Package 'GAD'

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Author Leonardo Sandrini-Neto & Mauricio G. Camargo

Maintainer Leonardo Sandrini-Neto <leonardosandrini@gmail.com>

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Description This package analyses complex ANOVA models with any combination of orthogonal/nested and fixed/random factors, as described by Underwood (1997). There are two restrictions: (i) data must be balanced; (ii) fixed nested factors are not allowed. Homogeneity of variances is checked using Cochran's C test and 'a posteriori' comparisons of means are done using Student-Newman-Keuls (SNK) procedure.

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GAD-package   *Analysis of variance from general principles*

Description

This package contains functions for the analysis of any complex ANOVA models with any combination of orthogonal/nested and fixed/random factors, based on general principles described by Underwood (1997).

Details

Package:	GAD
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License:	GPL (>= 2.0)

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)
Mauricio G. Camargo (<camargo.ufpr@gmail.com>)

Maintainer: leonardosandrini@gmail.com

References

Cornfield, J., Tukey, J.W. 1956. Average values of mean squares in factorials. *Annals of Mathematical Statistics*, **27**, 907-949.

Sokal, R.R., Rohlf, F.J. 1995. *Biometry: the principles and practice of statistics in biological research.* 3rd edition. W. H. Freeman and Co. New York. 887 pp.

Underwood, A.J. 1997. *Experiments in Ecology: Their Logical Design and Interpretation Using Analysis of Variance.* Cambridge University Press, Cambridge.

See Also

gad, estimates, C.test, snk.test

Examples

```
#Example 1
```

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
model <- lm(wing ~ CG + CG%in%MQ, data = rohlf95)
gad(model)
##
##
#Example 2
data(rats)
names(rats)
TR <- as.fixed(rats$treat)
RA <- as.random(rats$rat)
LI <- as.random(rats$liver)
model <- lm(glycog ~ TR + RA%in%TR + LI%in%RA%in%TR, data=rats)
gad(model)
##
##
#Example 3
data(snails)
O <- as.random(snails$origin)
S <- as.random(snails$shore)
B <- as.random(snails$boulder)
C <- as.random(snails$cage)
model <- lm(growth ~ O + S + O*S + B%in%S + O*(B%in%S) + C%in%(O*(B%in%S)),
            data = snails)
gad(model)
```

---

as.fixed   *Encodes a vector as a "fixed factor"*

Description

Assigns a class "fixed" to a vector

Usage

```
as.fixed(x)
```

Arguments

x   a vector of data

Details

The function works the same way as *as.factor*, but assigns an additional class informing that it is a fixed factor.

Value

as.factor returns an object of class "factor" and "fixed".

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

See Also

[as.random](#)

Examples

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
```

---

as.random   *Encodes a vector as a "random factor"*

Description

Assigns a class "random" to a vector

Usage

```
as.random(x)
```

Arguments

x   a vector of data

Details

The function works the same way as *as.factor*, but assigns an additional class informing that it is a random factor.

Value

as.factor returns an object of class "factor" and "random".

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

See Also

[as.fixed](#)

Examples

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
```

C.test   *Cochran's C test of homogeneity of variances*

Description

Performs a Cochran's test of the null hypothesis that the largest variance in several sampled variances are the same.

Usage

```
C.test(object)
```

Arguments

object   An object of class lm, containing the specified design.

Details

The test statistic is a ratio that relates the largest variance to the sum of the sampled variances.

Value

A list of class htest containing the following components:

statistic	Cochran's C test statistic
p-value	The p-value of the test
alternative	A character string describing the alternative hypothesis
method	The character string Cochran test of homogeneity of variances
data.name	A character string giving the name of the lm object
estimate	Sample estimates of variances

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

See Also

[gad](gad)

Examples

```
library(GAD)
data(rohlf95)
cg <- as.fixed(rohlf95$cages)
mq <- as.random(rohlf95$mosquito)
model <- lm(wing ~ cg + mq%in%cg, data = rohlf95)
C.test(model)
```

---

estimates   *Estimates of an ANOVA design*

Description

This function is used to construct the mean squares estimates of an ANOVA design, considering the complications imposed by nested/orthogonal and fixed/random factors.

Usage

```
estimates(object)
```

Arguments

object   an object of class lm, containing the specified design with random and/or fixed factors

Details

Determines what each mean square estimates in an ANOVA design by a set of procedures originally described by Cornfield and Tukey (1956). This version is a modification proposed by Underwood (1997), which does not allow for the use of fixed nested factors. The steps involve the construction of a table of multipliers with a row for each source of variation and a column for each term in the model that is not an interaction. The mean square estimates for each source of variation is obtained by determining which components belong to each mean square and what is their magnitude. This enables the recognition of appropriate F-ratios.

Value

A list of length 3, containing the table of multipliers ($tm), the mean squares estimates ($mse) and the F-ratio versus ($f.versus) for the model.

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

References

Cornfield, J., Tukey, J.W. 1956. Average values of mean squares in factorials. *Annals of Mathematical Statistics*, **27**, 907-949.

Underwood, A.J. 1997. *Experiments in Ecology: Their Logical Design and Interpretation Using Analysis of Variance.* Cambridge University Press, Cambridge.

See Also

gad, estimates

Examples

```
#Example 1
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
model_R <- lm(wing ~ CG + CG%in%MQ, data = rohlf95)
estimates(model_R)
##
##
#Example 2
data(snails)
O <- as.random(snails$origin)
S <- as.random(snails$shore)
B <- as.random(snails$boulder)
C <- as.random(snails$cage)
model_C <- lm(growth ~ O + S + O*S + B%in%S + O*(B%in%S) + C%in%(O*(B%in%S)),
              data = snails)
estimates(model_C)
```

---

gad   *General ANOVA Design*

Description

Fits a general ANOVA design with any combination of orthogonal/nested and fixed/random factors through function estimates

Usage

```
gad(object)
```

Arguments

object   an object of class lm, containing the specified design with random and/or fixed factors

Details

Function *gad* returns an analysis of variance table using the `estimates` function to identify the appropriate F-ratios and consequently p-values for any complex model of orthogonal or nested, fixed or random factors as described by Underwood(1997).

Value

An object of class "anova" inheriting from class "data.frame"

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

References

Underwood, A.J. 1997. *Experiments in Ecology: Their Logical Design and Interpretation Using Analysis of Variance.* Cambridge University Press, Cambridge.

See Also

`estimates`

Examples

```
#Example 1
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
model <- lm(wing ~ CG + CG%in%MQ, data = rohlf95)
gad(model)
##
##
#Example 2
data(rats)
names(rats)
TR <- as.fixed(rats$treat)
RA <- as.random(rats$rat)
LI <- as.random(rats$liver)
model <- lm(glycog ~ TR + RA%in%TR + LI%in%RA%in%TR, data=rats)
gad(model)
##
##
#Example 3
data(snails)
O <- as.random(snails$origin)
S <- as.random(snails$shore)
B <- as.random(snails$boulder)
C <- as.random(snails$cage)
model <- lm(growth ~ O + S + O*S + B%in%S + O*(B%in%S) + C%in%(O*(B%in%S)),
            data = snails)
gad(model)
```

---

is.fixed *Tests if a factor is fixed*

Description

This function works the same way of *is.factor*.

Usage

```
is.fixed(x)
```

Arguments

x   a vector of data

Value

is.fixed returns "TRUE" or "FALSE" depending on whether its argument is a fixed factor or not

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

See Also

is.random

Examples

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
is.fixed(CG)
is.random(MQ)
```

---

is.random *Tests if a factor is ramdom*

Description

This function works the same way of *is.factor*

Usage

```
is.random(x)
```

Arguments

x   a vector of data

Value

is.fixed returns "TRUE" or "FALSE" depending on whether its argument is a fixed factor or not

Author(s)

Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

See Also

[is.fixed](#)

Examples

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
is.fixed(CG)
is.random(MQ)
```

---

rats   *Dataset - Glycogen content of rat livers.*

Description

Duplicate readings were made on each of three preparations of rat livers from each of two rats for three different treatments (Sokal & Rohlf, 1995).

Usage

```
data(rats)
```

Format

A data frame with 36 observations on the following 4 variables.

treat a fixed factor

rat a random factor nested in treat

liver sample size

glycog response variable

References

Sokal, R.R., Rohlf, F.J. 1995. *Biometry: the principles and practice of statistics in biological research.* 3rd edition. W. H. Freeman and Co. New York. 887 pp.

Examples

```
data(rats)
```

| rohlf95 | *Dataset - Mosquitos' wing data colleted by Rohlf and cited in Sokal & Rohlf (1995)* |

Description

Three different types of cage are tested on the growth of *Aedes intrudens*, a kind of mosquito pupae. In each one, four mosquitos are added and its wings measured twice. There are 24 observations (3 cages X 4 jars X 2 measures).

Usage

```
data(rohlf95)
```

Format

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

cages a fixed factor with levels `cage1 cage2 cage3`

mosquito a random factor with levels `m1 m2 m3 m4` nested in cages

measure sample size

wing response variable

References

Sokal, R.R., Rohlf, F.J. 1995. *Biometry: the principles and practice of statistics in biological research.* 3rd edition. W. H. Freeman and Co. New York. 887 pp.

Examples

```
data(rohlf95)
```

---

snails   *Dataset - Growth rates of snails on large boulders on different rock shores.*

Description

This design was extracted from Underwood (1997) but data are artificial. Snails were transplanted from origin to different shores. Several boulders were used on each shore. Cages with snail of each origin on each boulder were replicated. All factors (origin, shore, boulder and cage) are random.

Usage

```
data(snails)
```

Format

A data frame with 240 observations on the following 6 variables.

origin a random factor with levels O1 O2

shore a random factor with levels S1 S2 S3 S4 orthogonal to origin

boulder a random factor with levels B1 B2 B3 nested in shore

cage a random factor with levels C1 C2 nested in the combination of boulder and origin

replicate Sample size

growth response variable

References

Underwood, A.J. 1997. *Experiments in Ecology: Their Logical Design and Interpretation Using Analysis of Variance.* Cambridge University Press, Cambridge.

Examples

```
data(snails)
```

---

snk.test   *Student-Newman-Keuls (SNK) procedure*

Description

This function perforns a SNK post-hoc test of means on the factors of a chosen term of the model, comparing among levels of one factor within each level of other factor or combination of factors.

Usage

```
snk.test(object, term, among = NULL, within = NULL)
```

Arguments

`object`	An object of class lm, containing the specified design.
`term`	Term of the model to be analysed. Use [estimates](#) to see the right form to inform it.
`among`	Specifies the factor which levels will be compared among. Need to be specified if the term to be analysed envolves more than one factor.
`within`	Specifies the factor or combination of factors that will be compared within level among.

Details

SNK is a stepwise procedure for hypothesis testing. First the sample means are sorted, then the pair-wise studentized range (q) is calculated by dividing the differences between means by the standard error, which is based upon the average variance of the two sample.

Value

A list containing the standard error, the degree of freedom and pairwise comparisons among levels of one factor within each level of other(s) factor(s).

Author(s)

Mauricio G. Camargo (<camargo.ufpr@gmail.com>)
Leonardo Sandrini-Neto (<leonardosandrini@gmail.com>)

References

Underwood, A.J. 1997. *Experiments in Ecology: Their Logical Design and Interpretation Using Analysis of Variance.* Cambridge University Press, Cambridge.

See Also

[gad](#), [estimates](#)

Examples

```
library(GAD)
data(rohlf95)
CG <- as.fixed(rohlf95$cages)
MQ <- as.random(rohlf95$mosquito)
model <- lm(wing ~ CG + CG%in%MQ, data = rohlf95)
gad(model)
##Check estimates to see model structure
estimates(model)
snk.test(model,term = 'CG:MQ', among = 'MQ', within = 'CG')
##
##
##Example using snails dataset
data(snails)
```

```
O <- as.random(snails$origin)
S <- as.random(snails$shore)
B <- as.random(snails$boulder)
C <- as.random(snails$cage)
model <- lm(growth ~ O + S + O*S + B%in%S + O*(B%in%S) + C%in%(O*(B%in%S)),
            data = snails)
gad(model)
##Check estimates to see model structure
estimates(model)
snk.test(model, term = 'O')
snk.test(model,term = 'O:S', among = 'S', within = 'O')
#if term O:S:B were significant, we could try
snk.test(model, term = 'O:S:B', among = 'B', within = 'O:S')
```

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