12 = NA,
  grau13 = NA,
  grau23 = NA,
  grau21 = NA,
  grau31 = NA,
  grau32 = NA,
  grau123 = NA,
  grau213 = NA,
  grau312 = NA,
  fill = "lightblue",
  theme = theme_classic(),
  angulo = 0,
  errorbar = TRUE,
  addmean = TRUE,
  family = "sans",
  dec = 3,
  geom = "bar",
  textsize = 12,
  labelsize = 4,
  point = "mean_sd",
  angle.label = 0
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`transf`	Applies data transformation (*default* is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`names.fat`	Allows labeling the factors 1, 2 and 3 (this argument uses the *parse* function).
`ylab`	Variable response name (this argument uses the *parse* function)
`sup`	Number of units above the standard deviation or average bar on the graph

`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau13`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f3 and qualitative factor 3 and quantitative factor 1.
`grau23`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f2 x f3 and qualitative factor 3 and quantitative factor 2.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`grau31`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f3 and qualitative factor 1 and quantitative factor 3.
`grau32`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f2 x f3 and qualitative factor 2 and quantitative factor 3.
`grau123`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 x f3 and quantitative factor 1.
`grau213`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 x f3 and quantitative factor 2.
`grau312`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f2 x f3 and quantitative factor 3.
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`theme`	ggplot2 theme (*default* is theme_classic())
`angulo`	x-axis scale text rotation
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`addmean`	Plot the average value on the graph (*default* is TRUE)
`family`	Font family
`dec`	Number of cells
`geom`	Graph type (columns or segments)
`textsize`	Font size
`labelsize`	Label Size

`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`angle.label`	label angle

Value

The analysis of variance table, the Shapiro-Wilk error normality test, the Bartlett homogeneity test of variances, the Durbin-Watson error independence test, multiple comparison test (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.For significant triple interaction only, no graph is returned.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two or more quantitative factors. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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References

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Ferreira, E. B., Cavalcanti, P. P., and Nogueira, D. A. (2014). ExpDes: an R package for ANOVA and experimental designs. Applied Mathematics, 5(19), 2952.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

Examples

```
library(AgroR)
data(enxofre)
with(enxofre, FAT3DBC(f1, f2, f3, bloco, resp))
```

`FAT3DBC.ad` *Analysis: DBC experiments in triple factorial with aditional*

Description

Analysis of an experiment conducted in a randomized block design in a triple factorial scheme with one aditional control using analysis of variance of fixed effects.

Usage

```
FAT3DBC.ad(
  f1,
  f2,
  f3,
  block,
  response,
  responseAd,
  norm = "sw",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE, TRUE),
  mcomp = "tukey",
  transf = 1,
  constant = 0,
  names.fat = c("F1", "F2", "F3"),
  ylab = "Response",
  sup = NA,
  grau = c(NA, NA, NA),
  grau12 = NA,
  grau13 = NA,
  grau23 = NA,
  grau21 = NA,
  grau31 = NA,
  grau32 = NA,
  grau123 = NA,
  grau213 = NA,
  grau312 = NA,
  fill = "lightblue",
  theme = theme_classic(),
  ad.label = "Additional",
  angulo = 0,
  errorbar = TRUE,
```

```
    addmean = TRUE,
    family = "sans",
    dec = 3,
    geom = "bar",
    textsize = 12,
    labelsize = 4,
    point = "mean_sd",
    angle.label = 0
  )
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`block`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`responseAd`	Numerical vector containing the aditional response
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`transf`	Applies data transformation (*default* is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`names.fat`	Allows labeling the factors 1, 2 and 3 (this argument uses the *parse* function).
`ylab`	Variable response name (this argument uses the *parse* function)
`sup`	Number of units above the standard deviation or average bar on the graph
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau13`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f3 and qualitative factor 3 and quantitative factor 1.
`grau23`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f2 x f3 and qualitative factor 3 and quantitative factor 2.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.

`grau31`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f3 and qualitative factor 1 and quantitative factor 3.
`grau32`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f2 x f3 and qualitative factor 2 and quantitative factor 3.
`grau123`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 x f3 and quantitative factor 1.
`grau213`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 x f3 and quantitative factor 2.
`grau312`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f2 x f3 and quantitative factor 3.
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`theme`	ggplot2 theme (*default* is theme_classic())
`ad.label`	Aditional label
`angulo`	x-axis scale text rotation
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`addmean`	Plot the average value on the graph (*default* is TRUE)
`family`	Font family
`dec`	Number of cells
`geom`	Graph type (columns or segments)
`textsize`	Font size
`labelsize`	Label size
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`angle.label`	label angle

Value

The analysis of variance table, the Shapiro-Wilk error normality test, the Bartlett homogeneity test of variances, the Durbin-Watson error independence test, multiple comparison test (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.For significant triple interaction only, no graph is returned.

Note

The order of the chart follows the alphabetical pattern. Please use 'scale_x_discrete' from package ggplot2, 'limits' argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two or more quantitative factors. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Ferreira, E. B., Cavalcanti, P. P., and Nogueira, D. A. (2014). ExpDes: an R package for ANOVA and experimental designs. Applied Mathematics, 5(19), 2952.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package 'agricolae'. R Package, Version, 1-2.

Examples

```
library(AgroR)
data(enxofre)
respAd=c(2000,2400,2530,2100)
attach(enxofre)
with(enxofre, FAT3DBC.ad(f1, f2, f3, bloco, resp, respAd))
```

`FAT3DIC` *Analysis: DIC experiments in triple factorial*

Description

Analysis of an experiment conducted in a completely randomized design in a triple factorial scheme using analysis of variance of fixed effects.

Usage

```
FAT3DIC(
  f1,
  f2,
  f3,
  response,
  norm = "sw",
  alpha.t = 0.05,
  alpha.f = 0.05,
  quali = c(TRUE, TRUE, TRUE),
  mcomp = "tukey",
  grau = c(NA, NA, NA),
  grau12 = NA,
  grau13 = NA,
  grau23 = NA,
  grau21 = NA,
  grau31 = NA,
  grau32 = NA,
  grau123 = NA,
  grau213 = NA,
  grau312 = NA,
  transf = 1,
  constant = 0,
  names.fat = c("F1", "F2", "F3"),
  ylab = "Response",
  sup = NA,
  fill = "lightblue",
  theme = theme_classic(),
  angulo = 0,
  family = "sans",
  addmean = TRUE,
  errorbar = TRUE,
  dec = 3,
  geom = "bar",
  textsize = 12,
  labelsize = 4,
  point = "mean_sd",
  angle.label = 0
```

```
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`response`	Numerical vector containing the response of the experiment.
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau13`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f3 and qualitative factor 3 and quantitative factor 1.
`grau23`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f2 x f3 and qualitative factor 3 and quantitative factor 2.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`grau31`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f3 and qualitative factor 1 and quantitative factor 3.
`grau32`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f2 x f3 and qualitative factor 2 and quantitative factor 3.
`grau123`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 x f3 and quantitative factor 1.
`grau213`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 x f3 and quantitative factor 2.
`grau312`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f2 x f3 and quantitative factor 3.

`transf`	Applies data transformation (*default* is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`names.fat`	Allows labeling the factors 1, 2 and 3 (this argument uses the *parse* function).
`ylab`	Variable response name (this argument uses the *parse* function)
`sup`	Number of units above the standard deviation or average bar on the graph
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`theme`	ggplot2 theme (*default* is theme_classic())
`angulo`	x-axis scale text rotation
`family`	Font family
`addmean`	Plot the average value on the graph (*default* is TRUE)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`dec`	Number of cells
`geom`	Graph type (columns or segments)
`textsize`	Font size
`labelsize`	Label Size
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`angle.label`	label angle

Value

The analysis of variance table, the Shapiro-Wilk error normality test, the Bartlett homogeneity test of variances, the Durbin-Watson error independence test, multiple comparison test (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.For significant triple interaction only, no graph is returned.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two or more quantitative factors. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

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Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Ferreira, E. B., Cavalcanti, P. P., and Nogueira, D. A. (2014). ExpDes: an R package for ANOVA and experimental designs. Applied Mathematics, 5(19), 2952.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

Examples

```
library(AgroR)
data(enxofre)
with(enxofre, FAT3DIC(f1, f2, f3, resp))
```

`FAT3DIC.ad` *Analysis: DIC experiments in triple factorial with aditional*

Description

Analysis of an experiment conducted in a completely randomized design in a triple factorial scheme with one aditional control using analysis of variance of fixed effects.

Usage

```
FAT3DIC.ad(
  f1,
  f2,
  f3,
  repe,
  response,
  responseAd,
  norm = "sw",
```

```
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE, TRUE),
  mcomp = "tukey",
  transf = 1,
  constant = 0,
  names.fat = c("F1", "F2", "F3"),
  ylab = "Response",
  sup = NA,
  grau = c(NA, NA, NA),
  grau12 = NA,
  grau13 = NA,
  grau23 = NA,
  grau21 = NA,
  grau31 = NA,
  grau32 = NA,
  grau123 = NA,
  grau213 = NA,
  grau312 = NA,
  fill = "lightblue",
  theme = theme_classic(),
  ad.label = "Additional",
  angulo = 0,
  errorbar = TRUE,
  addmean = TRUE,
  family = "sans",
  dec = 3,
  geom = "bar",
  textsize = 12,
  labelsize = 4,
  point = "mean_sd",
  angle.label = 0
)
```

Arguments

`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`repe`	Numerical or complex vector with blocks
`response`	Numerical vector containing the response of the experiment.
`responseAd`	Numerical vector containing the aditional response
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)

`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`transf`	Applies data transformation (*default* is 1; for log consider 0; ‘angular‘ for angular transformation)
`constant`	Add a constant for transformation (enter value)
`names.fat`	Allows labeling the factors 1, 2 and 3 (this argument uses the *parse* function).
`ylab`	Variable response name (this argument uses the *parse* function)
`sup`	Number of units above the standard deviation or average bar on the graph
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau13`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f3 and qualitative factor 3 and quantitative factor 1.
`grau23`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f2 x f3 and qualitative factor 3 and quantitative factor 2.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`grau31`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f3 and qualitative factor 1 and quantitative factor 3.
`grau32`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f2 x f3 and qualitative factor 2 and quantitative factor 3.
`grau123`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 x f3 and quantitative factor 1.
`grau213`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 x f3 and quantitative factor 2.
`grau312`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 3, in the case of interaction f1 x f2 x f3 and quantitative factor 3.
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`theme`	ggplot2 theme (*default* is theme_classic())
`ad.label`	Aditional label
`angulo`	x-axis scale text rotation
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE

`addmean`	Plot the average value on the graph (*default* is TRUE)
`family`	Font family
`dec`	Number of cells
`geom`	Graph type (columns or segments)
`textsize`	Font size
`labelsize`	Label size
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, 'mean_sd' and 'mean_se' change which information will be displayed in the error bar.
`angle.label`	label angle

Value

The analysis of variance table, the Shapiro-Wilk error normality test, the Bartlett homogeneity test of variances, the Durbin-Watson error independence test, multiple comparison test (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned.For significant triple interaction only, no graph is returned.

Note

The order of the chart follows the alphabetical pattern. Please use 'scale_x_discrete' from package ggplot2, 'limits' argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

The function does not perform multiple regression in the case of two or more quantitative factors. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Ferreira, E. B., Cavalcanti, P. P., and Nogueira, D. A. (2014). ExpDes: an R package for ANOVA and experimental designs. Applied Mathematics, 5(19), 2952.

Mendiburu, F., and de Mendiburu, M. F. (2019). Package ‘agricolae’. R Package, Version, 1-2.

Examples

```
library(AgroR)
data(enxofre)
respAd=c(2000,2400,2530,2100)
with(enxofre, FAT3DIC.ad(f1, f2, f3, bloco, resp, respAd))
```

`grid.onefactor` *utils: group graphs of the output of simple experiments in dic, dbc or dql*

Description

group graphs of the output of simple experiments into dic, dbc or dql. It is possible to group up to 6 graphs in different arrangements (see model argument)

Usage

```
grid.onefactor(output, model = "type1")
```

Arguments

`output`	List with the outputs of the DIC, DBC or DQL functions
`model`	Graph arrangement model, see in detail.

Details

- ‘type1‘: Two graphs next to each other - ‘type2‘: Two graphs one below the other - ‘type3‘: Three graphs, two top and one centered below - ‘type4‘: Three graphs one below the other - ‘type5‘: Four graphs, two at the top and two at the bottom - ‘type6‘: Four graphs one below the other - ‘type7‘: Five graphs, two at the top, two in the middle and one centered at the bottom - ‘type8‘: Five graphs, three at the top, two centered at the bottom - ‘type9‘: Six graphs, three at the top, three centered at the bottom - ‘type10‘: Six graphs, two at the top, two in the middle and two at the bottom

Value

returns grouped graphs

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("pomegranate")
attach(pomegranate)
a=DIC(trat, WL, geom = "point", ylab = "WL")
b=DIC(trat, SS, geom = "point", ylab="SS")
c=DIC(trat, AT, geom = "point", ylab = "AT")
grid.onefactor(list(a,b),model = "type1")
grid.onefactor(list(a,b),model = "type2")
grid.onefactor(list(a,b,c),model = "type3")
grid.onefactor(list(a,b,c),model = "type4")
```

`ibarplot.double` *Graph: Invert letters for two factor chart*

Description

invert uppercase and lowercase letters in graph for factorial scheme the subdivided plot with significant interaction

Usage

```
ibarplot.double(analysis)
```

Arguments

`analysis`	FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC object

Value

Return column chart for two factors

Examples

```
data(covercrops)
attach(covercrops)
a=FAT2DBC(A, B, Bloco, Resp, ylab=expression("Yield"~(Kg~"100 m"^2)),
legend = "Cover crops",alpha.f = 0.3,family = "serif")
ibarplot.double(a)
```

`jointcluster` *Analysis: Method to evaluate similarity of experiments based on QMres*

Description

This function presents a method to evaluate similarity of experiments based on a matrix of QMres of all against all. This is used as a measure of similarity and applied in clustering.

Usage

```
jointcluster(qmres, information = "matrix", method.cluster = "ward.D")
```

Arguments

`qmres`	Vector containing mean squares of residuals or output from list DIC or DBC function
`information`	Option to choose the return type. ‘matrix‘, ‘bar‘ or ‘cluster‘
`method.cluster`	Grouping method

Value

Returns a residual mean square ratio matrix, bar graph with ratios sorted in ascending order, or cluster analysis.

Author(s)

Gabriel Danilo Shimizu, <`gabrieldd.shimizu@gmail.com`>

Examples

```
qmres=c(0.344429, 0.300542, 0.124833, 0.04531, 0.039571, 0.011812, 0.00519)
jointcluster(qmres,information = "cluster")
jointcluster(qmres,information = "matrix")
jointcluster(qmres,information = "bar")

data(mirtilo)
m=lapply(unique(mirtilo$exp),function(x){
  m=with(mirtilo[mirtilo$exp==x,],DBC(trat,bloco,resp))})
jointcluster(m)
```

`laranja` *Dataset: Orange plants under different rootstocks*

Description

An experiment was conducted with the objective of studying the behavior of nine rootstocks for the Valencia orange tree. The data set refers to the 1973 evaluation (12 years old). The rootstocks are: T1: Tangerine Sunki; T2: National rough lemon; T3: Florida rough lemon; T4: Cleopatra tangerine; T5: Citranger-troyer; T6: Trifoliata; T7: Clove Tangerine; T8: Country orange; T9: Clove Lemon. The number of fruits per plant was evaluated.

Usage

```
data(laranja)
```

Format

data.frame containing data set

`f1`	Categorical vector with treatments
`bloco`	Categorical vector with block
`resp`	Numeric vector with number of fruits per plant

References

Planejamento e Analise Estatistica de Experimentos Agronomicos (2013) - Decio Barbin - pg. 72

See Also

cloro, enxofre, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(laranja)
```

`line_plot` *Graph: Line chart*

Description

Performs a descriptive line graph with standard deviation bars

Usage

```
line_plot(
  time,
  response,
  factor = NA,
  errorbar = "sd",
  ylab = "Response",
  xlab = "Time",
  legend.position = "right",
  theme = theme_classic()
)
```

Arguments

`time`	Vector containing the x-axis values
`response`	Vector containing the y-axis values
`factor`	Vector containing a categorical factor
`errorbar`	Error bars (sd or se)
`ylab`	y axis title (this argument uses the *parse* function)
`xlab`	x axis title (this argument uses the *parse* function)
`legend.position`	Legend position
`theme`	ggplot2 theme (*default* is theme_classic())

Value

Returns a line chart with error bars

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

sk_graph, plot_TH, corgraph, spider_graph

Examples

```
dose=rep(c(0,2,4,6,8,10),e=3,2)
resp=c(seq(1,18,1),seq(2,19,1))
fator=rep(c("A","B"),e=18)
line_plot(dose,resp,fator)
```

`logistic` *Analysis: Logistic regression*

Description

Logistic regression is a very popular analysis in agrarian sciences, such as in fruit growth curves, seed germination, etc...The logistic function performs the analysis using 3 or 4 parameters of the logistic model, being imported from the LL function .3 or LL.4 of the drc package (Ritz & Ritz, 2016).

Usage

```
logistic(
  trat,
  resp,
  npar = "LL.3",
  error = "SE",
  ylab = "Dependent",
  xlab = expression("Independent"),
  theme = theme_classic(),
  legend.position = "top",
  r2 = "all",
  width.bar = NA,
  scale = "none",
  textsize = 12,
  font.family = "sans"
)
```

Arguments

`trat`	Numerical or complex vector with treatments
`resp`	Numerical vector containing the response of the experiment.
`npar`	Number of model parameters
`error`	Error bar (It can be SE - *default*, SD or FALSE)
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	Treatments name (Accepts the *expression*() function)
`theme`	ggplot2 theme (*default* is theme_bw())
`legend.position`	Legend position (*default* is c(0.3,0.8))

`r2`	Coefficient of determination of the mean or all values (*default* is all)
`width.bar`	Bar width
`scale`	Sets x scale (*default* is none, can be "log")
`textsize`	Font size
`font.family`	Font family (*default* is sans)

Details

The three-parameter log-logistic function with lower limit 0 is

$$f(x) = 0 + \frac{d}{1 + \exp(b(\log(x) - \log(e)))}$$

The four-parameter log-logistic function is given by the expression

$$f(x) = c + \frac{d - c}{1 + \exp(b(\log(x) - \log(e)))}$$

The function is symmetric about the inflection point (e).

Value

The function allows the automatic graph and equation construction of the logistic model, provides important statistics, such as the Akaike (AIC) and Bayesian (BIC) inference criteria, coefficient of determination (r2), square root of the mean error (RMSE).

Author(s)

Model imported from the drc package (Ritz et al., 2016)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

References

Seber, G. A. F. and Wild, C. J (1989) Nonlinear Regression, New York: Wiley and Sons (p. 330).

Ritz, C.; Strebig, J.C.; Ritz, M.C. Package ‘drc’. Creative Commons: Mountain View, CA, USA, 2016.

Examples

```
data("emerg")
with(emerg, logistic(time, resp,xlab="Time (days)",ylab="Emergence (%)"))
with(emerg, logistic(time, resp,npar="LL.4",xlab="Time (days)",ylab="Emergence (%)"))
```

`mirtilo` *Dataset: Cutting blueberry data*

Description

An experiment was carried out in order to evaluate the rooting (resp1) of blueberry cuttings as a function of the cutting size (Treatment Colume). This experiment was repeated three times (Location column) and a randomized block design with four replications was adopted.

Usage

```
data(mirtilo)
```

Format

data.frame containing data set

`trat` Categorical vector with treatments

`exp` Categorical vector with experiment

`bloco` Categorical vector with block

`resp` Numeric vector

See Also

cloro, enxofre, laranja, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(mirtilo)
attach(mirtilo)
```

`orchard` *Dataset: Orchard*

Description

An experiment was carried out to analyze the treatments in orchards applied in the rows and between the rows, in a split-plot scheme according to a randomized block design. For this case, the line and leading are considered the levels of the factor applied in the plots and the treatments are considered the levels of the factor applied in the subplots. Microbial biomass carbon was analyzed.

Usage

```
data(orchard)
```

Format

data.frame containing data set

- `A` Categorical vector with plot
- `B` Categorical vector with split-plot
- `Bloco` Categorical vector with block
- `Resp` Numeric vector with microbial biomass carbon

See Also

enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(orchard)
```

`passiflora` *Dataset: Substrate data in the production of passion fruit seedlings*

Description

An experiment was carried out in order to evaluate the influence of the substrate on the dry mass of aerial part and root in yellow sour passion fruit. The experiment was conducted in a randomized block design with four replications. The treatments consisted of five substrates (Vermiculite, MC Normal, Carolina Soil, Mc organic and sand)

Usage

```
data(passiflora)
```

Format

data.frame containing data set

- `trat` Categorical vector with substrate
- `bloco` Categorical vector with block
- `MSPA` Numeric vector with dry mass of aerial part
- `MSR` Numeric vector with dry mass of root

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(passiflora)
```

PCA_function *Analysis: Principal components analysis*

Description

This function performs principal component analysis.

Usage

```
PCA_function(
  data,
  scale = TRUE,
  text = TRUE,
  pointsize = 5,
  textsize = 12,
  labelsize = 4,
  linesize = 0.6,
  repel = TRUE,
  ylab = NA,
  xlab = NA,
  groups = NA,
  sc = 1,
  font.family = "sans",
  theme = theme_bw(),
  label.legend = "Cluster",
  type.graph = "biplot"
)
```

Arguments

`data`	Data.frame with data set. Line name must indicate the treatment
`scale`	Performs data standardization (*default* is TRUE)
`text`	Add label (*default* is TRUE)
`pointsize`	Point size (*default* is 5)
`textsize`	Text size (*default* is 12)
`labelsize`	Label size (*default* is 4)
`linesize`	Line size (*default* is 0.8)
`repel`	Avoid text overlay (*default* is TRUE)
`ylab`	Names y-axis (this argument uses the *parse* function)
`xlab`	Names x-axis (this argument uses the *parse* function)
`groups`	Define grouping
`sc`	Secondary axis scale ratio (*default* is 1)
`font.family`	Font family (*default* is sans)

`theme`	Theme ggplot2 (*default* is theme_bw())
`label.legend`	Legend title (when group is not NA)
`type.graph`	Type of chart (*default* is biplot)

Details

The type.graph argument defines the graph that will be returned, in the case of "biplot" the biplot graph is returned with the first two main components and with eigenvalues and eigenvectors. In the case of "scores" only the treatment scores are returned, while for "cor" the correlations are returned. For "corPCA" a correlation between the vectors with the components is returned.

Value

The eigenvalues and eigenvectors, the explanation percentages of each principal component, the correlations between the vectors with the principal components, as well as graphs are returned.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Examples

```
data(pomegranate)
medias=tabledesc(pomegranate)
PCA_function(medias)
```

`pepper` *Dataset: Pepper*

Description

A vegetable breeder is characterizing five mini pepper accessions from the State University of Londrina germplasm bank for agronomic and biochemical variables. The experiment was conducted in a completely randomized design with four replications

Usage

```
data(pepper)
```

Format

data.frame containing data set

`Acesso`	Categorical vector with accessions
`MS`	Numeric vector com dry mass
`VitC`	Numeric vector with Vitamin C

See Also

enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(pepper)
```

`phao` *Dataset: Osmocote in* Phalaenopsis *sp.*

Description

The objective of the work was to evaluate the effect of doses of osmocote (15-09-12-N-P2O5-K2O, respectively) on the initial development of the orchid *Phalaenopsis* sp. The osmocote fertilizer was added in the following doses: 0, 2, 4, 6 and 8 g vase-1. After twelve months, leaf length was evaluated.

Usage

```
data(phao)
```

Format

data.frame containing data set

`dose` Numeric vector with doses

`comp` Numeric vector with leaf length

References

de Paula, J. C. B., Junior, W. A. R., Shimizu, G. D., Men, G. B., & de Faria, R. T. (2020). Fertilizante de liberacao controlada no crescimento inicial da orquidea *Phalaenopsis* sp. Revista Cultura Agronomica, 29(2), 289-299.

See Also

pomegranate, passiflora, cloro, enxofre, laranja, mirtilo, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(phao)
```

`plot_cor` *Graph: Plot correlation*

Description

Correlation analysis function (Pearson or Spearman)

Usage

```
plot_cor(
  x,
  y,
  method = "pearson",
  ylab = "Dependent",
  xlab = "Independent",
  theme = theme_classic(),
  pointsize = 5,
  shape = 21,
  fill = "gray",
  color = "black",
  axis.size = 12,
  ic = TRUE,
  title = NA,
  family = "sans"
)
```

Arguments

`x`	Numeric vector with independent variable
`y`	Numeric vector with dependent variable
`method`	Method correlation (*default* is Pearson)
`ylab`	Variable response name (Accepts the *expression*() function)
`xlab`	Treatments name (Accepts the *expression*() function)
`theme`	ggplot2 theme (*default* is theme_classic())
`pointsize`	Point size
`shape`	shape format
`fill`	Fill point
`color`	Color point
`axis.size`	Axis text size
`ic`	add interval of confidence
`title`	title
`family`	Font family

Value

The function returns a graph for correlation

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("pomegranate")
with(pomegranate, plot_cor(WL, SS, xlab="WL", ylab="SS"))
```

`plot_interaction` *Graph: Interaction plot*

Description

Performs an interaction graph from an output of the FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC commands.

Usage

```
plot_interaction(
  a,
  box_label = TRUE,
  repel = FALSE,
  pointsize = 3,
  linesize = 0.8,
  width.bar = 0.05,
  add.errorbar = TRUE,
  family = "sans"
)
```

Arguments

`a`	FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC object
`box_label`	Add box in label
`repel`	a boolean, whether to use ggrepel to avoid overplotting text labels or not.
`pointsize`	Point size
`linesize`	Line size (Trendline and Error Bar)
`width.bar`	width of the error bars.
`add.errorbar`	Add error bars.
`family`	Font family

Value

Returns an interaction graph with averages and letters from the multiple comparison test

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data(cloro)
a=with(cloro, FAT2DIC(f1, f2, resp))
plot_interaction(a)
```

`plot_jitter` *Graph: Column, box or segment chart with observations*

Description

The function performs the construction of graphs of boxes, columns or segments with all the observations represented in the graph.

Usage

```
plot_jitter(model)
```

Arguments

`model`	DIC, DBC or DQL object

Value

Returns with graph of boxes, columns or segments with all the observations represented in the graph.

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data("pomegranate")
a=with(pomegranate,DIC(trat,WL,geom="point"))
plot_jitter(a)
```

---

plot_TH *Graph: Climate chart of temperature and humidity*

Description

The plot_TH function allows the user to build a column/line graph with climatic parameters of temperature (maximum, minimum and average) and relative humidity (UR) or precipitation. This chart is widely used in scientific work in agrarian science

Usage

```
plot_TH(
  tempo,
  Tmed,
  Tmax,
  Tmin,
  UR,
  xlab = "Time",
  yname1 = expression("Humidity (%)"),
  yname2 = expression("Temperature ("^o * "C)"),
  legend.H = "Humidity",
  legend.tmed = "Tmed",
  legend.tmin = "Tmin",
  legend.tmax = "Tmax",
  colormax = "red",
  colormin = "blue",
  colormean = "darkgreen",
  fillbar = "gray80",
  limitsy1 = c(0, 100),
  x = "days",
  breaks = "1 months",
  textsize = 12,
  legendsize = 12,
  titlesize = 12,
  linesize = 1,
  date_format = "%m-%Y",
  sc = 2.5,
  angle = 0,
  legend.position = "bottom",
  theme = theme_classic()
)
```

Arguments

`tempo`	Vector with times
`Tmed`	Vector with mean temperature

`Tmax`	Vector with maximum temperature
`Tmin`	Vector with minimum temperature
`UR`	Vector with relative humidity or precipitation
`xlab`	x axis name
`yname1`	y axis name
`yname2`	Secondary y-axis name
`legend.H`	Legend column
`legend.tmed`	Legend mean temperature
`legend.tmin`	Legend minimum temperature
`legend.tmax`	Legend maximum temperature
`colormax`	Maximum line color (*default* is "red")
`colormin`	Minimum line color (*default* is "blue")
`colormean`	Midline color (*default* is "darkgreen")
`fillbar`	Column fill color (*default* is "gray80")
`limitsy1`	Primary y-axis scale (*default* is c(0,100))
`x`	x scale type (days or data, default is "days")
`breaks`	Range for x scale when x = "date" (default is 1 months)
`textsize`	Axis text size
`legendsize`	Legend text size
`titlesize`	Axis title size
`linesize`	Line size
`date_format`	Date format for x="data"
`sc`	Scale for secondary y-axis in relation to primary y-axis (declare the number of times that y2 is less than or greater than y1, the default being 2.5)
`angle`	x-axis scale text rotation
`legend.position`	Legend position
`theme`	ggplot2 theme

Value

Returns row and column graphs for graphical representation of air temperature and relative humidity. Graph normally used in scientific articles

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

sk_graph, barplot_positive, corgraph, plot_TH1, spider_graph, line_plot

Examples

```
library(AgroR)
data(weather)
with(weather, plot_TH(tempo, Tmed, Tmax, Tmin, UR))
```

---

plot_TH1 *Graph: Climate chart of temperature and humidity (Model 2)*

Description

The plot_TH1 function allows the user to build a column/line graph with climatic parameters of temperature (maximum, minimum and average) and relative humidity (UR) or precipitation. This chart is widely used in scientific work in agrarian science

Usage

```
plot_TH1(
  tempo,
  Tmed,
  Tmax,
  Tmin,
  UR,
  xlab = "Time",
  yname1 = expression("Humidity (%)"),
  yname2 = expression("Temperature ("^o * "C)"),
  legend.T = "Temperature",
  legend.H = "Humidity",
  legend.tmed = "Tmed",
  legend.tmin = "Tmin",
  legend.tmax = "Tmax",
  colormax = "red",
  colormin = "blue",
  colormean = "darkgreen",
  fillarea = "darkblue",
  facet.fill = "#FF9933",
  panel.grid = FALSE,
  x = "days",
  breaks = "1 months",
  textsize = 12,
  legendsize = 12,
  titlesize = 12,
  linesize = 1,
  date_format = "%m-%Y",
```

```
  angle = 0,
  legend.position = c(0.1, 0.3)
)
```

Arguments

`tempo`	Vector with times
`Tmed`	Vector with mean temperature
`Tmax`	Vector with maximum temperature
`Tmin`	Vector with minimum temperature
`UR`	Vector with relative humidity or precipitation
`xlab`	x axis name
`yname1`	y axis name
`yname2`	Secondary y-axis name
`legend.T`	faceted title legend 1
`legend.H`	faceted title legend 2
`legend.tmed`	Legend mean temperature
`legend.tmin`	Legend minimum temperature
`legend.tmax`	Legend maximum temperature
`colormax`	Maximum line color (*default* is "red")
`colormin`	Minimum line color (*default* is "blue")
`colormean`	Midline color (*default* is "darkgreen")
`fillarea`	area fill color (*default* is "darkblue")
`facet.fill`	faceted title fill color (*default* is #FF9933)
`panel.grid`	remove grid line (*default* is FALSE)
`x`	x scale type (days or data, default is "days")
`breaks`	Range for x scale when x = "date" (default is 1 months)
`textsize`	Axis text size
`legendsize`	Legend text size
`titlesize`	Axis title size
`linesize`	Line size
`date_format`	Date format for x="data"
`angle`	x-axis scale text rotation
`legend.position`	Legend position

Value

Returns row and column graphs for graphical representation of air temperature and relative humidity. Graph normally used in scientific articles

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

sk_graph, barplot_positive, corgraph, spider_graph, line_plot

Examples

```
library(AgroR)
data(weather)
with(weather, plot_TH1(tempo, Tmed, Tmax, Tmin, UR))
```

`plot_tonetest` *Graphics: Graphic for t test to compare means with a reference value*

Description

Sometimes the researcher wants to test whether the treatment mean is greater than/equal to or less than a reference value. For example, I want to know if the average productivity of my treatment is higher than the average productivity of a given country. For this, this function allows comparing the means with a reference value using the t test.

Usage

```
plot_tonetest(tonetest, alpha = 0.95)
```

Arguments

`tonetest`	t.one.test object
`alpha`	confidence level.

Value

returns a density plot and a column plot to compare a reference value with other treatments.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Examples

```
library(AgroR)
data("pomegranate")
resu=tonetest(resp=pomegranate$WL, trat=pomegranate$trat, mu=2)
plot_tonetest(resu)
```

`polynomial` *Analysis: Linear regression graph*

Description

Linear regression analysis of an experiment with a quantitative factor or isolated effect of a quantitative factor

Usage

```
polynomial(
  trat,
  resp,
  ylab = "Response",
  xlab = "Independent",
  yname.poly = "y",
  xname.poly = "x",
  grau = NA,
  theme = theme_classic(),
  point = "mean_sd",
  color = "gray80",
  posi = "top",
  textsize = 12,
  se = FALSE,
  ylim = NA,
  family = "sans",
  pointsize = 4.5,
  linesize = 0.8,
  width.bar = NA,
  n = NA,
  SSq = NA,
  DFres = NA,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`trat`	Numerical vector with treatments (Declare as numeric)
`resp`	Numerical vector containing the response of the experiment.
`ylab`	Dependent variable name (this argument uses the *parse* function)
`xlab`	Independent variable name (this argument uses the *parse* function)
`yname.poly`	Y name in equation
`xname.poly`	X name in equation
`grau`	Degree of the polynomial (1, 2 or 3)

`theme`	ggplot2 theme (*default* is theme_classic())
`point`	Defines whether to plot mean ("mean"), all repetitions ("all"),mean with standard deviation ("mean_sd") or mean with standard error (*default* - "mean_se").
`color`	Graph color (*default* is gray80)
`posi`	Legend position
`textsize`	Font size
`se`	Adds confidence interval (*default* is FALSE)
`ylim`	y-axis scale
`family`	Font family
`pointsize`	Point size
`linesize`	line size (Trendline and Error Bar)
`width.bar`	width of the error bars of a regression graph.
`n`	Number of decimal places for regression equations
`SSq`	Sum of squares of the residue
`DFres`	Residue freedom degrees
`print.on`	Print output
`plot.on`	Plot output

Value

Returns linear, quadratic or cubic regression analysis.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

polynomial2, polynomial2_color

Examples

```
data("phao")
with(phao, polynomial(dose,comp, grau = 2))
```

---

polynomial2 *Analysis: Linear regression graph in double factorial*

Description

Linear regression analysis for significant interaction of an experiment with two factors, one quantitative and one qualitative

Usage

```
polynomial2(
  fator1,
  resp,
  fator2,
  color = NA,
  grau = NA,
  ylab = "Response",
  xlab = "Independent",
  theme = theme_classic(),
  se = FALSE,
  point = "mean_sd",
  legend.title = "Treatments",
  posi = "top",
  textsize = 12,
  ylim = NA,
  family = "sans",
  width.bar = NA,
  pointsize = 3,
  linesize = 0.8,
  separate = c("(\"", "\")"),
  n = NA,
  DFres = NA,
  SSq = NA,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`fator1`	Numeric or complex vector with factor 1 levels
`resp`	Numerical vector containing the response of the experiment.
`fator2`	Numeric or complex vector with factor 2 levels
`color`	Graph color (*default* is NA)
`grau`	Degree of the polynomial (1,2 or 3)
`ylab`	Dependent variable name (this argument uses the *parse* function)

`xlab`	Independent variable name (this argument uses the *parse* function)
`theme`	ggplot2 theme (*default* is theme_classic())
`se`	Adds confidence interval (*default* is FALSE)
`point`	Defines whether to plot all points ("all"), mean ("mean"), mean with standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se").
`legend.title`	Title legend (this argument uses the *parse* function)
`posi`	Legend position
`textsize`	Font size (*default* is 12)
`ylim`	y-axis scale
`family`	Font family (*default* is sans)
`width.bar`	width of the error bars of a regression graph.
`pointsize`	Point size (*default* is 4)
`linesize`	line size (Trendline and Error Bar)
`separate`	Separation between treatment and equation (*default* is c("(\"","\")"))
`n`	Number of decimal places for regression equations
`DFres`	Residue freedom degrees
`SSq`	Sum of squares of the residue
`print.on`	Print output
`plot.on`	Plot output

Value

Returns two or more linear, quadratic or cubic regression analyzes.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

polynomial, polynomial2_color

Examples

```
dose=rep(c(0,0,0,2,2,2,4,4,4,6,6,6),3)
resp=c(8,7,5,23,24,25,30,34,36,80,90,80,
12,14,15,23,24,25,50,54,56,80,90,40,
12,14,15,3,4,5,50,54,56,80,90,40)
trat=rep(c(”A”,”B”,”C”),e=12)
polynomial2(dose, resp, trat, grau=c(1,2,3))
```

`polynomial2_color` *Analysis: Linear regression graph in double factorial with color graph*

Description

Linear regression analysis for significant interaction of an experiment with two factors, one quantitative and one qualitative

Usage

```
polynomial2_color(
  fator1,
  resp,
  fator2,
  color = NA,
  grau = NA,
  ylab = "Response",
  xlab = "independent",
  theme = theme_classic(),
  se = FALSE,
  point = "mean_se",
  legend.title = "Treatments",
  posi = "top",
  textsize = 12,
  ylim = NA,
  family = "sans",
  width.bar = NA,
  pointsize = 5,
  linesize = 0.8,
  separate = c("(\"", "\")"),
  n = NA,
  DFres = NA,
  SSq = NA,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`fator1`	Numeric or complex vector with factor 1 levels
`resp`	Numerical vector containing the response of the experiment.
`fator2`	Numeric or complex vector with factor 2 levels
`color`	Graph color (*default* is NA)
`grau`	Degree of the polynomial (1,2 or 3)
`ylab`	Dependent variable name (this argument uses the *parse* function)

`xlab`	Independent variable name (this argument uses the *parse* function)
`theme`	ggplot2 theme (*default* is theme_classic())
`se`	Adds confidence interval (*default* is FALSE)
`point`	Defines whether to plot all points ("all"), mean ("mean"), mean with standard deviation ("mean_sd") or mean with standard error (*default* - "mean_se").
`legend.title`	Title legend (this argument uses the *parse* function)
`posi`	Legend position
`textsize`	Font size (*default* is 12)
`ylim`	y-axis scale
`family`	Font family (*default* is sans)
`width.bar`	width of the error bars of a regression graph.
`pointsize`	Point size (*default* is 4)
`linesize`	line size (Trendline and Error Bar)
`separate`	Separation between treatment and equation (*default* is c("(\"","\")"))
`n`	Number of decimal places for regression equations
`DFres`	Residue freedom degrees
`SSq`	Sum of squares of the residue
`print.on`	Print output
`plot.on`	Plot output

Value

Returns two or more linear, quadratic or cubic regression analyzes.

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

polynomial, polynomial2

Examples

```
dose=rep(c(0,0,0,2,2,2,4,4,4,6,6,6),3)
resp=c(8,7,5,23,24,25,30,34,36,80,90,80,
12,14,15,23,24,25,50,54,56,80,90,40,
12,14,15,3,4,5,50,54,56,80,90,40)
trat=rep(c(”A”,”B”,”C”),e=12)
polynomial2_color(dose, resp, trat, grau=c(1,2,3))
```

`pomegranate` *Dataset: Pomegranate data*

Description

An experiment was conducted with the objective of studying different products to reduce the loss of mass in postharvest of pomegranate fruits. The experiment was conducted in a completely randomized design with four replications. Treatments are: T1: External Wax; T2: External + Internal Wax; T3: External Orange Oil; T4: Internal + External Orange Oil; T5: External sodium hypochlorite; T6: Internal + External sodium hypochlorite

Usage

```
data(pomegranate)
```

Format

data.frame containing data set

`trat` Categorical vector with treatments

`WL` Numeric vector weights loss

`SS` Numeric vector solid soluble

`AT` Numeric vector titratable acidity

`ratio` Numeric vector with ratio (SS/AT)

See Also

cloro, enxofre, laranja, mirtilo, porco, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora

Examples

```
data(pomegranate)
```

`porco` *Dataset: Pig development and production*

Description

An experiment whose objective was to study the effect of castration age on the development and production of pigs, evaluating the weight of the piglets. Four treatments were studied: A - castration at 56 days of age; B - castration at 7 days of age; C - castration at 36 days of age; D - whole (not castrated); E - castration at 21 days of age. The Latin square design was used in order to control the variation between litters (lines) and the variation in the initial weight of the piglets (columns), with the experimental portion consisting of a piglet.

Usage

```
data(porco)
```

Format

data.frame containing data set

`trat` Categorical vector with treatments

`linhas` Categorical vector with lines

`colunas` Categorical vector with columns

`resp` Numeric vector

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, sensorial, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(porco)
```

PSUBDBC *Analysis: DBC experiments in split-plot*

Description

Analysis of an experiment conducted in a randomized block design in a split-plot scheme using fixed effects analysis of variance.

Usage

```
PSUBDBC(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
```

```
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  color = "rainbow",
  textsize = 12,
  labelsize = 4,
  dec = 3,
  errorbar = TRUE,
  addmean = TRUE,
  ylim = NA,
  point = "mean_se",
  fill = "lightblue",
  angle = 0,
  family = "sans",
  posi = "right",
  angle.label = 0,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`f1`	Numeric or complex vector with plot levels
`f2`	Numeric or complex vector with subplot levels
`block`	Numeric or complex vector with blocks
`response`	Numeric vector with responses
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.
`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))
`theme`	ggplot2 theme (*default* is theme_classic())

`ylab`	Variable response name (this argument uses the *parse* function)
`color`	When the columns are different colors (Set fill-in argument as "trat")
`textsize`	Font size (*default* is 12)
`labelsize`	Font size (*default* is 4)
`dec`	Number of cells (*default* is 3)
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`addmean`	Plot the average value on the graph (*default* is TRUE)
`ylim`	y-axis limit
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family (*default* is sans)
`posi`	Legend position
`angle.label`	Label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett), the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned. The function also returns a standardized residual plot.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Examples

```
#==============================
# Example tomate
#==============================
library(AgroR)
data(tomate)
with(tomate, PSUBDBC(parc, subp, bloco, resp, ylab="Dry mass (g)"))

#==============================
# Example orchard
#==============================
library(AgroR)
data(orchard)
with(orchard, PSUBDBC(A, B, Bloco, Resp, ylab="CBM"))
```

`PSUBDIC` *Analysis: DIC experiments in split-plot*

Description

Analysis of an experiment conducted in a completely randomized design in a split-plot scheme using fixed effects analysis of variance.

Usage

```
PSUBDIC(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
```

```
  names.fat = c("F1", "F2"),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  lab.factor = c("F1", "F2"),
  fill = "lightblue",
  angle = 0,
  family = "sans",
  color = "rainbow",
  errorbar = TRUE,
  addmean = TRUE,
  textsize = 12,
  labelsize = 4,
  dec = 3,
  ylim = NA,
  posi = "right",
  point = "mean_se",
  angle.label = 0,
  print.on = TRUE,
  plot.on = TRUE
)
```

Arguments

`f1`	Numeric or complex vector with plot levels
`f2`	Numeric or complex vector with subplot levels
`block`	Numeric or complex vector with blocks
`response`	Numeric vector with responses
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`quali`	Defines whether the factor is quantitative or qualitative (*qualitative*)
`names.fat`	Name of factors (this argument uses the *parse* function)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD, Scott-Knott and Duncan)
`grau`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with three elements.
`grau12`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 2, in the case of interaction f1 x f2 and qualitative factor 2 and quantitative factor 1.

`grau21`	Polynomial degree in case of quantitative factor (*default* is 1). Provide a vector with n levels of factor 1, in the case of interaction f1 x f2 and qualitative factor 1 and quantitative factor 2.
`transf`	Applies data transformation (default is 1; for log consider 0)
`constant`	Add a constant for transformation (enter value)
`geom`	Graph type (columns or segments (For simple effect only))
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`lab.factor`	Provide a vector with two observations referring to the x-axis name of factors 1 and 2, respectively, when there is an isolated effect of the factors. This argument uses ‘parse‘.
`fill`	Defines chart color (to generate different colors for different treatments, define fill = "trat")
`angle`	x-axis scale text rotation
`family`	Font family (*default* is sans)
`color`	When the columns are different colors (Set fill-in argument as "trat")
`errorbar`	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE
`addmean`	Plot the average value on the graph (*default* is TRUE)
`textsize`	Font size (*default* is 12)
`labelsize`	Label size (*default* is 4)
`dec`	Number of cells (*default* is 3)
`ylim`	y-axis limit
`posi`	Legend position
`point`	This function defines whether the point must have all points ("all"), mean ("mean"), standard deviation (*default* - "mean_sd") or mean with standard error ("mean_se") if quali= FALSE. For quali=TRUE, ‘mean_sd‘ and ‘mean_se‘ change which information will be displayed in the error bar.
`angle.label`	Label angle
`print.on`	Print output
`plot.on`	Plot output

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett), the test of multiple comparisons (Tukey, LSD, Scott-Knott or Duncan) or adjustment of regression models up to grade 3 polynomial, in the case of quantitative treatments. The column chart for qualitative treatments is also returned. The function also returns a standardized residual plot.

Note

The order of the chart follows the alphabetical pattern. Please use ‘scale_x_discrete‘ from package ggplot2, ‘limits‘ argument to reorder x-axis. The bars of the column and segment graphs are standard deviation.

In the final output when transformation (transf argument) is different from 1, the columns resp and respo in the mean test are returned, indicating transformed and non-transformed mean, respectively.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Examples

```
#===================================
# Example tomate
#===================================
# Obs. Consider that the "tomato" experiment is a completely randomized design.
library(AgroR)
data(tomate)
with(tomate, PSUBDIC(parc, subp, bloco, resp, ylab="Dry mass (g)"))
```

PSUBFAT2DBC *Analysis: Plot subdivided into randomized blocks with a subplot in a double factorial scheme*

Description

This function performs the analysis of a randomized block design in a split-plot with a subplot in a double factorial scheme.

Usage

```
PSUBFAT2DBC(
  f1,
  f2,
  f3,
  block,
  resp,
  alpha.f = 0.05,
  alpha.t = 0.05,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey"
)
```

Arguments

`f1`	Numeric or complex vector with plot levels
`f2`	Numeric or complex vector with splitplot levels
`f3`	Numeric or complex vector with splitsplitplot levels
`block`	Numeric or complex vector with blocks
`resp`	Numeric vector with responses
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`norm`	Error normality test (*default* is Shapiro-Wilk)
`homog`	Homogeneity test of variances (*default* is Bartlett)
`mcomp`	Multiple comparison test (Tukey (*default*), LSD and Duncan)

Value

Analysis of variance of fixed effects and multiple comparison test of Tukey, Scott-Knott, LSD or Duncan.

Examples

```
f1=rep(c("PD","PDE","C"), e = 40);f1=factor(f1,unique(f1))
f2=rep(c(300,400), e = 20,3);f2=factor(f2,unique(f2))
f3=rep(c("c1", "c2", "c3", "c4"), e = 5,6);f3=factor(f3,unique(f3))
bloco=rep(paste("B",1:5),24); bloco=factor(bloco,unique(bloco))
set.seed(10)
resp=rnorm(120,50,5)
PSUBFAT2DBC(f1,f2,f3,bloco,resp,alpha.f = 0.5) # force triple interaction
PSUBFAT2DBC(f1,f2,f3,bloco,resp,alpha.f = 0.4) # force double interaction
```

PSUBSUBDBC *Analysis: DBC experiments in split-split-plot*

Description

Analysis of an experiment conducted in a randomized block design in a split-split-plot scheme using analysis of variance of fixed effects.

Usage

```
PSUBSUBDBC(
  f1,
  f2,
  f3,
  block,
  response,
  alpha.f = 0.05,
  alpha.t = 0.05,
  dec = 3,
  mcomp = "tukey"
)
```

Arguments

`f1`	Numeric or complex vector with plot levels
`f2`	Numeric or complex vector with splitplot levels
`f3`	Numeric or complex vector with splitsplitplot levels
`block`	Numeric or complex vector with blocks
`response`	Numeric vector with responses
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`alpha.t`	Significance level of the multiple comparison test (*default* is 0.05)
`dec`	Number of cells
`mcomp`	Multiple comparison test (Tukey (*default*), LSD and Duncan)

Value

Analysis of variance of fixed effects and multiple comparison test of Tukey, LSD or Duncan.

Note

The PSUBSUBDBC function does not present residual analysis, interaction breakdown, graphs and implementations of various multiple comparison or regression tests. The function only returns the analysis of variance and multiple comparison test of Tukey, LSD or Duncan.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
library(AgroR)
data(enxofre)
with(enxofre, PSUBSUBDBC(f1, f2, f3, bloco, resp))
```

`quant.fat2.desd` *Analysis: Polynomial splitting for double factorial in DIC and DBC*

Description

Splitting in polynomials for double factorial in DIC and DBC. Note that f1 must always be qualitative and f2 must always be quantitative. This function is an easier way to visualize trends for dual factor schemes with a quantitative and a qualitative factor.

Usage

```
quant.fat2.desd(factors = list(f1, f2, block), response, dec = 3)
```

Arguments

`factors`	Define f1 and f2 and/or block factors in list form. Please note that in the list it is necessary to write ‘f1‘, ‘f2‘ and ‘block‘. See example.
`response`	response variable
`dec`	Number of cells

Value

Returns the coefficients of the linear, quadratic and cubic models, the p-values of the t test for each coefficient (p.value.test) and the p-values for the linear, quadratic, cubic model splits and the regression deviations.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

See Also

FAT2DIC, FAT2DBC

Examples

```
library(AgroR)
data(cloro)
quant.fat2.desd(factors = list(f1=cloro$f1,
f2=rep(c(1:4),e=5,2), block=cloro$bloco),
response=cloro$resp)
```

`seg_graph` *Graph: Point graph for one factor*

Description

This is a function of the point graph for one factor

Usage

```
seg_graph(model, fill = "lightblue", horiz = TRUE, pointsize = 4.5)
```

Arguments

`model`	DIC, DBC or DQL object
`fill`	fill bars
`horiz`	Horizontal Column (*default* is TRUE)
`pointsize`	Point size

Value

Returns a point chart for one factor

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

barplot_positive, plot_TH, corgraph, spider_graph, line_plot

Examples

```
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
       mcomp = "sk",angle=45,sup=10,
       ylab = "Number of fruits/plants"))
seg_graph(a,horiz = FALSE)
```

`seg_graph2` *Graph: Point graph for one factor model 2*

Description

This is a function of the point graph for one factor

Usage

```
seg_graph2(
  model,
  theme = theme_gray(),
  pointsize = 4,
  pointshape = 16,
  horiz = TRUE,
  vjust = -0.6
)
```

Arguments

`model`	DIC, DBC or DQL object
`theme`	ggplot2 theme
`pointsize`	Point size
`pointshape`	Format point (default is 16)
`horiz`	Horizontal Column (*default* is TRUE)
`vjust`	vertical adjusted

Value

Returns a point chart for one factor

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

barplot_positive, plot_TH, corgraph, spider_graph, line_plot

Examples

```
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
       mcomp = "sk",angle=45,
       ylab = "Number of fruits/plants"))
seg_graph2(a,horiz = FALSE)
```

`sensorial` *Dataset: Sensorial data*

Description

Set of data from a sensory analysis with six participants in which different combinations (blend) of the grape cultivar bordo and niagara were evaluated. Color (CR), aroma (AR), flavor (SB), body (CP) and global (GB) were evaluated. The data.frame presents the averages of the evaluators.

Usage

```
data(sensorial)
```

Format

data.frame containing data set

`Blend`	Categorical vector with treatment
`variable`	Categorical vector with variables
`resp`	Numeric vector

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, simulate1, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(sensorial)
```

`simulate1` *Dataset: Simulated data dict*

Description

Simulated data from a completely randomized experiment with multiple assessments over time

Usage

```
data(simulate1)
```

Format

data.frame containing data set

`tempo`	Categorical vector with time
`trat`	Categorical vector with treatment
`resp`	Categorical vector with response

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate2, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(simulate1)
```

`simulate2` *Dataset: Simulated data dbct*

Description

Simulated data from a latin square experiment with multiple assessments over time

Usage

```
data(simulate2)
```

Format

data.frame containing data set

`tempo`	Categorical vector with time
`trat`	Categorical vector with treatment
`bloco`	Categorical vector with block
`resp`	Categorical vector with response

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate3, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(simulate2)
```

`simulate3` *Dataset: Simulated data dqlt*

Description

Simulated data from a completely randomized experiment with multiple assessments over time

Usage

```
data(simulate3)
```

Format

data.frame containing data set

- `tempo` Categorical vector with time
- `trat` Categorical vector with treatment
- `linhas` Categorical vector with line
- `colunas` Categorical vector with column
- `resp` Categorical vector with response

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, tomate, weather, phao, passiflora, aristolochia

Examples

```
data(simulate3)
```

sketch *Utils: Experimental sketch*

Description

Experimental sketching function

Usage

```
sketch(
  trat,
  trat1 = NULL,
  trat2 = NULL,
  r,
  design = "DIC",
  pos = "line",
  color.sep = "all",
  ID = FALSE,
  print.ID = TRUE,
  add.streets.y = NA,
  add.streets.x = NA,
  label.x = "",
  label.y = "",
  axissize = 12,
  legendsize = 12,
  labelsize = 4,
  export.csv = FALSE,
  comment.caption = NULL
)
```

Arguments

`trat`	Vector with factor A levels
`trat1`	Vector with levels of factor B (Set to NULL if not factorial or psub)
`trat2`	Vector with levels of factor C (Set to NULL if not factorial)
`r`	Number of repetitions
`design`	Experimental design (see note)
`pos`	Repeat position (line or column),
`color.sep`	Color box
`ID`	plot Add only identification in sketch
`print.ID`	Print table ID
`add.streets.y`	Adds streets by separating treatments in row or column. The user must supply a numeric vector grouping the rows or columns that must be together. See the example.

`add.streets.x`	Adds streets by separating treatments in row or column. The user must supply a numeric vector grouping the rows or columns that must be together. See the example.
`label.x`	text in x
`label.y`	text in y
`axissize`	Axis size
`legendsize`	Title legend size
`labelsize`	Label size
`export.csv`	Save table template based on sketch in csv
`comment.caption`	Add comment in caption

Value

Returns an experimental sketch according to the specified design.

Note

The sketches have only a rectangular shape, and the blocks (in the case of randomized blocks) can be in line or in a column.

For the design argument, you can choose from the following options:

`design="DIC"`	Completely randomized design
`design="DBC"`	Randomized block design
`design="DQL"`	Latin square design
`design="FAT2DIC"`	DIC experiments in double factorial
`design="FAT2DBC"`	DBC experiments in double factorial
`design="FAT3DIC"`	DIC experiments in triple factorial
`design="FAT3DBC"`	DBC experiments in triple factorial
`design="PSUBDIC"`	DIC experiments in split-plot
`design="PSUBDBC"`	DBC experiments in split-plot
`design="PSUBSUBDBC"`	DBC experiments in split-split-plot
`design="STRIP-PLOT"`	Strip-plot DBC experiments

For the color.sep argument, you can choose from the following options:

`design="DIC"`	use "all" or "none"
`design="DBC"`	use "all","bloco" or "none"
`design="DQL"`	use "all", "column", "line" or "none"
`design="FAT2DIC"`	use "all", "f1", "f2" or "none"
`design="FAT2DBC"`	use "all", "f1", "f2", "block" or "none"
`design="FAT3DIC"`	use "all", "f1", "f2", "f3" or "none"
`design="FAT3DBC"`	use "all", "f1", "f2", "f3", "block" or "none"
`design="PSUBDIC"`	use "all", "f1", "f2" or "none"
`design="PSUBDBC"`	use "all", "f1", "f2", "block" or "none"
`design="PSUBSUBDBC"`	use "all", "f1", "f2", "f3", "block" or "none"

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

Mendiburu, F., & de Mendiburu, M. F. (2019). Package 'agricolae'. R Package, Version, 1-2.

Examples

```
Trat=paste("Tr",1:6)

#=============================
# Completely randomized design
#=============================
sketch(Trat,r=3)
sketch(Trat,r=3,pos="column")
sketch(Trat,r=3,color.sep="none")
sketch(Trat,r=3,color.sep="none",ID=TRUE,print.ID=TRUE)
sketch(Trat,r=3,pos="column",add.streets.x=c(1,1,2,2,3,3))

#=============================
# Randomized block design
#=============================
sketch(Trat, r=3, design="DBC")
sketch(Trat, r=3, design="DBC",pos="column")
sketch(Trat, r=3, design="DBC",pos="column",add.streets.x=c(1,1,2))
sketch(Trat, r=3, design="DBC",pos="column",add.streets.x=c(1,2,3), add.streets.y=1:6)
sketch(Trat, r=3, design="DBC",pos="line",add.streets.y=c(1,2,3), add.streets.x=1:6)

#=============================
# Completely randomized experiments in double factorial
#=============================
sketch(trat=c("A","B"),
       trat1=c("A","B","C"),
       design = "FAT2DIC",
       r=3)

sketch(trat=c("A","B"),
       trat1=c("A","B","C"),
       design = "FAT2DIC",
       r=3,
       pos="column")
```

---

sk_graph *Graph: Scott-Knott graphics*

Description

This is a function of the bar graph for the Scott-Knott test

Usage

```
sk_graph(model, horiz = TRUE, fill.label = "lightyellow")
```

Arguments

`model`	DIC, DBC or DQL object
`horiz`	Horizontal Column (*default* is TRUE)
`fill.label`	fill Label box fill color

Value

Returns a bar chart with columns separated by color according to the Scott-Knott test

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

barplot_positive, plot_TH, corgraph, spider_graph, line_plot

Examples

```
data("laranja")
a=with(laranja, DBC(trat, bloco, resp,
       mcomp = "sk",angle=45,
       ylab = "Number of fruits/plants"))
sk_graph(a,horiz = FALSE)
library(ggplot2)
sk_graph(a,horiz = TRUE)+scale_fill_grey(start=1,end=0.5)
```

`soybean` *Dataset: Soybean*

Description

An experiment was carried out to evaluate the grain yield (kg ha-1) of ten different commercial soybean cultivars in the municipality of Londrina/Parana. The experiment was carried out in the design of randomized complete blocks with four replicates per treatment.

Usage

```
data("soybean")
```

Format

data.frame containing data set

`cult`	numeric vector with treatment
`bloc`	numeric vector with block
`prod`	Numeric vector with grain yield

See Also

cloro, laranja, enxofre, laranja, mirtilo, passiflora, phao, porco, pomegranate, simulate1, simulate2, simulate3, tomate, weather

Examples

```
data(soybean)
```

`spider_graph` *Graph: Spider graph for sensorial analysis*

Description

Spider chart or radar chart. Usually used for graphical representation of acceptability in sensory tests

Usage

```
spider_graph(
  resp,
  vari,
  blend,
  legend.title = "",
  xlab = "",
  ylab = "",
  ymin = 0
)
```

Arguments

`resp`	Vector containing notes
`vari`	Vector containing the variables
`blend`	Vector containing treatments
`legend.title`	Caption title

`xlab`	x axis title (this argument uses the *parse* function)
`ylab`	y axis title (this argument uses the *parse* function)
`ymin`	Minimum value of y

Value

Returns a spider or radar chart. This graph is commonly used in studies of sensory analysis.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

sk_graph, plot_TH, corgraph, barplot_positive, line_plot

Examples

```
library(AgroR)
data(sensorial)
with(sensorial, spider_graph(resp, variable, Blend))
```

STRIPLOT *Analysis: DBC experiments in strip-plot*

Description

Analysis of an experiment conducted in a block randomized design in a strit-plot scheme using fixed effects analysis of variance.

Usage

```
STRIPLOT(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  alpha.f = 0.05,
  transf = 1,
  textsize = 12,
  labelsize = 4,
  constant = 0
)
```

Arguments

`f1`	Numeric or complex vector with plot levels
`f2`	Numeric or complex vector with subplot levels
`block`	Numeric or complex vector with blocks
`response`	Numeric vector with responses
`norm`	Error normality test (*default* is Shapiro-Wilk)
`alpha.f`	Level of significance of the F test (*default* is 0.05)
`transf`	Applies data transformation (default is 1; for log consider 0)
`textsize`	Font size (*default* is 12)
`labelsize`	Label size (*default* is 4)
`constant`	Add a constant for transformation (enter value)

Value

The table of analysis of variance, the test of normality of errors (Shapiro-Wilk, Lilliefors, Anderson-Darling, Cramer-von Mises, Pearson and Shapiro-Francia), the test of homogeneity of variances (Bartlett). The function also returns a standardized residual plot.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

Ramalho M.A.P., Ferreira D.F., Oliveira A.C. 2000. Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA.

Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. Biometrics, 30, 507-512.

Examples

```
#===================================
# Example tomate
#===================================
# Obs. Consider that the "tomato" experiment is a block randomized design in strip-plot.
library(AgroR)
data(tomate)
with(tomate, STRIPLOT(parc, subp, bloco, resp))
```

`summarise_anova` *Utils: Summary of Analysis of Variance and Test of Means*

Description

Summarizes the output of the analysis of variance and the multiple comparisons test for completely randomized (DIC), randomized block (DBC) and Latin square (DQL) designs.

Usage

```
summarise_anova(
  analysis,
  inf = "p",
  design = "DIC",
  round = 3,
  divisor = FALSE
)
```

Arguments

`analysis`	List with the analysis outputs of the DIC, DBC, DQL, FAT2DIC, FAT2DBC, PSUBDIC and PSUBDBC functions
`inf`	Analysis of variance information (can be "p", "f", "QM" or "SQ")
`design`	Type of experimental project (DIC, DBC, DQL, FAT2DIC, FAT2DBC, PSUBDIC or PSUBDBC)
`round`	Number of decimal places
`divisor`	Add divider between columns

Value

returns a data.frame or print with a summary of the analysis of several experimental projects.

Note

Adding table divider can help to build tables in microsoft word. Copy console output, paste into MS Word, Insert, Table, Convert text to table, Separated text into:, Other: `|`.

The column names in the final output are imported from the ylab argument within each function.

This function is only for declared qualitative factors. In the case of a quantitative factor and the other qualitative in projects with two factors, this function will not work.

Triple factorials and split-split-plot do not work in this function.

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Examples

```
library(AgroR)

#=====================================
# DIC
#=====================================
data(pomegranate)
attach(pomegranate)
a=DIC(trat, WL, geom = "point", ylab = "WL")
b=DIC(trat, SS, geom = "point", ylab="SS")
c=DIC(trat, AT, geom = "point", ylab = "AT")
summarise_anova(analysis = list(a,b,c), divisor = TRUE)
library(knitr)
kable(summarise_anova(analysis = list(a,b,c), divisor = FALSE))

#=====================================
vari=c("WL","SS","AT")
output=lapply(vari,function(x){
output=DIC(trat,response = unlist(pomegranate[,x]),ylab = parse(text=x),print.on=FALSE)})
summarise_anova(analysis = output, divisor = TRUE)

#=====================================
# DBC
#=====================================
data(soybean)
attach(soybean)
a=DBC(cult,bloc,prod,ylab = "Yield")
summarise_anova(list(a),design = "DBC")

#=====================================
# FAT2DIC
#=====================================
data(corn)
attach(corn)
a=FAT2DIC(A, B, Resp, quali=c(TRUE, TRUE))
summarise_anova(list(a),design="FAT2DIC")
```

`summarise_conj` *Utils: Summary of Analysis of Variance and Test of Means for Joint analysis*

Description

Summarizes the output of the analysis of variance and the multiple comparisons test for completely randomized (DIC) and randomized block (DBC) designs for Joint analysis with qualitative factor.

Usage

```
summarise_conj(analysis, design = "DBC", info = "p")
```

Arguments

`analysis`	List with the analysis outputs of the conjdic and conjdbc functions
`design`	Type of experimental project (DIC or DBC)
`info`	Analysis of variance information (can be "p", "f", "QM" or "SQ")

Note

The column names in the final output are imported from the ylab argument within each function.

This function is only for declared qualitative factors. In the case of a quantitative factor and the other qualitative in projects with two factors, this function will not work.

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Examples

```
library(AgroR)
data(mirtilo)
set.seed(1); resp1=rnorm(36,10,4)
set.seed(4); resp2=rnorm(36,10,3)
set.seed(8); resp3=rnorm(36,100,40)
type1=with(mirtilo, conjdbc(trat, bloco, exp, resp, ylab = "var1"))
type2=with(mirtilo, conjdbc(trat, bloco, exp, resp1, ylab = "var2"))
type3=with(mirtilo, conjdbc(trat, bloco, exp, resp2, ylab = "var3"))
type4=with(mirtilo, conjdbc(trat, bloco, exp, resp3, ylab = "var4"))
summarise_conj(analysis = list(type1,type2,type3,type4))
```

`summarise_dunnett` *Utils: Dunnett's Test Summary*

Description

Performs a summary in table form from a list of Dunnett's test outputs

Usage

```
summarise_dunnett(variable, colnames = NA, info = "sig")
```

Arguments

`variable`	List object Dunnett test
`colnames`	Names of column
`info`	Information of table

Value

A summary table from Dunnett's test is returned

Examples

```
library(AgroR)
data("pomegranate")
a=with(pomegranate,dunnett(trat=trat,resp=WL,control="T1"))
b=with(pomegranate,dunnett(trat=trat,resp=SS,control="T1"))
c=with(pomegranate,dunnett(trat=trat,resp=AT,control="T1"))
d=with(pomegranate,dunnett(trat=trat,resp=ratio,control="T1"))
summarise_dunnett(list(a,b,c,d))
```

`tabledesc` *Descriptive: Table descritive analysis*

Description

Function for generating a data.frame with averages or other descriptive measures grouped by a categorical variable

Usage

```
tabledesc(data, fun = mean)
```

Arguments

`data`	data.frame containing the first column with the categorical variable and the remaining response columns
`fun`	Function of descriptive statistics (default is mean)

Value

Returns a data.frame with a measure of dispersion or position from a dataset and separated by a factor

Author(s)

Gabriel Danilo Shimizu, <`gabrield.shimizu@gmail.com`>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
data(pomegranate)
tabledesc(pomegranate)
library(knitr)
kable(tabledesc(pomegranate))
```

`TBARPLOT.reverse` *Graph: Reverse graph of DICT, DBCT and DQL output when geom="bar"*

Description

The function performs the construction of a reverse graph on the output of DICT, DBCT and DQL when geom="bar".

Usage

```
TBARPLOT.reverse(plot.t)
```

Arguments

`plot.t`	DICT, DBCT or DQLT output when geom="bar"

Value

Returns a reverse graph of the output of DICT, DBCT or DQLT when geom="bar".

Note

All layout and subtitles are imported from DICT, DBCT and DQLT functions

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

See Also

DICT, DBCT, DQLT

Examples

```
data(simulate1)
a=with(simulate1, DICT(trat, tempo, resp,geom="bar",sup=40))
TBARPLOT.reverse(a)
```

`test_two` *Analysis: Test for two samples*

Description

Test for two samples (paired and unpaired t test, paired and unpaired Wilcoxon test)

Usage

```
test_two(
  trat,
  resp,
  paired = FALSE,
  correct = TRUE,
  test = "t",
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  var.equal = FALSE,
  pointsize = 2,
  yposition.p = NA,
  xposition.p = NA,
  fill = "white"
)
```

Arguments

`trat`	Categorical vector with the two treatments
`resp`	Numeric vector with the response
`paired`	A logical indicating whether you want a paired t-test.
`correct`	A logical indicating whether to apply continuity correction in the normal approximation for the p-value.
`test`	Test used (t for test t or w for Wilcoxon test)
`alternative`	A character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
`conf.level`	Confidence level of the interval.
`theme`	ggplot2 theme (*default* is theme_classic())
`ylab`	Variable response name (this argument uses the *parse* function)
`xlab`	Treatments name (this argument uses the *parse* function)
`var.equal`	A logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.

`pointsize`	Point size
`yposition.p`	Position p-value in y
`xposition.p`	Position p-value in x
`fill`	fill box

Details

Alternative = "greater" is the alternative that x has a larger mean than y. For the one-sample case: that the mean is positive.

If paired is TRUE then both x and y must be specified and they must be the same length. Missing values are silently removed (in pairs if paired is TRUE). If var.equal is TRUE then the pooled estimate of the variance is used. By default, if var.equal is FALSE then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

If the input data are effectively constant (compared to the larger of the two means) an error is generated.

Value

Returns the test for two samples (paired or unpaired t test, paired or unpaired Wilcoxon test)

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

Examples

```
resp=rnorm(100,100,5)
trat=rep(c("A","B"),e=50)
test_two(trat,resp)
test_two(trat,resp,paired = TRUE)
```

`tomate` *Dataset: Tomato data*

Description

An experiment conducted in a randomized block design in a split plot scheme was developed in order to evaluate the efficiency of bacterial isolates in the development of tomato cultivars. The experiment counted a total of 24 trays; each block (in a total of four blocks), composed of 6 trays, in which each tray contained a treatment (6 isolates). Each tray was seeded with 4 different genotypes, each genotype occupying 28 cells per tray. The trays were randomized inside each block and the genotypes were randomized inside each tray.

Usage

```
data(tomate)
```

Format

data.frame containing data set

`parc`	Categorical vector with plot
`subp`	Categorical vector with split-plot
`bloco`	Categorical vector with block
`resp`	Numeric vector

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, weather, aristolochia, phao, passiflora

Examples

```
data(tomate)
```

`tonetest` *Analysis: t test to compare means with a reference value*

Description

Sometimes the researcher wants to test whether the treatment mean is greater than/equal to or less than a reference value. For example, I want to know if the average productivity of my treatment is higher than the average productivity of a given country. For this, this function allows comparing the means with a reference value using the t test.

Usage

```
tonetest(response, trat, mu = 0, alternative = "two.sided", conf.level = 0.95)
```

Arguments

`response`	Numerical vector containing the response of the experiment.
`trat`	Numerical or complex vector with treatments
`mu`	A number indicating the true value of the mean
`alternative`	A character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less"
`conf.level`	confidence level of the interval.

Value

returns a list with the mean per treatment, maximum, minimum, sample standard deviation, confidence interval, t-test statistic and its p-value.

Note

No treatment can have zero variability. Otherwise the function will result in an error.

Author(s)

Gabriel Danilo Shimizu, <gabrield.shimizu@gmail.com>

Examples

```
library(AgroR)
data("pomegranate")
tonetest(resp=pomegranate$WL,
trat=pomegranate$trat,
mu=2,
alternative = "greater")
```

`transf` *Utils: Data transformation (Box-Cox, 1964)*

Description

Estimates the lambda value for data transformation

Usage

```
transf(response, f1, f2 = NA, f3 = NA, block = NA, line = NA, column = NA)
```

Arguments

`response`	Numerical vector containing the response of the experiment.
`f1`	Numeric or complex vector with factor 1 levels
`f2`	Numeric or complex vector with factor 2 levels
`f3`	Numeric or complex vector with factor 3 levels
`block`	Numerical or complex vector with blocks
`line`	Numerical or complex vector with lines
`column`	Numerical or complex vector with columns

Value

Returns the value of lambda and/or data transformation approximation, according to Box-Cox (1964)

Author(s)

Gabriel Danilo Shimizu, `<gabrield.shimizu@gmail.com>`

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

References

Box, G. E., Cox, D. R. (1964). An analysis of transformations. Journal of the Royal Statistical Society: Series B (Methodological), 26(2), 211-243.

Examples

```
#===============================================================
# Completely randomized design
#===============================================================
data("pomegranate")
with(pomegranate, transf(WL,f1=trat))

#===============================================================
# Randomized block design
#===============================================================
data(soybean)
with(soybean, transf(prod, f1=cult, block=bloc))

#===============================================================
# Completely randomized design in double factorial
#===============================================================
data(cloro)
with(cloro, transf(resp, f1=f1, f2=f2))

#===============================================================
# Randomized block design in double factorial
#===============================================================
data(cloro)
with(cloro, transf(resp, f1=f1, f2=f2, block=bloco))
```

`weather` *Dataset: Weather data*

Description

Climatic data from 01 November 2019 to 30 June 2020 in the municipality of Londrina-PR, Brazil. Data from the Instituto de Desenvolvimento Rural do Parana (IDR-PR)

Usage

```
data(weather)
```

Format

data.frame containing data set

`Data` POSIXct vector with dates

`tempo` Numeric vector with time

`Tmax` Numeric vector with maximum temperature

`Tmed` Numeric vector with mean temperature

`Tmin` Numeric vector with minimum temperature

`UR` Numeric vector with relative humidity

See Also

cloro, enxofre, laranja, mirtilo, pomegranate, porco, sensorial, simulate1, simulate2, simulate3, tomate, aristolochia, phao, passiflora

Examples

```
data(weather)
```

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