

Package ‘eba’

January 2, 2012

Version 1.7-0

Date 2011-08-31

Title Elimination-by-Aspects (EBA) Models

Author Florian Wickelmaier

Maintainer Florian Wickelmaier <wickelmaier@web.de>

Depends R (>= 2.0.0), stats

Imports nlme

Description Fitting and testing multi-attribute probabilistic choice models, especially the Bradley-Terry-Luce (BTL) model (Bradley & Terry, 1952; Luce, 1959), elimination-by-aspects (EBA) models (Tversky, 1972), and preference tree (Pretree) models (Tversky & Sattath, 1979).

License GPL (>= 2)

URL <http://www.r-project.org>,
<http://homepages.uni-tuebingen.de/florian.wickelmaier>

Repository CRAN

Date/Publication 2011-09-01 08:43:44

R topics documented:

| | |
|-----------------------------|----|
| balanced.pcdesign | 2 |
| boot | 3 |
| celebrities | 4 |
| circular | 5 |
| cov.u | 6 |
| drugrisk | 7 |
| eba | 8 |
| eba.order | 10 |
| group.test | 13 |

| | |
|-------------------------|----|
| heaviness | 14 |
| kendall.u | 15 |
| linear2btl | 17 |
| logLik.eba | 18 |
| mbt | 19 |
| pcX | 20 |
| plot.eba | 21 |
| pork | 22 |
| residuals.eba | 23 |
| simulate.eba | 24 |
| strans | 25 |
| tartness | 26 |
| thurstone | 27 |
| uscale | 28 |
| wald.test | 29 |

| | |
|--------------|-----------|
| Index | 31 |
|--------------|-----------|

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

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

| | |
|--------------------|--|
| <code>pairs</code> | a character array holding the balanced pairs; see David (1988) for details how it is constructed |
| <code>listA</code> | the vector pairs in the original within-pair order |
| <code>listB</code> | 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.

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 indices of inconsistency.

Usage

`circular(mat)`

Arguments

| | |
|------------------|---|
| <code>mat</code> | a square matrix or a data frame consisting of (individual) binary choice data; row stimuli are chosen over column stimuli |
|------------------|---|

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 judged.

The null hypothesis in the chi-square test is that the inconsistencies in the paired-comparison judgments are by chance. The sampling distribution, however, 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 `chi2`. The chi-square approximation might be incorrect if $n < 8$.

Value

| | |
|--------------------|---|
| <code>T</code> | number of circular triads |
| <code>T.max</code> | maximum possible number of circular triads |
| <code>zeta</code> | Kendall's coefficient of consistency |
| <code>chi2</code> | the chi-square statistic for a test that the consistency is by chance |
| <code>df</code> | the degrees of freedom |
| <code>pval</code> | one minus the p-value for <code>chi2</code> (see Details) |

References

- David, H. (1988). *The method of paired comparisons*. London: Griffin.
- Kendall, M.G., & Smith, B.B. (1940). On the method of paired comparisons. *Biometrika*, **31**, 324–345.

See Also

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

Examples

```
# A dog's preferences for six samples of food: meat, biscuit, chocolate,
# apple, pear, and cheese (Kendall & Smith, 1940, p. 326)
mat <- 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)
circular(mat) # moderate consistency
```

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 <code>eba</code> , typically the result of a call to eba |
| norm | either <code>sum</code> (default), a number from 1 to number of stimuli, or <code>NULL</code> ; 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 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(bt1, 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="grey")
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 & 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 & Sattath, 1979), and elimination-by-aspects (EBA) models (Tversky, 1972), the former being special cases of the latter.

A 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 `fdHess[nlme]`. 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 |

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.
- 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.
- Tversky, A., & Sattath, S. (1979). Preference trees. *Psychological Review*, **86**, 542–573.
- 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.

See Also

[strans](#), [uscale](#), [cov.u](#), [group.test](#), [wald.test](#), [plot.eba](#), [residuals.eba](#), [logLik.eba](#), [simulate.eba](#), [kendall.u](#), [circular](#), [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 & 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 & 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 & Choisel (2006) describe a model that generalizes the Davidson-Beaver model and allows for an order effect in Pretree and EBA models.

Value

| | |
|---------------------------|---|
| <code>coefficients</code> | a vector of parameter estimates, the last component holds the order-effect estimate |
| <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 |

| | |
|-----------------|--|
| 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 |
| 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 ($y_1 + y_0$) |
| 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 equal 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, & King (2000) for further details, and Choisel & 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.

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.

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.

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="Estimated perceived heaviness (BTL model)",
     main="Weights judging experiment")
mtext("(Beaver & 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, "grey")
arrows(xval, uscale(bt12) - 1.96*sqrt(diag(cov.u(bt12))),
       xval, uscale(bt12) + 1.96*sqrt(diag(cov.u(bt12))), .05, 90, 3, "grey")

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)

```

kendall.u

Kendall's Coefficient of Agreement

Description

Kendall's u coefficient of agreement between judges.

Usage

```
kendall.u(M, cont.correct = FALSE)
```

Arguments

| | |
|---------------------------|---|
| <code>M</code> | a square matrix or a data frame consisting of absolute choice frequencies; row stimuli are chosen over column stimuli |
| <code>cont.correct</code> | logical, if TRUE a correction for continuity is applied (by deducting 1 from <code>chi2</code>), default is FALSE |

Details

Kendall's `u` takes values between `min.u` (when agreement is minimum) and 1 (when agreement is maximum). 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

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

References

Kendall, M.G., & Smith, B.B. (1940). On the method of paired comparisons. *Biometrika*, **31**, 324–345.

See Also

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

Examples

```
data(celebrities)
kendall.u(celebrities) # moderate 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

| | |
|---------------------|---|
| <code>object</code> | an object of class <code>glm</code> or <code>lm</code> specifying a BTL model |
| <code>order</code> | 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, & 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.

See Also

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

Examples

```
data(celebrities)
y1 <- t(celebrities)[lower.tri(celebrities)]
y0 <- celebrities[lower.tri(celebrities)]

## Fit BTL model using glm (maximum likelihood)
btl.glm <- glm(cbind(y1, y0) ~ pcX(9) - 1, binomial)
```

```
linear2bt1(bt1.glm)

## Fit BTL model using lm (weighted least squares)
bt1.lm <- lm(log(y1/y0) ~ pcX(9) - 1, 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)
```

| | |
|-----|------------------------------------|
| mbt | <i>Mallows-Bradley-Terry Model</i> |
|-----|------------------------------------|

Description

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

Usage

```
mbt(data)
```

Arguments

| | |
|------|--|
| data | a data frame, the first t columns containing the ranks, the (t + 1)th column containing the frequencies. |
|------|--|

Details

mbt provides a front end for glm.

See Critchlow & 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, and the p-value of the corresponding chi-square distribution |
| perm.idx | a vector of indices of 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.

Mallows, C.L. (1957). Non-null ranking models. I. *Biometrika*, **44**, 114–130.

See Also

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

Examples

```
data(tartness) # tartness rankings of salad dressings (Vargo, 1989)
mbt(tartness)  # 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 & Fligner (1991) for more details.

Value

A matrix having $(nstimuli - 1) * nstimuli / 2$ rows and $nstimuli$ columns.

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.

See Also

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

Examples

```

data(celebrities)      # absolute choice frequencies
btl <- eba(celebrities) # fit Bradley-Terry-Luce model using eba
summary(btl)

y1 <- t(celebrities)[lower.tri(celebrities)]
y0 <- celebrities[lower.tri(celebrities)]

## Fit Bradley-Terry-Luce model using glm
btl.glm <- glm(cbind(y1, y0) ~ pcX(9) - 1, binomial)
summary(btl.glm) # BTL model does not fit these data!

## Fit Thurstone Case V model using glm
tm.glm <- glm(cbind(y1, y0) ~ pcX(9) - 1, binomial(probit))
summary(tm.glm) # neither fits the TM model

```

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 = c(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**

This data set provides 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.

Examples

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

Description

Computes deviance and Pearson residuals for eba objects.

Usage

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

Arguments

| | |
|--------|--|
| object | an object of class eba, typically the result of a call to eba |
| type | the type of residuals which should be returned; the alternatives are: "deviance" (default) and "pearson" |
| ... | 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  
sum( resid(bt11, "pearson")^2 ) # Pearson X2
```

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, eba(simulate(eba1), A)$good[1])

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

```
xlim=c(0, 60), main="Parametric bootstrap")
curve(dchisq(x, df=eba1$good[2]), add=TRUE)
abline(v=eba1$good[1], 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

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); a more exact test of WST is suggested by Iverson & 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.
- 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.

See Also

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

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 # log transitivity violations
```

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

Description

The data were collected by Vargo (1989). 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.

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 & 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.

See Also

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

Examples

```
## Taste data (David, 1988, p. 116)
dat <- matrix(c( 0, 3, 2, 2,
               12, 0, 11, 3,
               13, 4, 0, 5,
               13, 12, 10, 0), 4, 4, byrow=TRUE)
thurstone(dat) # Thurstone-Mosteller model fits OK
```

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

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

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 <- matrix(c(0,0,0,1,-1,0,0,0,0,
              0,0,0,1,0,-1,0,0,0), 2, 9, TRUE)
wald.test(eba1, C1)

## Test whether the three branch parameters are different
C2 <- matrix(c(0,0,0,0,0,0,0,0,1,-1,0,
              0,0,0,0,0,0,0,0,1,0,-1), 2, 12, TRUE)
wald.test(eba1, C2, u.scale = FALSE)
```

Index

*Topic **datasets**

celebrities, 4
drugrisk, 7
heaviness, 14
pork, 22
tartness, 26

*Topic **models**

balanced.pcdesign, 2
boot, 3
circular, 5
cov.u, 6
eba, 8
eba.order, 10
group.test, 13
kendall.u, 15
linear2bt1, 17
logLik.eba, 18
mbt, 19
pcX, 20
plot.eba, 21
residuals.eba, 23
simulate.eba, 24
strans, 25
thurstone, 27
uscale, 28
wald.test, 29

AIC, 18

anova.eba (eba), 8
anova.eba.order (eba.order), 10

balanced.pcdesign, 2, 20
boot, 3, 24

celebrities, 4
circular, 5, 10, 16, 26, 28
cov.u, 6, 10, 29, 30

drugrisk, 7

eba, 3, 4, 6, 8, 8, 11, 12, 14, 16–18, 20, 21, 23,
24, 26, 28–30

eba.boot (boot), 3
eba.order, 10, 11, 17

glm, 17, 19, 20, 28
group.test, 9, 10, 12, 13, 30

heaviness, 14

kendall.u, 6, 10, 15, 26, 28

L (eba), 8
L.constrained.order (eba.order), 10
L.order (eba.order), 10
linear2bt1, 17, 20
lm, 20
logLik.eba, 10, 12, 18
logLik.eba.order (eba.order), 10
logLik.lm, 18

mbt, 19

nlm, 10

OptiPt (eba), 8

pcX, 3, 17, 20, 28
plot.eba, 10, 12, 21, 23
plot.eba.order (eba.order), 10
pork, 22
print.circular (circular), 5
print.eba (eba), 8
print.eba.order (eba.order), 10
print.group.test (group.test), 13
print.kendall.u (kendall.u), 15
print.mbt (mbt), 19
print.strans (strans), 25
print.summary.eba (eba), 8
print.summary.eba.order (eba.order), 10
print.thurstone (thurstone), 27

`print.wald.test` (`wald.test`), 29

`rbinom`, 24

`residuals.eba`, 10, 12, 21, 23

`residuals.eba.order` (`eba.order`), 10

`residuals.glm`, 23

`simulate.eba`, 4, 10, 24

`strans`, 6, 10, 16, 25, 28

`summary.eba`, 11

`summary.eba` (`eba`), 8

`summary.eba.order` (`eba.order`), 10

`tartness`, 19, 26

`thurstone`, 10, 20, 27

`uscale`, 6, 10, 28, 30

`vcov.eba` (`eba`), 8

`vcov.eba.order` (`eba.order`), 10

`wald.test`, 6, 10, 14, 29, 29