

# Package ‘AgroR’

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**Type** Package

**Title** Experimental Statistics and Graphics for Agricultural Sciences

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

**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), Anova of aligned ranks (Wobbrock, JO, Findlater, L., Gergle, D., Higgins, JJ (2011), <doi:10.1145/1978942.1978963>) 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** 7.1.1

**Imports** ggplot2, lmtest, nortest, ScottKnott, lme4, crayon, grid, gridExtra, stringr, Hmisc, emmeans, ARTool, multcomp, ggrepel, reshape2, MASS, cowplot, multcompView, hnp, RColorBrewer, drc

**Suggests** DT, knitr, rmarkdown, roxygen2

**Depends** R (>= 3.6.0)

**License** GPL (>= 2)

**URL** [https://agronomiar.github.io/AgroR\\_package/index.html](https://agronomiar.github.io/AgroR_package/index.html)

**NeedsCompilation** no

**Author** Gabriel Danilo Shimizu [aut, cre]  
 (<<https://orcid.org/0000-0001-8524-508X>>),  
 Rodrigo Yudi Palhaci Marubayashi [aut, ctb]  
 (<<https://orcid.org/0000-0003-2778-8654>>),  
 Leandro Simoes Azeredo Goncalves [aut, ctb]  
 (<<https://orcid.org/0000-0001-9700-9375>>)

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---

aacp

*Utils: Area under the curve*

---

### Description

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

### Usage

```
aacp(data)
```

### Arguments

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

### Value

Returns a vector with the area values under the curve

### Note

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

### Author(s)

Gabriel Danilo Shimizu, <shimizu@ue1.br>

### References

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

### See Also

[transf](#), [sketch](#)

### Examples

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

# Converting to readable format for function
dados=cbind(simulate1[simulate1$tempo==1,3],
```

```
simulate1[simulate1$tempo==2,3],
simulate1[simulate1$tempo==3,3],
simulate1[simulate1$tempo==4,3],
simulate1[simulate1$tempo==5,3],
simulate1[simulate1$tempo==6,3])
colnames(dados)=c(1,2,3,4,5,6)
dados

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

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

---

aristolochia

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

---

## Description

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

## Usage

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

## Format

data.frame containing data set

trat numeric vector with factor 1

resp Numeric vector with response

## See Also

[cloro](#), [laranja](#), [enxofre](#), [laranja](#), [mirtilo](#), [passiflora](#), [phao](#), [porco](#), [pomegranate](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

## Examples

```
data(aristolochia)
```

---

barplot\_positive      *Graph: Positive barplot*

---

### Description

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

### Usage

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

### 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@ue1.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)")
```

---

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 ( <i>default</i> 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

**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)
```

---

bean

*Dataset: bean*

---

### Description

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

### Usage

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

### Format

data.frame containing data set

trat numeric vector with treatment

prod Numeric vector with grain production per plant

### See Also

[aristolochia](#), [cloro](#), [laranja](#), [enxofre](#), [laranja](#), [mirtilo](#), [passiflora](#), [phao](#), [porco](#), [pomegranate](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

### Examples

```
data(bean)
```

---

cloro

*Dataset: Sodium dichloroisocyanurate in soybean*

---

### Description

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

### Usage

```
data(cloro)
```



**Format**

data.frame containing data set  
f1 Categorical vector with factor 1  
f2 Categorical vector with factor 2  
bloco Categorical vector with block  
resp Numeric vector with number nodules

**References**

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

**See Also**

[enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(cloro)
```

---

conjdbc

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

---

**Description**

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

**Usage**

```
conjdbc(  
  trat,  
  block,  
  local,  
  response,  
  transf = 1,  
  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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
theme	ggplot2 theme ( <i>default</i> is theme_classic())
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
ylab	Variable response name (Accepts the <i>expression()</i> function)
title	Graph title
xlab	Treatments name (Accepts the <i>expression()</i> 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) - <i>default</i> 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@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**References**

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

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

**Examples**

```
library(AgroR)
data(mirtilo)
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**

```

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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
title	Graph title

xlab	Treatments name (Accepts the <i>expression()</i> 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) - <i>default</i> 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**

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

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

**Examples**

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

---

corgraph

*Graph: Correlogram*

---

**Description**

Correlation analysis function (Pearson or Spearman)

**Usage**

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

**Arguments**

data	data.frame with responses
axissize	Axes font size ( <i>default</i> is 12)
legendsize	Legend font size ( <i>default</i> is 12)
legendposition	Legend position ( <i>default</i> is c(0.9,0.2))
legendtitle	Legend title ( <i>default</i> is "Correlation")
method	Method correlation ( <i>default</i> 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**

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

---

`corn`*Dataset: corn*

---

**Description**

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

**Usage**

```
data(corn)
```

**Format**

data.frame containing data set

A Categorical vector with hybrids

B Categorical vector with density

resp Numeric vector with response

**See Also**

[enxfre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(corn)
```

---

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

---

**Description**

Graph: Plot Pearson correlation with interval of confidence

**Usage**

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

**Arguments**

data	data.frame with responses
background	background fill ( <i>default</i> is TRUE)
axis.size	Axes font size ( <i>default</i> is 12)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)

**Value**

The function returns a new graphical approach to correlation.

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.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 m<sup>2</sup> plots.

**Usage**

```
data(covercrops)
```

**Format**

data.frame containing data set

A Categorical vector with cultivars

B Categorical vector with green manure

Bloco Categorical vector with block

Resp Numeric vector with yield



**See Also**

[enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(covercrops)
```

---

DBC

*Analysis: Randomized block design*

---

**Description**

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

**Usage**

```
DBC(  
  trat,  
  block,  
  response,  
  norm = "sw",  
  homog = "bt",  
  mcomp = "tukey",  
  quali = TRUE,  
  alpha.f = 0.05,  
  alpha.t = 0.05,  
  transf = 1,  
  test = "parametric",  
  grau = 1,  
  geom = "bar",  
  theme = theme_classic(),  
  sup = NA,  
  CV = TRUE,  
  ylab = "response",  
  xlab = "",  
  textsize = 12,  
  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
block	Numerical or complex vector with blocks
response	Numerical vector containing the response of the experiment.
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
transf	Applies data transformation (default is 1; for log consider 0)
test	"parametric" - Parametric test or "nparametric" - non-parametric test
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
geom	graph type (columns, boxes or segments)
theme	ggplot2 theme ( <i>default</i> 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 ( <i>default</i> is TRUE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
textsize	Font 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 ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
posi	Legend position
point	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - <i>default</i> ) or mean with standard error ( <i>default</i> - "mean_se").
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. 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**

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@ue1.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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

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

**See Also**

[DIC, DQL](#)

**Examples**

```
library(AgroR)

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

#####
# Friedman test
#####
DBC(trat, bloco, resp, test="nparametric", 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

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

### Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

### Examples

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

## Description

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

## Usage

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

<code>alpha.t</code>	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
<code>theme</code>	ggplot2 theme ( <i>default</i> is <code>theme_classic()</code> )
<code>geom</code>	Graph type (columns - "bar" or segments "point")
<code>fill</code>	Defines chart color (to generate different colors for different treatments, define <code>fill = "trat"</code> )
<code>ylab</code>	Variable response name (Accepts the <i>expression()</i> function)
<code>xlab</code>	Treatments name (Accepts the <i>expression()</i> function)
<code>mcomp</code>	Multiple comparison test (Tukey ( <i>default</i> ), LSD ("lsd"), Scott-Knott ("sk"), Duncan ("duncan") and Friedman ("fd"))
<code>textsize</code>	Font size of the texts and titles of the axes
<code>labelsize</code>	Font size of the labels
<code>error</code>	Add error bar
<code>family</code>	Font family
<code>sup</code>	Number of units above the standard deviation or average bar on the graph
<code>addmean</code>	Plot the average value on the graph ( <i>default</i> is TRUE)
<code>posi</code>	Legend position
<code>legend</code>	Legend title
<code>ylim</code>	y-axis scale
<code>width.bar</code>	width errorbar
<code>dec</code>	Number of cells
<code>xnumeric</code>	Declare x as numeric ( <i>default</i> is FALSE)

### 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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

## See Also

[DBC](#), [DICT](#), [DQLT](#)

## Examples

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

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

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

---

desc

*Descriptive: Descriptive analysis*

---

## Description

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

## Usage

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



**Arguments**

trat	Numerical or complex vector with treatments
response	Numerical vector containing the response of the experiment.
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	x name (Accepts the <i>expression()</i> function)
ylim	y-axis scale

**Value**

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

**Author(s)**

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

**See Also**

[desc2fat](#), [tabledesc](#), [dispvar](#)

**Examples**

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

---

desc2fat

*Descriptive: Descriptive analysis (Two factors)*

---

**Description**

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

**Usage**

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

**Arguments**

f1	Numeric or complex vector with factor 1 levels
f2	Numeric or complex vector with factor 2 levels
response	Numerical vector containing the response of the experiment.
ylab	Variable response name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme ( <i>default</i> 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

**Examples**

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

---

desc3fat

*Descriptive: Descriptive analysis (Three factors)*

---

**Description**

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

**Usage**

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

**Arguments**

f1	Numeric or complex vector with factor 1 levels
f2	Numeric or complex vector with factor 2 levels
f3	Numeric or complex vector with factor 3 levels
response	Numerical vector containing the response of the experiment.
legend.title	Legend title
xlab	x name (Accepts the <i>expression()</i> function)

y1ab	Variable response name (Accepts the <i>expression()</i> function)
theme	ggplot theme
plot	"interaction" or "box"

**Value**

The function returns a triple interaction graph.

**Author(s)**

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

**Examples**

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

---

DIC

*Analysis: Completely randomized design*

---

**Description**

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

**Usage**

```
DIC(
  trat,
  response,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  quali = TRUE,
  alpha.f = 0.05,
  alpha.t = 0.05,
  grau = 1,
  transf = 1,
  test = "parametric",
  p.adj = "holm",
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  CV = TRUE,
```

```

ylab = "Response",
xlab = "",
fill = "lightblue",
angle = 0,
family = "sans",
textsize = 12,
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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
transf	Applies data transformation ( <i>default</i> is 1; for log consider 0)
test	"parametric" - Parametric test or "noparametric" - non-parametric test
p.adj	Method for adjusting p values for Kruskal-Wallis ("none","holm","hommel", "hochberg", "bonferroni", "BH", "BY", "fdr")
geom	Graph type (columns, boxes or segments)
theme	ggplot2 theme ( <i>default</i> 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 ( <i>default</i> is TRUE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> 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
dec	Number of cells
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)

errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
posi	Legend position
point	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - <i>default</i> ) or mean with standard error ( <i>default</i> - "mean_se"). Only for quali=F.
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. 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

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 ( $p\text{-adj} = "holm"$ ).

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

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W.J. Conover, Practical Nonparametrics Statistics. 1999

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

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

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

**See Also**[DBC DQL](#)**Examples**

```

library(AgroR)
data(pomegranate)

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

#####
# Kruskal-Wallis
#####
with(pomegranate, DIC(trat, WL, test = "noparametric", ylab = "Weight loss (%)"))

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

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

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

```

**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,
  dec = 3,
  addmean = TRUE,
  errorbar = TRUE,
  posi = "top",
  point = "mean_sd",
  angle.label = 0
)

```

**Arguments**

trat	Numerical or complex vector with treatments
response	Numerical vector containing the response of the experiment. Use <code>cbind(resp, n- resp)</code> for binomial or quasibinomial family.
glm.family	distribution family considered ( <i>default</i> is binomial)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
geom	Graph type (columns, boxes or segments)
theme	ggplot2 theme ( <i>default</i> is <code>theme_classic()</code> )
sup	Number of units above the standard deviation or average bar on the graph
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
fill	Defines chart color (to generate different colors for different treatments, define <code>fill = "trat"</code> )
angle	x-axis scale text rotation
family	Font family
textsize	Font size

dec	Number of cells
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
posi	Legend position
point	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - <i>default</i> ) or mean with standard error ( <i>default</i> - "mean_se").
angle.label	label angle

### Author(s)

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

### Examples

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

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

#####
# Use the DIC.glm function
#####

resp=resp/4 # tttotal germinated seeds

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

---

DICT

*Analysis: Completely randomized design evaluated over time*

---

### Description

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



**Usage**

```

DICT(
  trat,
  time,
  response,
  alpha.f = 0.05,
  alpha.t = 0.05,
  mcomp = "tukey",
  theme = theme_classic(),
  geom = "bar",
  xlab = "Independent",
  ylab = "Response",
  p.adj = "holm",
  dec = 3,
  fill = "gray",
  error = TRUE,
  textsize = 12,
  labelsize = 5,
  family = "sans",
  sup = 0,
  addmean = FALSE,
  legend = "Legend",
  ylim = NA,
  width.bar = 0.1,
  posi = c(0.1, 0.8),
  xnumeric = 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 ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD ("lsd"), Scott-Knott ("sk"), Duncan ("duncan") and Kruskal-Wallis ("kw"))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
geom	Graph type (columns - "bar" or segments "point")
xlab	treatments name (Accepts the <i>expression()</i> function)
ylab	Variable response name (Accepts the <i>expression()</i> function)
p.adj	Method for adjusting p values for Kruskal-Wallis ("none", "holm", "hommel", "hochberg", "bonferroni", "BH", "BY", "fdr")
dec	Number of cells

fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
error	Add error bar
textsize	Font size of the texts and titles of the axes
labelsize	Font size of the labels
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 ( <i>default</i> is TRUE)
legend	Legend title
ylim	y-axis scale
width.bar	width errorbar
posi	Legend position
xnumeric	Declare x as numeric ( <i>default</i> is FALSE)

**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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

**See Also**

[DIC](#), [DBCT](#), [DQLT](#)

**Examples**

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

---

dispvar

*Descriptive: Boxplot with standardized data*


---

**Description**

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

**Usage**

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

**Arguments**

data	data.frame containing the response of the experiment.
trat	Numerical or complex vector with treatments
theme	ggplot2 theme ( <i>default</i> is theme_bw())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> 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**

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

---

DQL

*Analysis: Latin square design*

---

**Description**

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

**Usage**

```
DQL(
  trat,
  line,
  column,
  response,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = TRUE,
  transf = 1,
  grau = 1,
  geom = "bar",
  theme = theme_classic(),
  sup = NA,
  CV = TRUE,
  ylab = "Response",
  xlab = "",
  textsize = 12,
  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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>default</i> is qualitative)
transf	Applies data transformation (default is 1; for log consider 0)
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
geom	Graph type (columns, boxes or segments)
theme	ggplot2 theme ( <i>default</i> 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 ( <i>default</i> is TRUE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
textsize	Font 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 ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
posi	Legend position
point	Defines whether to plot mean ("mean"), mean with standard deviation ("mean_sd" - <i>default</i> ) or mean with standard error ( <i>default</i> - "mean_se").
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, 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

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

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

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

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

**See Also**

[DIC](#), [DBC](#)

**Examples**

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

**Description**

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

**Usage**

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

<code>alpha.f</code>	Level of significance of the F test ( <i>default</i> is 0.05)
<code>alpha.t</code>	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
<code>mcomp</code>	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
<code>error</code>	Add error bar
<code>xlab</code>	Treatments name (Accepts the <i>expression()</i> function)
<code>ylab</code>	Variable response name (Accepts the <i>expression()</i> function)
<code>textsize</code>	Font size of the texts and titles of the axes
<code>labelsize</code>	Font size of the labels
<code>family</code>	Font family
<code>sup</code>	Number of units above the standard deviation or average bar on the graph
<code>addmean</code>	Plot the average value on the graph ( <i>default</i> is TRUE)
<code>posi</code>	Legend position
<code>geom</code>	Graph type (columns - "bar" or segments "point")
<code>fill</code>	Defines chart color (to generate different colors for different treatments, define <code>fill = "trat"</code> )
<code>legend</code>	Legend title
<code>ylim</code>	y-axis scale
<code>width.bar</code>	width errorbar
<code>dec</code>	Number of cells
<code>theme</code>	ggplot2 theme ( <i>default</i> is <code>theme_classic()</code> )
<code>xnumeric</code>	Declare x as numeric ( <i>default</i> is FALSE)

### 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@ue1.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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

## See Also

[DQL](#), [DICT](#), [DBCT](#)

## Examples

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

---

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,
  label = "Response"
)
```

**Arguments**

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
control	Treatment considered control (write identical to the name in the vector)
model	Experimental design (DIC, DBC or DQL)
block	Numerical or complex vector with blocks
column	Numerical or complex vector with columns
line	Numerical or complex vector with lines
alpha.t	Significance level ( <i>default</i> is 0.05)
label	Variable label

**Value**

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

**Note**

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

**Examples**

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

#####
# randomized block design in factorial double
#####
library(AgroR)
data(cloro)
attach(cloro)
respAd=c(268, 322, 275, 350, 320)
a=FAT2DBC.ad(f1, f2, bloco, resp, respAd,
             ylab="Number of nodules",
             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",
                 block=bloco,model = "DBC"))
```

---

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

---

**Description**

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

**Usage**

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

**Format**

`data.frame` containing data set

`time` numeric vector with time

`resp` Numeric vector with emergence

**See Also**

[aristolochia](#), [cloro](#), [laranja](#), [enxofre](#), [laranja](#), [mirtilo](#), [passiflora](#), [phao](#), [porco](#), [pomegranate](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

**Examples**

```
data(emerg)
```

---

`enxofre`*Dataset: Sulfur data*

---

**Description**

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

**Usage**

```
data(enxofre)
```

**Format**

data.frame containing data set

f1 Categorical vector with factor 1

f2 Categorical vector with factor 2

f2 Categorical vector with factor 3

bloco Categorical vector with block

resp Numeric vector

**See Also**

[cloro](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(enxofre)
```

---

FAT2DBC

*Analysis: DBC experiments in double factorial*

---

**Description**

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

**Usage**

```
FAT2DBC(  
  f1,  
  f2,  
  block,  
  response,  
  transf = 1,  
  norm = "sw",  
  homog = "bt",  
  mcomp = "tukey",  
  alpha.f = 0.05,  
  alpha.t = 0.05,  
  quali = c(TRUE, TRUE),  
  grau = NA,  
  geom = "bar",  
  theme = theme_classic(),  
  ylab = "Response",  
  xlab = "",  
  legend = "Legend",
```

```

    fill = "lightblue",
    angle = 0,
    textsize = 12,
    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.
transf	Applies data transformation (default is 1; for log consider 0)
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
legend	Legend title name
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
angle	x-axis scale text rotation
textsize	font size
dec	number of cells
family	font family

point	if quali=FALSE, defines whether to plot all points ("all"), mean ("mean"), standard deviation ("mean_sd" - <i>default</i> ) or mean with standard error ( <i>default</i> - "mean_se").
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
CV	Plotting the coefficient of variation and p-value of Anova ( <i>default</i> is TRUE)
sup	Number of units above the standard deviation or average bar on the graph
color	Column chart color ( <i>default</i> is "rainbow")
posi	Legend position
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 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.

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 and Dickey. Third Edition 1997

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

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

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

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

### See Also

[FAT2DBC.ad](#), [FAT2DBC.art](#)

[FAT2DBC.art](#)

### Examples

```
#=====
# Example cloro
#=====
library(AgroR)
data(cloro)
attach(cloro)
FAT2DBC(f1, f2, bloco, resp, 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.ad

*Analysis: DBC experiment in double factorial design with an additional treatment*

---

### Description

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

### Usage

```
FAT2DBC.ad(
  f1,
  f2,
  block,
  response,
  responseAd,
  norm = "sw",
  homog = "bt",
```

```

mcomp = "tukey",
alpha.f = 0.05,
alpha.t = 0.05,
quali = c(TRUE, TRUE),
grau = NA,
transf = 1,
geom = "bar",
theme = theme_classic(),
ylab = "Response",
xlab = "",
legend = "Legend",
ad.label = "Additional",
color = "rainbow",
fill = "lightblue",
textsize = 12,
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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
transf	Applies data transformation (default is 1; for log consider 0)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())



ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
legend	Legend title name
ad.label	Additional label
color	Column chart color ( <i>default</i> is "rainbow")
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
textsize	Font size
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
CV	Plotting the coefficient of variation and p-value of Anova ( <i>default</i> 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 ( <i>default</i> - "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 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.

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@ue1.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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

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

**See Also**

[FAT2DBC.art](#)

[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"))
```

---

FAT2DBC.art

*Analysis: Analysis of Variance of Aligned Rank Transformed Data in  
FAT2DBC*

---

**Description**

Apply the aligned rank transform to a factorial model (with optional grouping terms). Usually done in preparation for a nonparametric analyses of variance on models with numeric or ordinal responses, which can be done by following up with anova.art.

**Usage**

```
FAT2DBC.art(  
  f1,  
  f2,  
  block,  
  response,  
  decreasing = TRUE,  
  xlab = " ",  
  ylab = "Sum of posts",  
  legend.title = "Factor",  
  sup = NA,  
  theme = theme_classic()  
)
```

**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.
decreasing	letter order ( <i>default</i> is TRUE)
xlab	Treatments name (Accepts the <i>expression()</i> function)
ylab	Variable response name (Accepts the <i>expression()</i> function)
legend.title	legend title name
sup	Number of units above the standard deviation or average bar on the graph
theme	ggplot2 theme ( <i>default</i> is theme_classic())

**Value**

The function returns the Anova of aligned ranks, the multiple comparison test and the interaction graph.

**Author(s)**

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

**References**

Wobbrock, J. O., Findlater, L., Gergle, D., Higgins, J. J. (2011, May). The aligned rank transform for nonparametric factorial analyses using only anova procedures. In Proceedings of the SIGCHI conference on human factors in computing systems (pp. 143-146).

Kay, M., Wobbrock, J. O. (2020). Package 'ARTool'.

**See Also**[FAT2DBC](#)**Examples**

```
data(cloro)
with(cloro, FAT2DBC.art(f1,f2,bloco,resp))
```

---

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",
  mcomp = "tukey",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  grau = NA,
  transf = 1,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  legend = "Legend",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  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
response	Numerical vector containing the response of the experiment.
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
transf	Applies data transformation (default is 1; for log consider 0)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
legend	Legend title name
color	Column chart color ( <i>default</i> is "rainbow")
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
textsize	Font size
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
CV	Plotting the coefficient of variation and p-value of Anova ( <i>default</i> 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 ( <i>default</i> - "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 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.

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@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**References**

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

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

**See Also**

[FAT2DIC.art](#), [FAT2DIC.ad](#)

**Examples**

```
#=====
# 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="Height (cm)"))

```

---

FAT2DIC.ad

*Analysis: DIC experiment in double factorial design with an additional treatment*


---

### Description

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

### Usage

```

FAT2DIC.ad(
  f1,
  f2,
  repe,
  response,
  responseAd,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  grau = NA,
  transf = 1,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  legend = "Legend",
  ad.label = "Additional",
  color = "rainbow",
  fill = "lightblue",
  textsize = 12,
  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
response	Numerical vector containing the response of the experiment.
responseAd	Numerical vector with additional treatment responses
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
transf	Applies data transformation (default is 1; for log consider 0)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
legend	Legend title name
ad.label	Additional label
color	Column chart color ( <i>default</i> is "rainbow")
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
textsize	Font size
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
CV	Plotting the coefficient of variation and p-value of Anova ( <i>default</i> 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 ( <i>default</i> - "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 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.

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@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

### References

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

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

**See Also**[FAT2DIC.art](#)[FAT2DIC](#)[dunnnett](#)**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"))
```

FAT2DIC.art

---

*Analysis: Analysis of Variance of Aligned Rank Transformed Data in  
FAT2DIC*

---

**Description**

Apply the aligned rank transform to a factorial model (with optional grouping terms). Usually done in preparation for a nonparametric analyses of variance on models with numeric or ordinal responses, which can be done by following up with `anova.art`.

**Usage**

```
FAT2DIC.art(
  f1,
  f2,
  response,
  decreasing = TRUE,
  sup = NA,
  xlab = " ",
  ylab = "Sum of posts",
  legend.title = "Factor",
  theme = theme_classic()
)
```

**Arguments**

<code>f1</code>	Numeric or complex vector with factor 1 levels
<code>f2</code>	Numeric or complex vector with factor 2 levels
<code>response</code>	Numerical vector containing the response of the experiment.
<code>decreasing</code>	Letter order ( <i>default</i> is TRUE)
<code>sup</code>	Number of units above the standard deviation or average bar on the graph
<code>xlab</code>	Treatments name (Accepts the <i>expression()</i> function)
<code>ylab</code>	Variable response name (Accepts the <i>expression()</i> function)
<code>legend.title</code>	Legend title name
<code>theme</code>	ggplot2 theme ( <i>default</i> is <code>theme_classic()</code> )

**Value**

The function returns the Anova of aligned ranks, the multiple comparison test and the interaction graph.

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**References**

Wobbrock, J. O., Findlater, L., Gergle, D., Higgins, J. J. (2011, May). The aligned rank transform for nonparametric factorial analyses using only anova procedures. In Proceedings of the SIGCHI conference on human factors in computing systems (pp. 143-146).

Kay, M., Wobbrock, J. O. (2020). Package 'ARTool'.

**See Also**

[FAT2DIC](#)

**Examples**

```
data(cloro)
with(cloro, FAT2DIC.art(f1, f2, resp))
```

---

FAT3DBC

*Analysis: DBC experiments in triple factorial*

---

**Description**

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

**Usage**

```
FAT3DBC(
  f1,
  f2,
  f3,
  block,
  response,
  quali = c(TRUE, TRUE, TRUE),
  names.fat = c("F1", "F2", "F3"),
  mcomp = "tukey",
  transf = 1,
```

```

norm = "sw",
homog = "bt",
alpha.f = 0.05,
alpha.t = 0.05,
ylab = "Response",
xlab = "",
sup = NA,
grau = NA,
fill = "lightblue",
theme = theme_classic(),
angulo = 0,
errorbar = TRUE,
addmean = TRUE,
family = "sans",
dec = 3,
geom = "bar",
textsize = 12,
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.
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
names.fat	Allows labeling the factors 1, 2 and 3.
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
transf	Applies data transformation ( <i>default</i> is 1; for log consider 0)
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
sup	Number of units above the standard deviation or average bar on the graph
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
theme	ggplot2 theme ( <i>default</i> is theme_classic())
angulo	x-axis scale text rotation

errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
family	Font family
dec	Number of cells
geom	Graph type (columns or segments)
textsize	Font 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 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

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

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

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

## Examples

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

---

FAT3DIC

*Analysis: DIC experiments in triple factorial*

---

## Description

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

## Usage

```
FAT3DIC(
  f1,
  f2,
  f3,
  response,
  quali = c(TRUE, TRUE, TRUE),
  names.fat = c("F1", "F2", "F3"),
  mcomp = "tukey",
  alpha.t = 0.05,
  alpha.f = 0.05,
  transf = 1,
  norm = "sw",
  homog = "bt",
  ylab = "Response",
  xlab = "",
  sup = NA,
  grau = NA,
  fill = "lightblue",
  theme = theme_classic(),
  angulo = 0,
  family = "sans",
  addmean = TRUE,
  errorbar = TRUE,
  dec = 3,
  geom = "bar",
  textsize = 12,
  angle.label = 0
)
```

**Arguments**

f1	Numeric or complex vector with factor 1 levels
f2	Numeric or complex vector with factor 2 levels
f3	Numeric or complex vector with factor 3 levels
response	Numerical vector containing the response of the experiment.
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
names.fat	Allows labeling the factors 1, 2 and 3.
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
transf	Applies data transformation ( <i>default</i> is 1; for log consider 0)
norm	Error normality test ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	treatments name (Accepts the <i>expression()</i> function)
sup	Number of units above the standard deviation or average bar on the graph
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
theme	ggplot2 theme ( <i>default</i> is theme_classic())
angulo	x-axis scale text rotation
family	Font family
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
dec	Number of cells
geom	Graph type (columns or segments)
textsize	Font 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 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@ue1.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

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

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

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

**Examples**

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

---

laranja

*Dataset: Orange plants under different rootstocks*

---

**Description**

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



**Usage**

```
data(laranja)
```

**Format**

data.frame containing data set

f1 Categorical vector with treatments

bloco Categorical vector with block

resp Numeric vector with number of fruits per plant

**References**

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

**See Also**

[cloro](#), [enxofre](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(laranja)
```

---

line\_plot

*Graph: Line chart*

---

**Description**

Performs a descriptive line graph with standard deviation bars

**Usage**

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

**Arguments**

time	Vector containing the x-axis values
response	Vector containing the y-axis values
factor	Vector containing a categorical factor
errorbar	Error bars (sd or se)
ylab	y axis title
xlab	x axis title
legend.position	Legend position
theme	ggplot2 theme ( <i>default</i> is theme_classic())

**Value**

Returns a line chart with error bars

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.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)
```

---

logistic

---

*Analysis: Logistic regression*


---

**Description**

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

**Usage**

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

**Arguments**

trat	Numerical or complex vector with treatments
resp	Numerical vector containing the response of the experiment.
npar	Number of model parameters
error	Error bar (It can be SE - <i>default</i> , SD or FALSE)
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme ( <i>default</i> is theme_bw())
legend.position	Legend position ( <i>default</i> is c(0.3,0.8))
r2	Coefficient of determination of the mean or all values ( <i>default</i> is all)
width.bar	Bar width
scale	Sets x scale ( <i>default</i> is none, can be "log")
textsize	Font size
font.family	Font family ( <i>default</i> 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 ( $r^2$ ), 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**

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

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

**Examples**

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

---

mirtilo

*Dataset: Cutting blueberry data*

---

**Description**

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

**Usage**

```
data(mirtilo)
```

**Format**

data.frame containing data set

trat Categorical vector with treatments

exp Categorical vector with experiment

bloco Categorical vector with block

resp Numeric vector

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

**Examples**

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

---

orchard

*Dataset: orchard*

---

**Description**

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

**Usage**

```
data(orchard)
```

**Format**

data.frame containing data set

A Categorical vector with plot

B Categorical vector with split-plot

Bloco Categorical vector with block

Resp Numeric vector with microbial biomass carbon

**See Also**

[enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(orchard)
```

passiflora

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

---

**Description**

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

**Usage**

```
data(passiflora)
```

**Format**

data.frame containing data set

trat Categorical vector with substrate

bloco Categorical vector with block

MSPA Numeric vector with dry mass of aerial part

MSR Numeric vector with dry mass of root

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

**Examples**

```
data(passiflora)
```

---

PCA\_function

*Analysis: Principal components analysis*

---

**Description**

This function performs principal component analysis.

**Usage**

```

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

```

**Arguments**

data	Data.frame with data set. Line name must indicate the treatment
scale	Performs data standardization ( <i>default</i> is TRUE)
text	Add label ( <i>default</i> is TRUE)
pointsize	Point size ( <i>default</i> is 5)
textsize	Text size ( <i>default</i> is 12)
labelsize	Label size ( <i>default</i> is 4)
linesize	Line size ( <i>default</i> is 0.8)
repel	Avoid text overlay ( <i>default</i> is TRUE)
ylab	Names y-axis
xlab	Names x-axis
groups	Define grouping
sc	Secondary axis scale ratio ( <i>default</i> is 1)
font.family	Font family ( <i>default</i> is sans)
theme	Theme ggplot2 ( <i>default</i> is theme_bw())
label.legend	Legend title (when group is not NA)
type.graph	Type of chart ( <i>default</i> 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**

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

---

pepper

*Dataset: pepper*

---

**Description**

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

**Usage**

```
data(pepper)
```

**Format**

```
data.frame containing data set
Acesso Categorical vector with accessions
MS Numeric vector com dry mass
Vi tC Numeric vector with Vitamin C
```

**See Also**

[enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(pepper)
```



---

phao

*Dataset: Osmocote in Phalaenopsis sp.*

---

### Description

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

### Usage

```
data(phao)
```

### Format

data.frame containing data set

dose Numeric vector with doses

comp Numeric vector with leaf length

### References

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

### See Also

[pomegranate](#), [passiflora](#), [cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

### Examples

```
data(phao)
```

---

plot\_cor

*Graph: Plot correlation*

---

### Description

Correlation analysis function (Pearson or Spearman)

**Usage**

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

**Arguments**

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

**Value**

The function returns a graph for correlation

**Author(s)**

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

**Examples**

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

---

plot\_interaction      *Graph: Interaction plot*

---

**Description**

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

**Usage**

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

**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@ue1.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

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

### Arguments

tempo	Vector with times
Tmed	Vector with mean temperature

Tmax	Vector with maximum temperature
Tmin	Vector with minimum temperature
UR	Vector with relative humidity or precipitation
xlab	x axis name
yname1	y axis name
yname2	Secondary y-axis name
legend.H	Legend column
legend.tmed	Legend mean temperature
legend.tmin	Legend minimum temperature
legend.tmax	Legend maximum temperature
colormax	Maximum line color ( <i>default</i> is "red")
colormin	Minimum line color ( <i>default</i> is "blue")
colormean	Midline color ( <i>default</i> is "darkgreen")
fillbar	Column fill color ( <i>default</i> is "gray80")
limitsy1	Primary y-axis scale ( <i>default</i> is c(0,100))
x	x scale type (days or data, <i>default</i> is "days")
breaks	Range for x scale when x = "date" ( <i>default</i> 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 <i>default</i> 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@ue1.br>  
 Leandro Simoes Azeredo Goncalves  
 Rodrigo Yudi Palhaci Marubayashi

**See Also**

[radargraph](#), [sk\\_graph](#), [barplot\\_positive](#), [corgraph](#), [plot\\_TH1](#), [spider\\_graph](#), [line\\_plot](#)

**Examples**

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

---

plot\_TH1

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

---

**Description**

The plot\_TH1 function allows the user to build a column/line graph with climatic parameters of temperature (maximum, minimum and average) and relative humidity (UR) or precipitation. This chart is widely used in scientific work in agrarian science

**Usage**

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

```

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

```

### Arguments

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

### Value

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



**Author(s)**

Gabriel Danilo Shimizu, <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
)
```

**Arguments**

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

**Value**

Returns linear, quadratic or cubic regression analysis.

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**See Also**

[polynomial2](#), [polynomial2\\_color](#)

**Examples**

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

**Description**

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

**Usage**

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

**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 ( <i>default</i> is NA)
grau	Degree of the polynomial (1,2 or 3)
ylab	Dependent variable name (Accepts the <i>expression()</i> function)
xlab	Independent variable name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme ( <i>default</i> is theme_classic())
se	Adds confidence interval ( <i>default</i> is FALSE)

point	Defines whether to plot all points ("all"), mean ("mean"), mean with standard deviation ("mean_sd") or mean with standard error ( <i>default</i> - "mean_se").
legend.title	Title legend
posi	Legend position
textsize	Font size ( <i>default</i> is 12)
ylim	y-axis scale
family	Font family ( <i>default</i> is sans)
width.bar	width of the error bars of a regression graph.
pointsize	Point size ( <i>default</i> is 4)
linesize	line size (Trendline and Error Bar)
separate	Separation between treatment and equation ( <i>default</i> is c("\", "\"))
n	Number of decimal places for regression equations

**Value**

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

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**See Also**

[polynomial](#), [polynomial2\\_color](#)

**Examples**

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

---

polynomial2\_color      *Analysis: Linear regression graph in double factorial with color graph*

---

### Description

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

### Usage

```
polynomial2_color(
  fator1,
  resp,
  fator2,
  color = NA,
  grau = NA,
  ylab = "Response",
  xlab = "independent",
  theme = theme_classic(),
  se = FALSE,
  point = "mean_se",
  legend.title = "Tratamentos",
  posi = "top",
  textsize = 12,
  ylim = NA,
  family = "sans",
  width.bar = NA,
  pointsize = 5,
  linesize = 0.8,
  separate = c("\\", "\\"),
  n = 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 ( <i>default</i> is NA)
grau	Degree of the polynomial (1,2 or 3)
ylab	Dependent variable name (Accepts the <i>expression()</i> function)
xlab	Independent variable name (Accepts the <i>expression()</i> function)
theme	ggplot2 theme ( <i>default</i> is theme_classic())
se	Adds confidence interval ( <i>default</i> is FALSE)

point	Defines whether to plot all points ("all"), mean ("mean"), mean with standard deviation ("mean_sd") or mean with standard error ( <i>default</i> - "mean_se").
legend.title	Title legend
posi	Legend position
textsize	Font size ( <i>default</i> is 12)
ylim	y-axis scale
family	Font family ( <i>default</i> is sans)
width.bar	width of the error bars of a regression graph.
pointsize	Point size ( <i>default</i> is 4)
linesize	line size (Trendline and Error Bar)
separate	Separation between treatment and equation ( <i>default</i> is c("\", "\"))
n	Number of decimal places for regression equations

**Value**

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

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.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,
12,14,15,23,24,25,50,54,56,80,90,40,
12,14,15,3,4,5,50,54,56,80,90,40)
trat=rep(c("A","B","C"),e=12)
polynomial2_color(dose, resp, trat, grau=c(1,2,3))
```

---

pomegranate

*Dataset: Pomegranate data*

---

### Description

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

### Usage

```
data(pomegranate)
```

### Format

```
data.frame containing data set  
trat Categorical vector with treatments  
WL Numeric vector weights loss  
SS Numeric vector solid soluble  
AT Numeric vector titratable acidity  
ratio Numeric vector with ratio (SS/AT)
```

### See Also

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#)

### Examples

```
data(pomegranate)
```

---

porco

*Dataset: Pig development and production*

---

### Description

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

**Usage**

```
data(porco)
```

**Format**

```
data.frame containing data set  
trat Categorical vector with treatments  
linhas Categorical vector with lines  
colunas Categorical vector with columns  
resp Numeric vector
```

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(porco)
```

---

PSUBDBC

*Analysis: DBC experiments in split-plot*

---

**Description**

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

**Usage**

```
PSUBDBC(  
  f1,  
  f2,  
  block,  
  response,  
  norm = "sw",  
  homog = "bt",  
  alpha.f = 0.05,  
  alpha.t = 0.05,  
  mcomp = "tukey",  
  quali = c(TRUE, TRUE),  
  grau = NA,  
  transf = 1,  
  geom = "bar",  
  theme = theme_classic(),  
  ylab = "Response",
```



```

xlab = "",
color = "rainbow",
textsize = 12,
dec = 3,
legend = "Legend",
errorbar = TRUE,
addmean = TRUE,
ylim = NA,
point = "mean_se",
fill = "lightblue",
angle = 0,
family = "sans",
posi = "right",
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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
transf	Applies data transformation (default is 1; for log consider 0)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
color	When the columns are different colors (Set fill-in argument as "trat")
textsize	Font size ( <i>default</i> is 12)
dec	Number of cells ( <i>default</i> is 3)
legend	Legend title name
errorbar	Plot the standard deviation bar on the graph (In the case of a segment and column graph) - <i>default</i> is TRUE
addmean	Plot the average value on the graph ( <i>default</i> 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 ( <i>default</i> 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 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. Non-parametric analysis can be used by the Friedman test. The column 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.

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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

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

### Examples

```
#=====
# Example tomate
#=====
```

```

library(AgroR)
data(tomate)
with(tomate, PSUBDBC(perc, subp, bloco, resp, ylab="Dry mass (g)"))

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

```

---

PSUBDIC

---

*Analysis: DIC experiments in split-plot*


---

### Description

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

### Usage

```

PSUBDIC(
  f1,
  f2,
  block,
  response,
  norm = "sw",
  homog = "bt",
  mcomp = "tukey",
  alpha.f = 0.05,
  alpha.t = 0.05,
  quali = c(TRUE, TRUE),
  transf = 1,
  grau = NA,
  geom = "bar",
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  fill = "lightblue",
  angle = 0,
  family = "sans",
  color = "rainbow",
  legend = "Legend",
  errorbar = TRUE,
  addmean = TRUE,
  textsize = 12,
  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 ( <i>default</i> is Shapiro-Wilk)
homog	Homogeneity test of variances ( <i>default</i> is Bartlett)
mcomp	Multiple comparison test (Tukey ( <i>default</i> ), LSD, Scott-Knott and Duncan)
alpha.f	Level of significance of the F test ( <i>default</i> is 0.05)
alpha.t	Significance level of the multiple comparison test ( <i>default</i> is 0.05)
quali	Defines whether the factor is quantitative or qualitative ( <i>qualitative</i> )
transf	Applies data transformation (default is 1; for log consider 0)
grau	Degree of polynomial in case of quantitative factor ( <i>default</i> is 1)
geom	Graph type (columns or segments (For simple effect only))
theme	ggplot2 theme ( <i>default</i> is theme_classic())
ylab	Variable response name (Accepts the <i>expression()</i> function)
xlab	Treatments name (Accepts the <i>expression()</i> function)
fill	Defines chart color (to generate different colors for different treatments, define fill = "trat")
angle	x-axis scale text rotation
family	Font family ( <i>default</i> 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) - <i>default</i> is TRUE
addmean	Plot the average value on the graph ( <i>default</i> is TRUE)
textsize	Font size ( <i>default</i> is 12)
dec	Number of cells ( <i>default</i> 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 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. Non-parametric analysis can be used by the Friedman test. The column 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.

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@ue1.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

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

Practical Nonparametrics Statistics. W.J. Conover, 1999

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

**Examples**

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

---

 PSUBSUBDBC

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


---

**Description**

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

**Usage**

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

**Arguments**

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

```
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 ( <i>default</i> 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**

```
data("laranja")
a=with(laranja, DBC(trat,bloco,resp, mcomp = "sk"))
radargraph(a)
```

---

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

---

**Description**

This is a function of the bar graph for one factor

**Usage**

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

**Arguments**

<code>model</code>	DIC, DBC or DQL object
<code>fill</code>	fill bars
<code>horiz</code>	Horizontal Column ( <i>default</i> is TRUE)
<code>pointsize</code>	Point size

**Value**

Returns a segment chart for one factor

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@ue1.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)
```



---

sensorial	<i>Dataset: Sensorial data</i>
-----------	--------------------------------

---

**Description**

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

**Usage**

```
data(sensorial)
```

**Format**

data.frame containing data set  
Blend Categorical vector with treatment  
variable Categorical vector with variables  
resp Numeric vector

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(sensorial)
```

---

simulate1	<i>Dataset: Simulated data dict</i>
-----------	-------------------------------------

---

**Description**

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

**Usage**

```
data(simulate1)
```

**Format**

data.frame containing data set  
tempo Categorical vector with time  
trat Categorical vector with treatment  
resp Categorical vector with response

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(simulate1)
```

---

simulate2

*Dataset: Simulated data dbct*

---

**Description**

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

**Usage**

```
data(simulate2)
```

**Format**

data.frame containing data set

tempo Categorical vector with time

trat Categorical vector with treatment

bloco Categorical vector with block

resp Categorical vector with response

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate3](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(simulate2)
```

---

`simulate3`*Dataset: Simulated data dqlt*

---

**Description**

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

**Usage**

```
data(simulate3)
```

**Format**

`data.frame` containing data set

`tempo` Categorical vector with time

`trat` Categorical vector with treatment

`linhas` Categorical vector with line

`colunas` Categorical vector with column

`resp` Categorical vector with response

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [tomate](#), [weather](#), [phao](#), [passiflora](#), [aristolochia](#)

**Examples**

```
data(simulate3)
```

---

`sketch`*Utils: Experimental sketch*

---

**Description**

Experimental sketching function

**Usage**

```
sketch(trat, trat1 = NULL, trat2 = NULL, r, design = "dic", pos = "line")
```

**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 ("dic", "dbc", "dql", "psubdic", "psubdbc", "fat2dic", "fat2dbc")
pos	Repeat position (line or column)

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

**Author(s)**

Gabriel Danilo Shimizu, <shimizu@uel.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**Examples**

```

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

#=====
# Completely randomized design
#=====
sketch(Trat,r=3)
sketch(Trat,r=3,pos="column")

#=====
# Randomized block design
#=====
sketch(Trat, r=3, design="dbc")
sketch(Trat, r=3, design="dbc",pos="column")

#=====
# Completely randomized experiments in double factorial
#=====
sketch(trat=c("A","B"),
      trat1=c("A","B","C"),
      design = "fat2dic",
      r=3)

sketch(trat=c("A","B"),

```

```
trat1=c("A","B","C"),
design = "fat2dic",
r=3,
pos="column")
```

---

sk\_graph

*Graph: Scott-Knott graphics*

---

### Description

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

### Usage

```
sk_graph(model, horiz = TRUE)
```

### Arguments

model	DIC, DBC or DQL object
horiz	Horizontal Column ( <i>default</i> is TRUE)

### Value

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

### Author(s)

Gabriel Danilo Shimizu, <shimizu@ue1.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<sup>-1</sup>) of ten different commercial soybean cultivars in the municipality of Londrina/Parana. The experiment was carried out in the design of randomized complete blocks with four replicates per treatment.

### Usage

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

### Format

data.frame containing data set

cult numeric vector with treatment

bloc numeric vector with block

prod Numeric vector with grain yield

### See Also

[cloro](#), [laranja](#), [enxofre](#), [laranja](#), [mirtilo](#), [passiflora](#), [phao](#), [porco](#), [pomegranate](#), [simulate1](#), [simulate2](#), [simulate3](#), [tomate](#), [weather](#)

### Examples

```
data(soybean)
```

---

spider\_graph

*Graph: Spider graph for sensorial analysis*

---

### Description

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

**Usage**

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

**Arguments**

resp	Vector containing notes
vari	Vector containing the variables
blend	Vector containing treatments
legend.title	Caption title
xlab	x axis title
ylab	y axis title
ymin	Minimum value of y

**Value**

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

**Author(s)**

Gabriel Danilo Shimizu, <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))
```

---

 summarise\_anova

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


---

**Description**

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

**Usage**

```
summarise_anova(analysis, inf = "p", design = "DIC", round = 3, divisor = 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: l.

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**

```
library(AgroR)

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



```

a=DIC(trat, WL, geom = "point", ylab = "WL")
b=DIC(trat, SS, geom = "point", ylab="SS")
c=DIC(trat, AT, geom = "point", ylab = "AT")
summarise_anova(analysis = list(a,b,c), divisor = TRUE)

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

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

```

---

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@ue1.br>  
Leandro Simoes Azeredo Goncalves  
Rodrigo Yudi Palhaci Marubayashi

**Examples**

```
data(pomegranate)
tabledesc(pomegranate)
```

---

TBARPLOT.reverse	<i>Graph: Reverse graph of DICT, DBCT and DQL output when geom="bar"</i>
------------------	--

---

**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@ue1.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)
```

---

test_two	<i>Analysis: Test for two samples</i>
----------	---------------------------------------

---

## Description

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

## Usage

```
test_two(
  trat,
  resp,
  paired = FALSE,
  test = "t",
  alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95,
  theme = theme_classic(),
  ylab = "Response",
  xlab = "",
  var.equal = FALSE
)
```

## Arguments

<code>trat</code>	Categorical vector with the two treatments
<code>resp</code>	Numeric vector with the response
<code>paired</code>	A logical indicating whether you want a paired t-test.
<code>test</code>	Test used (t for test t or w for Wilcoxon test)
<code>alternative</code>	A character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
<code>conf.level</code>	Confidence level of the interval.
<code>theme</code>	ggplot2 theme ( <i>default</i> is <code>theme_classic()</code> )
<code>ylab</code>	Variable response name (Accepts the <i>expression()</i> function)
<code>xlab</code>	Treatments name (Accepts the <i>expression()</i> function)
<code>var.equal</code>	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@ue1.br>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

### Examples

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

---

tomate

*Dataset: Tomato data*

---

### Description

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

### Usage

```
data(tomate)
```

### Format

data.frame containing data set

parc Categorical vector with plot

subp Categorical vector with split-plot

bloco Categorical vector with block

resp Numeric vector

**See Also**

[cloro](#), [enxofre](#), [laranja](#), [mirtilo](#), [pomegranate](#), [porco](#), [sensorial](#), [simulate1](#), [simulate2](#), [simulate3](#), [weather](#), [aristolochia](#), [phao](#), [passiflora](#)

**Examples**

```
data(tomate)
```

---

transf

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

---

**Description**

Estimates the lambda value for data transformation

**Usage**

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

**Arguments**

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

**Value**

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

**Author(s)**

Gabriel Danilo Shimizu, <[shimizu@ue1.br](mailto:shimizu@ue1.br)>

Leandro Simoes Azeredo Goncalves

Rodrigo Yudi Palhaci Marubayashi

**References**

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

**Examples**

```
data("pomegranate")
with(pomegranate, transf(WL, trat))
```

---

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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