

Package ‘ExpDes’

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Imports stargazer

Description Package for analysis of simple experimental designs (CRD, RBD and LSD), experiments in double factorial schemes (in CRD and RBD), experiments in a split plot in time schemes (in CRD and RBD), experiments in double factorial schemes with an additional treatment (in CRD and RBD), experiments in triple factorial scheme (in CRD and RBD) and experiments in triple factorial schemes with an additional treatment (in CRD and RBD), performing the analysis of variance and means comparison by fitting regression models until the third power (quantitative treatments) or by a multiple comparison test, Tukey test, test of Student-Newman-Keuls (SNK), Scott-Knott, Duncan test, t test (LSD) and Bonferroni t test (protected LSD)(qualitative treatments); residual analysis (Ferreira, Cavalcanti and Nogueira, 2014) <doi:10.4236/am.2014.519280>.

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ExpDes-package *Experimental Designs*

Description

Package for analysis of simple experimental designs (CRD, RBD and LSD), experiments in double factorial schemes (in CRD and RBD), experiments in a split plot in time schemes (in CRD and RBD), experiments in double factorial schemes with an additional treatment (in CRD and RBD), experiments in triple factorial scheme (in CRD and RBD) and experiments in triple factorial schemes with an additional treatment (in CRD and RBD), performing the analysis of variance and means comparison by fitting regression models until the third power (quantitative treatments) or by a multiple comparison test, Tukey test, test of Student-Newman-Keuls (SNK), Scott-Knott, Duncan test, t test (LSD), Bonferroni t test (protected LSD) and bootstrap multiple comparison's test (qualitative treatments); residual analysis (Ferreira, Cavalcanti and Nogueira, 2014) <doi:10.4236/am.2014.519280>.

Details

| | |
|-----------|------------|
| Package: | ExpDes |
| Type: | Package |
| Version: | 1.2 |
| Date: | 2018-05-17 |
| License: | GPL 2 |
| LazyLoad: | yes |

Author(s)

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- FERREIRA, E. B.; CAVALCANTI, P. P. Funcao em codigo R para analisar experimentos em DIC simples, em uma so rodada. In: REUNIAO ANUAL DA REGIAO BRASILEIRA DA SOCIEDADE INTERNACIONAL DE BIOMETRIA, 54o SIMPOSIO DE ESTATISTICA APLICADA A EXPERIMENTACAO AGRONOMICA, 13, 2009, Sao Carlos. Programas e resumos... Sao Carlos, SP: UFSCar, 2009. p. 1-5.
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- RODRIGUES, R. B. Danos do percevejo-barriga-verde *Dichelops melacanthus* (Dallas, 1851) (Hemiptera: Pentatomidae) na cultura do milho. 2011. 105f. Dissertacao (Mestrado em Agronomia - Universidade Federal de Santa Maria, Santa Maria, 2011.

STEEL, R. G. D.; TORRIE, J. H.; DICKEY, D. A. Principles and procedures of statistics: a biometrical approach. 3rd Edition. 1997. 666 p.

VENABLES, W. N.; RIPLEY, B. D. Modern Applied Statistics with S-PLUS. Third Edition. Springer. 1999. p. 100.

See Also

see: [crd](#), [rbd](#), [fat2.crd](#), [fat3.crd](#), [split2.crd](#), [fat2.ad.crd](#), [fat3.ad.crd](#), [fat2.rbd](#), [fat3.rbd](#), [split2.rbd](#), [strip](#), [fat2.ad.rbd](#) e [fat3.ad.rbd](#)

anscombetukey

Test for homogeneity of variances of Anscombe and Tukey

Description

Performs the test for homogeneity of variances of Anscombe and Tukey (1963).

Usage

```
anscombetukey(resp, trat, block, glres, msres, sstrat, ssblock, residuals, fitted.values)
```

Arguments

| | |
|----------------------------|---|
| <code>resp</code> | Numeric or complex vector containing the response variable. |
| <code>trat</code> | Numeric or complex vector containing the treatments. |
| <code>block</code> | Numeric or complex vector containing the blocks. |
| <code>glres</code> | Residual degrees of freedom. |
| <code>msres</code> | Residual Mean Square. |
| <code>sstrat</code> | Residual Sum of Squares. |
| <code>ssblock</code> | Sum of Squares for blocks. |
| <code>residuals</code> | Numeric or complex vector containing the residuals. |
| <code>fitted.values</code> | Numeric or complex vector containing the fitted values. |

Value

Returns the p-value of Anscombe and Tukey's test of homogeneity of variances and its practical interpretation for 5% of significance.

Author(s)

Denismar Alves Nogueira

Eric Batista Ferreira

Marcos Costa de Paula

Mateus Pimenta Siqueira Lima

References

ANSCOMBE, F. J.; TUKEY, J. W. *The examination and analysis of residuals*. Technometrics, 5:141-160, 1963.

RIBEIRO, R. *Proposta e comparação do desempenho de testes para homogeneidade de variância de modelos de classi cação one-way e two-way*. Iniciação Científica. (Iniciação Científica) - Universidade Federal de Alfenas. 2012.

See Also

See also: [han](#), [oneillmathews](#)

Examples

```
data(ex2)
attach(ex2)
rbd(trat, provador, aparencia, hvar='anscombetukey')
```

bartlett

Test for Homogeneity of Variances: Bartlett

Description

Performs the test for homogeneity of variances of Bartlett (1937).

Usage

```
bartlett(trat, resp, t, r)
```

Arguments

| | |
|------|--|
| trat | Numeric or complex vector containing the treatments. |
| resp | Numeric or complex vector containing the response variable. |
| t | Number of treatments. |
| r | Numeric or complex vector containing the number of replications of each treatment. |

Value

Returns the p-value of Bartlett's test of homogeneity of variances and its practical interpretation for 5% of significance.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

BARTLETT, M. S. Properties of sufficiency and statistical tests. *Proceedings of the Royal Statistical Society - Serie A*, 60:268-282, 1937.

NOGUEIRA, D, P.; PEREIRA, G, M. Desempenho de testes para homogeneidade de variâncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

See Also

See also: [levene](#), [layard](#), [oneillmathews](#), [samiuddin](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar='bartlett')
```

ccboot

Multiple comparison: Bootstrap

Description

Performs the Ramos and Ferreira (2009) multiple comparison bootstrap test.

Usage

```
ccboot(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL, B = 1000)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance of the test. |
| group | TRUE or FALSE |
| main | Title |
| B | Number of bootstrap resamples. |

Value

Multiple means comparison for the bootstrap test.

Author(s)

Patricia de Siqueira Ramos
 Daniel Furtado Ferreira
 Eric Batista Ferreira

References

RAMOS, P. S., FERREIRA, D. F. Agrupamento de medias via bootstrap de populacoes normais e nao-normais, Revista Ceres, v.56, p.140-149, 2009.

See Also

[snk](#), [duncan](#), [lsd](#), [lsdb](#), [tukey](#), [scottknott](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='ccboot', sigT = 0.05)
```

 ccf

Multiple comparison: Calinski and Corsten

Description

Performs the Calinski and Corsten test based on the F distribution.

Usage

```
ccf(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance of the test. |
| group | TRUE or FALSE |
| main | Title |

Value

Multiple means comparison for the Calinski and Corsten test.

Author(s)

Patricia de Siqueira Ramos
 Daniel Furtado Ferreira
 Eric Batista Ferreira

References

CALIV'NSKI, T.; CORSTEN, L. C. A. Clustering means in ANOVA by Simultaneous Testing. *Biometrics*. v. 41, p. 39-48, 1985.

See Also

[snk](#), [duncan](#), [lsd](#), [lsdb](#), [tukey](#), [scottknott](#), [ccboot](#)

Examples

```
data(ex2)
attach(ex2)
rbd(trat, provador, aparencia, quali = TRUE, mcomp='ccf', sigT = 0.05)
```

 crd

One factor Completely Randomized Design

Description

Analyses balanced experiments in Completely Randomized Design under one single factor, considering a fixed model.

Usage

```
crd(treat, resp, quali = TRUE, mcomp = "tukey", nl = FALSE, hvar='bartlett',
sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-------|---|
| treat | Numeric or complex vector containing the treatments. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knot ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('ccboot'). |
| nl | Logic. If FALSE (<i>default</i>) linear regression models are adjusted. IF TRUE, non-linear regression models are adjusted. |

| | |
|------|--|
| hvar | Allows choosing the test for homogeneity of variances; the <i>default</i> is the test of Bartlett, however there are other options: test of Levene ('levener'), test of Samiuddin ('samiuddin'), test of O'Neill and Mathews ('oneillmathews') and the Layard test ('layard'). |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

- BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.
- FERREIRA, E. B.; CAVALCANTI, P. P. Funcao em codigo R para analisar experimentos em DIC simples, em uma so rodada. In: REUNIAO ANUAL DA REGIAO BRASILEIRA DA SOCIEDADE INTERNACIONAL DE BIOMETRIA, 54./SIMPOSIO DE ESTATISTICA APLICADA A EXPERIMENTACAO AGRONOMICA, 13., 2009, Sao Carlos. Programas e resumos... Sao Carlos, SP: UFSCar, 2009. p. 1-5.

See Also

For more examples, see: [fat2.crd](#), [fat3.crd](#), [split2.crd](#), [fat2.ad.crd](#) and [fat3.ad.crd](#).

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, sigF = 0.05)
```

duncan *Multiple comparison: Duncan test*

Description

Performs the test of Duncan for multiple comparison of means.

Usage

```
duncan(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance level. |
| group | TRUE or FALSE |
| main | Title |

Value

Returns the multiple comparison of means according to the test of Duncan.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

See Also

[snk](#), [tukey](#), [lsd](#), [lsdb](#), [ccboot](#), [scottknott](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='duncan', sigT = 0.05)
```

est21Ad *Stink bugs in corn: additional treatment*

Description

Additional treatment response variable (height of corn plants) of the experiment on stink bugs.

Usage

```
data(est21Ad)
```

Format

The format is: num [1:4] 32.5 32.1 30.3 29.8

Examples

```
data(est21Ad)
## maybe str(est21Ad) ; plot(est21Ad) ...
```

ex *Vines: Split-Plot in Randomized Blocks Design*

Description

Experiment about vines (not published) where one studied the effects of different fertilizers and harvest dates on the pH of grapes.

Usage

```
data(ex)
```

Format

A data frame with 24 observations on the following 4 variables.

trat a factor with levels A B

dose a numeric vector

rep a numeric vector

resp a numeric vector

Examples

```
data(ex)
## maybe str(ex) ; plot(ex) ...
```

ex1

Yacon: CRD

Description

Experiment aiming to evaluate the influence of the yacon flour consumption on the glicemic index.

Usage

```
data(ex1)
```

Format

A data frame with 24 observations on the following 2 variables.

trat a numeric vector

ig a numeric vector

References

RIBEIRO, J. de A. Estudos Quimicos e bioquimicos do Yacon (*Samallanthus sonchifolius*) in natura e Processado e Influencia do seu Consumo sobre Niveis Glicemicos e Lipideos Fecais de Ratos. 2008. 166p. Dissertation (Master in Food Science) - Universidade Federal de Lavras, UFLA, Lavras, 2008.

Examples

```
data(ex1)
## maybe str(ex1) ; plot(ex1) ...
```

ex2

Food bars: RBD

Description

Sensory evaluation of food bars where panelists (blocks) evaluated their appearance.

Usage

```
data(ex2)
```

Format

A data frame with 350 observations on the following 3 variables.

provador a numeric vector

trat a factor with levels A B C D E

aparencia a numeric vector

References

PAIVA, A. P. de. Estudos Tecnológicos, Químico, Físico-químico e Sensorial de Barras Alimentícias Elaboradas com Subprodutos e Resíduos Agroindustriais. 2008. 131p. Dissertation (Master in Food Science) - Universidade Federal de Lavras, UFLA, Lavras, 2008.

Examples

```
data(ex2)
## maybe str(ex2) ; plot(ex2) ...
```

ex3

Forage: LSD

Description

Data from an experiment aiming to select forage for minimizing the intake problem of feeding cattle in the sub-region of Paiaguas.

Usage

```
data(ex3)
```

Format

A data frame with 49 observations on the following 4 variables.

trat a factor with levels A B C D E F G

linha a numeric vector

coluna a numeric vector

resp a numeric vector

References

COMASTRI FILHO, J. A. Avaliação de espécies de forrageiras nativas e exóticas na sub-região dos paiaguas no pantanal mato-grossense. *Pesq. Agropec. Bras.*, Brasília, v.29, n.6, p. 971-978, jun. 1994.

Examples

```
data(ex3)
## maybe str(ex3) ; plot(ex3) ...
```

ex4

Composting: Doble Factorial scheme in CRD

Description

Field experiment to test the composting of coffee husk with or without cattle manure at different revolving intervals.

Usage

```
data(ex4)
```

Format

A data frame with 24 observations on the following 11 variables.

revol a numeric vector

esterco a factor with levels c s

rep a numeric vector

c a numeric vector

n a numeric vector

k a numeric vector

p a numeric vector

zn a numeric vector

b a numeric vector

ca a numeric vector

cn a numeric vector

References

REZENDE, F. A. de. Aproveitamento da Casca de Cafe e Borra da Purificacao de Gorduras e Oleos Residuarios em Compostagem. 2010. 74p. Thesis (Doctorate in Agronomy/Fitotecny) - Universidade Federal de Lavras, UFLA, Lavras, 2010.

Examples

```
data(ex4)
## maybe str(ex4) ; plot(ex4) ...
```

`ex5`*Food bars: Double Factorial scheme in RBD*

Description

Data adapted from a sensorial experiment where panelists of different genders evaluated the taste of food bars.

Usage

```
data(ex5)
```

Format

A data frame with 160 observations on the following 4 variables.

`trat` a factor with levels 10g 15g 15t 20t

`genero` a factor with levels F M

`bloco` a numeric vector

`sabor` a numeric vector

References

MOREIRA, D. K. T. Extrudados Expandidos de Arroz, Soja e Gergelim para Uso em Barras Alimenticias. 2010. 166p. Dissertation (Master in Food Science) - Universidade Federal de Lavras, UFLA, Lavras, 2010.

Examples

```
data(ex5)
## maybe str(ex5) ; plot(ex5) ...
```

`ex6`*Fictional data 1*

Description

Data simulated from a standard normal distribution for an experiment in triple factorial scheme.

Usage

```
data(ex6)
```


Format

A data frame with 24 observations on the following 5 variables.

fatorA a numeric vector

fatorB a numeric vector

fatorC a numeric vector

rep a numeric vector

resp a numeric vector

Examples

```
data(ex6)
## maybe str(ex6) ; plot(ex6) ...
```

ex7

Height of corn plants 21 days after emergence.

Description

We evaluated the height of corn plants 21 days after emergence under infestation of stink bugs (*Dichelops*) at different times of coexistence (period) and infestation levels (level). Additional treatment is period zero and level zero.

Usage

```
data(ex7)
```

Format

Data frame with 80 observations on the following 4 variables.

periodo a factor with levels 0-7DAE 0-14DAE 0-21DAE 7-14DAE 7-21DAE

nivel a numeric vector

bloco a numeric vector

est21 a numeric vector

References

RODRIGUES, R. B. Danos do percevejo-barriga-verde *Dichelops melacanthus* (Dallas, 1851) (Hemiptera: Pentatomidae) na cultura do milho. 2011. 105f. Dissertacao (Mestrado em Agronomia - Universidade Federal de Santa Maria, Santa Maria, 2011.

Examples

```
data(ex7)
```

ex8 *Composting: double factorial scheme plus one additional treatment in CRD.*

Description

Experiment in greenhouses to observe the performance of the obtained composting for fertilizing sorghum.

Usage

```
data(ex8)
```

Format

A data frame with 24 observations on the following 5 variables.

inoculante a factor with levels esterco mamona

biodiesel a numeric vector

vaso a numeric vector

fresca a numeric vector

seca a numeric vector

References

REZENDE, F. A. de. Aproveitamento da Casca de Cafe e Borra da Purificacao de Gorduras e Oleos Residuarios em Compostagem. 2010. 74p. Thesis (Doctorate in Agronomy/Fitotecny) - Universidade Federal de Lavras, UFLA, Lavras, 2010.

Examples

```
data(ex8)
## maybe str(ex8) ; plot(ex8) ...
```

ex9 *Vegetated: Split-plot in CRD*

Description

Subset of data from an experiment that studied the effect on soil pH of cover crops subjected to trampling by cattle predominantly under continuous grazing system, analyzed at different depths.

Usage

```
data(ex9)
```

Format

A data frame with 48 observations on the following 4 variables.

cobertura a factor with levels T1 T2 T3 T4 T5 T6

prof a numeric vector

rep a numeric vector

pH a numeric vector

References

GUERRA, A. R. Atributos de Solo sob Coberturas Vegetais em Sistema Silvopastoril em Lavras - MG. 2010. 141p. Dissertation (Master in Forest Engineering) - Universidade Federal de Lavras, UFLA, Lavras, 2010.

Examples

```
data(ex9)
## maybe str(ex9) ; plot(ex9) ...
```

ex_nl

Example of fictitious data mass

Description

Example of fictitious data mass for non-linear regression model fit

Usage

```
data(ex_nl)
```

Format

A data frame with 30 observations of the following 3 variables

trat numeric vector

rep numeric vector

resp numeric vector

References

fictitious data

Examples

```
data(ex_nl)
```

fat2.ad.crd

*Double factorial scheme plus one additional treatment in CRD***Description**

Analyses experiments in balanced Completely Randomized Design in double factorial scheme with an additional treatment, considering a fixed model.

Usage

```
fat2.ad.crd(factor1, factor2, repet, resp, respAd, quali = c(TRUE, TRUE),
mcomp = "tukey", fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| repet | Numeric or complex vector containing the replications. |
| resp | Numeric or complex vector containing the response variable. |
| respAd | Numeric or complex vector containing the additional treatment. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
 Eric Batista Ferreira
 Portya Piscitelli Cavalcanti

References

HEALY, M. J. R. The analysis of a factorial experiment with additional treatments. *Journal of Agricultural Science, Cambridge*, v. 47, p. 205-206. 1956.

FERREIRA, E. B.; CAVALCANTI, P. P.; NOGUEIRA D. A. Funcao para analisar experimentos em fatorial duplo com um tratamento adicional, em uma so rodada. In: CONGRESSO DE POS-GRADUACAO DA UNIVERSIDADE FEDERAL DE LAVRAS, 19., 2010, Lavras. Resumos... Lavras: UFLA, 2010.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex8)
attach(ex8)
data(secaAd)
fat2.ad.crd(inoculante, biodiesel, vaso, seca, secaAd, quali = c(TRUE,FALSE), mcomp = "tukey",
  fac.names = c("Inoculant", "Biodiesel"), sigT = 0.05, sigF = 0.05)
```

 fat2.ad.rbd

Double factorial scheme plus one additional treatment in RBD

Description

Analyses experiments in balanced Randomized Blocks Designs in double factorial scheme with an additional treatment, considering a fixed model.

Usage

```
fat2.ad.rbd(factor1, factor2, block, resp, respAd, quali = c(TRUE, TRUE),
  mcomp = "tukey", fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|---------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| block | Numeric or complex vector containing the blocks. |
| resp | Numeric or complex vector containing the response variable. |

| | |
|-----------|---|
| respAd | Numeric or complex vector containing the additional treatment. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

HEALY, M. J. R. The analysis of a factorial experiment with additional treatments. Journal of Agricultural Science, Cambridge, v. 47, p. 205-206. 1956.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex7)
attach(ex7)
data(est21Ad)
fat2.ad.rbd(periodo, nivel, bloco, est21, est21Ad, quali=c(TRUE, FALSE), mcomp = "tukey",
  fac.names = c("Period", "Level"), sigT = 0.05, sigF = 0.05)
```

fat2.crd

*Double factorial scheme in CRD***Description**

Analyses experiments in balanced Completely Randomized Design in double factorial scheme, considering a fixed model.

Usage

```
fat2.crd(factor1, factor2, resp, quali = c(TRUE, TRUE), mcomp = "tukey",
fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|--|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('ccboot'). |
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
 Eric Batista Ferreira
 Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

For more examples, see: [crd](#), [fat3.crd](#), [split2.crd](#), [fat2.ad.crd](#) and [fat3.ad.crd](#).

Examples

```
data(ex4)
attach(ex4)
fat2.crd(revol, estercos, zn, quali=c(FALSE,TRUE), mcomp="tukey",
  fac.names=c("Revolving","Manure"), sigT = 0.05, sigF = 0.05)
```

 fat2.rbd

Double factorial scheme in RBD

Description

Analyses experiments in balanced Randomized Blocks Designs in double factorial scheme, considering a fixed model.

Usage

```
fat2.rbd(factor1, factor2, block, resp, quali = c(TRUE, TRUE), mcomp = "tukey",
  fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|---------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| block | Numeric or complex vector containing the blocks. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |

| | |
|-----------|--|
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

For more examples, see: [fat2.rbd](#), [fat3.rbd](#), [split2.rbd](#), [strip](#), [fat2.ad.rbd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex5)
attach(ex5)
fat2.rbd(trat, genero, bloco, sabor ,quali=c(TRUE,TRUE), mcomp="lsd",
  fac.names=c("Samples","Gender"), sigT = 0.05, sigF = 0.05)
```

fat3.ad.crd

*Triple factorial scheme plus an additional treatment in CRD***Description**

Analyses experiments in balanced Completely Randomized Design in triple factorial scheme with an additional treatment, considering a fixed model.

Usage

```
fat3.ad.crd(factor1, factor2, factor3, repet, resp, respAd,
quali = c(TRUE, TRUE, TRUE), mcomp = "tukey", fac.names = c("F1", "F2", "F3"),
sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|--|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| factor3 | Numeric or complex vector containing the factor 3 levels. |
| repet | Numeric or complex vector containing the replications. |
| resp | Numeric or complex vector containing the response variable. |
| respAd | Numeric or complex vector containing the additional treatment. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('ccboot'). |
| fac.names | Allows labeling the factors 1, 2 and 3. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

HEALY, M. J. R. The analysis of a factorial experiment with additional treatments. *Journal of Agricultural Science, Cambridge*, v. 47, p. 205-206. 1956.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex6)
attach(ex6)
data(respAd)
fat3.ad.crd(fatorA, fatorB, fatorC, rep, resp, respAd, quali = c(TRUE, TRUE, TRUE),
mcomp = "duncan", fac.names = c("Factor A", "Factor B", "Factor C"), sigT = 0.05, sigF = 0.05)
```

fat3.ad.rbd

Triple factorial scheme plus an additional treatment in RBD

Description

Analyses experiments in balanced Randomized Blocks Designs in triple factorial scheme with an additional treatment, considering a fixed model.

Usage

```
fat3.ad.rbd(factor1, factor2, factor3, block, resp, respAd, quali = c(TRUE, TRUE, TRUE),
mcomp = "tukey", fac.names = c("F1", "F2", "F3"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|---------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| factor3 | Numeric or complex vector containing the factor 3 levels. |
| block | Numeric or complex vector containing the blocks. |

| | |
|-----------|---|
| resp | Numeric or complex vector containing the response variable. |
| respAd | Numeric or complex vector containing the additional treatment. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1, 2 and 3. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

HEALY, M. J. R. The analysis of a factorial experiment with additional treatments. Journal of Agricultural Science, Cambridge, v. 47, p. 205-206. 1956.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex6)
attach(ex6)
data(respAd)
fat3.ad.rbd(fatorA, fatorB, fatorC, rep, resp, respAd, quali = c(TRUE, TRUE, TRUE),
  mcomp = "snk", fac.names = c("Factor A", "Factor B", "Factor C"), sigT = 0.05, sigF = 0.05)
```

fat3.crd

*Triple factorial scheme in CRD***Description**

Analyses experiments in balanced Completely Randomized Design in triple factorial scheme, considering a fixed model.

Usage

```
fat3.crd(factor1, factor2, factor3, resp, quali = c(TRUE, TRUE, TRUE),
  mcomp = "tukey", fac.names = c("F1", "F2", "F3"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| factor3 | Numeric or complex vector containing the factor 3 levels. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1, 2 and 3. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex6)
attach(ex6)
fat3.crd(fatorA, fatorB, fatorC, resp, quali = c(TRUE, TRUE, TRUE), mcomp = "lsdb",
fac.names = c("Factor A", "Factor B", "Factor C"), sigT = 0.05, sigF = 0.05)
```

fat3.rbd

Triple factorial scheme in RBD

Description

Analyses experiments in balanced Randomized Blocks Designs in triple factorial scheme, considering a fixed model.

Usage

```
fat3.rbd(factor1, factor2, factor3, block, resp, quali = c(TRUE, TRUE, TRUE),
mcomp = "tukey", fac.names = c("F1", "F2", "F3"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|---------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| factor3 | Numeric or complex vector containing the factor 3 levels. |
| block | Numeric or complex vector containing the blocks. |
| resp | Numeric or complex vector containing the response variable. |

| | |
|-----------|---|
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1, 2 and 3. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

For more examples, see: [fat2.crd](#), [fat2.rbd](#), [fat3.crd](#), [fat3.rbd](#), [fat2.ad.crd](#), [fat2.ad.rbd](#), [fat3.ad.crd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex6)
attach(ex6)
fat3.rbd(fatorA, fatorB, fatorC, rep, resp, quali = c(TRUE, TRUE, TRUE),
mcomp = "tukey", fac.names = c("Factor A", "Factor B", "Factor C"), sigT = 0.05, sigF = 0.05)
```

 ginv

Generalized inverse

Description

Calculates the Moore-Penrose generalized inverse of a matrix X .

Usage

```
ginv(X, tol = sqrt(.Machine$double.eps))
```

Arguments

| | |
|------------------|---|
| <code>X</code> | Matrix for which the Moore-Penrose inverse is required. |
| <code>tol</code> | A relative tolerance to detect zero singular values. |

Value

A MP generalized inverse matrix for X .

References

Venables, W. N. and Ripley, B. D. (1999) Modern Applied Statistics with S-PLUS. Third Edition. Springer. p.100.

See Also

See also: solve, svd, eigen.

Examples

```
## Not run:
# The function is currently defined as
function(X, tol = sqrt(.Machine$double.eps))
{
## Generalized Inverse of a Matrix
  dnx <- dimnames(X)
  if(is.null(dnx)) dnx <- vector("list", 2)
  s <- svd(X)
  nz <- s$d > tol * s$d[1]
  structure(
    if(any(nz)) s$v[, nz] %*% (t(s$u[, nz])/s$d[nz]) else X, dimnames = dnx[2:1])
  )
}

## End(Not run)
```

 graphics

Regression model plots

Description

Plots from regression models fitted in ANOVA

Usage

```
graphics(a, degree = 1, mod = TRUE, main = " ", sub = " ",
         xlab = "Levels (X)", ylab = "Response var (Y)", pch = 19,
         xlim = NULL, ylim = NULL, bty = "o")
```

Arguments

| | |
|--------|--|
| a | Output from anova (performed in ExpDes) |
| degree | For polynomial models, 1 (linear model) is the <i>default</i> , 2 (quadratic model), 3 (cubic model), "pot" (Power model), "log" (Logistic model), "gom" (Gompertz model) and "exp" (Exponential model). |
| mod | Logic. Print the model expression and its R2 on the top of the graphic. The <i>default</i> is TRUE. |
| main | Title of the plot. Empty is the <i>default</i> . |
| sub | Subtitle of the plot. Empty is the <i>default</i> . |
| xlab | Name for axis X. |
| ylab | Name for axis Y. |
| pch | Character type to be used on the observed values. |
| xlim | Limits for axis X. |
| ylim | Limits for axis Y. |
| bty | Type of box the plot is fitted in. |

Author(s)

Eric Batista Ferreira

References

STEEL, R. G. D.; TORRIE, J. H. *Principles and procedures in Statistics: a biometrical approach*. McGraw-Hill, New York, NY. 1980.

See Also

[reg.poly](#), [plotres](#)

Examples

```
data(ex1)
attach(ex1)
a<-crd(trat, ig, quali=FALSE, nl=FALSE)
graphics(a, degree=1)
graphics(a, degree=2)
graphics(a, degree=3)
```

han

Test for homogeneity of variances of Han

Description

Performs the test for homogeneity of variances of Han (1969).

Usage

```
han(resp, trat, block)
```

Arguments

| | |
|-------|---|
| resp | Numeric or complex vector containing the response variable. |
| trat | Numeric or complex vector containing the treatments. |
| block | Numeric or complex vector containing the blocks. |

Value

Returns the p-value of Han's test of homogeneity of variances and its practical interpretation for 5% of significance.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

HAN, C. P. Testing the homogeneity of variances in a two-way classification. *Biometrics*, 25:153-158, Mar. 1969.

RIBEIRO, R. *Proposta e comparacao do desempenho de testes para homogeneidade de variancia de modelos de classificacao one-way e two-way*. Iniciacao Cientifica. (Iniciacao Cientifica) - Universidade Federal de Alfenas. 2012.

See Also

See also: [anscombetukey](#), [oneillmathews](#)

Examples

```
data(ex2)
attach(ex2)
rbd(trat, provador, aparencia, hvar='han')
```

lastC

Setting the last character of a chain

Description

A special function for the group of treatments in the multiple comparison tests. Use `order.group`.

Usage

```
lastC(x)
```

Arguments

x letters

Value

x character

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
(Adapted from Felipe de Mendiburu - GPL)

See Also

`order.group`

Examples

```
x<-c("a", "ab", "b", "c", "cd")
lastC(x)
# "a" "b" "b" "c" "d"
```

| | |
|-------|----------------------------|
| latsd | <i>Latin Square Design</i> |
|-------|----------------------------|

Description

Analyses experiments in balanced Latin Square Design, considering a fixed model.

Usage

```
latsd(treat, row, column, resp, quali = TRUE, mcomp = "tukey", sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|--------|---|
| treat | Numeric or complex vector containing the treatments. |
| row | Numeric or complex vector containing the rows. |
| column | Numeric or complex vector containing the columns. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the LSD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

- GOMES, F. P. Curso de Estatística Experimental. 10a ed. Piracicaba: ESALQ/USP. 1982. 430.
- FERREIRA, E. B.; CAVALCANTI, P. P.; NOGUEIRA D. A. Funcao em codigo R para analisar experimentos em DQL simples, em uma so rodada. In: CONGRESSO DE POS-GRADUACAO DA UNIVERSIDADE FEDERAL DE LAVRAS, 18., 2009, Lavras. Annals... Lavras: UFLA, 2009.

See Also

For more examples, see: [crd](#), [rbd](#)

Examples

```
data(ex3)
attach(ex3)
latsd(trat, linha, coluna, resp, quali=TRUE, mcomp="snk", sigT=0.05, sigF=0.05)
```

layard

Test for homogeneity of variances of Layard

Description

Performs the test for homogeneity of variances of Layard for Jackknife (1973).

Usage

```
layard(trat, resp, t, r)
```

Arguments

| | |
|------|--|
| trat | Numeric or complex vector containing treatments. |
| resp | Numeric or complex vector containing the response variable. |
| t | Number of treatments. |
| r | Numeric or complex vector containing the number of replications of each treatment. |

Value

Returns the p-value of the Layard test of homogeneity of variances and its practical interpretation for the significance level of 5%.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

LAYARD, M. N. J. Robust large-sample tests for homogeneity of variances. *Journal of the American Statistical Association*, v.68, n.341, p.195-198, 1973.

NOGUEIRA, D, P.; PEREIRA, G, M. Desempenho de testes para homogeneidade de variâncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

See Also

See also: [bartlett](#), [samiuddin](#), [levene](#), [oneillmathews](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar='layard')
```

levene

Test for homogeneity of variances of Levene

Description

Performs the test for homogeneity of variances of Levene (1960).

Usage

```
levene(trat, resp, t, r)
```

Arguments

| | |
|------|--|
| trat | Numeric or complex vector containing treatments. |
| resp | Numeric or complex vector containing the response variable. |
| t | Number of treatments. |
| r | Numeric or complex vector containing the number of replications of each treatment. |

Value

Returns the p-value of Levene's test of homogeneity of variances and its practical interpretation for significance level of 5%.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

LEVENE, H. Robust tests for equality of variances. in: Olkin, i.; ghurye, s.g.; hoeffding, w.; madow, w.g.; mann, h.b. (eds.). *Contribution to Probability and Statistics*. Stanford, CA: Stanford University Press, pages 278-292, 1960.

NOGUEIRA, D, P.; PEREIRA, G, M. Desempenho de testes para homogeneidade de variâncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

See Also

See also: [bartlett](#), [layard](#), [oneillmathews](#), [samiuddin](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar='levne')
```

lsd

Multiple comparison: Least Significant Difference test

Description

Performs the t test (LSD) for multiple comparison of means.

Usage

```
lsd(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance level. |
| group | TRUE or FALSE |
| main | Title |

Value

Returns the multiple comparison of means according to the LSD test.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

See Also

see: [snk](#), [duncan](#), [ccboot](#), [lsdb](#), [scottknott](#), [tukey](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='lsd', sigT = 0.05)
```

lsdb

Multiple comparison: Bonferroni's Least Significant Difference test

Description

Performs the t test (LSD) with Bonferroni's protection, for multiple comparison of means

Usage

```
lsdb(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance level. |
| group | TRUE or FALSE |
| main | Title |

Value

Returns the multiple comparison of means according to the LSDB test.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

See Also

See: [snk](#), [duncan](#), [lsd](#), [ccboot](#), [scottknott](#), [tukey](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='lsdb', sigT = 0.05)
```

oneilldb

Test for homogeneity of variances of O'Neill and Mathews (RBD)

Description

Performs the test for homogeneity of variances of O'Neill and Mathews (2002).

Usage

```
oneilldb(resp, trat, block)
```

Arguments

| | |
|-------|---|
| resp | Numeric or complex vector containing the response variable. |
| trat | Numeric or complex vector containing treatments. |
| block | Numeric or complex vector containing blocks. |

Value

Returns the p-value of O'Neill and Mathews' test of homogeneity of variances and its practical interpretation for significance level of 5%.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

O'NEILL, M. E.; MATHEWS, K. L. Levene tests of homogeneity of variance for general block and treatment designs. *Biometrics*, 58:216-224, Mar. 2002.

RIBEIRO, R. *Proposta e comparacao do desempenho de testes para homogeneidade de variancia de modelos de classi cação one-way e two-way*. Iniciação Científica. (Iniciação Científica) - Universidade Federal de Alfenas. 2012.

See Also

see: [anscombetukey](#), [han](#)

Examples

```
data(ex2)
attach(ex2)
rbd(trat, provador, aparencia, hvar='oneillmathews')
```

oneillmathews

Test for homogeneity of variances of O'Neill and Mathews (CRD)

Description

Performs the test for homogeneity of variances of O'Neill and Mathews (2000).

Usage

```
oneillmathews(trat, resp, t, r)
```

Arguments

| | |
|------|--|
| trat | Numeric or complex vector containing treatments. |
| resp | Numeric or complex vector containing the response variable. |
| t | Number of treatments. |
| r | Numeric or complex vector containing the number of replications of each treatment. |

Value

Returns the p-value of O'Neill and Mathews' test of homogeneity of variances and its practical interpretation for significance level of 5%.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

O'NEILL, M. E.; MATHEWS, K. L. A weighted least squares approach to levene test of homogeneity of variance. *Australian e New Zealand Journal Statistical*, 42(1):81-100, 2000.

NOGUEIRA, D, P.; PEREIRA, G, M. Desempenho de testes para homogeneidade de variâncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

See Also

See also: [bartlett](#), [layard](#), [levene](#), [samiuddin](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar='oneillmathews', sigF = 0.05)
```

order.group

Ordering the treatments according to the multiple comparison

Description

Orders the groups os means.

Usage

```
order.group(trt, means, N, MSerror, Tprob, std.err, parameter = 1)
```

Arguments

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

Value

trt Factor means Numeric N Numeric MSerror Numeric Tprob value between 0 and 1 std.err Numeric parameter Constant

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
(Adapted from Felipe de Mendiburu - GPL)

See Also

order.stat

| | |
|----------------|--|
| order.stat.SNK | <i>Grouping the treatments averages in a comparison with a minimum value</i> |
|----------------|--|

Description

Orders the groups of means according to the test of SNK.

Usage

```
order.stat.SNK(treatment, means, minimum)
```

Arguments

| | |
|-----------|----------------------------------|
| treatment | treatment |
| means | means of treatment |
| minimum | minimum value for the comparison |

Value

trt Factor means Numeric minimum Numeric

Author(s)

Denismar Alves Nogueira
 Eric Batista Ferreira
 Portya Piscitelli Cavalcanti
 (Adapted from Felipe de Mendiburu - GPL)

See Also

order.group

| | |
|---------|-------------------------------|
| plotres | <i>Set of plots residuals</i> |
|---------|-------------------------------|

Description

Residual plots for a output model. Four sets of plots are produced: (1) Histogram, (2) normal probability plot for the residual, (3) Standardized Residuals versus Fitted Values, and (4) box-plot (Standardized Residuals).

Usage

```
plotres(x)
```

Arguments

x Output from anova (performed in ExpDes)

Note

The default "printing" of the result will produce four plots of any model of the

Author(s)

Denismar Alves Nogueira

References

STEEL, R. G. D.; TORRIE, J. H. *Principles and procedures in Statistics: a biometrical approach*. McGraw-Hill, New York, NY. 1980.

See Also

See also:[graphics](#)

Examples

```
data(ex1)
attach(ex1)
a<-crd(trat, ig)
plotres(a)
```

rbd

Randomized Blocks Design

Description

Analyses experiments in balanced Randomized Blocks Designs under one single factor, considering a fixed model.

Usage

```
rbd(treat, block, resp, quali = TRUE, mcomp = "tukey", nl = FALSE,
hvar='oneillmathews', sigT = 0.05, sigF = 0.05)
```

Arguments

treat Numeric or complex vector containing the treatments.
block Numeric or complex vector containing the blocks.
resp Numeric or complex vector containing the response variable.
quali Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives.

| | |
|-------|---|
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| n1 | Logic. If FALSE (<i>default</i>) linear regression models are adjusted. If TRUE, non-linear regression models are adjusted. |
| hvar | Allows choosing a test for homogeneity of variances; the <i>default</i> is the test of O'Neill and Mathews ('oneillmathews'), however, there are other options: test of Han ('han') and test of Ascombe and Tukey ('anscombetukey'). |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira

Eric Batista Ferreira

Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

FERREIRA, E. B.; CAVALCANTI, P. P.; NOGUEIRA D. A. Funcao em codigo R para analisar experimentos em DBC simples, em uma so rodada. In: JORNADA CIENTIFICA DA UNIVERSIDADE FEDERAL DE ALFENAS-MG, 2., 2009, Alfenas. Annals... ALFenas: Unifal-MG, 2009.

See Also

For more examples, see: [fat2.rbd](#), [fat3.rbd](#), [split2.rbd](#), [strip](#), [fat2.ad.rbd](#) and [fat3.ad.rbd](#).

Examples

```
data(ex2)
attach(ex2)
rbd(trat, provador, aparencia, quali = TRUE, mcomp='lsd',
    hvar='oneillmathews', sigT = 0.05, sigF = 0.05)
```

`reg.nl`*Non-linear Regression*

Description

Adjusts non-linear regression models in Anova (Models: Power, Exponential, Logistic, Gompertz).

Usage

```
reg.nl(resp, treat)
```

Arguments

| | |
|--------------------|---|
| <code>resp</code> | Numeric or complex vector containing the response variable. |
| <code>treat</code> | Numeric or complex vector containing the treatments. |

Value

Returns coefficients, significance and ANOVA of the fitted regression models.

Author(s)

Luiz Alberto Beijo
Eric Batista Ferreira

References

DRAPER, N.R.; SMITH, H. *Applied regression analysis*. 3ed. New York : John Wiley, 1998. 706p.

See Also

See too: [graphics](#)

Examples

```
data(ex_nl)
attach(ex_nl)
x<-crd(trat, resp, quali=FALSE, nl=TRUE)
graphics(x,degree = "log")
```

`reg.poly`*Polinomial Regression*

Description

Fits sequential regression models until the third power.

Usage

```
reg.poly(resp, treat, DFerror, SSerror, DFtreat, SStreat)
```

Arguments

| | |
|----------------------|---|
| <code>resp</code> | Numeric or complex vector containing the response variable. |
| <code>treat</code> | Numeric or complex vector containing the treatments. |
| <code>DFerror</code> | Error degrees of freedom |
| <code>SSerror</code> | Error sum of squares |
| <code>DFtreat</code> | Treatments' degrees of freedom |
| <code>SStreat</code> | Treatments' sum of squares |

Value

Returns coefficients, significance and ANOVA of the fitted regression models.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

GOMES, F. P. Curso de Estatística Experimental. 10a ed. Piracicaba: ESALQ/USP. 1982. 430.

See Also

See: [graphics](#)

| | |
|--------|---|
| respAd | <i>Fictional data: additional treatment</i> |
|--------|---|

Description

Response variable form the additional treatment.

Usage

```
data(respAd)
```

Format

The format is: num [1:3] 10.6 10.6 10.4

Examples

```
data(respAd)
## maybe str(respAd) ; plot(respAd) ...
```

| | |
|-----------|---|
| samiuddin | <i>Test for homogeneity of variances of Samiuddin</i> |
|-----------|---|

Description

Performs the test for homogeneity of variances of Samiuddin (1976).

Usage

```
samiuddin(trat, resp, t, r)
```

Arguments

| | |
|------|--|
| trat | Numeric or complex vector containing treatments. |
| resp | Numeric or complex vector containing the response variable. |
| t | Number of treatments. |
| r | Numeric or complex vector containing the number of replications of each treatment. |

Value

Returns the p-value of Samiuddin's test of homogeneity of variances and its practical interpretation for significance level of 5%.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Marcos Costa de Paula
Mateus Pimenta Siqueira Lima

References

SAMIUDDIN, M. Bayesian test of homogeneity of variance. *Journal of the American Statistical Association*, 71(354):515-517, Jun. 1976.

NOGUEIRA, D, P.; PEREIRA, G, M. Desempenho de testes para homogeneidade de variâncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

See Also

See also: [bartlett](#), [layard](#), [levene](#), [oneillmathews](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar='samiuddin', sigF = 0.05)
```

scottknott

Multiple comparison: Scott-Knott test

Description

Performs the test of Scott-Knott, for multiple comparison of means.

Usage

```
scottknott(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance level. |
| group | TRUE or FALSE |
| main | Title |

Value

Returns the multiple comparison of means according to the test of Scott-Knott.

Author(s)

Denismar Alves Nogueira

Eric Batista Ferreira

Portya Piscitelli Cavalcanti

(Adapted from Laercio Junio da Silva - GPL(>=2))

References

RAMALHO, M. A. P.; FERREIRA, D. F.; OLIVEIRA, A. C. de. Experimentacao em Genetica e Melhoramento de Plantas. 2a ed. Lavras: UFLA. 2005. 300p.

See Also

[snk](#), [duncan](#), [lsd](#), [lsdb](#), [ccboot](#), [tukey](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='sk', sigT = 0.05)
```

secaAd

Composting: additional treatment

Description

Response variable (dry biomass) of the additional treatment of the experiment about composting.

Usage

```
data(secaAd)
```

Format

The format is: num [1:3] 0.13 0.1 0.1

Examples

```
data(secaAd)
## maybe str(secaAd) ; plot(secaAd) ...
```

`snk`*Multiple comparison: Student-Newman-Keuls test*

Description

Performs the test of SNK, for multiple comparison of means.

Usage

```
snk(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|----------------------|---|
| <code>y</code> | Numeric or complex vector containing the response variable. |
| <code>trt</code> | Numeric or complex vector containing the treatments. |
| <code>DFerror</code> | Error degrees of freedom. |
| <code>SSerror</code> | Error sum of squares. |
| <code>alpha</code> | Significance level. |
| <code>group</code> | TRUE or FALSE |
| <code>main</code> | Title |

Value

Returns the multiple comparison of means according to the test of SNK.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

See Also

[tukey](#), [duncan](#), [lsd](#), [lsdb](#), [ccboot](#), [scottknott](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='snk', sigT = 0.05)
```

split2.crd

*Split-plots in CRD***Description**

Analyses experiments in Split-plot scheme in balanced Completely Randomized Design, considering a fixed model.

Usage

```
split2.crd(factor1, factor2, repet, resp, quali = c(TRUE, TRUE), mcomp = "tukey",
fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| repet | Numeric or complex vector containing the replications. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred CRD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Denismar Alves Nogueira
 Eric Batista Ferreira
 Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

[split2.rbd](#) and [strip](#)

Examples

```
data(ex9)
attach(ex9)
split2.crd(cobertura, prof, rep, pH, quali = c(TRUE, TRUE), mcomp = "lsd",
  fac.names = c("Cover", "Depth"), sigT = 0.05, sigF = 0.05)
```

split2.rbd

Split-plots in RBD

Description

Analyses experiments in Split-plot scheme in balanced Randomized Blocks Design, considering a fixed model.

Usage

```
split2.rbd(factor1, factor2, block, resp, quali = c(TRUE, TRUE), mcomp = "tukey",
  fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|---------|---|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| block | Numeric or complex vector containing the blocks. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('cboot'). |

| | |
|-----------|--|
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Details

The arguments sigT and mcomp will be used only when the treatment are qualitative.

Value

The output contains the ANOVA of the referred RBD, the Shapiro-Wilk normality test for the residuals of the model, the fitted regression models (when the treatments are quantitative) and/or the multiple comparison tests (when the treatments are qualitative).

Note

The [graphics](#) can be used to construct regression plots.

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

BANZATTO, D. A.; KRONKA, S. N. Experimentacao Agricola. 4 ed. Jaboticabal: Funep. 2006. 237 p.

See Also

[split2.crd](#) and [strip](#)

Examples

```
data(ex)
attach(ex)
split2.rbd(trat, dose, rep, resp, quali = c(TRUE, FALSE), mcomp = "tukey",
  fac.names = c("Treatment", "Dose"), sigT = 0.05, sigF = 0.05)
```

| | |
|-------|-------------------------------|
| strip | <i>Strip-plot experiments</i> |
|-------|-------------------------------|

Description

Analysis Strip-plot experiments

Usage

```
strip(factor1, factor2, block, resp, quali = c(TRUE, TRUE), mcomp = "tukey",
fac.names = c("F1", "F2"), sigT = 0.05, sigF = 0.05)
```

Arguments

| | |
|-----------|--|
| factor1 | Numeric or complex vector containing the factor 1 levels. |
| factor2 | Numeric or complex vector containing the factor 2 levels. |
| block | Numeric or complex vector containing the blocks. |
| resp | Numeric or complex vector containing the response variable. |
| quali | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| mcomp | Allows choosing the multiple comparison test; the <i>default</i> is the test of Tukey, however, the options are: the LSD test ('lsd'), the LSD test with Bonferroni protection ('lsdb'), the test of Duncan ('duncan'), the test of Student-Newman-Keuls ('snk'), the test of Scott-Knott ('sk'), the Calinski and Corsten test ('ccf') and bootstrap multiple comparison's test ('ccboot'). |
| fac.names | Allows labeling the factors 1 and 2. |
| sigT | The significance to be used for the multiple comparison test; the default is 5%. |
| sigF | The significance to be used for the F test of ANOVA; the default is 5%. |

Note

The [graphics](#) can be used to construct regression plots and [plotres](#) for residuals plots

Author(s)

Eric B Ferreira

Lais B S Ferreira

See Also

[rbd](#) and [split2.rbd](#)

Examples

```
data(ex5)
attach(ex5)
strip(trat, genero, bloco, sabor, quali=c(TRUE,TRUE), mcomp="tukey",
      fac.names=c("Amostras","Genero"), sigT = 0.05, sigF = 0.05)
```

| | |
|-------------|--|
| tapply.stat | <i>Statistics of data grouped by factors</i> |
|-------------|--|

Description

This process lies in finding statistics which consist of more than one variable, grouped or crossed by factors. The table must be organized by columns between variables and factors.

Usage

```
tapply.stat(y, x, stat = "mean")
```

Arguments

| | |
|------|----------------------|
| y | data.frame variables |
| x | data.frame factors |
| stat | Method |

Value

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

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
(Adapted from Felipe de Mendiburu - GPL)

tukey

Multiple comparison: Tukey's test

Description

Performs the test of Tukey, for multiple comparison of means.

Usage

```
tukey(y, trt, DFerror, SSerror, alpha = 0.05, group = TRUE, main = NULL)
```

Arguments

| | |
|---------|---|
| y | Numeric or complex vector containing the response variable. |
| trt | Numeric or complex vector containing the treatments. |
| DFerror | Error degrees of freedom. |
| SSerror | Error sum of squares. |
| alpha | Significance level. |
| group | TRUE or FALSE |
| main | Title |

Details

It is necessary first makes a analysis of variance.

Value

y Numeric trt factor DFerror Numeric MSerror Numeric alpha Numeric group Logic main Text

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
(Adapted from Felipe de Mendiburu - GPL)

References

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

See Also

[snk](#), [duncan](#), [lsd](#), [lsdb](#), [ccboot](#), [scottknott](#), [ccf](#)

Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='tukey', sigT = 0.05)
```

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