Package ‘GAD’

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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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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
Type: Package
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References


See Also

gad, estimates, C.test, snk.test

Examples

#Example 1
```r
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**

```r
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".
as.random

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
C.test

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
estimates

Examples

```r
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)
```

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

```r
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>)
gad

References


See Also

gad, estimates

Examples

```r
#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


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 random

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

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

### 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

```r
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

Examples

```r
data(rats)
```

**rohlf95**

*Dataset - Mosquitos' wing data collected 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**

```r
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**


**Examples**

```r
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

Examples
data(snails)

snk.test

Student-Newman-Keuls (SNK) procedure

Description
This function performs 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 involves 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 pairwise 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)

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

References


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)
0 <- 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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