Package ‘ExpDes’

February 19, 2015

Type  Package
Title  Experimental Designs package
Version  1.1.2
Date  2013-04-06
Author  Eric Batista Ferreira, Portya Piscitelli Cavalcanti, Denismar
        Alves Nogueira
Maintainer  Eric Batista Ferreira <eric.ferreira@unifal-mg.edu.br>
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.
License  GPL-2
LazyLoad  yes
Encoding  latin1
NeedsCompilation  no
Repository  CRAN
Date/Publication  2013-05-07 17:22:18

R topics documented:

ExpDes-package  .................................................. 2
ccboot  .......................................................... 5
crd  .............................................................. 6
<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>duncan</td>
<td>7</td>
</tr>
<tr>
<td>est21Ad</td>
<td>8</td>
</tr>
<tr>
<td>ex</td>
<td>8</td>
</tr>
<tr>
<td>ex1</td>
<td>9</td>
</tr>
<tr>
<td>ex2</td>
<td>9</td>
</tr>
<tr>
<td>ex3</td>
<td>10</td>
</tr>
<tr>
<td>ex4</td>
<td>11</td>
</tr>
<tr>
<td>ex5</td>
<td>12</td>
</tr>
<tr>
<td>ex6</td>
<td>12</td>
</tr>
<tr>
<td>ex7</td>
<td>13</td>
</tr>
<tr>
<td>ex8</td>
<td>14</td>
</tr>
<tr>
<td>ex9</td>
<td>14</td>
</tr>
<tr>
<td>fat2_ad.crd</td>
<td>15</td>
</tr>
<tr>
<td>fat2_ad.rbd</td>
<td>17</td>
</tr>
<tr>
<td>fat2_crd</td>
<td>18</td>
</tr>
<tr>
<td>fat2_rbd</td>
<td>19</td>
</tr>
<tr>
<td>fat3_ad.crd</td>
<td>21</td>
</tr>
<tr>
<td>fat3_ad.rbd</td>
<td>22</td>
</tr>
<tr>
<td>fat3_crd</td>
<td>24</td>
</tr>
<tr>
<td>fat3_rbd</td>
<td>25</td>
</tr>
<tr>
<td>ginv</td>
<td>26</td>
</tr>
<tr>
<td>lastC</td>
<td>27</td>
</tr>
<tr>
<td>latsd</td>
<td>28</td>
</tr>
<tr>
<td>lsd</td>
<td>29</td>
</tr>
<tr>
<td>lsdB</td>
<td>30</td>
</tr>
<tr>
<td>order.group</td>
<td>31</td>
</tr>
<tr>
<td>order.stat.SNK</td>
<td>32</td>
</tr>
<tr>
<td>rbd</td>
<td>32</td>
</tr>
<tr>
<td>reg.poly</td>
<td>34</td>
</tr>
<tr>
<td>respAd</td>
<td>35</td>
</tr>
<tr>
<td>scottknott</td>
<td>35</td>
</tr>
<tr>
<td>secaAd</td>
<td>36</td>
</tr>
<tr>
<td>snk</td>
<td>36</td>
</tr>
<tr>
<td>split2_crd</td>
<td>37</td>
</tr>
<tr>
<td>split2_rbd</td>
<td>38</td>
</tr>
<tr>
<td>tapply.stat</td>
<td>40</td>
</tr>
<tr>
<td>tukey</td>
<td>40</td>
</tr>
</tbody>
</table>

**Index**

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>ExpDes-package</td>
<td></td>
</tr>
<tr>
<td>Experimental Designs package</td>
<td>42</td>
</tr>
</tbody>
</table>
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 - for qualitative treatments.

Details

Package: ExpDes
Type: Package
Version: 1.0
Date: 2010-11-09
License: GPL 2
LazyLoad: yes

Author(s)

Eric Batista Ferreira
Portya Piscitelli Cavalcanti
Denismar Alves Nogueira

Maintainer: Eric Batista Ferreira <eric@unifal-mg.edu.br>

References


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

Usage
ccboot(y, trt, DError, 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.
- `DError`: 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

Examples
```r
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp='ccboot', sigF = 0.05)
```
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", 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 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') and bootstrap multiple comparison's test ('ccboot').
- `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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
References


See Also

For more examples, see: fat2.crd, fat3.crd, split2.crd, split2.ad.crd and fat3.ad.crd.

Examples

```r
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

```r
duncan(y, trt, DError, 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.
**est21Ad**  
*Stink bugs in corn: additional treatment*

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

**Usage**
```r
data(est21Ad)
```

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

**Examples**
```r
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**
```r
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

```r
data(ex1)
## 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

```r
data(ex1)
```

Format

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

- `trat` a numeric vector
- `ig`  a numeric vector

References


Examples

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

ex2 

Food bars: RBD

Description

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

Usage

```r
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


Examples

dataHexRI
## maybe strHexRI 
plotHexRI

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


Examples

data(ex3)
## maybe str(ex3) ; plot(ex3) ...
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
c a   numeric vector
ca  a numeric vector

References


Examples

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

Examples

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

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) ...

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


Examples

data(ex7)
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


Examples

data(ex8)

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

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**


**Examples**

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

---

**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**

```r
fat2.ad.crd(factor1, factor2, repet, resp, respAd, quali = c(TRUE, TRUE), mcomp = "tukey", fac.names = ...
```

**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") 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: 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("Inoculante", "Biodiesel", "Vaso", "Seca", "SecaAd"))
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 = FALSE, 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 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") 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 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
References


See Also

For more examples, see: 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 = "sk", fac.names = c("Period", "Nivel", "Bloco", "Est1", "Est21", "Qualitative"))

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, quantitative.
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") 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: fat2.rbd, fat3.crd, fat3.rbd, fat2.ad.crd, fat2.ad.rbd, fat3.ad.crd and fat3.ad.rbd.

Examples

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

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') 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 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).

Author(s)

Denismar Alves Nogueira

Eric Batista Ferreira

Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: fat2.crd, fat3.crd, fat3.rbd, fat2.ad.crd, fat2.ad.rbd, fat3.ad.crd 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.
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", facNames)

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, quantitative.
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") and bootstrap multiple comparison’s test ("ccboot").
facNames 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).
Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: fat2.crd, fat2.rbd, fat3.crd, fat3.rbd, fat2.ad.crd, fat2.ad.rbd and fat3.ad.rbd.

Examples

data(ex6)
attach(ex6)
data(respAd)
fat3.ad.crd(factorA, factorB, factorC, rep, resp, respAd, quali = c(TRUE, TRUE, TRUE), mcomp = "duncan", fac.names =

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 = "tukene"
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") 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 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: fat2.crd, fat2.rbd, fat3.crd, fat3.rbd, fat2.ad.crd, fat2.ad.rbd 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("fat3.ad.rbd")))
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(1,2,3))

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") 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).

Author(s)
Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti
References


See Also

For more examples, see: fat2.crd, fat2.rbd, fat2.ad.crd, fat2.ad.rbd, fat3.rbd, fat3.ad.crd and fat3.ad.rbd.

Examples

data(ex6)
attach(ex6)
fat3.crd(factorA, factorB, factorC, resp, quali = c(TRUE, TRUE, TRUE), mcomp = "1sdb", fac.names = c("Factor A", "Factor B", "Factor C"))

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("Factor 1", "Factor 2", "Factor 3"), sigf = 0.05, sigt = 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, quantitative.

mcomp Allows choosing the multiple comparison test; the default is the test of Tukey, however, the options are: 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') 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 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

For more examples, see: fat2.crd, fat2.rbd, fat2.ad.crd, fat2.ad.rbd, fat3.crd, fat3.ad.crd and fat3.ad.rbd.

Examples

dataHex6I
attachHex6I
fatSNrbdHfatoraL fatorbL fatorcL repL respL quali 
] cHtrueL trueL trueIL mcomp 
] BtukeyBL facNnames 
] cHBfactor aBL Bfactor bBL Bfactor cBIL sigt 
] PNPUL sigf 
] PNPUI
ginv

Description

Calculates 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


See Also

See also: solve, svd, eigen.

Examples

```r
## 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)
```

---

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

```r
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

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

latsd

Latin Square Design

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

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>treat</td>
<td>Numeric or complex vector containing the treatments.</td>
</tr>
<tr>
<td>row</td>
<td>Numeric or complex vector containing the rows.</td>
</tr>
<tr>
<td>column</td>
<td>Numeric or complex vector containing the columns.</td>
</tr>
<tr>
<td>resp</td>
<td>Numeric or complex vector containing the response variable.</td>
</tr>
<tr>
<td>quali</td>
<td>Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitative.</td>
</tr>
<tr>
<td>mcomp</td>
<td>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') and bootstrap multiple comparison's test ('ccboot').</td>
</tr>
<tr>
<td>sigT</td>
<td>The significance to be used for the multiple comparison test; the default is 5%.</td>
</tr>
<tr>
<td>sigF</td>
<td>The significance to be used for the F test of ANOVA; the default is 5%.</td>
</tr>
</tbody>
</table>
The arguments sigT and mcomp will be used only when the treatment are qualitative.

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).

Denismar Alves Nogueira  
Eric Batista Ferreira  
Portya Piscitelli Cavalcanti


For more examples, see: crd and rbd

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

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

```
lsd(y, trt, Derror, 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

**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

```r
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

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  Grouping the treatments averages in a comparison with a minimum value

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

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", 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 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’) and bootstrap multiple comparison’s test (‘ccboot’).
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).

Author(s)
Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

See Also
For more examples, see: fat2.rbd, fat3.rbd, split2.rbd, split2.ad.rbd and fat3.ad.rbd.

Examples
```r
data(ex2)
attach(ex2)
rbd(trat, provador, aparenca, quali = TRUE, mcomp='lsd', sigT = 0.05, sigF = 0.05)
```
Description

Fits sequential regression models until the third power.

Usage

`reg.poly(resp, treat, DError, SSError, DFTreat, SSTreat)`

Arguments

- `resp` Numeric or complex vector containing the response variable.
- `treat` Numeric or complex vector containing the treatments.
- `DError` Error degrees of freedom
- `SSError` Error sum of squares
- `DFTreat` Treatments’ degrees of freedom
- `SSTreat` 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

**respAd**

_Fictional data: additional treatment_

---

**Description**

Response variable form the additional treatment.

**Usage**

```r
data(respAd)
```

**Format**

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

**Examples**

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

---

**scottknott**

_Multiple comparison: Scott-Knott test_

---

**Description**

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

**Usage**

```r
scottknott(y, trt, DError, 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

---

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, DError, 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.
- **DError**: Error degrees of freedom.
- **SError**: 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)**

- Denismar Alves Nogueira
- Eric Batista Ferreira
- Portya Piscitelli Cavalcanti

---

**Description**

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

**Usage**

```r
split2.crd(factor1, factor2, repet, resp, quali = c(TRUE, TRUE), mcomp = "tukey", fac.names = c("F1", "F2"), main = "Title")
```

---

**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') 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).

Author(s)
Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References

Examples
```
data(ex9)
attach(ex9)
split2.rbd(cobertura, prof, rep, pH, quali = c(TRUE, TRUE), mcomp = "1sd", fac.names = c("Cover", "Depth"), sigT = ...)
```

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", ...)```
split2.rbd

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') 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 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).

Author(s)

Denismar Alves Nogueira
Eric Batista Ferreira
Portya Piscitelli Cavalcanti

References


See Also

split2.crd

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)
tapplyNstat  

Statistics of data grouped by factors

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, DError, 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

LSD.test, waller.test
Index

*Topic package
  ExpDes-package, 2

ccboot, 5
crd, 6
duncan, 7
est21Ad, 8
ex, 8
ex1, 9
ex2, 9
ex3, 10
ex4, 11
ex5, 12
ex6, 12
ex7, 13
ex8, 14
ex9, 14
ExpDes (ExpDes-package), 2
ExpDes-package, 2

fat2.ad.crd, 15
fat2.ad.rbd, 17
fat2.crd, 18
fat2.rbd, 19
fat3.ad.crd, 21
fat3.ad.rbd, 22
fat3.crd, 24
fat3.rbd, 25
ginv, 26
lastC, 27
latsd, 28
lsd, 29
lsdb, 30

order.group, 31
order.stat.SNK, 32
rbd, 32
reg.poly, 34
respAd, 35
scottknott, 35
secaAd, 36
snk, 36
split2.crd, 37
split2.rbd, 38
tapply.stat, 40
tukey, 40