

Package ‘pairwise’

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Imports graphics, stats, methods

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Title Rasch Model Parameters by Pairwise Algorithm

Description Performs the explicit calculation

-- not estimation! -- of the Rasch item parameters for dichotomous and polytomous item responses, using a pairwise comparison approach. Person parameters (WLE) are calculated according to Warm's weighted likelihood approach.

Suggests psych, exhaustiveRasch

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andersentest.pers *Andersen's Likelihood Ratio Test for Object of class "pers"*

Description

The Andersen likelihood ratio test is based on splitting the dataset into subgroups of persons. One can argue that it is a significance testable version of the more descriptive graphical model check - see [grm](#).

Usage

```
andersentest.pers(
  pers_obj,
  split = "median",
  splitseed = "no",
  pot = NULL,
  zerocor = NULL
)
```

Arguments

<code>pers_obj</code>	an object of class "pers" - see function pers .
<code>split</code>	Specifies the splitting criterion. Basically there are three different options available - each with several modes - which are controlled by passing the corresponding character expression to the argument. <ol style="list-style-type: none"> Using the rawscore for splitting into subsamples with the following modes: <code>split = "median"</code> median raw score split - high score group and low score group; <code>split = "mean"</code> mean raw score split - high score group and low score group. Finally <code>split = "score"</code> that is splitting daten into as many subsamples as there are raw score groups - discarding min and max (theoretical) score group - which matches the concept proposed by Andersen (1973). Dividing the persons in daten into subsamples with equal size by random allocation with the following modes: <code>split = "random"</code> (which is equivalent to <code>split = "random.2"</code>) divides persons into two subsamples with equal size. In general the number of desired subsamples must be expressed after the dot in the character expression - e.g. <code>split = "random.6"</code> divides persons into 6 subsamples (with equal size) by random allocation etc. The third option is using a manifest variable as a splitting criterion. In this case a vector with the same length as number of cases in daten must be passed to the argument grouping the data into subsamples. This vector should be coded as "factor" or a "numeric" integer vector with <code>min = 1</code>.
<code>splitseed</code>	numeric, used for <code>set.seed(splitseed)</code> for random splitting - see argument <code>split</code> .
<code>pot</code>	optional argument, at default (<code>pot=NULL</code>) setting is read from <code>pers_obj</code> - see description for pair .

zerocor optional argument, at default (zerocor=NULL) setting is read from pers_obj - see description for `pair`.
 pot=pers_obj\$pair\$fuargs\$pot, zerocor=pers_obj\$pair\$fuargs\$zerocor

Details

Andersen (1973) proposed to split the dataset by [raw] score groups, which can be achieved setting the argument `split = "score"`. However as pointed out by Rost (2004) there might be several different splitting criteria for testing subsample invariance of the raschmodel. Thus the argument `split` provides some other options for splitting the data - see description of arguments.

Value

A (list) object of class "andersentest.pers" ...

References

Andersen, E. B. (1973). A goodness of fit test for the rasch model. *Psychometrika*, 38(1), 123–140.
 Rost, J. (2004). *Lehrbuch Testtheorie - Testkonstruktion* (2 nd Ed.) Huber: Bern.

Examples

```
## Not run:
data(bfiN) # loading example data set
data(bfi_cov) # loading covariates to bfiN data set
model <- pers(pair(bfiN,m=6))
andersentest.pers(model, split = bfi_cov$gender)
andersentest.pers(model, split = "random")
andersentest.pers(model, split = "median")
### using simulated data:
data("sim200x3")
model2 <- pers(pair(sim200x3))
andersentest.pers(model2, split = "median")

## End(Not run)
```

bfiN

5 polytomous personality items

Description

Data from 2800 subjects answering to 5 neuroticism items with 6 answer categories (0-5) of the bfi dataset originally included in the R-package {psych} - see <https://cran.r-project.org/package=psych>.

Usage

```
data(bfiN)
```

Format

A "data.frame" containing 5 variables and 2800 observations.

Details

The other variables from the original bfi dataset were skipped and the categories are 'downcoded' to '0,1,2,3,4,5' to have a simple, ready to use example data frame. For further Information on the original dataset see R-package {psych}.

The category meanings (after downcoding) are as follows:

score 0 Very Inaccurate
 score 1 Moderately Inaccurate
 score 2 Slightly Inaccurate
 score 3 Slightly Accurate
 score 4 Moderately Accurate
 score 5 Very Accurate

The Item meanings are as follows:

N1 Get angry easily.
 N2 Get irritated easily.
 N3 Have frequent mood swings.
 N4 Often feel blue.
 N5 Panic easily.

The covariates like gender, education and age are in a seperate dataset cov_bfi

Source

<https://cran.r-project.org/package=psych>

References

Revelle, William (2015), psych: Procedures for Psychological, Psychometric, and Personality Research. *R package version 1.5.1*

Examples

```
data(bfiN)
dim(bfiN)
#####
names(bfiN) # show all variable names of data.frame bfiN
range(bfiN,na.rm=TRUE) # checking the valid response range
```

bfiN_miss	<i>5 polytomous personality items</i>
-----------	---------------------------------------

Description

Data from 2800 subjects answering to 5 neuroticism items with 6 answer categories (0-5) of the bfi dataset originally included in the R-package {psych} with artificial missing data (see details).

Usage

```
data(bfiN_miss)
```

Format

A "data.frame" containing 5 variables and 2800 observations.

Details

This dataset is the same like the dataset {bfiN} included in this package, except for the amount of missing data, which were additional created in that way, having aprox. 15% missing for each of the 5 variables by random.

The other variables from the original bfi dataset were skipped and the categories are 'downcoded' to '0,1,2,3,4,5' to have a simple, ready to use example data frame. For further Information on the original dataset see R-package {psych}. The covariates like gender, education and age are in a separate dataset cov_bfi

Source

<https://cran.r-project.org/package=psych>

References

Revelle, William (2015), psych: Procedures for Psychological, Psychometric, and Personality Research. *R package version 1.5.1*

Examples

```
data(bfiN_miss)
dim(bfiN_miss)
#####
names(bfiN_miss) # show all variable names of data.frame bfiN_miss
range(bfiN_miss,na.rm=TRUE) # checking the valid response range
colSums(is.na(bfiN_miss))/dim(bfiN_miss)[1] # percentage of missing per variable
```

`bfi_cov`*Covariates to the bfiN Data*

Description

Covariates to the data from 2800 subjects answering to 5 neuroticism items of the bfi dataset originally included in the R-package {psych} - see <https://cran.r-project.org/package=psych>.

Usage

```
data(bfi_cov)
```

Format

A "data.frame" containing 3 variables (gender, education, and age) for 2800 observations.

Details

The covariates are in the same row (person) order as the responses to the 5 neuroticism items in the separate datasets `bfiN` and `bfiN_miss`. The coding is as follows:

gender Males = 1, Females = 2

education 1 = HS, 2 = finished HS, 3 = some college, 4 = college graduate 5 = graduate degree

age age in years

Source

<https://cran.r-project.org/package=psych>

References

Revelle, William (2015), psych: Procedures for Psychological, Psychometric, and Personality Research. *R package version 1.5.1*

Examples

```
data(bfi_cov)
dim(bfi_cov)
#####
names(bfi_cov) # show all variable names of data
```

`catprob`*Category Probability Plots*

Description

plotting function for plotting category probability curves.

Usage

```
catprob(pair_obj, itemnumber = 1, ra = 4, plot = TRUE, ...)
```

Arguments

<code>pair_obj</code>	an object of class "pair" as a result from function <code>pair</code> .
<code>itemnumber</code>	an integer, defining the number of the item to plot the respective category probability for. This is set to an arbitrary default value of <code>itemnumber = 1</code> to avoid error messages when you forget to choose an item to plot the expected score curves for.
<code>ra</code>	an integer, defining the (logit) range for x-axis
<code>plot</code>	a logical (default <code>plot = TRUE</code>), defining whether to suppress plotting and just return a matrix of category probabilities
<code>...</code>	arguments passed to plot

Details

no details in the moment.

Value

a plot or a matrix with category probabilities.

Examples

```
#####  
data(sim200x3)  
result <- pair(sim200x3)  
catprob(pair_obj = result, itemnumber = 2 )  
data(bfiN)  
result <- pair(bfiN)  
catprob(pair_obj = result, itemnumber = 3 )
```

cog	<i>Math PISA (2003) data</i>
-----	------------------------------

Description

Data from the german sample of the PISA 2003 survey, containing 31 dichotomous items from the math task.

Usage

```
data(cog)
```

Format

A data frame containing 34 variables and 4660 observations.

Details

The first 3 variables are ID variables. For further information on variables and their meaning see the codebook PDF file available at https://www.oecd.org/pisa/pisaproducts/PISA12_cogn_codebook.pdf

References

Database - PISA 2003, *Downloadable Data*, <https://www.oecd.org/pisa/data/pisa2012database-downloadabledata>

Examples

```
data(cog)
dim(cog)
#####
names(cog) # show all variable names of data.frame cog
names(cog[,4:34]) # show the variable names of the math items
names(cog[,1:3]) # show the variable names of the ID variables
```

cogBOOKLET	<i>Booklet allocation table for Math PISA (2003) data</i>
------------	---

Description

a data.frame containing a booklet allocation table for the cognitive Data `cog` in this package, which holds 31 dichotomous items from the math task from the german sample of the PISA 2003 survey.

Usage

```
data(cogBOOKLET)
```

Format

A data.frame containing 31 rows.

Details

For further Information on variables and their meaning see the codebook PDF file available at https://www.oecd.org/pisa/pisaproducts/PISA12_cogn_codebook.pdf

References

Database - PISA 2003, *Downloadable Data*, <https://www.oecd.org/pisa/data/pisa2012database-downloadabledata>

Examples

```
data(cogBOOKLET)
cogBOOKLET
```

deltapar

Compute delta parameters from thurstonian thresholds

Description

Calculation of delta parameters or rather item step parameters from thurstonian threshold parameters returned by the function `pair`.

Usage

```
deltapar(object, sigma = TRUE)
```

Arguments

object	an object of class "pair" as resulting from item parameter calculation using the function <code>pair</code> .
sigma	a logical whether to return item difficulties (sigma) or not

Details

The "Thurstone threshold" or rather thurstonian threshold for a category corresponds to a point on the latent variable at which the probability of being observed in that category or above equals that of being observed in the categories below. Thus these thurstonian threshold parameters can be interpreted in a strait forward and easy way. However, some other computer programs related to Rasch analysis don't return thurstonian threshold parameters from their estimation procedure, but rather so called delta parameters for the item steps. The later are also known as "step measures", "step calibrations", "step difficulties", "tau parameters", and "Rasch-Andrich thresholds". For a better comparability between different Rasch software and estimation procedures the thurstonian threshold parameters can be converted into delta or rather items step parameters.

Value

If `sigma=TRUE` an object of class `c("data.frame", "deltapar")` containing delta parameters for items and their difficulties (first column). Otherwise a matrix containing only the delta parameters.

References

Linacre J.M. (1992). Rasch-Andrich Thresholds and Rasch-Thurstone Thresholds. *Rasch Measurement Transactions*, 5:4, 191. <https://www.rasch.org/rmt/rmt54r.htm>

Linacre J.M. (2001). Category, Step and Threshold: Definitions & Disordering. *Rasch Measurement Transactions*, 15:1, 794. <https://www.rasch.org/rmt/rmt151g.htm>

Adams, R. J., Wu, M. L., & Wilson, M. (2012). The Rasch Rating Model and the Disordered Threshold Controversy. *Educational and Psychological Measurement*, 72(4), 547–573. <https://doi.org/10.1177/00131644114>

Linacre J.M. (2006). Item Discrimination and Rasch-Andrich Thresholds. *Rasch Measurement Transactions*, 20:1, 1054. <https://www.rasch.org/rmt/rmt201k.htm>

Examples

```
#####
data(sim200x3) # loading reponse data
ip <- pair(sim200x3,m = c(2,3,3)) # compute item parameters
summary(ip) # have a look at the results (thurstonian thresholds)
deltapar(ip) # compute delta parameters from these
```

 DEU_PISA2012

Data from PISA 2012 - German Sample

Description

Selecttd data for 5001 'subjects' who participated in the PISA 2012 survey.

Usage

```
data(DEU_PISA2012)
```

Format

A list containing

Details

The data is based on freely down loadable data on the official OECD page - see source. The general structure of the data in list format, is described in an PDF document available in the User guides, package vignettes and other documentation section.

References

Database - PISA 2003, *Downloadable Data*, <https://www.oecd.org/pisa/data/pisa2012database-downloadabledata>

Examples

```
#####
data(DEU_PISA2012)
str(DEU_PISA2012)
```

 esc

Expected Score Curves Plots

Description

plotting function for plotting expected score curves.

Usage

```
esc(pers_obj, itemnumber = 1, integ = 6, ra = 4, nodes = 100, lwd = 2, ...)
```

Arguments

<code>pers_obj</code>	an object of class "pers" as a result from function pers .
<code>itemnumber</code>	an integer, defining the number of the item to plot the respective category probability for. This is set to an arbitrary default value of <code>itemnumber = 1</code> to avoid error messages when you forget to choose an item to plot the expected score curves for.
<code>integ</code>	either an integer defining the number of (ability) groups to integrate the empirical theta vector or the character expression "all" to plot the empirical theta distribution at the respective item score using symbols (see example).
<code>ra</code>	an integer, defining the (logit) range for x-axis
<code>nodes</code>	number of integration nodes
<code>lwd</code>	see plot
<code>...</code>	arguments passed to plot

Details

no details in the moment.

Examples

```
#####
data(bfiN)
result <- pers(pair(bfiN))
esc(pers_obj=result,1,lwd=2) # plot for first item
esc(pers_obj=result,2,lwd=2) # plot for second item
for(i in 1:5){esc(pers_obj=result,i,lwd=2)}
#####
esc(pers_obj=result,2,integ="all",lwd=2) # plot for second item
```

ftab

Tabulating Answer Categories in Data

Description

function tabulating (answer) categories in X.

Usage

```
ftab(X, catgories = NULL, na.omit = FALSE)
```

Arguments

X	Data as a "matrix", a "data.frame" or even a "vector" or "factor". "vector" or "factor" are coerced to a "data.frame" with one column.
catgories	optional a vector ("numeric" or "character") containig the categories to tabulate. At default (catgories=NULL) the fuction looks for unique categories in X.
na.omit	logical (default: na.omit=FALSE) wether to return frequencies for missing values, NAs.

Details

X can either be a ("numeric" or "character") "matrix" containing response vectors of persons (rows) or a "data.frame" containing "numeric", "character" or "factor" variables (columns).

Value

a "matrix" with category frequencies

Examples

```
#####  
data(bfiN)  
ftab(bfiN)  
data(sim200x3)  
ftab(sim200x3)
```

gif

*Graphical Item Fit Plots***Description**

plotting function for plotting empirical and model derived category probability curves.

Usage

```
gif(pers_obj, itemnumber = 1, ra = 4, integ = "raw", kat = "all", ...)
```

Arguments

<code>pers_obj</code>	an object of class "pers" as a result from function pers .
<code>itemnumber</code>	an integer, defining the number of the item to plot the respective category probability for. This is set to an arbitrary default value of <code>itemnumber = 1</code> to avoid error messages when you forget to choose an item to plot the expected score curves for.
<code>ra</code>	an integer, defining the (logit) range for x-axis
<code>integ</code>	either an integer, defining the number of integration points along the (logit) range on the x-axis to integrate the empirical theta values, or the character expression "raw" (default) which will use the rawscore groups as integration points.
<code>kat</code>	either an integer, defining for which category the empirical category probabilities should be plotted over the model derived category probability curves, or the character expression "all" (default) which will plot the empirical category probabilities for all categories.
<code>...</code>	arguments passed to plot

Details

no details in the moment.

Value

a plot with category probabilities.

Examples

```
#####
data(bfiN)
pers_obj <- pers(pair(bfiN))
#### plot empirical category probabilities
gif(pers_obj = pers_obj, itemnumber = 1 )
gif(pers_obj = pers_obj, itemnumber = 1 , integ=8) # integration over 8 points
gif(pers_obj = pers_obj, itemnumber = 1 , integ=8, kat=1) # only for category number 1
```

Description

This function makes the basic calculations for the graphical model check for dichotomous or polytomous item response formats. It is more or less a wrapper function, internally calling the function `pairSE`. Several splitting options are available (see arguments).

Usage

```
grm(
  daten,
  m = NULL,
  w = NULL,
  split = "random",
  splitseed = "no",
  verbose = FALSE,
  ...
)
```

Arguments

- `daten` a data.frame or matrix with optionally named columns (names of items), potentially with missing values, comprising polytomous or dichotomous (or mixed category numbers) responses of n respondents (rows) on k items (columns) coded starting with 0 for lowest category to $m-1$ for highest category, with m being a vector (with length k) with the number of categories for the respective item.
- `m` an integer (will be recycled to a vector of length k) or a vector giving the number of response categories for all items - by default $m = \text{NULL}$, m is calculated from data, assuming that every response category is at least once present in data. For sparse data it is strongly recommended to explicitly define the number of categories by defining this argument.
- `w` an optional vector of case weights.
- `split` Specifies the splitting criterion. Basically there are three different options available - each with several modes - which are controlled by passing the corresponding character expression to the argument.

 - 1) Using the rawscore for splitting into subsamples with the following modes: `split = "median"` median raw score split - high score group and low score group; `split = "mean"` mean raw score split - high score group and low score group.
 - 2) Dividing the persons in `daten` into subsamples with equal size by random allocation with the following modes: `split = "random"` (which is equivalent to `split = "random.2"`) divides persons into two subsamples with equal size. In general the number of desired subsamples must be expressed after the dot

in the character expression - e.g. `split = "random.6"` divides persons into 6 subsamples (with equal size) by random allocation etc.

3) The third option is using a manifest variable as a splitting criterion. In this case a vector with the same length as number of cases in `daten` must be passed to the argument grouping the data into subsamples. This vector should be coded as "factor" or a "numeric" integer vector with `min = 1`.

<code>splitseed</code>	numeric, used for <code>set.seed(splitseed)</code> for random splitting - see argument <code>split</code> .
<code>verbose</code>	logical, if <code>verbose = TRUE</code> (default) a message about subsampling is sent to console when calculating standard errors.
<code>...</code>	additional arguments <code>nsample</code> , <code>size</code> , <code>seed</code> , <code>pot</code> for calling <code>pairSE</code> are passed through - see description for <code>pairSE</code> .

Details

The data is splitted in two or more subsamples and then item thresholds, the parameter (Sigma) and their standard errors (SE) for the items according the PCM are calculated for each subsample. Additional arguments (see description of function `pairSE`) for parameter calculation are passed through.

WARNING: When using data based on booklet designs with systematically missing values (by design) you have to ensure that in each of the booklet the maximum raw value to reach is equal while using the raw value as splitting criterion.

Value

A (list) object of class `c("grm", "list")` containing the item difficulty parameter `sigma` and their standard errors for two or more subsamples.

A note on standard errors

Estimation of standard errors is done by repeated calculation of item parameters for subsamples of the given data. This procedure is mainly controlled by the arguments `nsample` and `size` (see arguments). With regard to calculation time, the argument `nsample` is the 'time killer'. On the other hand, things (estimation of standard errors) will not necessarily get better when choosing large values for `nsample`. For example choosing `nsample=400` will only result in minimal change for standard error estimation in comparison to (`nsample=30`) which is the default setting (see examples).

References

description of function `pairSE{pairwise}`.

Examples

```
data(bfiN) # loading example data set

data(bfi_cov) # loading covariates to bfiN data set

# calculating itemparameters and SE for two random allocated subsamples
```



```

grm_gen <- grm(daten=bfiN, split = bfi_cov$gender)
summary(grm_gen)
#### plot(grm_gen)

grm_med <- grm(daten=bfiN, split = "median")
summary(grm_med)
#### plot(grm_med)

grm_ran<-grm(daten=bfiN, split = "random")

summary(grm_ran)

# some examples for plotting options
# plotting item difficulties for two subsamples against each other
# with ellipses for a CI = 95% .
#### plot(grm_ran)

# using triangles as plotting pattern
#### plot(grm_ran,pch=2)

#plotting without CI ellipses
#### plot(grm_ran,ci=0,pch=2)

# plotting with item names
#### plot(grm_ran,itemNames=TRUE)

# Changing the size of the item names
#### plot(grm_ran,itemNames=TRUE, cex.names = 1.3)

# Changing the color of the CI ellipses
plot(grm_ran,itemNames=TRUE, cex.names = .8, col.error="green")

##### example from details section 'Some Notes on Standard Errors' #####
## Not run:
grm_def<-grm(daten=bfiN, split = "random",splitseed=13)
plot(grm_def)
#####
grm_400<-grm(daten=bfiN, split = "random", splitseed=13 ,nsample=400)
plot(grm_400)

## End(Not run)

```

Description

plotting function for plotting the Item information function(IIF).

Usage

```
iff(
  pair_obj,
  itemnumber = 1,
  x = NULL,
  plot = TRUE,
  cat = FALSE,
  lwd = 2,
  col = 1,
  ...
)
```

Arguments

<code>pair_obj</code>	an object of class "pair" as a result from function pair .
<code>itemnumber</code>	an integer, defining the number of the item to plot the respective item information function for. This is set to an arbitrary default value of <code>itemnumber = 1</code> to avoid error messages when you forget to choose an item to plot the item information function for.
<code>x</code>	The value(s) of the latent variable, at which the IIF will be evaluated. <code>x</code> should be either a numeric vector of theta values or a single numeric value. If <code>x</code> is given as a single numeric value plotting is suppressed. If not given (default), 99 values spaced evenly between -4 and +4 will be used, handy for plotting.
<code>plot</code>	a logical (default <code>plot = TRUE</code>), defining whether to suppress plotting and just return a matrix of the values of the Item information function.
<code>cat</code>	a logical (default <code>cat = FALSE</code>), defining whether to plot or return the values of the Item information function based on item categories.
<code>lwd</code>	see parameters for plot
<code>col</code>	see parameters for plot
<code>...</code>	arguments passed to <code>plot</code>

Details

no details in the moment.

Value

a plot, a matrix or a single numeric with values of the Item information function.

Examples

```
#####
data(sim200x3)
result <- pair(sim200x3)
# IFF plot for Item No. 2
iff(pair_obj = result, itemnumber = 2 )
# IFF plot for Categories of Item No. 2
```

```

iff(pair_obj = result, itemnumber = 2 ,cat=TRUE)
# IFF at theta=0 for Item No. 2
iff(pair_obj = result, itemnumber = 2 ,x=0)
# IFF at theta=0 for Categories of Item No. 2
iff(pair_obj = result, itemnumber = 2 ,x=0,cat=TRUE)
# IFF of Item No. 2 for a given range of thetas
iff(pair_obj = result, itemnumber = 2 ,x=seq(0,4,.1))
# ... etc.
iff(pair_obj = result, itemnumber = 2 ,x=seq(0,4,.1),cat=TRUE)
##### examples with other data ...
data(bfiN)
result <- pair(bfiN)
iff(pair_obj = result, itemnumber = 3 )
iff(pair_obj = result, itemnumber = 3 ,cat=TRUE)

```

KCT

*Knox Cube Test Data from Wright & Stone (1979)***Description**

Data from the Book 'Best Test Design' from Wright & Stone (1979, p. 31, table 2.3.1) comprising responses from 35 subjects scored in 18 dichotomous items.

Usage

```
data(KCT)
```

Format

A "data.frame" containing 18 numeric variables (coded 0,1) and 35 observations.

Details

The so called 'Knox Cube Test' was initially developed as a cube imitation test around 1913 by Howard A. Knox as a nonverbal test of intelligence to screen and identify potential immigrants with mental deficits at the Ellis Island immigration station in New York Harbor – see Richardson (2005) for a historical review.

Quoted from Wright & Stone (1979):

"Success on this subtest requires the application of visual attention and short-term memory to a simple sequencing task. It appears to be free from school-related tasks and hence to be an indicator of nonverbal intellectual capacity." (Wright & Stone 1979, p. 28).

References

Wright, B. D. & Stone, M. H. (1979). *Best Test Design: Rasch Measurement*. Chicago: MESA Press.

Richardson, J. T. E. (2005). Knox's cube imitation test: A historical review and an experimental analysis. *Brain and Cognition*, 59(2), 183–213. <https://doi.org/10.1016/j.bandc.2005.06.001>

Examples

```

data(KCT)
dim(KCT)
##### some item calibrations #####
data(KCT)
IP_pair <- pair(daten = KCT[,4:17], m = 2)
summary(IP_pair)
#####
#####
#####MIKE error message never received#####
#####
#####

```

kft5

Dichotomous example data in Rost 2004

Description

Data for 300 subjects answering to 5 dichotomous items out of 'Kognitiver Fähigkeits Test' [Cognitive Skills Test] (KFT - Gaedike & Weinläder, 1976) . This data is used as an example in the textbook by J. Rost (2004) to demonstrate some principles of rasch measurement.

Usage

```
data(kft5)
```

Format

A "matrix" containing 5 columns (variables) and 300 rows (obsevation).

Details

The instrument KFT and the data are described in Rost (2004) at page 95.

References

Rost, J. (2004). *Lehrbuch Testtheorie - Testkonstruktion* (2 nd Ed.) Huber: Bern.
Heller, K, Gaedike, A.-K & Weinläder, H. (1976). *Kognitiver Fähigkeits-Test (KFT 4-13)*. Weinheim: Beltz.

Examples

```

data(kft5)
dim(kft5)
#####
# frequencies
ftab(kft5)
# Itemparameter to be compared with Rost (2004), page 120.

```

```
summary(pair(kft5))
# Itemparameter to be compared with Rost (2004), page 120.
summary(pers(pair(kft5)))
```

logLik.pers

S3 logLik for Object of class "pers"

Description

S3 logLik method to extract the log-likelihood for object of class "pers"

Usage

```
## S3 method for class 'pers'
logLik(object, sat = FALSE, p = FALSE, ...)
```

Arguments

object	object of class "pers"
sat	a "logical" with default set to sat=FALSE to return the Log-Likelihood of the data for the unrestricted model based on parameters estimated with function pers . If set to sat=TRUE the Log-Likelihood of the saturated model is returned instead.
p	a "logical" with default set to p=FALSE to return the category probabilities for the empirical data.
...	not used yet.

lrtest.pers

Likelihood Ratio Test for Object of class "pers"

Description

Function to perform a likelihood ratio test for the estimated model 'against' the saturated model for object of class "pers".

Usage

```
lrtest.pers(object, ...)
```

Arguments

object	an object of class "pers" - see function pers .
...	not used yet.

make.incidenz	<i>Converting a booklet allocation table into a incidence matrix</i>
---------------	--

Description

This function converts a booklet allocation table (like in [cogBOOKLET](#)) into a incidence matrix used in the function [pers](#).

Usage

```
make.incidenz(tab, bookid, item_order = NULL, info = FALSE)
```

Arguments

tab	a booklet allocation table as a <code>data.frame</code> . The first column is assumed to contain the item names as a character vector (not a factor!) the other columns must be integer vectors containing the information in which booklet(s) the respective item is allocated.
bookid	a integer vector with the same length as the number of persons in the response data giving the information which booklet was assigned to each person.
item_order	optional a character vector with the item names in the order of the items in the response data (from first to last column in the response data). By default it is assumed that the item order in the booklet allocation table is already the same as in the response data.
info	logical default: <code>info=FALSE</code> to return just the incidence matrix. If set to <code>info=TRUE</code> more detailed information about the booklet design is returned.

Details

It is assumed that there is an equal replicate factor for each item used, when constructing the bookletdesign - so every items occurs with the same frequency over all booklets of the entire set of booklets.

Value

an incidence matrix as an object of class "matrix" with 0,1 coding or a "list" with detailed information.

Examples

```
#####
data(cog);data(cogBOOKLET) # loading reponse and allocation data
table(cog$BOOKID)# show n persons per booklet
names(table(c(as.matrix(cogBOOKLET[,2:5])))) # show booklets in allocation data
d<-(cog[cog$BOOKID!=14,]) # skip persons which got booklet No.14.
inc<-make.incidenz(tab=cogBOOKLET, bookid=d$BOOKID) # make just the incidence matrix
inc
```

```

make.incidenz(tab=cogBOOKLET, bookid=d$BOOKID, info=TRUE) # get some info too
# in this case not necessary but just to show
# using the (item) names in cog to secure the item order in incidence matrix:
make.incidenz(tab=cogBOOKLET, bookid=d$BOOKID, item_order=names(cog)[4:34])
#####

```

Neoffi5

Polytomous example data in Rost 2004

Description

Data for 1000 subjects answering to 5 polytomous items assessing neuroticism contained in the german version of the NEO–five–factor–inventory (NEOFFI) by Borkenau and Ostendorf (1991). This data is used as an example in the textbook by J. Rost (2004) to demonstrate some principles of rasch measurement.

Usage

```
data(Neoffi5)
```

Format

A "matrix" containing 5 columns (variables) and 1000 rows (obsevation).

Details

An detailed description of the data can be found in Rost (2004) at page 202.

References

Rost, J. (2004). *Lehrbuch Testtheorie - Testkonstruktion* (2 nd Ed.) Huber: Bern.

Borkenau, P. & Ostendorf F. (1991). Ein Fragebogen zur Erfassung fünf robuster Persönlichkeitsfaktoren. *Diagnostica*, 37, (1), 29–41.

Examples

```

data(Neoffi5)
dim(Neoffi5)
#####
# frequencies
ftab(Neoffi5)
# Itemparameter to be compared with Rost (2004), page 211.
summary(pair(Neoffi5))
# Itemparameter to be compared with Rost (2004), page 213.
summary(pers(pair(Neoffi5)))

```

 pair

Item Parameter Calculation

Description

This is the (new) main function for calculation of the item parameter for the dichotomous Rasch Model (Rasch, 1960) and its extension for polytomous items (thurstonian thresholds) according to the Partial Credit Model (Masters, 1982).

The function implements a generalization (see Heine & Tarnai, 2015) of the pairwise comparison approach, that is based on the principle for item calibration introduced by Choppin (1968, 1985) – see also (Wright & Masters, 1982). The number of (response) categories may vary across items.

Missing values up to an high amount in data are allowed, as long as items are proper linked together.

Usage

```
pair(
  daten,
  m = NULL,
  w = NULL,
  pot = TRUE,
  zerocor = TRUE,
  ccf = FALSE,
  likelihood = NULL,
  pot2 = 2,
  delta = TRUE,
  conv = 1e-04,
  maxiter = 3000,
  progress = TRUE,
  init = NULL,
  zerosum = TRUE,
  ...
)
```

Arguments

daten	a single <code>data.frame</code> or <code>matrix</code> or a list with every list entry holding a <code>data.frame</code> or <code>matrix</code> . Row and column names may represent the names of items (columns) and persons (rows). Missing values (NA) are allowed. Item responses can be polytomous or dichotomous (or a mixture of a varying number of categories across all items). Responses of n respondents (rows) on k items (columns) must be coded (scored) starting with 0 for lowest category to $m-1$ for highest category. If a list is assigned to this argument each <code>data.frame</code> or <code>matrix</code> as respective list entry must have the same dimensionality. See details and examples.
m	an integer (will be recycled to a vector of length k) or a vector giving the number of response categories for all items - by default ($m = \text{NULL}$), m is calculated from data, assuming that every response category is at least once present in the data.

	For 'sparse' data it is <i>strongly recommended</i> to explicitly define the number of categories by defining this argument.
w	an optional vector of case weights.
pot	either a logical or an integer ≥ 2 defining the power to compute of the pairwise comparison matrix. If TRUE (default) a power of three of the pairwise comparison matrix is used for further calculations. If FALSE no powers are computed.
zerocor	either a logical or a numeric value between >0 and ≤ 1 . If (in case of a logical) zerocor is set to TRUE (default) unobserved combinations (1-0, 0-1) in the data for each pair of items are given a frequency of one conf. proposal by Alexandrowicz (2011, p.373). As an alternative option a numeric value between >0 and ≤ 1 can be assigned to unobserved combinations (1-0, 0-1) in the data for each pair of items (conf. to personal communication with A. Robitzsch; 29-03-2021).
ccf	logical with default ccf=FALSE to perform normal item parameter calculation, if set to ccf=TRUE just the conditional item (category) frequencies are returned.
likelihood	either NULL (default) or a character expression defining a likelihood estimation approach based on the pairwise comparison matrix. Currently only the so called MINCHI approach as described in Fischer (2006) is implemented, which can be selected by setting likelihood="minchi".
pot2	ignored when likelihood=NULL (default).
delta	ignored when likelihood=NULL (default).
conv	ignored when likelihood=NULL (default).
maxiter	ignored when likelihood=NULL (default).
progress	ignored when likelihood=NULL (default).
init	ignored when likelihood=NULL (default).
zerosum	ignored when likelihood=NULL (default).
...	additional parameters passed through.

Details

Parameter calculation is based on the construction of a paired comparison matrix M_{nicjc} with entries $ficjc$ representing the number of respondents who answered to item i in category c and to item j in category $c-1$ widening Choppin's (1968, 1985) conditional pairwise algorithm to polytomous item response formats. This algorithm is simply realized by matrix multiplication.

To avoid numerical problems with off diagonal zero's when constructing the pairwise comparison matrix M_{nij} , powers of the M_{nicjc} matrix, can be used (Choppin, 1968, 1985). Using powers k of M_{nicjc} - argument `pot=TRUE` (default), replaces the results of the direct comparisons between i and j with the sum of the indirect comparisons of i and j through an intermediate k . In general, it is recommended to use the argument with default value `pot=TRUE`.

If a list object is assigned to the argument `data`, the list entries (matrix or data.frame) must all have the same dimensionality. The individual list entries represent either r measurement times or raters. If such a list object is used, first the item parameters are calculated across all r measurement points or raters and additionally a threshold parameter is given for each of the r measurement points or raters (e.g. rater severity or overall item shift).

For a graphic representation of the item 'estimates' the plotting S3 method `plot.pair` is available. For plotting the item category probabilities the function `catprob` can be used.

Value

A (list) object of class "pair" containing the item category thresholds and difficulties sigma, also called item location.

References

- Choppin, B. (1968). Item Bank using Sample-free Calibration. *Nature*, 219(5156), 870-872.
- Choppin, B. (1985). A fully conditional estimation procedure for Rasch model parameters. *Evaluation in Education*, 9(1), 29-42.
- Heine, J. H. & Tarnai, Ch. (2015). Pairwise Rasch model item parameter recovery under sparse data conditions. *Psychological Test and Assessment Modeling*, 57(1), 3–36.
- Alexandrowicz, R. W. (2011). 'GANZ RASCH': A Free Software for Categorical Data Analysis. *Social Science Computer Review*, 30(3), 369-379.
- Masters, G. (1982). A Rasch model for partial credit scoring. *Psychometrika*, 47(2), 149–174.
- Rasch, G. (1960). *Probabilistic models for some intelligence and attainment tests*. Copenhagen: Danmarks pædagogiske Institut.
- Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.
- Fischer, Gerhard H. 2006. "Rasch Models". Pp. 515–85 in *Handbook of statistics (26): Psychometrics*. Vol. 26, edited by C. R. Rao and S. Sinharay. Amsterdam: Elsevier.

Examples

```
data(bfiN) # loading example data set
# calculating itemparameters for 5 neuroticism items with 6 answer categories (0-5).
neuro_itempar<-pair(daten = bfiN, m = 6)
summary(neuro_itempar)
summary(neuro_itempar, sortdif=TRUE) # ordered by difficulty
# plotting threshold profiles for 5 neuroticism items.
plot(neuro_itempar)
plot(neuro_itempar, sortdif=TRUE) # plotting ordered by difficulty
##### with unequal number of categories
data(sim200x3)
res<-pair(sim200x3)
summary(res)
plot(res)
```

 pairSE

Item Parameter Calculation with Standard Errors

Description

Calculation of the item parameters for dichotomous (difficulty) or polytomous items (thurstonian thresholds) and their standard errors (SE) respectively. All parameters are calculated using a generalization (see Heine & Tarnai, 2015) of the pairwise comparison algorithm (Choppin, 1968, 1985). Missing values up to an high amount in data matrix are allowed, as long as items are proper linked together.

Usage

```

pairSE(
  daten,
  m = NULL,
  w = NULL,
  nsample = 30,
  size = 0.5,
  seed = "no",
  pot = TRUE,
  zerocor = TRUE,
  verbose = TRUE,
  likelihood = NULL,
  pot2 = 2,
  delta = TRUE,
  conv = 1e-04,
  maxiter = 3000,
  progress = TRUE,
  init = NULL,
  zerosum = TRUE,
  ...
)

```

Arguments

daten	a data.frame or matrix with optionally named columns (names of items), potentially with missing values, comprising polytomous or dichotomous (or mixed category numbers) responses of n respondents (rows) on k items (columns) coded starting with 0 for lowest category to $m-1$ for highest category, with m being a vector (with length k) with the number of categories for the respective item.
m	an integer (will be recycled to a vector of length k) or a vector giving the number of response categories for all items - by default $m = \text{NULL}$, m is calculated from data, assuming that every response category is at least once present in data. For sparse data it is strongly recommended to explicitly define the number of categories by defining this argument.
w	an optional vector of case weights.
nsample	numeric specifying the number of subsamples sampled from data, which is the number of replications of the parameter calculation. WARNING! specifying high values for <code>nsample</code> (> 100) may result in long computing time without leading to "better" estimates for SE. This may also be the case when choosing argument <code>size="jack"</code> (see argument <code>size</code>) in combination with large datasets ($N > 5000$).
size	numeric with valid range between 0 and 1 (but not exactly 0 or 1) specifying the size of the subsample of data when bootstrapping for SE estimation. As an alternative, <code>size</code> can be set to the character "jack" (<code>size="jack"</code>). This will set the subsample size to $N-1$ and set <code>nsample=N</code> (see argument <code>nsample</code>), with N being the number of persons in <code>daten</code> .
seed	numeric used for <code>set.seed(seed)</code> .

pot	either a logical or an integer ≥ 2 defining the power to compute of the pairwise comparison matrix. If TRUE (default) a power of three of the pairwise comparison matrix is used for further calculations. If FALSE no powers are computed.
zerocor	either a logical or an numeric value between >0 and ≤ 1 . If (in case of a logical) zerocor is set to TRUE (default) unobserved combinations (1-0, 0-1) in the data for each pair of items are given a frequency of one conf. proposal by Alexandrowicz (2011, p.373). As an alternative option a numeric value between >0 and ≤ 1 can be assigned to unobserved combinations (1-0, 0-1) in the data for each pair of items (conf. to personal communication with A. Robitzsch; 29-03-2021).
verbose	logical, if verbose = TRUE (default) a message about subsampling is sent to console when calculating standard errors.
likelihood	see pair .
pot2	see pair .
delta	see pair .
conv	see pair .
maxiter	see pair .
progress	see pair .
init	see pair .
zerosum	see pair .
...	additional parameters passed through.

Details

Parameter calculation is based on the construction of a paired comparison matrix M_{nicjc} with entries $ficjc$, representing the number of respondents who answered to item i in category c and to item j in category $c-1$ widening Choppin's (1968, 1985) conditional pairwise algorithm to polytomous item response formats. This algorithm is simply realized by matrix multiplication.

Estimation of standard errors is done by repeated calculation of item parameters for sub samples of the given data.

To avoid numerical problems with off diagonal zeros when constructing the pairwise comparison matrix M_{nicjc} , powers of the M_{nicjc} matrix, can be used (Choppin, 1968, 1985). Using powers k of M_{nicjc} , argument `pot=TRUE` (default), replaces the results of the direct comparisons between i and j with the sum of the indirect comparisons of i and j through an intermediate k .

In general, it is recommended to use the argument with default value `pot=TRUE`.

Value

A (list) object of class `c("pairSE", "list")` containing the item category thresholds, difficulties sigma and their standard errors.

A note on standard errors

Estimation of standard errors is done by repeated calculation of item parameters for subsamples of the given data. This procedure is mainly controlled by the arguments `nsample` and `size` (see arguments). With regard to calculation time, the argument `nsample` may be the 'time killer'. On the other hand, things (estimation of standard errors) will not necessarily get better when choosing large values for `nsample`. For example choosing `nsample=400` will only result in minimal change for standard error estimation in comparison to (`nsample=30`) which is the default setting (see examples).

References

- Choppin, B. (1968). Item Bank using Sample-free Calibration. *Nature*, 219(5156), 870-872.
- Choppin, B. (1985). A fully conditional estimation procedure for Rasch model parameters. *Evaluation in Education*, 9(1), 29-42.
- Heine, J. H. & Tarnai, Ch. (2015). Pairwise Rasch model item parameter recovery under sparse data conditions. *Psychological Test and Assessment Modeling*, 57(1), 3–36.
- Alexandrowicz, R. W. (2011). 'GANZ RASCH': A Free Software for Categorical Data Analysis. *Social Science Computer Review*, 30(3), 369-379.
- Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.

Examples

```
data(bfiN) # loading example data set

# calculating item parameters and their SE for 5 neuroticism items with 6 answer categories (0-5).
neuro_itempar<-pairSE(daten = bfiN, m = 6)
summary(neuro_itempar) # summary for result

# plotting item thresholds with with their CI = 95%
plot(neuro_itempar)
plot(neuro_itempar,sortdif=TRUE)

##### example from details section 'Some Notes on Standard Errors' #####
neuro_itempar_400<-pairSE(daten = bfiN, m = 6,nsample=400)
plot(neuro_itempar)
plot(neuro_itempar_400)
```

pairwise.item.fit *Item Fit Indices*

Description

function for calculating item fit indices. The procedures for calculating the fit indices are based on the formulas given in Wright & Masters, (1982, P. 100), with further clarification given in <http://www.rasch.org/rmt/rmt34e.htm>.

Usage

```
pairwise.item.fit(pers_obj, na_treat = NA)
```

Arguments

`pers_obj` an object of class "pers" as a result from function [pers](#)

`na_treat` value to be assigned to residual cells which have missing data in the original response matrix. default is set to `na_treat=NA` to ignore these cells in further calculations. An option is to set these residuals to 0 using `na_treat=0`, which implies that they are imputed as 'fitting data', i.e., zero residuals. This can attenuate contrasts (see. <http://www.rasch.org/rmt/rmt142m.htm>).

Details

contrary to many IRT software using MI based item parameter estimation, `pairwise` will not exclude persons, showing perfect response vectors (e.g. `c(0,0,0)` for dataset with three variables), prior to the scaling. Therefore the fit statistics computed with `pairwise` may deviate somewhat from the fit statistics produced by IRT software using MI based item parameter estimation (e.g. R-package `eRm`), depending on the amount of persons with perfect response vectors in the data.

Value

an object of class `c("pifit", "data.frame")` containing item fit indices.

References

Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.

Wright, B. D., & Masters, G. N. (1990). Computation of OUTFIT and INFIT Statistics. *Rasch Measurement Transactions*, 3(4), 84–85.

Examples

```
#####
data(sim200x3)
result <- pers(pair(sim200x3))
pairwise.item.fit(pers_obj=result) # item fit statistic
```

`pairwise.person.fit` *Person Fit Indices*

Description

function for calculating person fit indices. The procedures for calculating the fit indices are based on the formulas given in Wright & Masters, (1982, P. 100), with further clarification given in <http://www.rasch.org/rmt/rmt34e.htm>.

Usage

```
pairwise.person.fit(pers_obj, na_treat = NA)
```

Arguments

`pers_obj` an object of class "pers" as a result from function [pers](#).

`na_treat` value to be assigned to residual cells which have missing data in the original response matrix. default is set to `na_treat=NA` to ignore these cells in further calculations. An option is to set these residuals to 0 using `na_treat=0`, which implies that they are imputed as 'fitting data', i.e., zero residuals. This can attenuate contrasts (see. <http://www.rasch.org/rmt/rmt142m.htm>).

Details

contrary to many IRT software using ML based item parameter estimation, `pairwise` will not exclude persons, showing perfect response vectors (e.g. `c(0,0,0)` for dataset with three variables), prior to scaling. Therefor the fit statistics computed with `pairwise` may deviate somewhat from the fit statistics produced by IRT software using ML based item parameter estimation (e.g. R-package `eRm`), depending on the amount of persons with perfect response vectors in the data.

Value

an object of class `c("ppfit", "data.frame")` containing person fit indices

References

Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.

Wright, B. D., & Masters, G. N. (1990). Computation of OUTFIT and INFIT Statistics. *Rasch Measurement Transactions*, 3(4), 84–85.

Examples

```
#####
data(sim200x3)
result <- pers(pair(sim200x3))
pairwise.person.fit(pers_obj=result) # item fit statistic
```

pairwise.S

The Fischer-Scheiblechner Statistic S on item level (Wald like Test)

Description

This function calculates the S-statistic on item level proposed by Fischer and Scheiblechner (1970) on item level for dichotomous or polytomous item response formats by splitting the data into two subsamples. For polytomous items the test is performed on item category level. Several splitting options are available (see arguments). The S-statistic is also mentioned in van den Wollenberg, (1982) – an article in *Psychometrika*, which might be available more easily (see details).

Usage

```
pairwise.S(
  daten,
  m = NULL,
  split = "random",
  splitseed = "no",
  verbose = FALSE,
  ...
)
```

Arguments

daten	a data.frame or matrix with optionally named columns (names of items), potentially with missing values, comprising polytomous or dichotomous (or mixed category numbers) responses of n respondents (rows) on k items (columns) coded starting with 0 for lowest category to $m-1$ for highest category, with m being a vector (with length k) with the number of categories for the respective item.
m	an integer (will be recycled to a vector of length k) or a vector giving the number of response categories for all items - by default $m = \text{NULL}$, m is calculated from data, assuming that every response category is at least once present in data. For sparse data it is strongly recommended to explicitly define the number of categories by defining this argument.
split	Specifies the splitting criterion. Basically there are three different options available - each with several modes - which are controlled by passing the corresponding character expression to the argument. <ol style="list-style-type: none"> 1) Using the rawscore for splitting into subsamples with the following modes: <code>split = "median"</code> median raw score split - high score group and low score group; <code>split = "mean"</code> mean raw score split - high score group and low score group. 2) Dividing the persons in <code>daten</code> into subsamples with equal size by random allocation with the following modes: <code>split = "random"</code> (which is equivalent to <code>split = "random.2"</code>) divides persons into two subsamples with equal size. In general the number of desired subsamples must be expressed after the dot in the character expression - e.g. <code>split = "random.6"</code> divides persons into 6 subsamples (with equal size) by random allocation etc. 3) The third option is using a manifest variable as a splitting criterion. In this case a vector with the same length as number of cases in <code>daten</code> must be passed to the argument grouping the data into subsamples. This vector should be coded as "factor" or a "numeric" integer vector with <code>min = 1</code>.
splitseed	numeric, used for <code>set.seed(splitseed)</code> for random splitting - see argument <code>split</code> .
verbose	logical, if <code>verbose = TRUE</code> (default) a message about subsampling is sent to console when calculating standard errors.
...	additional arguments <code>nsample</code> , <code>size</code> , <code>seed</code> , <code>pot</code> for caling <code>pairSE</code> are passed through - see description for <code>pairSE</code> .

Details

The data is splitted in two subsamples and then item thresholds, the parameter (Sigma) and their standard errors (SE) for the items according the PCM (or RM in case of dichotomies) are calculated for each subsample. This function internally calls the function `pairSE`. Additional arguments (see description of function `pairSE`) for parameter calculation are passed through. This item fit statistic is also (perhaps misleadingly) named as 'Wald test' in other R-packages. The S-statistic, as implemented in `pairwise`, is defined according to Fischer and Scheiblechner (1970); see also equation (3) in van den Wollenberg, (1982), p. 124 in the following equation:

$$S_i = \frac{\hat{\sigma}_i^{(1)} - \hat{\sigma}_i^{(2)}}{\sqrt{\left(S_{\hat{\sigma}_i}^{(1)}\right)^2 + \left(S_{\hat{\sigma}_i}^{(2)}\right)^2}}$$

where $\hat{\sigma}_i^{(1)}$ is the estimate of the item parameter of subsample 1, $\hat{\sigma}_i^{(2)}$ is the estimate of the item parameter of subsample 2 and $S_{\hat{\sigma}_i}^{(1)}$ and $S_{\hat{\sigma}_i}^{(2)}$ are the respective standard errors. In Fischer (1974), p. 297, the resulting test statistic (as defined above) is labeled with Z_i , as it is asymptotically normally distributed. Contrary to the 'Wald-type' test statistic W_i , which was derived by Glas and Verhelst (2005) from the (general) χ^2 distributed test of statistical hypotheses concerning several parameters, which was introduced by Wald (1943).

Value

A (list) object of class "pairs" containing the test statistic and item difficulty parameter sigma and their standard errors for the two or more subsamples.

A note on standard errors

Estimation of standard errors is done by repeated calculation of item parameters for subsamples of the given data. This procedure is mainly controlled by the arguments `nsample` and `size` (see arguments in `pairSE`). With regard to calculation time, the argument `nsample` is the 'time killer'. On the other hand, things (estimation of standard errors) will not necessarily get better when choosing large values for `nsample`. For example choosing `nsample=400` will only result in minimal change for standard error estimation in comparison to (`nsample=30`) which is the default setting (see examples).

References

- description of function `pairSE`{`pairwise`}.
- Fischer, G. H., & Scheiblechner, H. (1970). Algorithmen und Programme fuer das probabilistische Testmodell von Rasch. *Psychologische Beitrage*, (12), 23–51.
- van den Wollenberg, A. (1982). Two new test statistics for the rasch model. *Psychometrika*, 47(2), 123–140. <https://doi.org/10.1007/BF02296270>
- Glas, C. A. W., & Verhelst, N. D. (1995). *Testing the Rasch Model*. In G. Fischer & I. Molenaar (Eds.), *Rasch models: Foundations, recent developments, and applications*. New York: Springer.
- Wald, A. (1943). Tests of statistical hypotheses concerning several parameters when the number of observations is large. *Transactions of the American Mathematical Society*, 54(3), 426–482. <https://doi.org/10.1090/S0002-9947-1943-0012401-3>
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Examples

```
#####
data("kft5")
S_ran_kft <- pairwise.S(daten = kft5,m = 2,split = "random")
summary(S_ran_kft)
summary(S_ran_kft,thres = FALSE)
#### polytomous examples
data(bfiN) # loading example data set
data(bfi_cov) # loading covariates to bfiN data set

# calculating itemparameters and SE for two subsamples by gender
S_gen <- pairwise.S(daten=bfiN, split = bfi_cov$gender)
summary(S_gen)
summary(S_gen,thres = FALSE)

# other splitting criteria
## Not run:
S_med <- pairwise.S(daten=bfiN, split = "median")
summary(S_med)

S_ran<-pairwise.S(daten=bfiN, split = "random")
summary(S_ran)

S_ran.4<-pairwise.S(daten=bfiN, split = "random.4")
summary(S_ran.4) # currently not displayed

##### example from details section 'Some Notes on Standard Errors' #####
S_def<-pairwise.S(daten=bfiN, split = "random",splitseed=13)
summary(S_def)
#####
S_400<-pairwise.S(daten=bfiN, split = "random", splitseed=13 ,nsample=400)
summary(S_400)

## End(Not run)
```

pairwise.SepRel

Person Separation Reliability

Description

This function calculates an Index of Person Separation, that is the proportion of person variance that is not due to error.

Usage

```
pairwise.SepRel(pers_obj, na.rm = TRUE)
```

Arguments

`pers_obj` an object of class "pers" as a result from function `pers`.
`na.rm` a logical evaluating to TRUE or FALSE indicating whether NA values should be stripped before the computation proceeds.

Details

none

Value

An object of class `c("pairwiseSepRel", "list")`.

References

Andrich, D. (1982). An index of person separation in latent trait theory, the traditional KR.20 index, and the Guttman scale response pattern. *Education Research and Perspectives*, 9(1), 95–104.

Examples

```
#####
#####
data(bfiN) # loading reponse data
pers_obj <- pers(pair(bfiN))
result <- pairwise.SepRel(pers_obj)
result
str(result) # to see whats in ;-)
```

pairwise_PACKAGE *Rasch Model Parameters with pairwise*

Description

Performs the explicit calculation – not estimation! – of the Rasch item parameters for dichotomous and polytomous response formats using a pairwise comparison approach (see Heine & Tarnai, 2015) a procedure that is based on the principle for item calibration introduced by Choppin (1968, 1985). On the basis of the item parameters, person parameters (WLE) are calculated according to Warm's weighted likelihood approach (Warm, 1989). Item- and person fit statistics and several functions for plotting are available.

Details

In case of dichotomous answer formats the item parameter calculation for the Rasch Model (Rasch, 1960), is based on the construction of a pairwise comparison matrix M_{nij} with entries f_{ij} representing the number of respondents who got item i right and item j wrong according to Choppin's (1968, 1985) conditional pairwise algorithm.

For the calculation of the item thresholds and difficulty in case of polytomous answer formats, according to the Partial Credit Model (Masters, 1982), a generalization of the pairwise comparison algorithm is used. The construction of the pairwise comparison matrix is therefore extended to the comparison of answer frequencies for each category of each item. In this case, the pairwise comparison matrix M_{nicjc} with entries $ficjc$ represents the number of respondents who answered to item i in category c and to item j in category $c-1$ widening Choppin's (1968, 1985) conditional pairwise algorithm to polytomous item response formats. Within R this algorithm is simply realized by matrix multiplication.

In general, for both polytomous and dichotomous response formats, the benefit in applying this algorithm lies in it's capability to return stable item parameter 'estimates' even when using data with a relative high amount of missing values, as long as the items are still proper linked together.

The recent version of the package 'pairwise' computes item parameters for dichotomous and polytomous item responses – and a mixture of both – according the partial credit model using the function `pair`.

Based on the explicit calculated item parameters for a dataset, the person parameters may thereupon be estimated using any estimation approach. The function `pers` implemented in the package uses Warm's weighted likelihood approach (WLE) for estimation of the person parameters (Warm, 1989). When assessing person characteristics (abilities) using (rotated) booklet designs an 'incidence' matrix should be used, giving the information if the respective item was in the booklet (coded 1) given to the person or not (coded 0). Such a matrix can be constructed (out of a booklet allocation table) using the function `make.incidenz`.

Item- and person fit statistics, see functions `pairwise.item.fit` and `pairwise.person.fit` respectively, are calculated based on the squared and standardized residuals of observed and the expected person-item matrix. The implemented procedures for calculating the fit indices are based on the formulas given in Wright & Masters, (1982, p. 100), with further clarification given at <http://www.rasch.org/rmt/rmt34e.htm>.

Further investigation of item fit can be done by using the function `ptbis` for point biserial correlations. For a graphical representation of the item fit, the function `gif` for plotting empirical and model derived category probability curves, or the function `esc` for plotting expected (and empirical) score curves, can be used.

The function `iff` plots or returns values of the item information function and the function `tff` plots or returns values of the test information function.

To detect multidimensionality within a set of Items a rasch residual factor analysis proposed by Wright (1996) and further discussed by Linacre (1998) can be performed using the function `rfa`.

For a 'heuristic' model check the function `grm` makes the basic calculations for the graphical model check for dico- or polytomous item response formats. The corresponding S3 plotting method is `plot.grm`.

Author(s)

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References

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pers

WLE - Rasch Person Parameter

Description

This is the (new) main function for calculation of person estimates based on answering dichotomous or polytomous items according the Rasch Model (Rasch, 1960) and Partial Credit Model (Masters, 1982), given the item parameters (object of class "pair" - as a result of `pair()`) and the datamatrix (argument `daten`) containing the person response vectors (rows), using an WL approach, introduced by Warm (1989).

Usage

```

pers(
  itempar,
  daten = NULL,
  incidenz = NULL,
  na_treat = NULL,
  limit = 1e-05,
  iter = 50,
  Nrel = FALSE,
  tecout = FALSE
)

```

Arguments

<code>itempar</code>	The item parameter prior calculated or estimated. A list object of class "pair" as a result of applying the function <code>pair()</code> to the data. Or an 'ordinary' "matrix" with <code>nrow = k</code> (number of items) and <code>ncol = m</code> (maximum number of thresholds), holding the 'thurstonian' thresholds of the respective item. Some matrix entries may be NA, depending on the number of categories of the respective item.
<code>daten</code>	A "matrix" (or "data.frame") optionally with named cols (names of items) and named rows (person IDs). This argument can be left empty when the argument <code>itempar</code> (above) is of class "pair". <code>daten</code> holds polytomous or dichotomous (or mixed category numbers) responses of <code>n</code> respondents (rows) on <code>k</code> items (columns) coded starting with 0 for lowest category to <code>m-1</code> for highest category, with <code>m</code> being a vector (with length <code>k</code>) with the number of categories for the respective item. Responses in <code>daten</code> must be stored as "integers" (not "factors" !) and may have missing values.
<code>incidenz</code>	This argument is only relevant when items are assigned to different booklets. For such a booklet-design a "matrix" should be assigned to this argument, with the same dimensions like <code>daten</code> , containing 0 and 1 integer codes, giving the information (for every person) if the respective item was in the respective booklet (coded 1) given to the person or not (coded 0).
<code>na_treat</code>	optionally an integer (vector) defining the type of treatment to missing responses in the argument <code>daten</code> . If set to <code>na_treat=NULL</code> (default) missing responses are treated as missings and the respective person is assigned to an corresponding missing group for estimation. An option is to set <code>na_treat</code> to any integer value between 0 (lowest category) and the numeric code for the maximum category of the respective item.
<code>limit</code>	numeric giving the limit at which accuracy the WL-algorithm stops.
<code>iter</code>	numeric giving the maximum number of iteration to perform.
<code>Nrel</code>	logical with default set to <code>Nrel=FALSE</code> to include persons with perfect response vectors for calculating WLE reliability. If set to <code>Nrel=TRUE</code> persons with perfect response vectors are excluded for calculating WLE reliability.
<code>tecout</code>	logical default set to <code>FALSE</code> . If set to <code>TRUE</code> the result will be a (very) long list with estimation details for every case in <code>daten</code> . In case of a booklet-design the list entries will be divided by "booklet".

Details

no detail in the moment.

Value

An object of class `c("pers", "data.frame")` or a (very long) "list" (when setting on `techout=TRUE`) containing the person parameters.

References

Masters, G. (1982). A Rasch model for partial credit scoring. *Psychometrika*, 47(2), 149–174.

Rasch, G. (1960). *Probabilistic models for some intelligence and attainment tests*. Copenhagen: Danmarks pædagogiske Institut.

Warm, T. A. (1989). Weighted likelihood estimation of ability in item response theory. *Psychometrika*, 54(3), 427–450.

Examples

```
#####
data(sim200x3)
result <- pers(itempar=pair(sim200x3))
summary(result)
plot(result)
logLik(result) # Log-Likelihood for 'estimated' model
logLik(result, sat=TRUE) # Log-Likelihood for saturated model
AIC(logLik(result)) # AIC for 'estimated' model
AIC(logLik(result, sat=TRUE)) # AIC for saturated model
BIC(logLik(result)) # BIC for 'estimated' model
BIC(logLik(result, sat=TRUE)) # BIC for saturated model
##### following example requires package eRm #####
# require(eRm)
# # itemparameter with eRm:
# itempar_eRm <- thresholds(PCM(sim200x3))$ threshtable[[1]][,2:3]
# # pairwise personparameter with eRm-itemparameter and data:
# summary(pers(itempar=itempar_eRm, daten=sim200x3))
# # eRm personparameter:
# person.parameter(PCM(sim200x3))
# # personparameter with pairwise:
# summary(pers(pair(sim200x3)))
```

plot.grm

S3 Plotting Graphical Model Check

Description

S3 plotting method for object of class `("grm", "list")`

Usage

```
## S3 method for class 'grm'
plot(
  x,
  xmin = NULL,
  xmax = NULL,
  ci = 2,
  main = NULL,
  col.error = "blue",
  col.diag = "red",
  itemNames = TRUE,
  cex.names = 0.8,
  type = "b",
  xlab = NULL,
  ylab = NULL,
  pch = 43,
  las = 3,
  cex.axis = 0.5,
  ...
)
```

Arguments

x	object of classc("grm", "list")
xmin	optional lower limit for xy-axis
xmax	optional upper limit for xy-axis
ci	numeric defining confidence intervall for point estimator
main	see plot
col.error	vector of colors for error bars
col.diag	color for the diagonal of the plot
itemNames	logical wether to plot itemnames
cex.names	magnification factor for itemnames
type	see plot
xlab	see plot
ylab	see plot
pch	see plot
las	see plot
cex.axis	see plot
...	other parameters passed to plot

Description

S3 plotting method for object of class "pair"

Usage

```
## S3 method for class 'pair'
plot(
  x,
  sortdif = FALSE,
  ra = "auto",
  main = NULL,
  col.lines = (1:dim(x$threshold)[2]),
  type = "b",
  xlab = "items",
  ylab = "logits",
  pch = (1:dim(x$threshold)[2]),
  las = 3,
  cex.axis = 0.8,
  ...
)
```

Arguments

x	object of class "pair"
sortdif	logical wether to order items by difficulty
ra	either the character "auto" (default) or an numeric, defining the (logit) range for y-axis
main	see plot
col.lines	vector of colors for threshold profile lines
type	see plot
xlab	see plot
ylab	see plot
pch	see plot
las	see plot
cex.axis	see plot
...	other parameters passed to plot

plot.pairSE

S3 Plotting Thustonian Thresholds with SE

Description

S3 plotting method for object of class("pairSE", "list")

Usage

```
## S3 method for class 'pairSE'
plot(
  x,
  ci = 2,
  sortdif = FALSE,
  ra = "auto",
  main = NULL,
  col.lines = 1:(dim(x$threshold)[2]),
  col.error = 1:(dim(x$threshold)[2]),
  type = "b",
  xlab = "items",
  ylab = "logits",
  pch = 20,
  las = 3,
  cex.axis = 0.8,
  ...
)
```

Arguments

x	object of classc("pairSE", "list")
ci	numeric defining confidence intervall for point estimator
sortdif	logical wether to order items by difficulty
ra	either the character "auto" (default) or an numeric, defining the (logit) range for y-axis
main	see plot
col.lines	vector of colors for threshold profile lines
col.error	vector of colors for error bars
type	see plot
xlab	see plot
ylab	see plot
pch	see plot
las	see plot
cex.axis	see plot
...	other parameters passed to plot

Description

S3 plotting method for object of class "pers"

Usage

```
## S3 method for class 'pers'  
plot(  
  x,  
  ra = NULL,  
  sortdif = FALSE,  
  main = NULL,  
  ylab = "Logits",  
  itemNames = TRUE,  
  fillCol = "grey60",  
  lineCol = "grey40",  
  cex = 0.7,  
  pos = 4,  
  breaks = "Sturges",  
  pch = 1,  
  ...  
)
```

Arguments

x	object of class "pers"
ra	an integer, defining the (logit) range for y-axis
sortdif	logical wether to order items by difficulty
main	see plot
ylab	see plot
itemNames	logical wether to use itemnames in the resulting plot
fillCol	color for bar filling of the ability histogram
lineCol	color for bar lines of the ability histogram
cex	see text
pos	see text
breaks	see hist
pch	see points
...	other parameters passed to hist and text .

Description

S3 plotting Method for object of class "rfa"

Usage

```
## S3 method for class 'rfa'
plot(
  x,
  com = 1,
  ra = "auto",
  main = NULL,
  labels = NULL,
  xlab = "logits",
  ylab = "loadings",
  srt = 0,
  cex.axis = 0.8,
  cex.text = 0.8,
  col.text = NULL,
  ...
)
```

Arguments

x	object of class "rfa"
com	an integer giving the number of the principal component used for plotting
ra	either the character "auto" (default) or an numeric, defining the (logit) range for x-axis
main	see plot
labels	a character vector specifying the plotting pattern to use. see text . At default the itemnames are used.
xlab	see plot
ylab	see plot
srt	see text or par
cex.axis	see plot
cex.text	see argument cex in function text
col.text	see argument col in function text
...	other parameters passed through.

ptbis

Point Biserial Correlations

Description

Calculation of the point biserial correlations for dichotomous or polytomous item categories with total scale (person parameter).

Usage

```
ptbis(y, daten = NULL)
```

Arguments

y either an object of class "pers", or a numeric vector as a result of any scaling approach (WLE, MLE, Rawscore, etc.) relating to the Items (columns) in daten.

daten if argument y is not an object of class "pers", a "data.frame", potentially with missing values, comprising dichotomous or polytomous items (columns).

Details

no details in the moment.

Value

An object of class c("data.frame", "ptbis") containing item statistics.

Examples

```
#####  
#####  
data(sim200x3) # loading response data  
y <- rowSums(sim200x3)  
ptbis(y=y, daten=sim200x3)  
####  
result <- pers(pair(sim200x3))  
ptbis(y= result)
```

Q

*Person Fit Index Q***Description**

function for calculating the person fit index Q, which was proposed by Tarnai and Rost (1990).

Usage

```
Q(obj = NULL, data = NULL, threshold = NULL, ...)
```

Arguments

obj	an object of class "pers" or class "pair" as a result from function pers or pair respectively.
data	optional response data when object of class "pers" or class "pair" is not provided.
threshold	optional in case that object of class "pers" or class "pair" is not provided. Threshold values as matrix with row and columnnames !! – items as rows and thresholds as columns. Thresholds should be ordered from left to right, some items may have less thresholds than the others, in this case the respective row/column is filled with an NA value - see examples.
...	not used so far.

Details

The person Q-index proposed by Tarnai and Rost, (1990) is solely based on the empirical responses and the item parameters. Thus the computation of person parameters using the function [pers](#) is not required - see examples. But for convenience return objects of both functions are accepted in function Q.

Value

a vector holding the Q-index for every person.

References

Tarnai, C., & Rost, J. (1990). *Identifying aberrant response patterns in the Rasch model: the Q index*. Münster: ISF.

Examples

```
#####
data(bfiN) # get some data
ip <- pair(daten = bfiN, m = 6) # item parameters according the partial credit model
Q(ip)
```

```

### with data an thresholds as external objects #####
threshold <- matrix(seq(-3,3,length.out = 9),ncol = 3)
dimnames(threshold) <- list(c("I1","I2","I3"),c("1","2","2"))
threshold
resp_vec <- c(3,0,2,1,2,2,2,2,1,3,0,NA,NA,0,2,3,NA,2,NA,2,1,2,NA,1,2,2,NA)
resp_emp <- matrix(resp_vec,ncol = 3,byrow = TRUE)
colnames(resp_emp) <- c("I1","I2","I3")
resp_emp
Qindex <- Q(data = resp_emp,threshold = threshold)
cbind(resp_emp,Qindex)

##### unequal number of thresholds #####
threshold <- matrix(seq(-3,3,length.out = 9),ncol = 3)
dimnames(threshold) <- list(c("I1","I2","I3"),c("1","2","2"))
threshold[2,3] <- NA

resp_vec <- c(3,0,2,1,2,2,2,2,1,3,0,NA,NA,0,2,3,NA,2,NA,2,1,2,NA,1,2,2,NA)
resp_emp <- matrix(resp_vec,ncol = 3,byrow = TRUE)
colnames(resp_emp) <- c("I1","I2","I3")
resp_emp
Qindex <- Q(data = resp_emp,threshold = threshold)
cbind(resp_emp,Qindex)

```

q3

*Q3 Fit Statistic***Description**

Calculation of Q3 fit statistic for the rasch model based on the residuals, which was proposed by Yen (1984).

Usage

```

q3(
  pers_obj,
  na_treat = 0,
  use = "complete.obs",
  res = "stdr",
  method = "pearson"
)

```

Arguments

pers_obj an object of class "pers" as a result from function [pers](#).

na_treat value to be assigned to residual cells which have missing data in the original response matrix. default is set to na_treat=0 to set the residuals to 0, which implies that they are imputed as 'fitting data', i.e., zero residuals. This can attenuate contrasts (see. <http://www.rasch.org/rmt/rmt142m.htm>). An option is to set it to na_treat=NA.

use	a character string as used in function <code>cor</code> or <code>cov</code> , giving a method for computing covariances or correlations in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs". The default is set to <code>use="complete.obs"</code> which will exclude cases by listwise deletion to keep the correlation matrix positive definit.
res	a character string defining which type of (rasch-) residual to analyze when computing the correlations. This must be (exactly) one of the strings "sr" for score residuals, "stdr" for standardised residuals, "srsq" for score residuals squared, or "stdrsq" for standardised residuals squared. The default is set to <code>res="stdr"</code> referring to Linacre (1998).
method	a character string as used in function <code>cor</code> , indicating which correlation coefficient is to be computed. One of "pearson" (default), "kendall", or "spearman", can be abbreviated. The default is set to <code>method="pearson"</code> .

Details

The lower level letter 'q' was used (instead of 'Q') for naming the function because the name 'Q3' was already used in another IRT package – namely TAM. As perhaps some users like to use both packages simultaneously, an alternative naming convention was chosen for 'pairwise'. No other details in the moment.

Value

An object of class `c("Q3", "list")`.

References

Yen, W. M. (1984). Effects of Local Item Dependence on the Fit and Equating Performance of the Three-Parameter Logistic Model. *Applied Psychological Measurement*, 8(2), 125–145. <https://doi.org/10.1177/01466216840>

Examples

```
#####
#####
data(bfiN) # loading response data
pers_obj <- pers(pair(bfiN))
result <- q3(pers_obj)
str(result) # to see what's in ;-)
####
```

Qtest

Model Fit based on Person Fit Index Q

Description

function for performing a model fit test based on calculating the person fit index *Q* for sub samples. Persons are ranked according their fit and in turn a Kruskal-Wallis rank sum test (see `kruskal.test`) is performed to test if the parameters of the distribution of *Q* are the same in each group (sample).

Usage

```

Qtest(
  obj = NULL,
  data = NULL,
  threshold = NULL,
  split = "median",
  splitseed = "no",
  ...
)

```

Arguments

obj	an object of class "pers" or class "pair" as a result from function <code>pers</code> or <code>pair</code> respectively.
data	optional response data when object of class "pers" or class "pair" is not provided.
threshold	optional in case that object of class "pers" or class "pair" is not provided. Threshold values as matrix with row and columnnames !! – items as rows and thresholds as columns. Thresholds should be ordered from left to right, some items may have less thresholds than the others, in this case the respective row/column is filled with an NA value - see examples.
split	<p>Specifies the splitting criterion. Basically there are three different options available - each with several modes - which are controlled by passing the corresponding character expression to the argument.</p> <p>1) Using the rawscore for splitting into subsamples with the following modes: <code>split = "median"</code> median raw score split - high score group and low score group; <code>split = "mean"</code> mean raw score split - high score group and low score group. Finally <code>split = "score"</code> that is splitting daten into as many subsamples as there are raw score groups - discarding min and max (theoretical) score group - which matches the concept proposed by Andersen (1973).</p> <p>2) Dividing the persons in daten into subsamples with equal size by random allocation with the following modes: <code>split = "random"</code> (which is equivalent to <code>split = "random.2"</code>) divides persons into two subsamples with equal size. In general the number of desired subsamples must be expressed after the dot in the character expression - e.g. <code>split = "random.6"</code> divides persons into 6 subsamples (with equal size) by random allocation etc.</p> <p>3) The third option is using a manifest variable as a splitting criterion. In this case a vector with the same length as number of cases in daten must be passed to the argument grouping the data into subsamples. This vector should be coded as "factor" or a "numeric" integer vector with <code>min = 1</code>.</p>
splitseed	numeric, used for <code>set.seed(splitseed)</code> for random splitting - see argument <code>split</code> .
...	not used so far.

Details

The person Q-index proposed by Tarnai and Rost, (1990) is solely based on the empirical responses and the item parameters. Thus the computation of person parameters using the function `pers` is not required - see examples. But for convenience return objects of both functions are accepted in function `Q`. This offers the opportunity to get some inference on model fit only based on item parameters.

Value

A list with class "htest" containing the following components as returned by `kruskal.test`.

References

Tarnai, C., & Rost, J. (1990). *Identifying aberrant response patterns in the Rasch model: the Q index*. Münster: ISF.

Andersen, E. B. (1973). A goodness of fit test for the rasch model. *Psychometrika*, 38(1), 123–140.

Examples

```
#####
data(bfiN) # get some data
ip <- pair(daten = bfiN,m = 6) # item parameters according the partial credit model
Q(ip)

Qtest(ip)

### with data an thresholds as external objects #####
threshold <- matrix(seq(-3,3,length.out = 9),ncol = 3)
dimnames(threshold) <- list(c("I1","I2","I3"),c("1","2","2"))
threshold
resp_vec <- c(3,0,2,1,2,2,2,2,1,3,0,NA,NA,0,2,3,NA,2,NA,2,1,2,NA,1,2,2,NA)
resp_emp <- matrix(resp_vec,ncol = 3,byrow = TRUE)
colnames(resp_emp) <- c("I1","I2","I3")
resp_emp
Qindex <- Q(data = resp_emp,threshold = threshold)
cbind(resp_emp,Qindex)

Qtest_res <- Qtest(data = resp_emp,threshold = threshold)
Qtest_res

#### unequal number of thresholds #####
threshold <- matrix(seq(-3,3,length.out = 9),ncol = 3)
dimnames(threshold) <- list(c("I1","I2","I3"),c("1","2","2"))
threshold[2,3] <- NA

resp_vec <- c(3,0,2,1,2,2,2,2,1,3,0,NA,NA,0,2,3,NA,2,NA,2,1,2,NA,1,2,2,NA)
resp_emp <- matrix(resp_vec,ncol = 3,byrow = TRUE)
colnames(resp_emp) <- c("I1","I2","I3")
resp_emp
Qindex <- Q(data = resp_emp,threshold = threshold)
cbind(resp_emp,Qindex)
```

```
Qtest_res <- Qtest(data = resp_emp, threshold = threshold)
Qtest_res
```

residuals.pers	<i>S3 residuals for Object of class "pers"</i>
----------------	--

Description

S3 residuals method to extract the (Rasch) residuals for object of class "pers"

Usage

```
## S3 method for class 'pers'
residuals(object, res = "sr", na_treat = 0, ...)
```

Arguments

object	object of class "pers"
res	a character string defining which type of (rasch-) residual to return. This must be (exactly) one of the strings "exp" for expected scores "sr" for score residuals (default), "stdr" for standardised residuals, "srsq" for score residuals squared, or "stdrsq" for standardised residuals squared. The default is set to res="sr".
na_treat	value to be assigned to residual cells which have missing data in the original response matrix. Default is set to na_treat=0 to set the residuals to 0, which implies that they are imputed as 'fitting data', i.e., zero residuals. This can attenuate contrasts (see. http://www.rasch.org/rmt/rmt142m.htm). An option is to set it to na_treat=NA.
...	not used jet.

rfa	<i>Rasch Residual Factor Analysis</i>
-----	---------------------------------------

Description

Calculation of the rasch residual factor analysis proposed by Wright (1996) and further discussed by Linacre (1998) to detect multidimensionality.

Usage

```
rfa(
  pers_obj,
  na_treat = 0,
  tr = FALSE,
  use = "complete.obs",
  res = "stdr",
  method = "pearson",
  cor = TRUE
)
```

Arguments

<code>pers_obj</code>	an object of class "pers" as a result from function <code>pers</code> .
<code>na_treat</code>	value to be assigned to residual cells which have missing data in the original response matrix. default is set to <code>na_treat=0</code> to set the residuals to 0, which implies that they are imputed as 'fitting data', i.e., zero residuals. This can attenuate contrasts (see. http://www.rasch.org/rmt/rmt142m.htm). An option is to set it to <code>na_treat=NA</code> .
<code>tr</code>	a logical value indicating whether the data (the residual matrix) is transposed prior to calculation. This would perform a person analysis rather than a item analysis. The default is set to item analysis.
<code>use</code>	a character string as used in function <code>cor</code> or <code>cov</code> , giving a method for computing covariances or correlations in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs". The default is set to <code>use="complete.obs"</code> which will exclude cases by listwise deletion to keep the correlation matrix positive definit.
<code>res</code>	a character string defining which type of (rasch-) residual to analyze when computing covariances or correlations. This must be (exactly) one of the strings "sr" for score residuals, "stdr" for standardised residuals, "srsq" for score residuals squared, or "stdrsq" for standardised residuals squared. The default is set to <code>res="stdr"</code> referring to Linacre (1998).
<code>method</code>	a character string as used in function <code>cor</code> or <code>cov</code> , indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman", can be abbreviated. The default is set to <code>method="pearson"</code> .
<code>cor</code>	a logical value indicating whether the calculation should use the correlation matrix or the covariance matrix. The default is set to <code>cor=TRUE</code> to use the correlation matrix.

Details

no details in the moment.

Value

An object of class `c("rfa", "list")`.

References

- Wright, B. D. (1996). Comparing Rasch measurement and factor analysis. *Structural Equation Modeling: A Multidisciplinary Journal*, 3(1), 3–24.
- Linacre, J. M. (1998). Detecting multidimensionality: which residual data-type works best? *Journal of outcome measurement*, 2, 266–283.

Examples

```
#####
#####
data(bfiN) # loading reponse data
pers_obj <- pers(pair(bfiN))
result <- rfa(pers_obj)
summary(result)
plot(result)
####
```

sim200x3

Simulated Data

Description

Simulated data for 200 'subjects' 'answering' to 3 items with unequal number of categories – one dichotomous and two polytymous items.

Usage

```
data(sim200x3)
```

Format

A data.frame containing 3 variables and 200 observations.

Details

This simulated data is used as an example in the rasch module of the 'ALMO - Statistiksystem'.

Source

<https://www.almo-statistik.de/>

References

- Holm, K. (2014). ALMO Statistik-System. *P14.8 Das allgemeine ordinale Rasch-Modell* https://www.almo-statistik.de/download/Ordinales_Rasch_Modell.pdf

Examples

```

data(sim200x3)
dim(sim200x3)
#####
apply(sim200x3,2,table)

```

simra	<i>Simulate Response Pattern under Dichotomous and Polytomous Rasch Model</i>
-------	---

Description

function for simulation of response patterns following the dichotomous and/or polytomous Rasch model based on the category probabilities given the model parameters. At default, when just calling `simra()` 1 replication of responses to 5 items with difficulties -2, -1, 0, 1, 2 from 100 persons with ability drawn from $N(0|1)$ are sampled.

Usage

```

simra(
  itempar = matrix(seq(-2, 2, length = 5)),
  theta = 100,
  pers_obj = NULL,
  replicate = 1,
  seed = seq(1, replicate, 1),
  ...
)

```

Arguments

itempar	a "matrix" with <code>nrow = k</code> (number of items) and <code>ncol = m</code> (maximum number of thresholds), holding the 'thurstonian' thresholds of the respective item. Some of the rightmost matrix entries may be NA, depending on the number of categories of the respective item.
theta	either one of the following (1) a numeric vector of length <code>n</code> providing the values of the person parameter (ability) for <code>n</code> persons to be used in the simulation. (2) a integer defining the number of values <code>n</code> to draw from $N(0 1)$.
pers_obj	an object of class "pers" as a result from function <code>pers</code> . If an object of class "pers" is assigned to this argument the model parameters in it are taken to simulate the responses. At default (<code>pers_obj = NULL</code>) simulation is done by considering the model parameters given in the other arguments (see above).
replicate	an integer defining how many replicates (data matrices) <code>r</code> to draw based on the model parameters.
seed	a numeric vector with length of number of replications used for <code>set.seed</code> prior to each replicate to keep the result repeatable. If <code>seed = NULL</code> no seed is set.
...	arguments passed through.

Details

no details in the moment.

Value

an array with $\text{dim}(n, k, r)$ response patterns (k items in columns n persons in rows and r replications in the third dimension).

Examples

```
#####  
simra() # 100 dichotomous probabilistic response pattern  
### 100 polytomous response pattern (4 items; each 4 answer categories)  
v <- c(-1.0,-0.5,0.0,0.5,-0.75,-0.25,0.25,0.75,-0.5,0.0,0.5,1.0)  
itempar <- matrix(v,nrow = 4,ncol = 3)  
simra(itempar = itempar)  
simra(itempar = itempar,replicate = 10) # draw 10 replications
```

summary.grm

S3 Summary for graphical Model Check

Description

S3 summary method for object of classc("grm", "list")

Usage

```
## S3 method for class 'grm'  
summary(object, ci = 2, ...)
```

Arguments

object	object of classc("grm", "list")
ci	numeric with default ci=2 to return confidence intervals for point estimator.
...	other parameters passed through

 summary.pair

S3 Summary for Item Parameter

Description

S3 summary method for object of class "pair"

Usage

```
## S3 method for class 'pair'
summary(object, sortdif = FALSE, ...)
```

Arguments

object	object of class "pair"
sortdif	logical with default sortdif=FALSE whether to order items by difficulty.
...	other parameters passed trough

 summary.pairS

S3 Summary for S-Statistic Test (Wald Test)

Description

S3 summary method for object of class "pairS"

Usage

```
## S3 method for class 'pairS'
summary(object, thres = TRUE, ...)
```

Arguments

object	object of class "pairS"
thres	logical whether to output results based on the thresholds
...	other parameters passed trough

`summary.pairSE`*S3 Summary for Item Parameter with Standard Errors*

Description

S3 summary method for object of class("pairSE", "list")

Usage

```
## S3 method for class 'pairSE'  
summary(object, sortdif = FALSE, ...)
```

Arguments

<code>object</code>	object of class("pairSE", "list")
<code>sortdif</code>	logical with default <code>sortdif=FALSE</code> whether to order items by difficulty.
<code>...</code>	other parameters passed through

`summary.pairwiseSepRel`*S3 Summary for Person Separation Reliability*

Description

S3 summary method for object of class"pairwiseSepRel"

Usage

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

Arguments

<code>object</code>	object of class"pairwiseSepRel"
<code>...</code>	other parameters passed through

summary.pers

S3 Summary for Thetas

Description

S3 summary method for object of class "pers"

Usage

```
## S3 method for class 'pers'
summary(object, short = TRUE, sortwle = FALSE, ...)
```

Arguments

object	object of class "pers"
short	logical with default short=TRUE - if set to short=FALSE a "data.frame" with WLE estimates (and their respective standard errors) for every row (person) in the original dataset will be returned.
sortwle	logical whether to order persons by ability - ignored when short=TRUE
...	other parameters passed through

summary.pifit

S3 Summary for Item-Fit-Statistics

Description

S3 summary method for object of class ("pifit", "data.frame")

Usage

```
## S3 method for class 'pifit'
summary(
  object,
  sort = FALSE,
  by = "INFIT.ZSTD",
  decreasing = FALSE,
  relative = FALSE,
  ...
)
```

Arguments

object	object of class "ppfit", "data.frame"
sort	logical with default sort=FALSE - if set to sort=TRUE items are ordered by absolute FIT.
by	character passing the type of Fit-Statistic to sort by - ignored when sort=FALSE. valid options are: "INFIT.ZSTD" (default), "OUTFIT.MSQ", "OUTFIT.ZSTD" and "INFIT.MSQ".
decreasing	see order
relative	logical with default relative=FALSE to return the fit statistics as proposed by Wright & Masters, (1982, P. 100) with no further modifications. If relative=TRUE the sample adjusted fit statistics are returned in a way that their mean (for the present sample) equals 1 using formula: $fit_{i+} = 1 - \text{mean}(\text{fit})$.
...	other parameters passed through - see order

References

- Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.
- Wright, B. D., & Masters, G. N. (1990). Computation of OUTFIT and INFIT Statistics. *Rasch Measurement Transactions*, 3(4), 84–85.

summary.ppfif

S3 Summary for Person-Fit-Statistics

Description

S3 summary method for object of class("ppfit", "data.frame")

Usage

```
## S3 method for class 'ppfit'
summary(
  object,
  sort = FALSE,
  by = "INFIT.ZSTD",
  decreasing = FALSE,
  relative = FALSE,
  ...
)
```

Arguments

object	object of class "ppfit", "data.frame"
sort	logical with default sort=FALSE - if set to sort=TRUE persons are ordered by absolute FIT.

by	character passing the type of Fit-Statistic to sort by - ignored when sort=FALSE. valid options are: "INFIT.ZSTD" (default), "OUTFIT.MSQ", "OUTFIT.ZSTD" and "INFIT.MSQ".
decreasing	see order
relative	logical with default relative=FALSE to return the fit statistics as proposed by Wright & Masters, (1982, P. 100) with no further modifications. If relative=TRUE the sample adjusted fit statistics are returned in a way that their mean (for the present sample) equals 1 using formula: $fit_{i+} = 1 - \text{mean}(\text{fit})$.
...	other parameters passed trough - see order

References

- Wright, B. D., & Masters, G. N. (1982). *Rating Scale Analysis*. Chicago: MESA Press.
- Wright, B. D., & Masters, G. N. (1990). Computation of OUTFIT and INFIT Statistics. *Rasch Measurement Transactions*, 3(4), 84–85.

summary.q3

S3 Summary for Q3 Fit Statistic

Description

S3 summary method for object of class "q3"

Usage

```
## S3 method for class 'q3'
summary(object, maxrc = 3, ...)
```

Arguments

object	object of class "q3"
maxrc	numerical with default maxrc=3 to specify the output of the maximum number of highest residual correlations in terms of absolute value.
...	other parameters passed trough

`summary.rfa`*S3 Summary for Rasch Factor Analysis*

Description

S3 summary method for object of class "pair"

Usage

```
## S3 method for class 'rfa'  
summary(object, sortdif = FALSE, ...)
```

Arguments

<code>object</code>	object of class "pair"
<code>sortdif</code>	logical with default <code>sortdif=FALSE</code> whether to order items / persons by difficulty / ability.
<code>...</code>	other parameters passed through

`tff`*Test information function*

Description

plotting function for plotting the test information function (TIF).

Usage

```
tff(  
  pair_obj,  
  items = NULL,  
  x = NULL,  
  main = "Test Information Function",  
  plot = TRUE,  
  cat = FALSE,  
  lwd = 2,  
  col = 1,  
  ...  
)
```

Arguments

<code>pair_obj</code>	an object of class "pair" as a result from function <code>pair</code> .
<code>items</code>	optional a vector (character or numeric) identifying the items (according their order in the data) to use for plotting the test information function.
<code>x</code>	The value(s) of the latent variable, at which the TIF will be evaluated. <code>x</code> should be either a numeric vector of theta values or a single numeric value. If <code>x</code> is given as a single numeric value plotting is suppressed. If not given (default), 99 values spaced evenly between -4 and +4 will be used, handy for plotting.
<code>main</code>	see parameters for <code>plot</code>
<code>plot</code>	a logical (default <code>plot = TRUE</code>), defining whether to suppress plotting and just return a matrix of the values of the Item information function.
<code>cat</code>	a logical (default <code>cat = FALSE</code>), defining whether to plot as an overlay to the Test information function the item category information functions based on item categories. If <code>cat = TRUE</code> and <code>plot = FALSE</code> the values of the item category information functions are returned.
<code>lwd</code>	see parameters for <code>plot</code>
<code>col</code>	see parameters for <code>plot</code>
<code>...</code>	arguments passed to <code>plot</code>

Details

no details in the moment.

Value

a plot, a "data.frame" or a single numeric with values of the Test information function.

Examples

```
#####
data(sim200x3)
result <- pair(sim200x3)
tff(pair_obj = result) # TIF plot
tff(pair_obj = result, cat=TRUE) # TIF plot
tff(pair_obj = result, items=c("V1","V3"), cat=TRUE) # TIF plot
tff(pair_obj = result, x=0) # TIF at theta=0
tff(pair_obj = result, x=seq(0,4,.1)) # TIF for a given range of Thetas
##### examples with other data ...
data(bfiN)
result <- pair(bfiN)
tff(pair_obj = result)
tff(pair_obj = result, cat=TRUE) # TIF plot
```

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