Package ‘AgroR’

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Type Package

Title Experimental Statistics and Graphics for Agricultural Sciences

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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).

Encoding UTF-8

RoxygenNote 7.2.0

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

Suggests DT, knitr, rmarkdown, roxygen2

Depends R (>= 3.6.0)

License GPL (>= 2)


NeedsCompilation no
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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, <shimizu@uel.br>

References

See Also
transf, sketch
Examples

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

data = 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(data) = c(1, 2, 3, 4, 5, 6)
data

data = aacp(data)
trat = simulate1$trat[simulate1$tempo == 1]

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 35°C) 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)

**Description**

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

**Usage**

```r
def facets(
    model,
    facet = NULL,
    theme = theme_gray(),
    geom = "bar",
    fill = "lightblue",
    pointsize = 4.5,
    width.bar = 0.15
)
```

**Arguments**

- `model`
  - DIC, DBC or DQL object
- `facet`
  - vector with facets
- `theme`
  - ggplot2 theme
- `geom`
  - graph type (columns or segments)
- `fill`
  - fill bars
- `pointsize`
  - Point size
- `width.bar`
  - width of the error bars of a regression graph.

**Value**

Returns a bar chart for one factor

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
Examples

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

Description

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

Usage

```r
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 bar
- `sup`: Number of units above the standard deviation or average bar on the graph

Value

Returns a column chart grouped by facets
Examples

```r
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"), occult.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**

```r
bargraph_twofactor(
  analysis,
  labels = NULL,
  occult.facet = FALSE,
  occult.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
- **occult.facet**: Hide facets
- **occult.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

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

barplot_positive

<table>
<thead>
<tr>
<th>Graph: Positive barplot</th>
</tr>
</thead>
</table>

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

```r
barplot_positive(
  a,
  b,
  ylab = "Response",
  var_name = c("Var1", "Var2"),
  legend.title = "Variable",
  fill_color = c("darkgreen", "brown")
)
```

Arguments

- `a`: Object of DIC, DBC or DQL functions
- `b`: Object of DIC, DBC or DQL functions
- `ylab`: Y axis names
- `var_name`: Name of the variable
- `legend.title`: Legend title
- `fill_color`: Bar fill color

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, <shimizu@uel.br>
See Also

radargraph, 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)”)
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",
   legend = "Stages",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=resp))
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)

Arguments

model DIC, DBC or DQL object
fill fill bars
horiz Horizontal Column (default is TRUE)

Value

Returns a bar chart for one factor

Author(s)

Gabriel Danilo Shimizu, <shimizu@ue1.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
bar_graph2

See Also
radargraph, 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)

Description
This is a function of the bar graph for one factor

Usage
bar_graph2(
  model,  # DIC, DBC or DQL object
  point.color = "black",  # Point color
  point.size = 2,  # Point size
  point.shape = 16,  # Format point
  text.color = "black",  # Text color
  label.color = "black",  # Label color
  bar.color = "black",  # Bar color
  title.size = 14,  # Title size
  y.text = 0,  # Y-text
  add.info = NA,  # Add info
  y.info = 0,  # Y-info
  color.info = "black",  # Color info
  fill = "lightblue"  # Fill
)

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
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)

<table>
<thead>
<tr>
<th>cloro</th>
<th>Dataset: Sodium dichloroisocyanurate in soybean</th>
</tr>
</thead>
</table>

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
confinterval

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**

```r
conjdbc(
  trat,  
  block,  
  local,  
  response,  
  transf = 1,  
  norm = "sw",  
  homog = "bt",  
  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)
- **norm**: Error normality test (default is Shapiro-Wilk)
- **homog**: Homogeneity test of variances (default is Bartlett)
- **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 (Accepts the expression() function)
title  Graph title
xlab  Treatments name (Accepts the expression() 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
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)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References
Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

Examples

```r
library(AgroR)
data(mirtilo)
with(mirtilo, conjdbc(trat, bloco, 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**

```r
conjdic(
  trat,
  repet,
  local,
  response,
  transf = 1,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  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).
- **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).
- **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 (Accepts the expression() function).
- **title**: Graph title.
- **xlab**: Treatments name (Accepts the expression() 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**

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)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References
Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

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

---
corgraph

Graph: Correlogram

Description
Correlation analysis function (Pearson or Spearman)

Usage
corgraph(
data, 
aixissize = 12, 
legendsize = 12, 
legendposition = c(0.9, 0.2), 
legendtitle = "Correlation", 
method = "pearson"
)
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)

Value

The function returns a correlation matrix

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

```r
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

```r
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

```r
data(corn)
```

---

**cor_ic**

Graph: Plot Pearson correlation with interval of confidence

**Description**

Plot Pearson correlation with interval of confidence

**Usage**

```r
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)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
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)
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

```r
DBC(
  trat,  # Numerical or complex vector with treatments
  block,
  response,
  norm = "sw",  # Normality test
  homog = "bt",  # Homogeneity test
  alpha.f = 0.05,  # Type I error for F-test
  alpha.t = 0.05,  # Type I error for t-test
  quali = TRUE,  # Qualitative factor
  mcomp = "tukey",  # Multiple comparisons test
  grau = 1,  # Graphical output
  transf = 1,  # Data transformation
  constant = 0,  # Constant for transformation
  test = "parametric",  # Test type
  geom = "bar",  # Geometric representation
  theme = theme_classic(),  # Theme customization
  sup = NA,  # Superscript
  CV = TRUE,  # Confidence intervals
  ylab = "response",  # Y-axis label
  xlab = "",  # X-axis label
  textsize = 12,  # Text size
  labelsize = 4,  # Label size
  fill = "lightblue",  # Fill color
  angle = 0,  # Angle of text
  family = "sans",  # Font family
  dec = 3,  # Decimal places
  addmean = TRUE,  # Add mean
  errorbar = TRUE,  # Add error bars
  posi = "top",  # Position of bars
  point = "mean_sd",  # Symbol for point
  angle.label = 0  # Angle of label
)
```

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 (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
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

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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


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=expression("Grain yield"~(kg~ha^-1))))

---

**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**

```r
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 (Accepts the `expression()` function)
- **xlab**: Treatments name (Accepts the `expression()` 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)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

**Examples**

```r
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")
```
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

```r
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 ("ltd"), 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 (Accepts the expression() function)

**xlab**  Treatments name (Accepts the expression() 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)

**legend**  Legend title

**ylim**  y-axis scale

**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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Gonçalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


See Also

DBC, DICT, DQLT

Examples

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

#===================================
# default
#===================================
DBCT(trat, bloco, tempo, resp)

#===================================
# 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

```r
desc(trat, response, ylab = "Response", xlab = "Treatment", ylim = NA)
```
desc2fat

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)
- **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)

- Gabriel Danilo Shimizu, <shimizu@uel.br>
- Leandro Simoes Azeredo Goncalves
- Rodrigo Yudi Palhaci Marubayashi

See Also

- `desc2fat`, `tabledesc`, `dispvar`

Examples

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

---

**Description**

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

**Usage**

```r
desc2fat(f1, f2, response, ylab = "Response", theme = theme_classic())
```
desc3fat

Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

library(AgroR)
data(cloro)
with(cloro, desc2fat(f1,f2,resp))

desc3fat
**Description**

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

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>f1</td>
<td>Numeric or complex vector with factor 1 levels</td>
</tr>
<tr>
<td>f2</td>
<td>Numeric or complex vector with factor 2 levels</td>
</tr>
<tr>
<td>f3</td>
<td>Numeric or complex vector with factor 3 levels</td>
</tr>
<tr>
<td>response</td>
<td>Numerical vector containing the response of the experiment.</td>
</tr>
<tr>
<td>legend.title</td>
<td>Legend title</td>
</tr>
<tr>
<td>xlab</td>
<td>x name (Accepts the expression() function)</td>
</tr>
</tbody>
</table>
DIC

ylab Variable response name (Accepts the `expression()` function)
theme ggplot theme
plot "interaction" or "box"

Value

The function returns a triple interaction graph.

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

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

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

```r
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,
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.
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 "nonparametric" - non-parametric test
mcompNP Multiple comparison test (LSD (default) or dunn)
geom Graph type (columns, boxes or segments)
theme ggplot2 theme (default is theme_classic())
ylab Variable response name (Accepts the expression() 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 (Accepts the expression() 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"). For quali=FALSE or quali=TRUE.
angle.label label angle

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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
References

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


W.J. Conover, Practical Nonparametrics Statistics. 1999


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"))

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

#=============================  
# data transformation  
#=============================

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

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

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**Examples**

```r
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")

**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**

```r
DIC(  
  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 (Accepts the expression() function)

ylab  Variable response name (Accepts the expression() function)


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  y-axis scale

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)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References
Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

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, 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",
)
DQL

```r
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)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

**Examples**

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

---

**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,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  angle.label = 0
)

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)
alpfa.f Level of significance of the F test (default is 0.05)
alpfa.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)
graufdegree of polynomial in case of quantitative factor (default is 1)
transfdata transformation (default is 1; for log consider 0; ‘angular’ for angular transformation)
constantadd a constant for transformation (enter value)
geomgraph type (columns, boxes or segments)
themeggpplot2 theme (default is theme_classic())
supnumber of units above the standard deviation or average bar on the graph
CVplotting the coefficient of variation and p-value of anova (default is TRUE)
ylabvariable response name (accepts the expression() function)
xlabtreatments name (accepts the expression() function)
textsizefont size
labelsize label size
fill defines chart color (to generate different colors for different treatments, define fill = "trat")
agelex-axis scale text rotation
familyfont family
decnnumber of cells
addmeanplot the average value on the graph (default is TRUE)
errorbarplot the standard deviation bar on the graph (in the case of a segment and column graph) - default is TRUE
posielegend position
pointdefines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - default) or mean with standard error (default - "mean_se").
angle.labellabel angle

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)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

**References**

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


**See Also**

DIC, DBC

**Examples**

```r
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**

```r
DQLT(
  trat,
  line,
  column,
  time,
  response,
  alpha.f = 0.05,
)```
alpha.t = 0.05,
mcomp = "tukey",
error = TRUE,
xlab = "Independent",
ylab = "Response",
textsize = 12,
labels = 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 (Accepts the expression() function)
ylab Variable response name (Accepts the expression() function)
textsize Font size of the texts and titles of the axes
labels 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         y-axis scale
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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999
See Also

DQL, DICT, DBCT

Examples

```r
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

```r
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, <shimizu@uel.br>

Examples

```r
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",
  fontfamily = "sans"
)

Arguments

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

```r
#====================================================
# complete randomized design
#====================================================
# Data: Pomegranate
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",
legend = "Stages", 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", 
        bloco=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.
enxofre

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)

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)

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),
    mcomp = "tukey",
    grau = c(NA, NA),
    grau12 = NA,
    grau21 = NA,
    transf = 1,
    constant = 0,
    geom = "bar",
    theme = theme_classic(),
    ylab = "Response",
    xlab = "",
    xlab.factor = c("F1", "F2"),
    legend = "Legend",
    fill = "lightblue",
    angle = 0,
    textsize = 12,
    labelsize = 4,
    dec = 3,
    family = "sans",
    point = "mean_sd",
    addmean = TRUE,
    errorbar = TRUE,
    CV = TRUE,
    sup = NA,
color = "rainbow",
posi = "right",
ylim = NA,
angle.label = 0
}

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)
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; ‘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 (Accepts the expression() function)
xlab Treatments name (Accepts the expression() function)
xlab.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’.
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
<table>
<thead>
<tr>
<th>labelsize</th>
<th>label size</th>
</tr>
</thead>
<tbody>
<tr>
<td>dec</td>
<td>number of cells</td>
</tr>
<tr>
<td>family</td>
<td>font family</td>
</tr>
<tr>
<td>point</td>
<td>if quali=FALSE, defines whether to plot all points (&quot;all&quot;), mean (&quot;mean&quot;), standard deviation (&quot;mean_sd&quot; - default) or mean with standard error (default - &quot;mean_se&quot;).</td>
</tr>
<tr>
<td>addmean</td>
<td>Plot the average value on the graph (default is TRUE)</td>
</tr>
<tr>
<td>errorbar</td>
<td>Plot the standard deviation bar on the graph (In the case of a segment and column graph) - default is TRUE</td>
</tr>
<tr>
<td>sup</td>
<td>Number of units above the standard deviation or average bar on the graph</td>
</tr>
<tr>
<td>color</td>
<td>Column chart color (default is &quot;rainbow&quot;)</td>
</tr>
<tr>
<td>posi</td>
<td>Legend position</td>
</tr>
<tr>
<td>ylim</td>
<td>y-axis scale</td>
</tr>
<tr>
<td>angle.label</td>
<td>label angle</td>
</tr>
</tbody>
</table>

**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)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
References


Practical Nonparametrics Statistics. W.J. Conover, 1999


See Also

FAT2DBC.ad

Examples

#================================================
# Example cloro
#================================================
library(AgroR)
data(cloro)
attach(cloro)
FAT2DBC(f1, f2, bloco, resp, ylab="Number of nodules", legend = "Stages")
FAT2DBC(f1, f2, bloco, resp, mcomp="sk", ylab="Number of nodules", legend = "Stages")
#================================================
# Example covercrops
#================================================
library(AgroR)
data(covercrops)
attach(covercrops)
FAT2DBC(A, B, Bloco, Resp, ylab=expression("Yield"~(Kg~"100 m"^2)), legend = "Cover crops")
FAT2DBC(A, B, Bloco, Resp, mcomp="sk", ylab=expression("Yield"~(Kg~"100 m"^2)), legend = "Cover crops")

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),
    mcomp = "tukey",
    grau = c(NA, NA),
    grau12 = NA,
    grau21 = NA,
    transf = 1,
    constant = 0,
    geom = "bar",
    theme = theme_classic(),
    ylab = "Response",
    xlab = "",
    xlab.factor = c("F1", "F2"),
    legend = "Legend",
    ad.label = "Additional",
    color = "rainbow",
    fill = "lightblue",
    textsize = 12,
    labelsize = 4,
    addmean = TRUE,
    errorbar = TRUE,
    CV = TRUE,
    dec = 3,
    angle = 0,
    posi = "right",
    family = "sans",
    point = "mean_sd",
    sup = NA,
    ylim = NA,
    angle.label = 0
)

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)
mcomp  Multiple comparison test (Tukey (default), LSD 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; '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 (Accepts the expression() function)
xlab  Treatments name (Accepts the expression() function)
xlab.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'.
legend  Legend title name
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
angle  x-axis scale text rotation
posi  legend position
family  Font family
point   if quali=F, defines whether to plot all points ("all"), mean ("mean"), standard deviation ("mean_sd") or mean with standard error (default - "mean_se").
sup     Number of units above the standard deviation or average bar on the graph
ylim    y-axis scale
angle.label label angle

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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


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),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  xlab.factor = c("F1", "F2"),
  legend = "Legend",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  labelsize = 4,
  addmean = TRUE,
)

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", legend = "Stages"))
errorbar = TRUE,
CV = TRUE,
dec = 3,
angle = 0,
 posi = "right",
family = "sans",
point = "mean_sd",
sup = NA,
ylim = NA,
angle.label = 0
)

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)
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; ‘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 (Accepts the expression() function)
xlab Treatments name (Accepts the expression() function)
xlab.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’.
legend Legend title name
color Column chart color (default is "rainbow")
fill  Defines chart color (to generate different colors for different treatments, define fill = "trat")
textsize  Font size
labelsizelabel 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
angle x-axis scale text rotation
posi Legend position
family Font family
point if quali=F, defines whether to plot all points ("all"), mean ("mean"), standard deviation ("mean_sd") or mean with standard error (default - "mean_se").
sup Number of units above the standard deviation or average bar on the graph
ylim y-axis scale
angle.label Label angle

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)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


See Also

FAT2DIC.ad

Examples

```r
#====================================
# Example cloro
#====================================
library(AgroR)
data(cloro)
with(cloro, FAT2DIC(f1, f2, resp, ylab="Number of nodules", legend = "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)"))
```

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),
  mcomp = "tukey",
  grau = c(NA, NA),
  grau12 = NA,
  grau21 = NA,
  transf = 1,
  constant = 0,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  xlab.factor = c("F1", "F2"),
  legend = "Legend",
  ad.label = "Additional",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  labelsize = 4,
  addmean = TRUE,
  errorbar = TRUE,
  CV = TRUE,
  dec = 3,
  angle = 0,
  posi = "right",
  family = "sans",
  point = "mean_sd",
  sup = NA,
  ylim = NA,
  angle.label = 0
)

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
### FAT2DIC.ad

<table>
<thead>
<tr>
<th><strong>Response</strong></th>
<th>Numerical vector containing the response of the experiment.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ResponseAd</strong></td>
<td>Numerical vector with additional treatment responses</td>
</tr>
<tr>
<td><strong>Norm</strong></td>
<td>Error normality test (default is Shapiro-Wilk)</td>
</tr>
<tr>
<td><strong>Homog</strong></td>
<td>Homogeneity test of variances (default is Bartlett)</td>
</tr>
<tr>
<td><strong>Alpha.f</strong></td>
<td>Level of significance of the F test (default is 0.05)</td>
</tr>
<tr>
<td><strong>Alpha.t</strong></td>
<td>Significance level of the multiple comparison test (default is 0.05)</td>
</tr>
<tr>
<td><strong>Quali</strong></td>
<td>Defines whether the factor is quantitative or qualitative (qualitative)</td>
</tr>
<tr>
<td><strong>Mcomp</strong></td>
<td>Multiple comparison test (Tukey (default), LSD and Duncan)</td>
</tr>
<tr>
<td><strong>Grau</strong></td>
<td>Polynomial degree in case of quantitative factor (default is 1). Provide a vector with three elements.</td>
</tr>
<tr>
<td><strong>Grau12</strong></td>
<td>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.</td>
</tr>
<tr>
<td><strong>Grau21</strong></td>
<td>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.</td>
</tr>
<tr>
<td><strong>Transf</strong></td>
<td>Applies data transformation (default is 1; for log consider 0; 'angular' for angular transformation)</td>
</tr>
<tr>
<td><strong>Constant</strong></td>
<td>Add a constant for transformation (enter value)</td>
</tr>
<tr>
<td><strong>Geom</strong></td>
<td>Graph type (columns or segments (For simple effect only))</td>
</tr>
<tr>
<td><strong>Theme</strong></td>
<td>ggplot2 theme (default is theme_classic())</td>
</tr>
<tr>
<td><strong>Ylab</strong></td>
<td>Variable response name (Accepts the expression() function)</td>
</tr>
<tr>
<td><strong>Xlab</strong></td>
<td>Treatments name (Accepts the expression() function)</td>
</tr>
<tr>
<td><strong>Xlab.factor</strong></td>
<td>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'.</td>
</tr>
<tr>
<td><strong>Legend</strong></td>
<td>Legend title name</td>
</tr>
<tr>
<td><strong>Ad.label</strong></td>
<td>Additional label</td>
</tr>
<tr>
<td><strong>Color</strong></td>
<td>Column chart color (default is &quot;rainbow&quot;)</td>
</tr>
<tr>
<td><strong>Fill</strong></td>
<td>Defines chart color (to generate different colors for different treatments, define fill = &quot;trat&quot;)</td>
</tr>
<tr>
<td><strong>Textsize</strong></td>
<td>Font size</td>
</tr>
<tr>
<td><strong>Labelsize</strong></td>
<td>Label Size</td>
</tr>
<tr>
<td><strong>Addmean</strong></td>
<td>Plot the average value on the graph (default is TRUE)</td>
</tr>
<tr>
<td><strong>Errorbar</strong></td>
<td>Plot the standard deviation bar on the graph (In the case of a segment and column graph) - default is TRUE</td>
</tr>
<tr>
<td><strong>CV</strong></td>
<td>Plotting the coefficient of variation and p-value of Anova (default is TRUE)</td>
</tr>
<tr>
<td><strong>Dec</strong></td>
<td>Number of cells</td>
</tr>
<tr>
<td><strong>Angle</strong></td>
<td>x-axis scale text rotation</td>
</tr>
<tr>
<td><strong>Posi</strong></td>
<td>Legend position</td>
</tr>
</tbody>
</table>
family  Font family
point  if qual=1, defines whether to plot all points ("all"), mean ("mean"), standard deviation ("mean_sd") or mean with standard error (default - "mean_se").
sup  Number of units above the standard deviation or average bar on the graph
ylim  y-axis scale
angle.label  label angle

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)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


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", legend = "Stages"))

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",
  homog = "bt",
  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",
  xlab = "",
  xlab.factor = c("F1", "F2", "F3"),
  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,
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)
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)
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.
ylab Variable response name (Accepts the expression() function)
xlab Treatments name (Accepts the expression() function)
xlab.factor Provide a vector with two observations referring to the x-axis name of factors 1, 2 and 3, respectively, when there is an isolated effect of the factors. This argument uses 'parse'.
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.
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.

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.

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.

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 1.

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.

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.

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.

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.

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.

Defines chart color (to generate different colors for different treatments, define fill = "trat")

**ggplot2** theme (*default* is theme_classic())

x-axis scale text rotation

Plot the standard deviation bar on the graph (In the case of a segment and column graph) - *default* is TRUE

Plot the average value on the graph (*default* is TRUE)

Font family

Number of cells

Graph type (columns or segments)

Font size

Label Size

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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


Examples

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

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

Usage

FAT3DBC.ad(
  f1,
  f2,
  f3,
  block,
  response,
  responseAd,
  norm = "sw",
  homog = "bt",
  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",
  xlab = "",
  xlab.factor = c("F1", "F2", "F3"),
  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,
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 additional response
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)
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.
ylab Variable response name (Accepts the expression() function)
xlab Treatments name (Accepts the expression() function)
xlab.factor Provide a vector with two observations referring to the x-axis name of factors 1, 2 and 3, respectively, when there is an isolated effect of the factors. This argument uses 'parse'.
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.
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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


Examples

```r
library(AgroR)
data(enxofre)
respAd=c(2000,2400,2530,2100)
attach(enxofre)
with(enxofre, FAT3DBC.ad(f1, f2, f3, bloco, resp, respAd))
```
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",  
homog = "bt",  
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",  
xlab = "",  
xlab.factor = c("F1", "F2", "F3"),  
sup = NA,  
fill = "lightblue",  
theme = theme_classic(),  
angulo = 0,  
family = "sans",  
addmean = TRUE,  
errorbar = TRUE,  
dec = 3,  
geom = "bar",  
textsize = 12,
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)
homog Homogeneity test of variances (default is Bartlett)
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 quantitative 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.
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.

Applies data transformation (default is 1; for log consider 0; ‘angular’ for angular transformation)

Add a constant for transformation (enter value)

Allows labeling the factors 1, 2 and 3.

Variable response name (Accepts the expression() function)

Provide a vector with two observations referring to the x-axis name of factors 1, 2 and 3, respectively, when there is an isolated effect of the factors. This argument uses ‘parse’.

Number of units above the standard deviation or average bar on the graph

Defines chart color (to generate different colors for different treatments, define fill = "trat")

ggplot2 theme (default is theme_classic())

x-axis scale text rotation

Font family

Plot the average value on the graph (default is TRUE)

Plot the standard deviation bar on the graph (In the case of a segment and column graph) - default is TRUE

Number of cells

Graph type (columns or segments)

Font size

Label Size

label angle

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.

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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References
Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

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",
)
homog = "bt",
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",
xlab = "",
xlab.factor = c("F1", "F2", "F3"),
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,
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)
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)
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.
ylab    Variable response name (Accepts the expression() function)
xlab    Treatments name (Accepts the expression() function)
xlab.factor Provide a vector with two observations referring to the x-axis name of factors 1, 2 and 3, respectively, when there is an isolated effect of the factors. This argument uses 'parse'.
sup     Number of units above the standard deviation or average bar on the graph
grau1   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
labelszie
Label size
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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

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

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)
**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**

```r
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**

```r
data(laranja)
```
line_plot

*Graph: Line chart*

**Description**

Performs a descriptive line graph with standard deviation bars

**Usage**

```r
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
- `xlab` x axis title
- `legend.position` Legend position
- `theme` ggplot2 theme (*default* is `theme_classic()`)

**Value**

Returns a line chart with error bars

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

**See Also**

- `radargraph`
- `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)

---

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trat</td>
<td>Numerical or complex vector with treatments</td>
</tr>
<tr>
<td>resp</td>
<td>Numerical vector containing the response of the experiment.</td>
</tr>
<tr>
<td>npar</td>
<td>Number of model parameters</td>
</tr>
<tr>
<td>error</td>
<td>Error bar (It can be SE - default, SD or FALSE)</td>
</tr>
<tr>
<td>ylab</td>
<td>Variable response name (Accepts the expression() function)</td>
</tr>
<tr>
<td>xlab</td>
<td>Treatments name (Accepts the expression() function)</td>
</tr>
<tr>
<td>theme</td>
<td>ggplot2 theme (default is theme_bw())</td>
</tr>
<tr>
<td>legend.position</td>
<td>Legend position (default is c(0.3,0.8))</td>
</tr>
</tbody>
</table>
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
Leandro Simoes Azeredo Goncalves

References


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 (%)"))
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 Column). 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)

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)

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
xlab Names x-axis
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

Examples

```r
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

```r
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)

data frame containing data set
dose Numeric vector with doses
comp Numeric vector with leaf length

References


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
plot_interaction

Value
The function returns a graph for correlation

Author(s)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

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

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

Usage

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

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.
Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
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, <shimizu@uel.br>
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**

```r
plot_TH(
  tempo,            # Vector with times
  Tmed,             # Vector with mean temperature
  Tmax,             # Vector with maximum temperature
  Tmin,             # Vector with minimum temperature
  UR,               # Vector with relative humidity
  xlab = "Time",    # Label for the x-axis
  yname1 = expression("Humidity (%)"), # Label for the first y-axis
  yname2 = expression("Temperature ("^o * "C")", # Label for the second y-axis
  legend.H = "Humidity",  # Legend for relative humidity
  legend.tmed = "Tmed",   # Legend for mean temperature
  legend.tmin = "Tmin",   # Legend for minimum temperature
  legend.tmax = "Tmax",   # Legend for maximum temperature
  colormax = "red",      # Color for maximum temperature
  colormin = "blue",     # Color for minimum temperature
  colormean = "darkgreen", # Color for mean temperature
  fillbar = "gray80",    # Fill color for the bar
  limitsy1 = c(0, 100),  # Limits for the first y-axis
  x = "days",           # Label for the x-axis
  breaks = "1 months",  # Breaks for the x-axis
  textsize = 12,        # Text size
  legendsize = 12,      # Legend size
  titlesize = 12,       # Title size
  linesize = 1,         # Line size
  date_format = "%m-%Y", # Date format
  sc = 2.5,             # Scaling factor
  angle = 0,            # Angle
  legend.position = "bottom", # Position of the legend
  theme = theme_classic() # Theme
)
```

**Arguments**

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

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")
b 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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi
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

```r
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",
```

---

**See Also**

`radargraph, sk_graph, barplot_positive, corgraph, plot_TH1, spider_graph, line_plot`

---

**Examples**

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

Author(s)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also
radargraph, sk_graph, barplot_positive, corgraph, spider_graph, line_plot

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

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
)
polynomial

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trat</td>
<td>Numerical vector with treatments (Declare as numeric)</td>
</tr>
<tr>
<td>resp</td>
<td>Numerical vector containing the response of the experiment.</td>
</tr>
<tr>
<td>ylab</td>
<td>Dependent variable name (Accepts the expression() function)</td>
</tr>
<tr>
<td>xlab</td>
<td>Independent variable name (Accepts the expression() function)</td>
</tr>
<tr>
<td>yname.poly</td>
<td>Y name in equation</td>
</tr>
<tr>
<td>xname.poly</td>
<td>X name in equation</td>
</tr>
<tr>
<td>grau</td>
<td>Degree of the polynomial (1, 2 or 3)</td>
</tr>
<tr>
<td>theme</td>
<td>ggplot2 theme (default is theme_classic())</td>
</tr>
<tr>
<td>point</td>
<td>Defines whether to plot mean (&quot;mean&quot;), all repetitions (&quot;all&quot;), mean with standard deviation (&quot;mean_sd&quot;) or mean with standard error (default - &quot;mean_se&quot;).</td>
</tr>
<tr>
<td>color</td>
<td>Graph color (default is gray80)</td>
</tr>
<tr>
<td>posi</td>
<td>Legend position</td>
</tr>
<tr>
<td>textsize</td>
<td>Font size</td>
</tr>
<tr>
<td>se</td>
<td>Adds confidence interval (default is FALSE)</td>
</tr>
<tr>
<td>ylim</td>
<td>y-axis scale</td>
</tr>
<tr>
<td>family</td>
<td>Font family</td>
</tr>
<tr>
<td>pointsize</td>
<td>Point size</td>
</tr>
<tr>
<td>linesize</td>
<td>line size (Trendline and Error Bar)</td>
</tr>
<tr>
<td>width.bar</td>
<td>width of the error bars of a regression graph.</td>
</tr>
<tr>
<td>n</td>
<td>Number of decimal places for regression equations</td>
</tr>
<tr>
<td>SSq</td>
<td>Sum of squares of the residue</td>
</tr>
<tr>
<td>DFres</td>
<td>Residue freedom degrees</td>
</tr>
</tbody>
</table>

Value

Returns linear, quadratic or cubic regression analysis.

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
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**

```r
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
)
```

**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 *(Accepts the expression() function)*
- `xlab` Independent variable name *(Accepts the expression() 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
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","\n"))
n           Number of decimal places for regression equations
DFres       Residue freedom degrees
SSq         Sum of squares of the residue

Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also

polynomial, polynomial2_color

Examples

dose=rep(c(0,0,2,2,2,4,4,4,6,6,6),3)
resp=c(8,7,5,23,8,24,25,30,34,56,36,80,90,80,
12,14,15,23,24,50,54,56,80,90,40,
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))
Description

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

Usage

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

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 (Accepts the `expression()` function)
- `xlab`: Independent variable name (Accepts the `expression()` function)
- `theme`: ggplot2 theme (default is theme_classic())
polynomial2_color

- `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
- `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

Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
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,
  12,14,15,23,24,50,54,56,80,90,40,
  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
datatreatment 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",
homog = "bt",
alpha.f = 0.05,
alpha.t = 0.05,
quali = c(TRUE, TRUE),
mcomp = "tukey",
grau = c(NA, NA),
grau12 = NA,
grau21 = NA,
transf = 1,
constant = 0,
geom = "bar",
theme = theme_classic(),
ylab = "Response",
xlab = "",
xlab.factor = c("F1", "F2"),
color = "rainbow",
textsize = 12,
labelsize = 4,
dec = 3,
legend = "Legend",
errorbar = TRUE,
addmean = TRUE,
ylim = NA,
point = "mean_se",
fill = "lightblue",
angle = 0,
family = "sans",
angle.label = 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)
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)
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 1 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.
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 (Accepts the *expression()* function)

**xlab** Treatments name (Accepts the *expression()* function)

**xlab.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** 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)*

**legend** Legend title name

**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** Point type for regression ("mean_se","mean_sd","mean" or "all")

**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

---

**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
References

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


Practical Nonparametrics Statistics. W.J. Conover, 1999


Examples

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

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

Description

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

Usage

```r
PSUBDIC(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  homog = "bt",
  alpha.f = 0.05,
)```
alpha.t = 0.05,
quali = c(TRUE, TRUE),
mcomp = "tukey",
grau = c(NA, NA),
grau12 = NA,
grau21 = NA,
transf = 1,
constant = 0,
geom = "bar",
theme = theme_classic(),
ylab = "Response",
xlab = "",
xlab.factor = c("F1", "F2"),
fill = "lightblue",
angle = 0,
family = "sans",
color = "rainbow",
legend = "Legend",
errorbar = TRUE,
addmean = TRUE,
textsize = 12,
labelsize = 4,
dec = 3,
ylim = NA,
posi = "right",
point = "mean_se",
angle.label = 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)
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)
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 (Accepts the expression() function)
xlab  Treatments name (Accepts the expression() function)
xlab.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")
legend  Legend title name
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  Point type for regression ("mean_se","mean_sd","mean" or "all")
angle.label  Label angle

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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References
Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

Examples

```r
#===================================
# 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)"))
```

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

Usage

```r
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

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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

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

*Graph: Circular column chart*

**Description**

Circular column chart of an experiment with a factor of interest or isolated effect of a factor

**Usage**

```r
radargraph(model, ylim = NA, labelsize = 4, transf = FALSE)
```

**Arguments**

- **model**: DIC, DBC or DQL object
- **ylim**: y-axis limit
- **labelsize**: Font size of the labels
- **transf**: If the data has been transformed (*default* is FALSE)

**Value**

Returns pie chart with averages and letters from the Scott-Knott cluster test

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**See Also**

- `barplot_positive`, `sk_graph`, `plot_TH`, `corgraph`, `spider_graph`, `line_plot`

**Examples**

```r
data("laranja")
a=with(laranja, DBC(trat,bloco,resp, mcomp = "sk"))
radargraph(a)
```
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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also

radargraph, 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_graph(a,horiz = FALSE)
Description

This is a function of the point graph for one factor

Usage

```r
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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also

radargraph, barplot_positive, plot_TH, corgraph, spider_graph, line_plot
**Examples**

```r
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**

```r
data(sensorial)
```

**Format**

- `data.frame` containing data set
  - `Blend`  Categorical vector with treatment variable
  - `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**

```r
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)

data(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**

```r
sketch(
  trat,
  trat1 = NULL,
  trat2 = NULL,
  r,
  design = "DIC",
  pos = "line",
  color.sep = "all",
  ID = FALSE,
  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
- **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.
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"
**sk_graph**

**Graph: Scott-Knott graphics**

**Description**

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

Usage

sk_graph(model, horiz = TRUE)

Arguments

model DIC, DBC or DQL object
horiz Horizontal Column (default is TRUE)

Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also

radargraph, 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)

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")
spider_graph

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
ylab y axis title
ymin Minimum value of y
STRIPLOT

Value

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

Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

See Also

radargraph, 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 strip-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)
labelsizel 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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

Principles and procedures of statistics a biometrical approach Steel, Torry and Dickey. Third Edition 1997
Practical Nonparametrics Statistics. W.J. Conover, 1999

Examples

#===================================
# Example tomate
#===================================
# Obs. Consider that the "tomato" experiment is a block randomized design in strip-plot.
library(AgroR)
data(tomate)
with(tomate, STRIPLY(par, 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**

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

**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

**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

**Examples**

```r
library(AgroR)

#=====================================  
# DIC                                   
#=====================================  
data(pomegranate)  
attach(pomegranate)
```
summarise_dunnett

Usage

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

Arguments

variable
colnames
info

Description

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

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 descriptive 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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

data(pomegranate)
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, <shimizu@uel.br>
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)
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 (Accepts the expression() function)
xlab Treatments name (Accepts the expression() 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.
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, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

Examples

```r
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.
transf

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)

---

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)
weather

Author(s)
Gabriel Danilo Shimizu, <shimizu@uel.br>
Leandro Simoes Azeredo Goncalves
Rodrigo Yudi Palhaci Marubayashi

References

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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