Package ‘ExpDes’

October 5, 2021

Type Package
Title Experimental Designs Package
Version 1.2.2
Date 2021-10-04
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; 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:

anscombetukey ......................................................... 3
bartlett ................................................................. 4
ccboot ................................................................. 5
<table>
<thead>
<tr>
<th>R topics documented:</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>ccF</td>
<td>6</td>
</tr>
<tr>
<td>crd</td>
<td>7</td>
</tr>
<tr>
<td>duncan</td>
<td>9</td>
</tr>
<tr>
<td>est21Ad</td>
<td>10</td>
</tr>
<tr>
<td>ex</td>
<td>10</td>
</tr>
<tr>
<td>ex1</td>
<td>11</td>
</tr>
<tr>
<td>ex2</td>
<td>12</td>
</tr>
<tr>
<td>ex3</td>
<td>12</td>
</tr>
<tr>
<td>ex4</td>
<td>13</td>
</tr>
<tr>
<td>ex5</td>
<td>14</td>
</tr>
<tr>
<td>ex6</td>
<td>15</td>
</tr>
<tr>
<td>ex7</td>
<td>15</td>
</tr>
<tr>
<td>ex8</td>
<td>16</td>
</tr>
<tr>
<td>ex9</td>
<td>17</td>
</tr>
<tr>
<td>exnl</td>
<td>17</td>
</tr>
<tr>
<td>fat2.ad.crd</td>
<td>18</td>
</tr>
<tr>
<td>fat2.ad.rbd</td>
<td>20</td>
</tr>
<tr>
<td>fat2.ad2.crd</td>
<td>22</td>
</tr>
<tr>
<td>fat2.ad2.rbd</td>
<td>24</td>
</tr>
<tr>
<td>fat2.crd</td>
<td>26</td>
</tr>
<tr>
<td>fat2.rbd</td>
<td>27</td>
</tr>
<tr>
<td>fat3.ad.crd</td>
<td>29</td>
</tr>
<tr>
<td>fat3.ad.rbd</td>
<td>31</td>
</tr>
<tr>
<td>fat3.crd</td>
<td>33</td>
</tr>
<tr>
<td>fat3.rbd</td>
<td>35</td>
</tr>
<tr>
<td>ginv</td>
<td>36</td>
</tr>
<tr>
<td>graphics</td>
<td>37</td>
</tr>
<tr>
<td>han</td>
<td>38</td>
</tr>
<tr>
<td>lastC</td>
<td>39</td>
</tr>
<tr>
<td>latsd</td>
<td>40</td>
</tr>
<tr>
<td>layard</td>
<td>42</td>
</tr>
<tr>
<td>levene</td>
<td>43</td>
</tr>
<tr>
<td>lsd</td>
<td>44</td>
</tr>
<tr>
<td>lsdb</td>
<td>45</td>
</tr>
<tr>
<td>oneilldbc</td>
<td>46</td>
</tr>
<tr>
<td>oneillmathews</td>
<td>47</td>
</tr>
<tr>
<td>order.group</td>
<td>48</td>
</tr>
<tr>
<td>order.stat.SNK</td>
<td>49</td>
</tr>
<tr>
<td>plotres</td>
<td>49</td>
</tr>
<tr>
<td>rbd</td>
<td>50</td>
</tr>
<tr>
<td>reg.nl</td>
<td>52</td>
</tr>
<tr>
<td>reg.poly</td>
<td>53</td>
</tr>
<tr>
<td>respAd</td>
<td>54</td>
</tr>
<tr>
<td>samiuddin</td>
<td>54</td>
</tr>
<tr>
<td>scottknott</td>
<td>55</td>
</tr>
<tr>
<td>secaAd</td>
<td>56</td>
</tr>
<tr>
<td>snk</td>
<td>57</td>
</tr>
<tr>
<td>split2.crd</td>
<td>58</td>
</tr>
</tbody>
</table>
anscombetukey

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.
Description

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

Usage

bartlett(trat, resp, t, r)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trat</td>
<td>Numeric or complex vector containing the treatments.</td>
</tr>
<tr>
<td>resp</td>
<td>Numeric or complex vector containing the response variable.</td>
</tr>
<tr>
<td>t</td>
<td>Number of treatments.</td>
</tr>
<tr>
<td>r</td>
<td>Numeric or complex vector containing the number of replications of each treatment.</td>
</tr>
</tbody>
</table>
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

See Also
levene, oneillmathews, samiuddin

Examples
```r
data(ex1)
attach(ex1)
iccboot(trat, ig, quali = FALSE, hvar='Var, sigF = 0.05)
```

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

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

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

Value

Multiple means comparison for the bootstrap test.

Author(s)

Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br>
Patricia de Siqueira Ramos
Daniel Furtado Ferreira

References


Examples

```r
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

```r
ccf(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 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>
- Patrícia de Siqueira Ramos
- Daniel Furtado Ferreira

References


Examples

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

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 Numerical or complex vector containing the treatments.
resp Numerical 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 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%.
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).
duncan

Author(s)
Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br>
Denismar Alves Nogueira
Portya Piscitelli Cavalcanti

References

See Also
fat2.crd, fat3.crd, split2.crd, fat2.ad.crd and fat3.ad.crd.

Examples
```r
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)
**ex1**

**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**

**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**

---

**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


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
cn  a numeric vector
Author(s)

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

References


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

**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>

---

**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>

---

**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**

**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**


---

**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 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%.

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


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').
fat2.ad.rbd

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%.
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


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)
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 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%.
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 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 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%.
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

```r
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 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%.
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


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)

Description

fat2.rbd Analyses experiments in balanced Randomized Blocks Designs in double factorial scheme, considering a fixed model.
fat2.rbd

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 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%.
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 quantitatives) 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.
fat3.ad.crd

Author(s)
Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br>
Denismar Alves Nogueira
Portya Piscitelli Cavalcanti

References

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 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%.
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>
Denisimar Alves Nogueira
Portya Piscitelli Cavalcanti

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

```r
data(ex6)
attach(ex6)
data(respAd)
fat3.ad.crd(factorA, factorB, factorC, 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)
```

Description

fat3.ad.rbd Analyses experiments in balanced Randomized Blocks Designs in triple factorial scheme with an additional treatment, considering a fixed model.

Usage

```r
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 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%.

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


See Also

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

```r
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)
```

Description

fat3.crd Analyses experiments in balanced Completely Randomized Design in triple factorial scheme, considering a fixed model.

Usage

```r
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’).
fat3.crd

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%.
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


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)
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 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%.
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


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**


**See Also**

solve, svd, eigen

---

**Description**

**graphics** Plots from regression models fitted in ANOVA.

**Usage**

```r
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

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


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, aparenca, hvar = "han")

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"

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

Usage
  latsd(
    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 = TRUE,            # Logic. If TRUE (default), the treatments are assumed qualitative, if FALSE, quantitatives.
    mcomp = "tukey",         # mcomp = "tukey",
    sigT = 0.05,             # sigT = 0.05,
    sigF = 0.05,             # sigF = 0.05,
    unfold = NULL            # unfold = NULL
  )
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 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%.

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


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

```r
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


See Also

`bartlett`, `samiuddin`, `levene`, `oneillmathews`.

Examples

```r
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**

```r
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**


**See Also**

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

**Examples**

```r
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, 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)

Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br>
Denismar Alves Nogueira
Portya Piscitelli Cavalcanti

See Also

snk, duncan, ccboot, lsdb, scottknot, 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**

```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)**

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**

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


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, aparenca, hvar = "oneillmathews")
Test for homogeneity of variances of O'Neill and Mathews (CRD)

Description

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

Usage

oneillmathews(trat, resp, t, r)

Arguments

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

Value

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

Author(s)

Eric B Ferreira, <eric.ferreira@unifal-mg.edu.br> @author Denismar Alves Nogueira @author Marcos Costa de Paula @author Mateus Pimenta Siqueira Lima

References


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**  

- **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

- 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


See Also

- graphics.

Examples

```r
data(ex1)
attach(ex1)
a<-crd(trat, ig)
plotres(a)
```
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 O'Neill and Mathews (‘oneillmathews’), however there are other options: test of Han (‘han’), and the test of Anscombe and Tukey (‘anscombetukey’).
sigT The significance to be used for the multiple comparison test; the default is 5%.
sigF The significance to be used for the F test of ANOVA; the default is 5%.
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 quantitave) 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


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)

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

reg.poly

See Also

graphics.

Examples

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

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' degrees 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


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%.
scottknott

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


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.
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>
snk

Multiple comparison: Student-Newman-Keuls test

Description

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

Usage

```r
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.
- `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

```r
data(ex1)
attach(ex1)
crd(trat, ig, quali = TRUE, mcomp = "snk", sigT = 0.05)
```
split2.crd 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"),
  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 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%.
- `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


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)
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 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%.
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.
**strip**

Strip-plot experiments

**Description**

`strip` Analysis Strip-plot experiments.

**Usage**

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

**Examples**

```r
data(ex)
attach(ex)
strip2.rbd(trat, dose, rep, resp, quali = c(TRUE, FALSE),
mcomp = "tukey", fac.names = c("Treatament", "Dose"),
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 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%.
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)

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**

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

* datasets
  - est21Ad, 10
  - ex, 10
  - ex1, 11
  - ex2, 12
  - ex3, 12
  - ex4, 13
  - ex5, 14
  - ex6, 15
  - ex7, 15
  - ex8, 16
  - ex9, 17
  - exnl, 17
  - respAd, 54
  - secaAd, 56

anscombetukey, 3, 39, 46

bartlett, 4, 42, 43, 47, 55

cceboot, 5, 44, 45, 56, 57, 64
cCF, 6, 44, 45, 56, 57, 64
crd, 7, 27, 41

duncan, 9, 44, 45, 56, 57, 64

eigen, 37
est21Ad, 10
ex, 10
ex1, 11
ex2, 12
ex3, 12
ex4, 13
ex5, 14
ex6, 15
ex7, 15
ex8, 16
ex9, 17
exnl, 17
fat2.ad.crd, 9, 18, 21, 23, 25, 27, 31, 32, 34, 36
fat2.ad.rbd, 19, 20, 23, 25, 29, 31, 32, 34, 36, 39, 52
fat2.ad2.crd, 22
fat2.ad2.rbd, 24
fat2.crd, 9, 19, 21, 23, 25, 26, 31, 32, 34, 36
fat2.rbd, 19, 21, 23, 25, 27, 31, 32, 34, 36, 39, 52
fat3.ad.crd, 9, 19, 21, 23, 25, 27, 29, 31, 32, 34, 36
fat3.ad.rbd, 19, 21, 23, 25, 29, 31, 32, 34, 35, 52
fat3.crd, 9, 19, 21, 23, 25, 27, 31, 32, 33, 36
fat3.rbd, 19, 21, 23, 25, 29, 31, 32, 34, 35, 52
ginv, 36
graphics, 19, 21, 23, 25, 27, 28, 30, 32, 34, 36, 37, 41, 50, 51, 53, 59, 60, 62
han, 4, 38, 46

lasC, 39
latsd, 40
layard, 42, 43, 47, 55
levene, 5, 42, 43, 47, 55
lsd, 44, 45, 56, 57, 64
lsdb, 44, 45, 56, 57, 64

oneilldbc, 46
oneillmathews, 4, 5, 39, 42, 43, 47, 55
order.group, 40, 48, 49
order.stat.SNK, 48, 49

plotres, 19, 21, 23, 25, 27, 28, 30, 32, 34, 36, 38, 41, 49, 51, 59, 60, 62

rbd, 41, 50, 62
reg.nl, 52
reg.poly, 38, 53
respAd, 54

samiuddin, 5, 42, 43, 47, 54
INDEX

scottknot, 44, 45, 55, 57, 64
secaAd, 56
snk, 44, 45, 56, 57, 64
solve, 37
split2.crd, 9, 27, 58, 61
split2.rbd, 29, 52, 59, 62
strip, 29, 52, 59, 61, 61
svd, 37

tapply.stat, 63
tukey, 44, 45, 56, 57, 64