# Package ‘ExpDes’

October 12, 2022

**Type** Package

**Title** Experimental Designs Package

**Version** 1.2.2

**Date** 2021-10-04

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**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) - for qualitative treatments; residual analysis (Ferreira, Cavalcanti and Nogueira, 2014) <doi:10.4236/am.2014.519280>.

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

**Imports** stargazer

**Depends** R (>= 4.0)

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2021-10-05 04:30:02 UTC

## R topics documented:

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## `anscombetukey` *Test for homogeneity of variances of Anscombe and Tukey*

### Description

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

### Usage

```
anscombetukey(
  resp,
  Trat,
  Bloco,
  glres,
  msres,
  sstrat,
  ssbloco,
  residuals,
  fitted.values
)
```

### Arguments

| | |
|---|---|
| `resp` | Numeric or complex vector containing the response variable. |
| `Trat` | Numeric or complex vector containing the treatments. |
| `Bloco` | Numeric or complex vector containing the blocks. |
| `glres` | Residual degrees of freedom. |
| `msres` | Residual Mean Square. |
| `sstrat` | Residual Sum of Squares. |
| `ssbloco` | Sum of Squares for blocks. |
| `residuals` | Numeric or complex vector containing the residuals. |
| `fitted.values` | 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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 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

`han`, `oneillmathews`.

### Examples

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

---

## `bartlett` *Test for Homogeneity of Variances: Bartlett*

### Description

`bartlett` 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)

Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br>

Denismar Alves Nogueira

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 vari?ncias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

## See Also

`levene`, `oneillmathews`, `samiuddin`

## Examples

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

---

# `ccboot` *Multiple comparison: Bootstrap*

## Description

`ccboot` 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 varible. |
| `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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Patricia de Siqueira Ramos

Daniel Furtado 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.

### Examples

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

---

## `ccF` *Multiple comparison: Calinski and Corsten*

### Description

`ccF` 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 varible. |
| `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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Patricia de Siqueira Ramos

Daniel Furtado Ferreira

## References

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

## Examples

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

---

# `crd` *One factor Completely Randomized Design*

## Description

`crd` 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,
  unfold = NULL
)
```

## 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 *default* 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 (*default*) linear regression models are adjusted. IF TRUE, non-linear regression models are adjusted. |
| `hvar` | Allows choosing the test for homogeneity of variances; the *default* is the test of Bartlett, however there are other options: test of Levene ('levene'), test of Samiuddin ('samiuddin'), test of ONeill and Mathews ('oneillmathews') and the Layard test ('layard'). |
| `sigT` | The signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested. |

## 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).

### Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`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, unfold=NULL)
```

---

## `duncan` *Multiple comparison: Duncan test*

### Description

duncan 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

---

## `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

Numeric vector.

### Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

---

## `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

## Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

---

# `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

## Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## 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.

---

## `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

### Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

### References

PAIVA, A. P. de. Estudos Tecnologicos, Quimico, Fisico-quimico e Sensorial de Barras Alimenticias Elaboradas com Subprodutos e Residuos Agoindustriais. 2008. 131p. Dissertation (Master in Food Science) - Universidade Federal de Lavras, UFLA, Lavras, 2008.

---

## `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

## Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## References

COMASTRI FILHO, J. A. Avaliacao de especies de forrageiras nativas e exoticas na sub-regiao dos paiaguas no pantanal mato-grossense. Pesq. Agropec. Bras., Brasilia, v.29, n.6, p. 971-978, jun. 1994.

---

# `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

### Author(s)

Eric Batista Ferreira, <`eric.ferreira@unifal-mg.edu.br`>

### 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.

---

## `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 |

### Author(s)

Eric Batista Ferreira, <`eric.ferreira@unifal-mg.edu.br`>

### 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.

---

`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 |

### Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

---

`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.

## Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

---

# `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 |

## Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## 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.

---

## `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

### Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

### References

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

---

## `exnl` *Example of fictitious data set*

---

### Description

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

### Usage

```
data(exnl)
```

## Format

A data frame with 30 observations of the following 3 variables.

| | |
|---|---|
| `trat` | a numeric vector |
| `rep` | a numeric vector |
| `resp` | a numeric vector |

## Author(s)

Eric Batista Ferreira, <eric.ferreira@unifal-mg.edu.br>

---

# `fat2.ad.crd` *Double factorial scheme plus one additional treatment in CRD*

## Description

`fat2.ad.crd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat3.rbd`, `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,
unfold=NULL)
```

---

## `fat2.ad.rbd` *Double factorial scheme plus one additional treatment in RBD*

### Description

`fat2.ad.rbd` 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,
  unfold = NULL
)
```

### 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat3.rbd`, `fat2.ad.crd`, `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,
unfold=NULL)
```

---

`fat2.ad2.crd` *Double factorial scheme plus two additional treatments in CRD*

---

## Description

`fat2.ad2.crd` Analyses experiments in balanced Completely Randomized Design in double factorial scheme with two additional treatments, considering a fixed model.

## Usage

```
fat2.ad2.crd(
  factor1,
  factor2,
  repet,
  resp,
  respAd1,
  respAd2,
  quali = c(TRUE, TRUE),
  mcomp = "tukey",
  fac.names = c("F1", "F2"),
  sigT = 0.05,
  sigF = 0.05,
  unfold = NULL
)
```

## 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. |
| `respAd1` | Numeric or complex vector containing the additional treatment 1. |
| `respAd2` | Numeric or complex vector containing the additional treatment 2. |
| `quali` | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| `mcomp` | Allows choosing the multiple comparison test; the *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Portya Piscitelli Cavalcanti

Sônia Maria De Stefano Piedade

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## References

???

## See Also

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat3.rbd`, `fat2.ad.crd`, `fat2.ad.rbd`, `fat3.ad.crd` and `fat3.ad.rbd`.

## Examples

```
factor1<-c(rep(1,6),rep(2,6))
factor2<-c(rep(1,3),rep(2,3),rep(1,3),rep(2,3))
repet<-rep(1:3,4)
resp<-c(10.0,10.8,9.8,10.3,11.3,10.3,9.7,10.1,10.2,9.4,11.6,9.1)
respAd1<-c(10.6,10.6,10.4)
respAd2<-c(5.7,6,7.4)
data.frame(factor1,factor2,repet,resp)
fat2.ad2.crd(factor1, factor2, repet, resp, respAd1, respAd2,
quali=c(TRUE, FALSE), mcomp = "tukey", fac.names =
c("XXXX", "YYYY"), sigT = 0.05, sigF = 0.05, unfold=NULL)
```

## `fat2.ad2.rbd` *Double factorial scheme plus two additional treatments in RBD*

### Description

`fat2.ad2.rbd` Analyses experiments in balanced Randomized Blocks Design in double factorial scheme with two additional treatments, considering a fixed model.

### Usage

```
fat2.ad2.rbd(
  factor1,
  factor2,
  block,
  resp,
  respAd1,
  respAd2,
  quali = c(TRUE, TRUE),
  mcomp = "tukey",
  fac.names = c("F1", "F2"),
  sigT = 0.05,
  sigF = 0.05,
  unfold = NULL
)
```

### 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. |
| `respAd1` | Numeric or complex vector containing the additional treatment 1. |
| `respAd2` | Numeric or complex vector containing the additional treatment 2. |
| `quali` | Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives. |
| `mcomp` | Allows choosing the multiple comparison test; the *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Portya Piscitelli Cavalcanti

Sônia Maria De Stefano Piedade

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## References

???

## See Also

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat3.rbd`, `fat2.ad.crd`, `fat2.ad.rbd`, `fat3.ad.crd` and `fat3.ad.rbd`.

## Examples

```
factor1<-c(rep(1,6),rep(2,6))
factor2<-c(rep(1,3),rep(2,3),rep(1,3),rep(2,3))
block<-rep(1:3,4)
resp<-c(10.0,10.8,9.8,10.3,11.3,10.3,9.7,10.1,10.2,9.4,11.6,9.1)
respAd1<-c(10.6,10.6,10.4)
respAd2<-c(5.7,6,7.4)
data.frame(factor1,factor2,block,resp)
fat2.ad2.rbd(factor1, factor2, block, resp, respAd1, respAd2,
quali=c(TRUE, FALSE), mcomp = "tukey", fac.names =
c("XXXX", "YYYY"), sigT = 0.05, sigF = 0.05, unfold=NULL)
```

---

`fat2.crd` *Double factorial scheme in CRD*

---

## Description

`fat2.crd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

### References

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

### See Also

`crd`, `fat3.crd`, `split2.crd`, `fat2.ad.crd` and `fat3.ad.crd`.

### Examples

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

---

## `fat2.rbd` *Double factorial scheme in RBD*

### Description

`fat2.rbd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

## References

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

## See Also

`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, unfold=NULL)
```

---

# `fat3.ad.crd` *Triple factorial scheme plus an additional treatment in CRD*

## Description

`fat3.ad.crd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2.1', '2.2' or '2.3', the double interactions are unfolded; if '3', the triple interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`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, unfold=NULL)
```

---

# `fat3.ad.rbd` *Triple factorial scheme plus an additional treatment in RBD*

## Description

`fat3.ad.rbd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2.1', '2.2' or '2.3', the double interactions are unfolded; if '3', the triple interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat3.rbd`, `fat2.ad.crd`, `fat2.ad.rbd`, `fat3.ad.crd` and `fat3.ad.crd`.

## 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, unfold=NULL)
```

---

# `fat3.crd` *Triple factorial scheme in CRD*

---

## Description

`fat3.crd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2.1', '2.2' or '2.3', the double interactions are unfolded; if '3', the triple interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

## References

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

## See Also

`fat2.crd`, `fat2.rbd`, `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

`fat3.rbd` 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,
  unfold = NULL
)
```

### 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if ’0’, just ANOVA is performed; if ’1’, the simple effects are tested; if ’2.1’, ’2.2’ or ’2.3’, the double interactions are unfolded; if ’3’, the triple interaction is unfolded. |

### 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

### References

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

### See Also

`fat2.crd`, `fat2.rbd`, `fat3.crd`, `fat2.ad.crd`, `fat2.ad.rbd`, `fat3.ad.crd` and `fat3.ad.crd`.

### 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,
unfold=NULL)
```

---

## `ginv` *Generalized inverse*

### Description

`ginv` Computes the Moore-Penrose generalized inverse of a matrix X.

### Usage

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

### Arguments

| | |
|---|---|
| `X` | Matrix for which the Moore-Penrose inverse is required. |
| `tol` | 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

`solve`, `svd`, `eigen`

---

## `graphics` *Regression model plots*

### Description

`graphics` 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 *default*, 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 *default* is TRUE. |
| `main` | Title of the plot. Empty is the *default*. |
| `sub` | Subtitle of the plot. Empty is the *default*. |
| `xlab` | Name for axis X. |
| `ylab` | Name for axis Y. |
| `pch` | Caracter 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 B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

## 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

han 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 classicacao one-way e two-way*. Iniciacao Cientifica. (Iniciacao Cientifica) - Universidade Federal de Alfenas. 2012.

## See Also

`anscombetukey`, `oneillmathews`.

## Examples

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

---

# `lastC` *Setting the last character of a chain*

## Description

`lastC` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author 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` *Latin Square Design*

### Description

`lastd` 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,
  unfold = NULL
)
```

### 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 *default* 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'). |
| `sigT` | The signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested. |

## 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).

## Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Portya Piscitelli Cavalcanti @note The `graphics` can be used to construct regression plots and `plotres` for residuals plots.

## References

GOMES, F. P. Curso de Estatistica 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

`crd`, `rbd`.

## Examples

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

---

## `layard` *Test for homogeneity of variances of Layard*

---

### Description

`layard` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 variancias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

### 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

`levene` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 variancias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

### See Also

`bartlett`, `samiuddin`, `layard`, `oneillmathews`.

### Examples

```
data(ex1)
attach(ex1)
crd(trat, ig, quali = FALSE, hvar = "levene")
```

---

## `lsd` *Multiple comparison: Least Significant Difference test*

---

### Description

`lsd` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

### See Also

`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

`lsdb` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

## See Also

`snk`, `duncan`, `ccboot`, `lsd`, `scottknott`, `tukey`, `ccF`.

## Examples

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

---

`oneilldbc` *Test for homogeneity of variances of ONeill and Mathews (RBD)*

---

## Description

`oneilldbc` Performs the test for homogeneity of variances of ONeill and Mathews (2002).

## Usage

```
oneilldbc(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 ONeill and Mathews' test of homogeneity of variances and its practical interpretation for significance level of 5%.

## Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 classificacao one-way e two-way*. Iniciacao Cientifica. (Iniciacao Cientifica) - Universidade Federal de Alfenas. 2012.

## See Also

`anscombetukey`, `han`.

## Examples

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

---

## `oneillmathews` *Test for homogeneity of variances of ONeill and Mathews (CRD)*

---

### Description

`oneillmathews` Performs the test for homogeneity of variances of ONeill 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 ONeill and Mathews' test of homogeneity of variances and its practical interpretation for significance level of 5%.

### Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 variancias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

### 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

`order.group` It orders the groups of 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Portya Piscitelli Cavalcanti (Adapted from Felipe de Mendiburu - GPL)

## See Also

`order.stat.SNK`.

---

## `order.stat.SNK` *Grouping the treatments averages in a comparison with a minimum value*

---

### Description

`order.stat.SNK` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Portya Piscitelli Cavalcanti (Adapted from Felipe de Mendiburu - GPL)

### See Also

`order.group`.

---

## `plotres` *Residual plots*

---

### Description

`plotres` 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). |

### Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @note The default produces four plots regarding the ANOVA assumptions.

### References

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

### See Also

`graphics`.

### Examples

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

---

## `rbd` *Randomized Blocks Design*

### Description

`rbd` 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,
  unfold = NULL
)
```

## 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 *default* 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 (*default*) linear regression models are adjusted. IF TRUE, non-linear regression models are adjusted. |
| `hvar` | Allows choosing the test for homogeneity of variances; the *default* is the test of ONeill and Mathews ('oneillmathews'), however there are other options: test of Han ('han'), and the test of Anscombe and Tukey ('anscombetukey'). |
| `sigT` | The signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`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,
unfold=NULL)
```

---

# `reg.nl` *Non-linear Regression*

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| `resp` | Numeric or complex vector containing the response variable. |
| `treat` | Numeric or complex vector containing the treatments. |

## Value

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

## Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Luiz Alberto Beijo

## References

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

### See Also

`graphics`.

### Examples

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

---

## `reg.poly` *Polinomial Regression*

### Description

`reg.poly` Fits sequential regression models until the third power.

### Usage

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

### Arguments

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

### Value

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

### Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

### References

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

### See Also

`graphics`.

---

## `respAd` *Fictional data: additional treatment*

---

### Description

Response variable form the additional treatment.

### Usage

```
data(respAd)
```

### Format

Numeric vector.

### Author(s)

Eric Batista Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

---

## `samiuddin` *Test for homogeneity of variances of Samiuddin*

---

### Description

`samiuddin` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>` @author Denismar Alves Nogueira @author Marcos Costa de Paula @author 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 variancias em delineamentos inteiramente casualizados. *Sigmae*, Alfenas, v.2, n.1, p. 7-22. 2013.

## 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

`scottknott` 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)

Eric B Ferreira, <`eric.ferreira@unifal-mg.edu.br`>

Denismar Alves Nogueira

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

Numeric vector.

## Author(s)

Eric Batista Ferreira, <`eric.ferreira@unifal-mg.edu.br`>

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

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### Description

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

### Usage

```
snk(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 SNK.

### Author(s)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti

### See Also

`scottknott`, `duncan`, `lsd`, `lsdb`, `ccboot`, `tukey`, `ccF`.

### Examples

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

## `split2.crd` *Split-plots in CRD*

### Description

`split2.crd` 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,
  unfold = NULL
)
```

### 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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, unfold=NULL)
```

---

# `split2.rbd` *Split-plots in RBD*

## Description

`split2.rbd` 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,
  unfold = NULL
)
```

## 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

## 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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("Treatament", "Dose"),
sigT = 0.05, sigF = 0.05, unfold=NULL)
```

---

# `strip` *Strip-plot experiments*

## Description

`strip` 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,
  unfold = NULL
)
```

### 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 *default* 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 signficance to be used for the multiple comparison test; the default is 5%. |
| `sigF` | The signficance to be used for the F test of ANOVA; the default is 5%. |
| `unfold` | Says what must be done after the ANOVA. If NULL (*default*), recommended tests are performed; if '0', just ANOVA is performed; if '1', the simple effects are tested; if '2', the double interaction is unfolded. |

### 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Laís Brambilla Storti Ferreira

### See Also

`split2.rbd` and `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, unfold=NULL)
```

---

# `tapply.stat` *Statistics of data grouped by factors*

## Description

`tapply.stat` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

Portya Piscitelli Cavalcanti (Adapted from Felipe de Mendiburu - GPL)

---

## `tukey` *Multiple comparison: Tukey's test*

---

### Description

`tukey` 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)

Eric B Ferreira, `<eric.ferreira@unifal-mg.edu.br>`

Denismar Alves Nogueira

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

`scottknott`, `duncan`, `lsd`, `lsdb`, `ccboot`, `snk`, `ccF`.

## Examples

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

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