

Package ‘eba’

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Title Elimination-by-Aspects Models

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Imports nlme

Description Fitting and testing multi-attribute probabilistic choice models, especially the Bradley-Terry-Luce (BTL) model (Bradley & Terry, 1952 <doi:10.1093/biomet/39.3-4.324>; Luce, 1959), elimination-by-aspects (EBA) models (Tversky, 1972 <doi:10.1037/h0032955>), and preference tree (Pretree) models (Tversky & Sattath, 1979 <doi:10.1037/0033-295X.86.6.542>).

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R topics documented:

balanced.pcdesign	2
boot	3
celebrities	4
circular	5
cov.u	7
drugrisk	7
eba	9
eba.order	11
group.test	13
heaviness	15

inclusion.rule	16
kendall.u	17
linear2btl	18
logLik.eba	19
mbt	20
pcX	21
plot.eba	22
pork	23
residuals.eba	24
schoolsubjects	25
simulate.eba	26
strans	27
tartness	28
thurstone	29
trineq	30
uscale	31
wald.test	32
Index	34

balanced.pcdesign	<i>Balanced Paired-Comparison Design</i>
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Description

Creates a (completely) balanced paired-comparison design.

Usage

```
balanced.pcdesign(nstimuli)
```

Arguments

nstimuli number of stimuli in the paired-comparison design

Details

When nstimuli is odd, the presentation order is completely balanced, that is any given stimulus appears an equal number of times as the first and second member of a pair. When nstimuli is even, the presentation order is balanced as much as possible.

Subjects should be equally assigned to listA and listB for the purpose of balancing the within-pair presentation order across a sample of subjects.

Pairs should be re-randomized for each subject.

Value

pairs	a character array holding the balanced pairs; see David (1988) for details on how it is constructed
listA	the vector pairs in the original within-pair order
listB	the vector of pairs in the inverted within-pair order

References

David, H. (1988). *The method of paired comparisons*. London: Griffin.

See Also

[pcX](#), [eba](#).

Examples

```
## Create balanced design for 6 stimuli
bp <- balanced.pcdesign(6)

## Replicate each within-pair order 10 times and re-randomize
cbind(replicate(10, sample(bp$listA)), replicate(10, sample(bp$listB)))
```

boot

Bootstrap for Elimination-by-Aspects (EBA) Models

Description

Performs a bootstrap by resampling the individual data matrices.

Usage

```
boot(D, R = 100, A = 1:I, s = rep(1/J, J), constrained = TRUE)
```

Arguments

D	a 3d array consisting of the individual paired comparison matrices
R	the number of bootstrap samples
A	a list of vectors consisting of the stimulus aspects; the default is 1:I, where I is the number of stimuli
s	the starting vector with default 1/J for all parameters, where J is the number of parameters
constrained	logical, if TRUE (default), parameters are constrained to be positive

Details

The bootstrap functions `eba.boot.constrained` and `eba.boot` are called automatically by `boot`. The code is experimental and may change in the future.

Value

p the matrix of bootstrap vectors
 stat the matrix of bootstrap statistics, including parameter means, standard errors,
 and confidence limits

See Also

[eba](#), [simulate.eba](#).

Examples

```
data(pork) # pork tasting data, 10 individual paired comparison matrices
bt11 <- eba(apply(pork, 1:2, sum)) # fit Bradley-Terry-Luce model
b <- boot(pork, 200) # resample 200 times

plot(bt11$estimate, b$stat[, "mean"], log="xy")
abline(0, 1, lty=2)
```

celebrities

Choice among Celebrities

Description

This data set provides the absolute choice frequencies of 234 subjects choosing between pairs of nine celebrities. L. B. Johnson (LBJ), Harold Wilson (HW), and Charles De Gaulle (CDG) are politicians; Johnny Unitas (JU), Carl Yastrzemski (CY), and A. J. Foyt (AJF) are athletes; Brigitte Bardot (BB), Elizabeth Taylor (ET), and Sophia Loren (SL) are female movie stars. Subjects were instructed to choose the person with whom they would rather spend an hour of discussion. Row stimuli are chosen over column stimuli.

Usage

```
data(celebrities)
```

Format

A square data frame with a diagonal of zeros.

Source

Rumelhart, D.L., & Greeno, J.G. (1971). Similarity between stimuli: An experimental test of the Luce and Restle choice models. *Journal of Mathematical Psychology*, **8**, 370–381. doi: [10.1016/00222496\(71\)900381](https://doi.org/10.1016/00222496(71)900381)

Examples

```
data(celebrities)
celebrities[,"LBJ", "HW"] # 159 subjects choose LBJ over HW
```

circular	<i>Circular Triads (Intransitive Cycles)</i>
----------	--

Description

Number of circular triads and coefficient of consistency.

Usage

```
circular(mat, alternative = c("two.sided", "less", "greater"),
         exact = NULL, correct = TRUE, simulate.p.value = FALSE,
         nsim = 2000)
```

Arguments

mat	a square matrix or a data frame consisting of (individual) binary choice data; row stimuli are chosen over column stimuli
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "less" or "greater"
exact	a logical indicating whether an exact p-value should be computed
correct	a logical indicating whether to apply continuity correction in the chi-square approximation for the p-value
simulate.p.value	a logical indicating whether to compute p-values by Monte Carlo simulation
nsim	an integer specifying the number of replicates used in the Monte Carlo test

Details

Kendall's coefficient of consistency,

$$\zeta = 1 - T/T_{max},$$

lies between one (perfect consistency) and zero, where T is the observed number of circular triads, and the maximum possible number of circular triads is $T_{max} = n(n^2 - 4)/24$, if n is even, and $T_{max} = n(n^2 - 1)/24$ else, and n is the number of stimuli or objects being judged. For details, see Kendall and Babington Smith (1940) and David (1988).

Kendall (1962) discusses a test of the hypothesis that the number of circular triads T is different (smaller or greater) than expected when choosing randomly. For small n , an exact p-value is computed, based on the exact distributions listed in Alway (1962) and in Kendall (1962). Otherwise, an approximate chi-square test is computed. In this test, the sampling distribution is measured from lower to higher values of T , so that the probability that T will be exceeded is the complement of the probability for χ^2 . The chi-square approximation may be incorrect if $n < 8$ and is only available for $n > 4$.

Value

T	number of circular triads
T.max	maximum possible number of circular triads
T.exp	expected number of circular triads $E(T)$ when choices are totally random
zeta	Kendall's coefficient of consistency
chi2, df, correct	the chi-square statistic and degrees of freedom for the approximate test, and whether continuity correction has been applied
p.value	the p-value for the test (see Details)
simulate.p.value, nsim	whether the p-value is based on simulations, number of simulation runs

References

- Alway, G.G. (1962). The distribution of the number of circular triads in paired comparisons. *Biometrika*, **49**, 265–269. doi: [10.1093/biomet/49.12.265](https://doi.org/10.1093/biomet/49.12.265)
- David, H. (1988). *The method of paired comparisons*. London: Griffin.
- Kendall, M.G. (1962). *Rank correlation methods*. London: Griffin.
- Kendall, M.G., & Babington Smith, B. (1940). On the method of paired comparisons. *Biometrika*, **31**, 324–345. doi: [10.1093/biomet/31.34.324](https://doi.org/10.1093/biomet/31.34.324)

See Also

[eba](#), [strans](#), [kendall.u](#).

Examples

```
# A dog's preferences for six samples of food
# (Kendall and Babington Smith, 1940, p. 326)
dog <- matrix(c(0, 1, 1, 0, 1, 1,
               0, 0, 0, 1, 1, 0,
               0, 1, 0, 1, 1, 1,
               1, 0, 0, 0, 0, 0,
               0, 0, 0, 1, 0, 1,
               0, 1, 0, 1, 0, 0), 6, 6, byrow=TRUE)
dimnames(dog) <- setNames(rep(list(c("meat", "biscuit", "chocolate",
                                   "apple", "pear", "cheese")), 2),
                          c(">", "<"))
circular(dog, alternative="less") # moderate consistency
subset(strans(dog)$violdf, !wst) # list circular triads
```

 cov.u

Covariance Matrix of the EBA Utility Scale

Description

Computes the (normalized) covariance matrix of the utility scale from the covariance matrix of elimination-by-aspects (EBA) model parameters.

Usage

```
cov.u(object, norm = "sum")
```

Arguments

object	an object of class eba, typically the result of a call to eba
norm	either sum (default), a number from 1 to number of stimuli, or NULL; see uscale for details

Details

The additivity rule for covariances $cov(x + y, z) = cov(x, z) + cov(y, z)$ is used for the computations.

If norm is not NULL, the unnormalized covariance matrix is transformed using $a^2 cov(u)$, where the constant a results from the type of normalization applied.

Value

The (normalized) covariance matrix of the utility scale.

See Also

[uscale](#), [eba](#), [wald.test](#).

 drugrisk

Perceived Health Risk of Drugs

Description

In summer 2007, a survey was conducted at the Department of Psychology, University of Tuebingen. Hundred and ninety-two participants were presented with all 15 unordered pairs of the names of six drugs or substances and asked to choose the drug they judged as more dangerous for their health. The six drugs were alcohol (alc), tobacco (tob), cannabis (can), ecstasy (ecs), heroine (her), and cocaine (coc). Choice frequencies were aggregated in four groups defined by gender and age.

Usage

```
data(drugrisk)
```

Format

A 3d array consisting of four square matrices of choice frequencies (row drugs are judged over column drugs):

`drugrisk[, , group = "female30"]` holds the choices of the 48 female participants up to 30 years of age.

`drugrisk[, , group = "female31"]` holds the choices of the 48 female participants from 31 years of age.

`drugrisk[, , group = "male30"]` holds the choices of the 48 male participants up to 30 years of age.

`drugrisk[, , group = "male31"]` holds the choices of the 48 male participants from 31 years of age.

Source

Wickelmaier, F. (2008). Analyzing paired-comparison data in R using probabilistic choice models. Presented at the *R User Conference 2008*, August 12-14, Dortmund, Germany.

Examples

```
data(drugrisk)

## Bradley-Terry-Luce (BTL) model
btl <- eba(drugrisk[, , group = "male30"])

## Elimination-by-aspects (EBA) model, 1 additional aspect
A1 <- list(c(1), c(2,7), c(3,7), c(4,7), c(5,7), c(6,7))
eba1 <- eba(drugrisk[, , group = "male30"], A1)

## EBA model, 2 additional aspects
A2 <- list(c(1), c(2,7), c(3,7), c(4,7,8), c(5,7,8), c(6,7,8))
eba2 <- eba(drugrisk[, , group = "male30"], A2)

## Model selection
anova(btl, eba1, eba2)

## Utility scale values (BTL for females, EBA for males)
dotchart(cbind(
  apply(drugrisk[, ,1:2], 3, function(x) uscale(eba(x), norm=1, log=TRUE)),
  apply(drugrisk[, ,3:4], 3, function(x) uscale(eba(x, A2), norm=1, log=TRUE))
), xlab="log[ Utility scale value (BTL and EBA models) ]",
  main="Perceived health risk of drugs")
abline(v=0, col="gray")
mtext("Wickelmaier, 2008)", line=.5)
```

eba *Elimination-by-Aspects (EBA) Models*

Description

Fits a (multi-attribute) probabilistic choice model by maximum likelihood.

Usage

```
eba(M, A = 1:I, s = rep(1/J, J), constrained = TRUE)

OptiPt(M, A = 1:I, s = rep(1/J, J), constrained = TRUE)

## S3 method for class 'eba'
summary(object, ...)

## S3 method for class 'eba'
anova(object, ..., test = c("Chisq", "none"))
```

Arguments

M	a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli
A	a list of vectors consisting of the stimulus aspects; the default is 1:I, where I is the number of stimuli
s	the starting vector with default 1/J for all parameters, where J is the number of parameters
constrained	logical, if TRUE (default), parameters are constrained to be positive
object	an object of class eba, typically the result of a call to eba
test	should the p-values of the chi-square distributions be reported?
...	additional arguments; none are used in the summary method; in the anova method they refer to additional objects of class eba.

Details

eba is a wrapper function for OptiPt. Both functions can be used interchangeably. See Wickelmaier and Schmid (2004) for further details.

The probabilistic choice models that can be fitted to paired-comparison data are the Bradley-Terry-Luce (BTL) model (Bradley, 1984; Luce, 1959), preference tree (Pretree) models (Tversky & Satath, 1979), and elimination-by-aspects (EBA) models (Tversky, 1972), the former being special cases of the latter.

A represents the family of aspect sets. It is usually a list of vectors, the first element of each being a number from 1 to I; additional elements specify the aspects shared by several stimuli. A must have as many elements as there are stimuli. When fitting a BTL model, A reduces to 1:I (the default), i.e. there is only one aspect per stimulus.

The maximum likelihood estimation of the parameters is carried out by `nlm`. The Hessian matrix, however, is approximated by `nlme::fdHess`. The likelihood functions `L.constrained` and `L` are called automatically.

See `group.test` for details on the likelihood ratio tests reported by `summary.eba`.

Value

<code>coefficients</code>	a vector of parameter estimates
<code>estimate</code>	same as <code>coefficients</code>
<code>logL.eba</code>	the log-likelihood of the fitted model
<code>logL.sat</code>	the log-likelihood of the saturated (binomial) model
<code>goodness.of.fit</code>	the goodness of fit statistic including the likelihood ratio fitted vs. saturated model ($-2\log L$), the degrees of freedom, and the p-value of the corresponding chi-square distribution
<code>u.scale</code>	the unnormalized utility scale of the stimuli; each utility scale value is defined as the sum of aspect values (parameters) that characterize a given stimulus
<code>hessian</code>	the Hessian matrix of the likelihood function
<code>cov.p</code>	the covariance matrix of the model parameters
<code>chi.alt</code>	the Pearson chi-square goodness of fit statistic
<code>fitted</code>	the fitted paired-comparison matrix
<code>y1</code>	the data vector of the upper triangle matrix
<code>y0</code>	the data vector of the lower triangle matrix
<code>n</code>	the number of observations per pair ($y1 + y0$)
<code>mu</code>	the predicted choice probabilities for the upper triangle
<code>nobs</code>	the number of pairs

Author(s)

Florian Wickelmaier

References

- Bradley, R.A. (1984). Paired comparisons: Some basic procedures and examples. In P.R. Krishnaiah & P.K. Sen (eds.), *Handbook of Statistics, Volume 4*. Amsterdam: Elsevier. doi: [10.1016/S01697161\(84\)040165](https://doi.org/10.1016/S01697161(84)040165)
- Luce, R.D. (1959). *Individual choice behavior: A theoretical analysis*. New York: Wiley.
- Tversky, A. (1972). Elimination by aspects: A theory of choice. *Psychological Review*, **79**, 281–299. doi: [10.1037/h0032955](https://doi.org/10.1037/h0032955)
- Tversky, A., & Sattath, S. (1979). Preference trees. *Psychological Review*, **86**, 542–573. doi: [10.1037/0033295X.86.6.542](https://doi.org/10.1037/0033295X.86.6.542)
- Wickelmaier, F., & Schmid, C. (2004). A Matlab function to estimate choice model parameters from paired-comparison data. *Behavior Research Methods, Instruments, and Computers*, **36**, 29–40. doi: [10.3758/BF03195547](https://doi.org/10.3758/BF03195547)

See Also

[strans](#), [uscale](#), [cov.u](#), [group.test](#), [wald.test](#), [plot.eba](#), [residuals.eba](#), [logLik.eba](#), [simulate.eba](#), [kendall.u](#), [circular](#), [trineq](#), [thurstone](#), [nlm](#).

Examples

```

data(celebrities)                # absolute choice frequencies
bt11 <- eba(celebrities)         # fit Bradley-Terry-Luce model
A <- list(c(1,10), c(2,10), c(3,10),
          c(4,11), c(5,11), c(6,11),
          c(7,12), c(8,12), c(9,12)) # the structure of aspects
eba1 <- eba(celebrities, A)      # fit elimination-by-aspects model

summary(eba1)                   # goodness of fit
plot(eba1)                      # residuals versus predicted values
anova(bt11, eba1)               # model comparison based on likelihoods
confint(eba1)                   # confidence intervals for parameters
uscale(eba1)                    # utility scale

ci <- 1.96 * sqrt(diag(cov.u(eba1))) # 95% CI for utility scale values
dotchart(uscale(eba1), xlim=c(0, .3), main="Choice among celebrities",
          xlab="Utility scale value (EBA model)", pch=16) # plot the scale
arrows(uscale(eba1)-ci, 1:9, uscale(eba1)+ci, 1:9, .05, 90, 3) # error bars
abline(v=1/9, lty=2)           # indifference line
mtext("Rumelhart and Greeno, 1971)", line=.5)

```

eba.order

Elimination-by-Aspects (EBA) Models with Order-Effect

Description

Fits a (multi-attribute) probabilistic choice model that accounts for the effect of the presentation order within a pair.

Usage

```
eba.order(M1, M2 = NULL, A = 1:I, s = c(rep(1/J, J), 1),
          constrained = TRUE)
```

```
## S3 method for class 'eba.order'
summary(object, ...)
```

Arguments

M1, M2 two square matrices or data frames consisting of absolute choice frequencies in both within-pair orders; row stimuli are chosen over column stimuli. If M2 is empty (default), M1 is assumed to be a 3d array containing both orders

A see [eba](#)

s	the starting vector with default 1/J for all J aspect parameters, and 1 for the order effect
constrained	see eba
object	an object of class <code>eba.order</code> , typically the result of a call to eba.order
...	additional arguments

Details

The choice models include a single multiplicative order effect, `order`, that is constant for all pairs (see Davidson and Beaver, 1977). An order effect < 1 (> 1) indicates a bias in favor of the first (second) interval.

See [eba](#) for choice models without order effect.

Several likelihood ratio tests are performed (see also [summary.eba](#)).

`EBA.order` tests an order-effect EBA model against a saturated binomial model; this corresponds to a goodness of fit test of the former model.

`Order` tests an EBA model with an order effect constrained to 1 against an unconstrained order-effect EBA model; this corresponds to a test of the order effect.

`Effect` tests an order-effect indifference model (where all scale values are equal, but the order effect is free) against the order-effect EBA model; this corresponds to testing for a stimulus effect; `order0` is the estimate of the former model.

Wickelmaier and Choisel (2006) describe a model that generalizes the Davidson-Beaver model and allows for an order effect in Pretree and EBA models.

Value

coefficients	a vector of parameter estimates, the last component holds the order-effect estimate
estimate	same as <code>coefficients</code>
logL.eba	the log-likelihood of the fitted model
logL.sat	the log-likelihood of the saturated (binomial) model
goodness.of.fit	the goodness of fit statistic including the likelihood ratio fitted vs. saturated model ($-2\log L$), the degrees of freedom, and the p-value of the corresponding chi-square distribution
u.scale	the unnormalized utility scale of the stimuli; each utility scale value is defined as the sum of aspect values (parameters) that characterize a given stimulus
hessian	the Hessian matrix of the likelihood function
cov.p	the covariance matrix of the model parameters
chi.alt	the Pearson chi-square goodness of fit statistic
fitted	3d array of the fitted paired-comparison matrices
y1	the data vector of the upper triangle matrices
y0	the data vector of the lower triangle matrices
n	the number of observations per pair ($y1 + y0$)
mu	the predicted choice probabilities for the upper triangles
M1, M2	the data matrices

Author(s)

Florian Wickelmaier

References

Davidson, R.R., & Beaver, R.J. (1977). On extending the Bradley-Terry model to incorporate within-pair order effects. *Biometrics*, **33**, 693–702.

Wickelmaier, F., & Choisel, S. (2006). Modeling within-pair order effects in paired-comparison judgments. In D.E. Kornbrot, R.M. Msetfi, & A.W. MacRae (eds.), *Fechner Day 2006. Proceedings of the 22nd Annual Meeting of the International Society for Psychophysics* (p. 89–94). St. Albans, UK: The ISP.

See Also

[eba](#), [group.test](#), [plot.eba](#), [residuals.eba](#), [logLik.eba](#).

Examples

```
data(heaviness)           # weights judging data
ebao1 <- eba.order(heaviness) # Davidson-Beaver model
summary(ebao1)           # goodness of fit
plot(ebao1)              # residuals versus predicted values
confint(ebao1)           # confidence intervals for parameters
```

group.test

Group Effects in Elimination-by-Aspects (EBA) Models

Description

Tests for group effects in elimination-by-aspects (EBA) models.

Usage

```
group.test(groups, A = 1:I, s = rep(1/J, J), constrained = TRUE)
```

Arguments

groups	a 3d array containing one aggregate choice matrix per group
A	a list of vectors consisting of the stimulus aspects; the default is 1:I, where I is the number of stimuli
s	the starting vector with default 1/J for all parameters, where J is the number of parameters
constrained	logical, if TRUE (default), EBA parameters are constrained to be positive

Details

The five tests are all based on likelihood ratios.

Overall compares a 1-parameter Poisson model to a saturated Poisson model, thereby testing the equality of the frequencies in each cell of the array. This test corresponds to simultaneously testing for a null effect of (1) the context induced by a given pair, (2) the grouping factor, (3) the stimuli, and (4) the imbalance between pairs. The deviances of the remaining tests sum to the total deviance associated with the overall test.

EBA.g tests an EBA group model against a saturated binomial group model, which corresponds to a goodness of fit test of the EBA group model.

Group tests an EBA model having its parameters restricted to be equal across groups (single set of parameters) against the EBA group model allowing its parameters to vary freely across groups (one set of parameters per group); this corresponds to testing for group differences.

Effect tests an indifference model (where all choice probabilities are equal to 0.5) against the restricted EBA model, which corresponds to testing for a stimulus effect.

Imbalance tests for differences in the number of observations per pair by comparing the average sample size (1-parameter Poisson model) to the actual sample sizes (saturated Poisson model).

See Duineveld, Arents, and King (2000) for further details, and Choisel and Wickelmaier (2007) for an application.

Value

tests a table displaying the likelihood ratio test statistics

References

Choisel, S., & Wickelmaier, F. (2007). Evaluation of multichannel reproduced sound: Scaling auditory attributes underlying listener preference. *Journal of the Acoustical Society of America*, **121**, 388–400. doi: [10.1121/1.2385043](https://doi.org/10.1121/1.2385043)

Duineveld, C.A.A., Arents, P., & King, B.M. (2000). Log-linear modelling of paired comparison data from consumer tests. *Food Quality and Preference*, **11**, 63–70. doi: [10.1016/s0950-3293\(99\)000403](https://doi.org/10.1016/s0950-3293(99)000403)

See Also

[eba](#), [wald.test](#).

Examples

```
## Bradley-Terry-Luce model
data(pork)            # Is there a difference between Judge 1 and Judge 2?
groups <- array(c(apply(pork[, , 1:5], 1:2, sum),
                  apply(pork[, , 6:10], 1:2, sum)), c(3,3,2))
group.test(groups) # Yes, there is.

## Elimination-by-aspects model
data(drugrisk)        # Do younger and older males judge risk of drugs differently?
A2 <- list(c(1), c(2,7), c(3,7), c(4,7,8), c(5,7,8), c(6,7,8))
group.test(drugrisk[, , 3:4], A2) # Yes.
```

heaviness

Weights Judging Data

Description

Fifty subjects were presented with all 20 ordered pairs of bottles filled with lead shot and asked to choose the bottle that felt heavier. The mass of the bottles was 90, 95, 100, 105, and 110 grams, respectively. Choice frequencies were aggregated across subjects for the two within-pair presentation orders.

Usage

```
data(heaviness)
```

Format

A 3d array consisting of two square matrices:

`heaviness[, , order = 1]` holds the choices where the row stimulus was presented first for each pair (in the upper triangle, and vice versa in the lower triangle).

`heaviness[, , order = 2]` holds the choices where the column stimulus was presented first for each pair (in the upper triangle, and vice versa in the lower triangle).

Source

Beaver, R.J., & Gokhale, D.V. (1975). A model to incorporate within-pair order effects in paired comparisons. *Communications in Statistics*, **4**, 923–939. doi: [10.1080/03610927308827302](https://doi.org/10.1080/03610927308827302)

Examples

```
data(heaviness)
## 6 subjects chose 90g over 100g, when 90g was presented first.
heaviness["90g", "100g", order=1]

## 44 subjects chose 100g over 90g, when 90g was presented first.
heaviness["100g", "90g", order=1]

## 14 subjects chose 90g over 100g, when 90g was presented second.
heaviness["90g", "100g", order=2]

## 36 subjects chose 100g over 90g, when 90g was presented second.
heaviness["100g", "90g", order=2]

## Bradley-Terry-Luce (BTL) model for each within-pair order
bt11 <- eba(heaviness[, , 1])
bt12 <- eba(heaviness[, , 2])

xval <- seq(90, 110, 5)
plot(uscale(bt11) ~ xval, type="n", log="y",
```

```

      xlab="Mass of lead shot filled bottle (in g)",
      ylab="Perceived heaviness (BTL model)",
      main="Weights judging experiment")
mtext("(Beaver and Gokhale, 1975)", line=.5)

arrows(xval, uscale(bt11) - 1.96*sqrt(diag(cov.u(bt11))),
       xval, uscale(bt11) + 1.96*sqrt(diag(cov.u(bt11))), .05, 90, 3, "gray")
arrows(xval, uscale(bt12) - 1.96*sqrt(diag(cov.u(bt12))),
       xval, uscale(bt12) + 1.96*sqrt(diag(cov.u(bt12))), .05, 90, 3, "gray")

points(uscale(bt11) ~ xval, type="b", pch=16)
points(uscale(bt12) ~ xval, type="b", lty=2, pch=21, bg="white")

text(90.3, .01, "Lower weight judged first", adj=0)
text(90.3, .08, "Higher weight judged first", adj=0)

```

inclusion.rule

Inclusion Rule

Description

Checks if a family of sets fulfills the inclusion rule.

Usage

```
inclusion.rule(A)
```

Arguments

A a list of vectors consisting of the stimulus aspects of an elimination-by-aspects model

Details

The inclusion rule is necessary and sufficient for a tree structure on the aspect sets:

Structure theorem. A family $\{x' | x \in T\}$ of aspect sets is representable by a tree iff either $x' \cap y' \supset x' \cap z'$ or $x' \cap z' \supset x' \cap y'$ for all x, y, z in T . (Tversky & Sattath, 1979, p. 546)

Value

Either TRUE if the inclusion rule holds for A, or FALSE otherwise.

References

Tversky, A., & Sattath, S. (1979). Preference trees. *Psychological Review*, **86**, 542–573. doi: [10.1037/0033295X.86.6.542](https://doi.org/10.1037/0033295X.86.6.542)

See Also

[eba](#), [trineq](#), [strans](#).

Examples

```
A <- list(c(1, 5), c(2, 5), c(3, 6), c(4, 6)) # tree
inclusion.rule(A)

B <- list(c(1, 5), c(2, 5, 6), c(3, 6), c(4, 6)) # lattice
inclusion.rule(B)
```

kendall.u

*Kendall's Coefficient of Agreement***Description**

Kendall's u coefficient of agreement between judges.

Usage

```
kendall.u(M, correct = TRUE)
```

Arguments

M	a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli
correct	logical, if TRUE (default) a continuity correction is applied when computing the test statistic (by subtracting one from the sum of agreeing pairs)

Details

Kendall's u (Kendall and Babington Smith, 1940) takes on values between min.u (minimum agreement) and 1 (maximum agreement). The minimum min.u equals $-1/(m - 1)$, if m is even, and $-1/m$, if m is odd, where m is the number of subjects (judges).

The null hypothesis in the chi-square test is that the agreement between judges is by chance.

It is assumed that there is an equal number of observations per pair and that each subject judges each pair only once.

Value

u	Kendall's u coefficient of agreement
min.u	the minimum value for u
chi2	the chi-square statistic for a test that the agreement is by chance
df	the degrees of freedom
p.value	the p-value of the test

References

Kendall, M.G., & Babington Smith, B. (1940). On the method of paired comparisons. *Biometrika*, **31**, 324–345. doi: [10.1093/biomet/31.34.324](https://doi.org/10.1093/biomet/31.34.324)

See Also

[schoolsubjects](#), [eba](#), [strans](#), [circular](#).

Examples

```
data(schoolsubjects)
lapply(schoolsubjects, kendall.u) # better-than-chance agreement
```

linear2btl

Linear Coefficients to Bradley-Terry-Luce (BTL) Estimates

Description

Transforms linear model coefficients to Bradley-Terry-Luce (BTL) model parameter estimates.

Usage

```
linear2btl(object, order = FALSE)
```

Arguments

object	an object of class <code>glm</code> or <code>lm</code> specifying a BTL model
order	logical, does the model include an order effect? Defaults to <code>FALSE</code>

Details

The design matrix used by `glm` or `lm` usually results from a call to `pcX`. It is assumed that the reference category is the first level.

The covariance matrix is estimated by employing the delta method.

See Imrey, Johnson, and Koch (1976) for more details.

Value

<code>btl.parameters</code>	a matrix; the first column holds the BTL parameter estimates, the second column the approximate standard errors
<code>cova</code>	the approximate covariance matrix of the BTL parameter estimates
<code>linear.coefs</code>	a vector of the original linear coefficients as returned by <code>glm</code> or <code>lm</code>

References

Imrey, P.B., Johnson, W.D., & Koch, G.G. (1976). An incomplete contingency table approach to paired-comparison experiments. *Journal of the American Statistical Association*, **71**, 614–623. doi: [10.2307/2285591](https://doi.org/10.2307/2285591)

See Also

[eba](#), [eba.order](#), [glm](#), [pcX](#).

Examples

```

data(drugrisk)
y1 <- t(drugrisk[, , 1])[lower.tri(drugrisk[, , 1])]
y0 <- drugrisk[, , 1][ lower.tri(drugrisk[, , 1])]

## Fit BTL model using glm (maximum likelihood)
bt1.glm <- glm(cbind(y1, y0) ~ 0 + pcX(6), binomial)
linear2bt1(bt1.glm)

## Fit BTL model using lm (weighted least squares)
bt1.lm <- lm(log(y1/y0) ~ 0 + pcX(6), weights=y1*y0/(y1 + y0))
linear2bt1(bt1.lm)

```

logLik.eba

*Log-Likelihood of an eba Object***Description**

Returns the log-likelihood value of the (multi-attribute) probabilistic choice model represented by object evaluated at the estimated parameters.

Usage

```

## S3 method for class 'eba'
logLik(object, ...)

```

Arguments

object	an object inheriting from class eba, representing a fitted elimination-by-aspects model.
...	some methods for this generic require additional arguments. None are used in this method.

Value

The log-likelihood of the model represented by object evaluated at the estimated parameters.

See Also

[eba](#), [logLik.lm](#), [AIC](#).

Examples

```

data(heaviness)
bt11 <- eba(heaviness[, , order=1])
logLik(bt11)
AIC(bt11)
BIC(bt11)

```

mbt *Mallows-Bradley-Terry Model*

Description

Fits a Mallows-Bradley-Terry (MBT) model by maximum likelihood.

Usage

```
mbt(data, bootstrap = FALSE, nsim = 1000, ...)
```

Arguments

data	a data frame, the first t columns containing the ranks, the (t + 1)th column containing the frequencies.
bootstrap	logical. Return a parametric bootstrap p-value?
nsim	number of bootstrap replicates.
...	further arguments passed to simulate.

Details

mbt provides a front end for glm.

See Critchlow and Fligner (1991) for more details.

Value

coefficients	a vector of parameter estimates (scale values) constrained to sum to unity
goodness.of.fit	the goodness of fit statistic including the likelihood ratio fitted vs. saturated model (-2logL), the degrees of freedom, the p-value of the corresponding chi-square distribution, and if bootstrap is TRUE the bootstrap p-value
perm.idx	the names of the non-zero frequency ranks
y	the vector of rank frequencies including zeros
mbt.glm	the output from a call to glm

Author(s)

Florian Wickelmaier

References

Critchlow, D.E., & Fligner, M.A. (1991). Paired comparison, triple comparison, and ranking experiments as generalized linear models, and their implementation in GLIM. *Psychometrika*, **56**, 517–533. doi: [10.1007/bf02294488](https://doi.org/10.1007/bf02294488)

Mallows, C.L. (1957). Non-null ranking models. I. *Biometrika*, **44**, 114–130. doi: [10.1093/biomet/44.12.114](https://doi.org/10.1093/biomet/44.12.114)

See Also

[tartness](#), [glm](#).

Examples

```
data(tartness)      # tartness rankings of salad dressings (Vargo, 1989)
mbt(tartness, bootstrap=TRUE, nsim=500) # fit Mallows-Bradley-Terry model
```

pcX

Paired-Comparison Design Matrix

Description

Computes a paired-comparison design matrix.

Usage

```
pcX(nstimuli, omitRef = TRUE)
```

Arguments

nstimuli	number of stimuli in the paired-comparison design
omitRef	logical, if TRUE (default), the first column corresponding to the reference category is omitted

Details

The design matrix can be used when fitting a Bradley-Terry-Luce (BTL) model or a Thurstone-Mosteller (TM) model by means of [glm](#) or [lm](#).

See Critchlow and Fligner (1991) for more details.

Value

A matrix having $(nstimuli - 1) * nstimuli / 2$ rows and $nstimuli - 1$ columns (if the reference category is omitted).

References

Critchlow, D.E., & Fligner, M.A. (1991). Paired comparison, triple comparison, and ranking experiments as generalized linear models, and their implementation in GLIM. *Psychometrika*, **56**, 517–533. doi: [10.1007/bf02294488](https://doi.org/10.1007/bf02294488)

See Also

[eba](#), [thurstone](#), [glm](#), [balanced.pcdesign](#), [linear2btl](#).

Examples

```

data(drugrisk)           # absolute choice frequencies
btl <- eba(drugrisk[, , 1]) # fit Bradley-Terry-Luce model using eba
summary(btl)

y1 <- t(drugrisk[, , 1])[lower.tri(drugrisk[, , 1])]
y0 <- drugrisk[, , 1][ lower.tri(drugrisk[, , 1])]

## Fit Bradley-Terry-Luce model using glm
btl.glm <- glm(cbind(y1, y0) ~ 0 + pcX(6), binomial)
summary(btl.glm)

## Fit Thurstone Case V model using glm
tm.glm <- glm(cbind(y1, y0) ~ 0 + pcX(6), binomial(probit))
summary(tm.glm)

```

plot.eba

Diagnostic Plot for EBA Models

Description

Plots elimination-by-aspects (EBA) model residuals against fitted values.

Usage

```

## S3 method for class 'eba'
plot(x, xlab = "Predicted choice probabilities",
     ylab = "Deviance residuals", ...)

```

Arguments

`x` an object of class `eba`, typically the result of a call to [eba](#)

`xlab`, `ylab`, ... graphical parameters passed to `plot`.

Details

The deviance residuals are plotted against the predicted choice probabilities for the upper triangle of the paired-comparison matrix.

See Also

[eba](#), [residuals.eba](#).

Examples

```
## Compare two choice models

data(celebrities)           # absolute choice frequencies
bt11 <- eba(celebrities)    # fit Bradley-Terry-Luce model
A <- list(c(1,10), c(2,10), c(3,10),
          c(4,11), c(5,11), c(6,11),
          c(7,12), c(8,12), c(9,12)) # the structure of aspects
eba1 <- eba(celebrities, A) # fit elimination-by-aspects model
anova(bt11, eba1)          # model comparison based on likelihoods

par(mfrow = 1:2)           # residuals versus fitted values
plot(bt11, main = "BTL", ylim = c(-4, 4.5)) # BTL doesn't fit well
plot(eba1, main = "EBA", ylim = c(-4, 4.5)) # EBA fits better
```

pork

*Pork Tasting Data***Description**

Bradley and Terry (1952) provide the individual choice matrices of two judges choosing between pairs of three samples of pork meet. The pigs had been fed on either corn (C), corn plus peanut supplement (Cp), or corn plus a large peanut supplement (CP). Each judge does five repetitions. The data are stored in a 3d array, the first five matrices of which correspond to the five repetitions of the first judge, the last five to the repetitions of the second judge. Row stimuli are chosen (preferred) over column stimuli.

Usage

```
data(pork)
```

Format

A 3d array consisting of ten square matrices.

Source

Bradley, R.A., & Terry, M.E. (1952). Rank analysis of incomplete block designs. I. The method of paired comparisons. *Biometrika*, **39**, 324–345. doi: [10.1093/biomet/39.34.324](https://doi.org/10.1093/biomet/39.34.324)

Examples

```
data(pork)
apply(pork, 1:2, sum) # aggregate choice frequencies
```

`residuals.eba`*Residuals for EBA Models*

Description

Computes deviance and Pearson residuals for eba objects.

Usage

```
## S3 method for class 'eba'  
residuals(object, type = c("deviance", "pearson"), ...)
```

Arguments

<code>object</code>	an object of class eba, typically the result of a call to eba
<code>type</code>	the type of residuals which should be returned; the alternatives are: "deviance" (default) and "pearson"
<code>...</code>	further arguments passed to or from other methods. None are used in this method.

Details

Residuals are computed from the upper triangle of the paired-comparison matrix.

See [residuals.glm](#) for details.

Value

A vector of residuals having as many elements as pairs of stimuli.

See Also

[eba](#), [residuals.glm](#), [plot.eba](#).

Examples

```
data(celebrities)           # absolute choice frequencies  
bt11 <- eba(celebrities)    # fit Bradley-Terry-Luce model  
sum( resid(bt11)^2 )        # deviance G2  
deviance(bt11)  
sum( resid(bt11, "pearson")^2 ) # Pearson X2
```

 schoolsubjects

Preference for School Subjects

Description

Two classes of children (ages 11 to 13) were asked to state their preferences with respect to certain school subjects. Each child was given a sheet on which were written the possible pairs of subjects and asked to underline the one preferred in each case.

Usage

```
data(schoolsubjects)
```

Format

A list containing two square matrices of aggregate choice frequencies (row entries are preferred over column entries):

`schoolsubjects[["boys"]]` holds the frequencies of 21 boys choosing among 13 school subjects: woodwork, gymnastics, art, science, history, geography, arithmetic, religion, English literature, commercial subjects, algebra, English grammar, geometry.

`schoolsubjects[["girls"]]` holds the frequencies of 25 girls choosing among 11 school subjects: gymnastics, science, art, domestic science, history, arithmetic, geography, English literature, religion, algebra, English grammar.

Source

Kendall, M.G., & Babington Smith, B. (1940). On the method of paired comparisons. *Biometrika*, **31**, 324–345. doi: [10.1093/biomet/31.34.324](https://doi.org/10.1093/biomet/31.34.324)

Examples

```
data(schoolsubjects)

m <- lapply(schoolsubjects, eba) # Bradley-Terry-Luce (BTL) model

par(mfrow = 1:2)
dotchart(uscale(m$boys), main = "Boys' preferences",)
dotchart(uscale(m$girls), main = "Girls' preferences")
mtext("Utility scale value (BTL model)", outer = TRUE, side = 1,
      line = -2)
mtext("(Kendall and Babington Smith, 1940)", outer = TRUE, line = -4)
```

simulate.eba

*Simulate Responses from EBA Models***Description**

Simulates responses from the distribution corresponding to a fitted eba model object.

Usage

```
## S3 method for class 'eba'
simulate(object, nsim, seed, pool = TRUE, ...)
```

Arguments

object	an object of class eba, typically the result of a call to eba .
nsim	currently not used.
seed	currently not used.
pool	logical, if TRUE (default), pooled responses (summed across respondents) are returned.
...	further arguments passed to or from other methods. None are used in this method.

Details

Responses are simulated by [rbinom](#) with sizes taken from the original sample and probabilities computed from the model object.

Value

A paired-comparison matrix of (pooled) responses.

See Also

[eba](#), [boot](#).

Examples

```
data(celebrities) # absolute choice frequencies
A <- list(c(1,10), c(2,10), c(3,10),
         c(4,11), c(5,11), c(6,11),
         c(7,12), c(8,12), c(9,12)) # the structure of aspects
eba1 <- eba(celebrities, A) # fit elimination-by-aspects model

## Perform parametric bootstrap
LR.stat <- replicate(200, deviance(eba(simulate(eba1), A)))

hist(LR.stat, col="lightgray", border="white", freq=FALSE, breaks=20,
```

```
xlim=c(0, 60), main="Parametric bootstrap")
curve(dchisq(x, df=eba1$goodness.of.fit["df"]), add=TRUE)
abline(v=deviance(eba1), lty=2)
```

strans

*Stochastic Transitivity***Description**

Checks the weak, moderate, and strong stochastic transitivity.

Usage

```
strans(M)
```

Arguments

M a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli

Details

The weak (WST), moderate (MST), and strong (SST) stochastic transitivity hold for a set of choice probabilities P , whenever if $P_{ij} \geq 0.5$ and $P_{jk} \geq 0.5$, then

$P_{ik} \geq 0.5$ (WST),

$P_{ik} \geq \min(P_{ij}, P_{jk})$ (MST),

$P_{ik} \geq \max(P_{ij}, P_{jk})$ (SST).

See Suppes, Krantz, Luce, & Tversky (1989/2007, chap. 17) for an introduction to the representation of choice probabilities.

If WST holds, a permutation of the indices of the matrix exists such that the proportions in the upper triangular matrix are ≥ 0.5 . This re-arranged matrix is stored in `pcm`. If WST does not hold, cells in the upper triangular matrix that are smaller than 0.5 are replaced by 0.5. The deviance resulting from this restriction is reported in `wst.fit`.

The approximate likelihood ratio test for significance of the WST violations is according to Tversky (1969); for a more exact test of WST see Iverson and Falmagne (1985).

Value

A table displaying the number of violations of the weak, moderate, and strong stochastic transitivity, the number of tests, the error ratio (violations/tests), and the mean and maximum deviation from the minimum probability for which the corresponding transitivity would hold.

weak	number of violations of WST
moderate	number of violations of MST
strong	number of violations of SST

n.tests	number of transitivity tests performed
wst.violations	a vector containing $0.5 - P_{ik}$ for all triples that violate WST
mst.violations	a vector containing $\min(P_{ij}, P_{jk}) - P_{ik}$ for all triples that violate MST
sst.violations	a vector containing $\max(P_{ij}, P_{jk}) - P_{ik}$ for all triples that violate SST
pcm	the permuted square matrix of relative choice frequencies
ranking	the ranking of the objects, which corresponds to the colnames of pcm
chkdf	data frame reporting the choice proportions for each triple in each permutation
violdf	data frame reporting for each triple which type of transitivity holds or does not hold
wst.fit	likelihood ratio test of WST (see details)
wst.mat	restricted matrix that satisfies WST

References

- Iverson, G., & Falmagne, J.-C. (1985). Statistical issues in measurement. *Mathematical Social Sciences*, **10**, 131–153. doi: [10.1016/01654896\(85\)900319](https://doi.org/10.1016/01654896(85)900319)
- Suppes, P., Krantz, D.H., Luce, R.D., & Tversky, A. (1989/2007). *Foundations of measurement. Volume II*. Mineola, N.Y.: Dover Publications.
- Tversky, A. (1969). Intransitivity of preferences. *Psychological Review*, **76**, 31–48. doi: [10.1037/h0026750](https://doi.org/10.1037/h0026750)

See Also

[eba](#), [circular](#), [kendall.u](#), [trineq](#).

Examples

```
data(celebrities)          # absolute choice frequencies
strans(celebrities)       # WST and MST hold, but not SST
strans(celebrities)$pcm   # re-ordered relative frequencies
strans(celebrities)$violdf # transitivity violations
```

tartness	<i>Tartness Rankings of Salad Dressings</i>
----------	---

Description

The data were collected by Vargo (1989; as cited in Critchlow and Fligner, 1991). Each of 32 judges is asked to rank four salad dressing preparations according to tartness, with a rank of 1 being assigned to the formulation judged to be the most tart.

Usage

```
data(tartness)
```

Format

a data frame consisting the rankings and their frequencies.

Source

Critchlow, D.E., & Fligner, M.A. (1991). Paired comparison, triple comparison, and ranking experiments as generalized linear models, and their implementation in GLIM. *Psychometrika*, **56**, 517–533. doi: [10.1007/bf02294488](https://doi.org/10.1007/bf02294488)

References

Vargo, M.D. (1989). Microbiological spoilage of a moderate acid food system using a dairy-based salad dressing model. Unpublished masters thesis, Ohio State University, Department of Food Science and Nutrition, Columbus, OH.

Examples

```
data(tartness)
```

thurstone

Thurstone-Mosteller Model (Case V)

Description

Fits a Thurstone-Mosteller model (Case V) by maximum likelihood.

Usage

```
thurstone(M)
```

Arguments

M a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli

Details

thurstone provides a front end for glm.

See Critchlow and Fligner (1991) for more details.

Value

estimate a vector of parameter estimates (scale values), first element is set to zero

goodness.of.fit the goodness of fit statistic including the likelihood ratio fitted vs. saturated model (-2logL), the degrees of freedom, and the p-value of the corresponding chi-square distribution

tm.glm the output from a call to glm

Author(s)

Florian Wickelmaier

References

Critchlow, D.E., & Fligner, M.A. (1991). Paired comparison, triple comparison, and ranking experiments as generalized linear models, and their implementation in GLIM. *Psychometrika*, **56**, 517–533. doi: [10.1007/bf02294488](https://doi.org/10.1007/bf02294488)

See Also

[eba](#), [strans](#), [pcX](#), [kendall.u](#), [circular](#), [glm](#).

Examples

```
## Taste data (David, 1988, p. 116)
taste <- matrix(c( 0,  3,  2,  2,
                 12,  0, 11,  3,
                 13,  4,  0,  5,
                 13, 12, 10,  0), 4, 4, byrow=TRUE)
dimnames(taste) <- setNames(rep(list(c("A1", "A2", "A3", "A4")), 2),
                           c(">", "<"))
thurstone(taste) # Thurstone-Mosteller model fits OK
```

trineq

Trinary Inequality

Description

Checks if binary choice probabilities fulfill the trinary inequality.

Usage

```
trineq(M, A = 1:I)
```

Arguments

M	a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli
A	a list of vectors consisting of the stimulus aspects; the default is 1:I, where I is the number of stimuli

Details

For any triple of stimuli x, y, z , the ternary inequality states that, if $P(x, y) > 1/2$ and $(xy)z$, then

$$R(x, y, z) > 1,$$

where $R(x, y, z) = R(x, y)R(y, z)R(z, x)$, $R(x, y) = P(x, y)/P(y, x)$, and $(xy)z$ denotes that x and y share at least one aspect that z does not have (Tversky and Sattath, 1979, p. 554).

[inclusion.rule](#) checks if a family of aspect sets is representable by a tree.

Value

Results checking the ternary inequality.

n	number of tests of the ternary inequality
prop	proportion of triples confirming the ternary inequality
quant	quantiles of $R(x, y, z)$
n. tests	number of transitivity tests performed
chkdf	data frame reporting $R(x, y, z)$ for each triple where $P(x, y) > 1/2$ and $(xy)z$

References

Tversky, A., & Sattath, S. (1979). Preference trees. *Psychological Review*, **86**, 542–573. doi: [10.1037/0033295X.86.6.542](https://doi.org/10.1037/0033295X.86.6.542)

See Also

[eba](#), [inclusion.rule](#), [strans](#).

Examples

```
data(celebrities)          # absolute choice frequencies
A <- list(c(1,10), c(2,10), c(3,10),
          c(4,11), c(5,11), c(6,11),
          c(7,12), c(8,12), c(9,12)) # the structure of aspects
trineq(celebrities, A)     # check ternary inequality for tree A
trineq(celebrities, A)$chkdf # ternary inequality for each triple
```

 uscale

Utility Scale of an EBA Choice Model

Description

Extract the (normalized) utility scale for an elimination-by-aspects (EBA) model.

Usage

```
uscale(object, norm = "sum", log = FALSE)
```

Arguments

object	an object of class eba, typically the result of a call to eba
norm	either sum, so the scale values sum to unity (default); or a number from 1 to number of stimuli, so this scale value becomes one; or NULL (no normalization)
log	should the log of the utility scale values be returned? Defaults to FALSE.

Details

Each utility scale value is defined as the sum of aspect values (EBA model parameters) that characterize a given stimulus. First these sums are computed for all stimuli, then normalization (if any) is applied. As each type of normalization corresponds to a multiplication by a positive real, the ratio between scale values remains constant.

Value

The (normalized) utility scale of the stimuli.

See Also

[eba](#), [cov.u](#), [wald.test](#).

Examples

```
data(drugrisk)
A <- list(c(1), c(2,7), c(3,7), c(4,7,8), c(5,7,8), c(6,7,8))
eba1 <- eba(drugrisk[, ,group = "male30"], A) # EBA model

uscale(eba1) # sum-to-unity normalization
uscale(eba1, norm=1) # u(alcohol) := 1
uscale(eba1, norm=5) # u(heroine) := 1
uscale(eba1, norm=NULL) # no normalization
uscale(eba1, norm=1, log=TRUE) # log utility scale, log u(alcohol) := 0
```

wald.test

Testing Linear Hypotheses in Elimination-by-Aspects (EBA) Models

Description

Tests linear hypotheses of the form $Cp = 0$ in elimination-by-aspects (EBA) models using the Wald test.

Usage

```
wald.test(object, C, u.scale = TRUE)
```


Arguments

object	an object of class eba, typically the result of a call to eba
C	a matrix of contrasts, specifying the linear hypotheses
u.scale	logical, if TRUE the test is performed on the utility scale, if FALSE the test is performed on the EBA parameters directly

Details

The Wald test statistic,

$$W = (Cp)'[Ccov(p)C']^{-1}(Cp),$$

is approximately chi-square distributed with $rk(C)$ degrees of freedom.

C is usually of full rank and must have as many columns as there are parameters in p.

Value

C	the matrix of contrasts, specifying the linear hypotheses
W	the Wald test statistic
df	the degrees of freedom ($rk(C)$)
pval	the p-value of the test

See Also

[eba](#), [group.test](#), [uscale](#), [cov.u](#).

Examples

```
data(celebrities) # absolute choice frequencies
A <- list(c(1,10), c(2,10), c(3,10),
         c(4,11), c(5,11), c(6,11),
         c(7,12), c(8,12), c(9,12)) # the structure of aspects
eba1 <- eba(celebrities, A) # fit elimination-by-aspects model

## Test whether JU, CY, and AJF have equal utility scale values
C1 <- rbind(c(0,0,0,1,-1, 0,0,0,0),
           c(0,0,0,1, 0,-1,0,0,0))
wald.test(eba1, C1)

## Test whether the three branch parameters are different
C2 <- rbind(c(0,0,0,0,0,0,0,0,1,-1, 0),
           c(0,0,0,0,0,0,0,0,0,1, 0,-1))
wald.test(eba1, C2, u.scale = FALSE)
```

Index

*Topic **datasets**

celebrities, 4
drugrisk, 7
heaviness, 15
pork, 23
schoolsubjects, 25
tartness, 28

*Topic **models**

balanced.pcdesign, 2
boot, 3
circular, 5
cov.u, 7
eba, 9
eba.order, 11
group.test, 13
inclusion.rule, 16
kendall.u, 17
linear2bt1, 18
logLik.eba, 19
mbt, 20
pcX, 21
plot.eba, 22
residuals.eba, 24
simulate.eba, 26
strans, 27
thurstone, 29
trineq, 30
uscale, 31
wald.test, 32

AIC, 19

anova.eba (eba), 9
anova.eba.order (eba.order), 11

balanced.pcdesign, 2, 21
boot, 3, 26

celebrities, 4
circular, 5, 11, 18, 28, 30
cov.u, 7, 11, 32, 33

deviance.eba (eba), 9

deviance.eba.order (eba.order), 11
drugrisk, 7

eba, 3, 4, 6, 7, 9, 9, 11–14, 16, 18, 19, 21, 22,
24, 26, 28, 30–33

eba.boot (boot), 3
eba.order, 11, 12, 18

glm, 18, 21, 30
group.test, 10, 11, 13, 13, 33

heaviness, 15

inclusion.rule, 16, 31

kendall.u, 6, 11, 17, 28, 30

L (eba), 9
L.constrained.order (eba.order), 11
L.order (eba.order), 11
linear2bt1, 18, 21
lm, 21
logLik.eba, 11, 13, 19
logLik.eba.order (eba.order), 11
logLik.lm, 19

mbt, 20

nlm, 11

nobs.eba (logLik.eba), 19

OptiPt (eba), 9

pcX, 3, 18, 21, 30
plot.eba, 11, 13, 22, 24
plot.eba.order (eba.order), 11
pork, 23
print.circular (circular), 5
print.eba (eba), 9
print.eba.order (eba.order), 11

print.group.test (group.test), 13
print.kendall.u (kendall.u), 17
print.mbt (mbt), 20
print.strans (strans), 27
print.summary.eba (eba), 9
print.summary.eba.order (eba.order), 11
print.thurstone (thurstone), 29
print.trineq (trineq), 30
print.wald.test (wald.test), 32

rbinom, 26
residuals.eba, 11, 13, 22, 24
residuals.eba.order (eba.order), 11
residuals.glm, 24

schoolsubjects, 18, 25
simulate.eba, 4, 11, 26
strans, 6, 11, 16, 18, 27, 30, 31
summary.eba, 12
summary.eba (eba), 9
summary.eba.order (eba.order), 11

tartness, 21, 28
thurstone, 11, 21, 29
trineq, 11, 16, 28, 30

uscale, 7, 11, 31, 33

vcov.eba (eba), 9
vcov.eba.order (eba.order), 11

wald.test, 7, 11, 14, 32, 32