Package ‘conquestr’

July 24, 2024

Type Package

Title An R Package to Extend 'ACER ConQuest'

Version 1.3.4

Description Extends 'ACER ConQuest' through a family of functions designed to improve graphical outputs and help with advanced analysis (e.g., differential item functioning). Allows R users to call 'ACER ConQuest' from within R and read 'ACER ConQuest' System Files (generated by the command ‘put’ <https://conquestmanual.acer.org/s4-00.html#put>). Requires 'ACER ConQuest' version 5.39 or later. A demonstration version can be downloaded from <https://shop.acer.org/acer-conquest-5.html>.

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Imports dplyr, ggplot2 (>= 3.5.1), ggrepel, kableExtra, magrittr, methods, Rcpp, rlang, stats, stringr, tidyr, tidyselect, zlib

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VignetteBuilder knitr

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Encoding UTF-8

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SystemRequirements ACER ConQuest (>=5.40.0)


NeedsCompilation yes
Contents

checkItemRespValid ............................................. 3
checkVars ......................................................... 4
cnvrtItemParam .................................................. 4
ConQuestCall ..................................................... 5
ConQuestRout ..................................................... 6
ConQuestSys ....................................................... 7
createConQuestProject ........................................... 8
DecompressSys ..................................................... 8
fisherTrnsfrm ..................................................... 9
fmtCqItanal ....................................................... 9
genItems .......................................................... 10
genResponses ..................................................... 12
getCqChain ......................................................... 13
getCqData ......................................................... 14
getCqDataDf ....................................................... 15
getCqFit ........................................................... 16
getCqHist ........................................................ 16
genCqItanal ........................................................ 17
genCqItanalFacility .............................................. 17
genCqItanalSummary .............................................. 18
genCqRespModel ................................................... 19
genCqTerms ........................................................ 19
genCqVars .......................................................... 20
ginsOnDims ........................................................ 20
informationWrightMap .......................................... 21
infoWI ............................................................ 22
itemInfoAtTheta ................................................... 23
itemInfoOverTheta ............................................... 23
itemListToThresholds ............................................ 24
makeItemList ....................................................... 25
plotCCC ........................................................... 27
plotCqHist ........................................................ 28
plotDif ............................................................. 30
plotItemMap ......................................................... 31
plotModelCCC ...................................................... 32
plotModelExp ...................................................... 32
plotRout .......................................................... 34
pvMeanVar ........................................................ 35
q3ExpCorrect ...................................................... 35
**checkItemRespValid**

Check that the item responses in raw data are: (1) valid, (2) each valid response mapped to an item appears at least once, and (3) each valid response mapped to an item has sufficiently many responses (defaults to a minimum of 10 observations for each response category).

### Usage

```r
checkItemRespValid(data, caseID, validMap, varLabel, validLabel)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>data</code></td>
<td>Raw data, a data frame.</td>
</tr>
<tr>
<td><code>caseID</code></td>
<td>A string indicating the name of the case id variable in the data.</td>
</tr>
<tr>
<td><code>validMap</code></td>
<td>A data frame which contains a mapping of valid responses to item labels. This data frame should be in long format, with each valid response * item combination representing a row.</td>
</tr>
<tr>
<td><code>varLabel</code></td>
<td>A string indicating the name of the variable in validMap that identifies the valid items names/lables.</td>
</tr>
<tr>
<td><code>validLabel</code></td>
<td>A string indicating the name of the variable in validMap that contains the valid codes/responses for each item. This should include missing values (e.g., &quot;99&quot;)</td>
</tr>
</tbody>
</table>
Value
A list of lists: one list per item in validMap$varLabel. Within each list, there can be up to three dfs: (1) the case ids and invalid responses for the item, (2) the valid codes not observed in the data set, and (3) the valid codes observed fewer than 10 times in the data. NOTE: a warning is thrown if the validMap$varLabel is not found in the data.

Description
Check raw data: are all required variables present and ensure there are no extraneous variables.

Usage
checkVars(data, varNames, except = NULL)

Arguments
- data: Raw data, a data frame.
- varNames: Vector of valid variable names.
- except: A vector of variable names to be excluded from the check.

Value
A list.

cnvrtItemParam
Description
takes an item in one model's parameterisation and returns it in another parameterisation.

Usage
cnvrtItemParam(item, from = "muraki", to = "conquest", D = 1)
Arguments

item  an item design matrix that is of size response categories (m) by four:

- column one is category values, usually from 0 to m. Sometimes referred to as 'x', and in this case, this value times the discrimination is the category score.
- column two is the delta dot parameter repeated m times (the average difficulty of the item)
- column three is the tau (step) parameter where for the first response category (x = 0) tau = 0, and for m >= 2, entries are deviations from delta dot. In the dichotomous case, all items in this column are zero.
- column four is the discrimination parameter ("a")

from  a string, either "muraki" or "conquest" (default) (see 10.1177/0146621697211001).

Describing the parameterisation of item to  a string, either "muraki" or "conquest" (default) (see 10.1177/0146621697211001).

Describing the output parameterisation of the returned item parameter matrix

Note that "muraki" assumes the scaling constant D = 1.7 (to give the normal ogive metric)

D  a number, giving the scaling constant. Default is 1 (logistic metric). Other common values are D = 1.7 (to give the normal ogive metric)

Value

an m x 4 matrix of item parameters. The same dimensions as the input, item

Examples

myTheta <- 0
myDelta <- 1.5
a <- 1.5
m <- 3
itemParamX <- seq(0, m-1, 1)
itemParamD <- rep(myDelta, m)
itemParamT <- c(0, -0.5, 0.5)
itemParamA <- rep(a, m)
itemParam <- cbind(itemParamX, itemParamD, itemParamT, itemParamA)
colnames(itemParam)<- c("x", "d", "t", "a")
myItem <- cnvrtItemParam(itemParam, from = "conquest", to = "muraki")

Description

Call an instance of 'ACER ConQuest' at the command line and run a control file (syntax).
ConQuestCall(cqc, cqExe, stdout = "")

Arguments

- **cqc**: The location of the control file (syntax) to be run.
- **cqExe**: The path to the 'ACER ConQuest' executable. Note, if this argument is missing, conquestr will find a local installation of ACER ConQuest by first searching the default installation locations (Program Files on Windows and Applications on Mac) then searching other local directories (Appdata and the HOME path).
- **stdout**: On Mac only, can be toggled to NULL (or a connection) to suppress output to R console.

Value

prints 'ACER ConQuest' output to stdout.

Examples

```r
## Not run:
ConQuestCall()
## End(Not run)
```

ConQuestRout

ConQuestRout

Description

Read an "ACER ConQuest" rout file created by a plot command in 'ACER ConQuest'.

Usage

ConQuestRout(myRout)

Arguments

- **myRout**: The location of an 'ACER ConQuest' rout file created by 'ACER ConQuest'

Value

A list containing the data objects created by 'ACER ConQuest' plot command.
Examples

myPlot <- ConQuestRout()
## Not run:
# if you run the above example you will have the points from a plot ICC command.
str(myPlot)

## End(Not run)

Description

Read an "ACER ConQuest" system file created by a put command in 'ACER ConQuest'. The system file must not be compressed. Use the option ‘compressed=no’ in the put command within 'ACER ConQuest'.

Usage

ConQuestSys(myCqs, isMini = FALSE)

Arguments

myCqs The location of an uncompressed 'ACER ConQuest' system file created by 'ACER ConQuest' > 4.35.
isMini A boolean, set to TRUE if the system file is a mini system file created by 'ACER ConQuest' command put with option "mini = yes".

Value

A list containing the data objects created by 'ACER ConQuest'.

Examples

mySysData <- ConQuestSys()
myEx1SysData <- ConQuestSys(myCqs = system.file("extdata", "mysysfile.cqs", package = "conquestr"))
## Not run:
# if you run the above example this will return your original 'ACER ConQuest' syntax.
cat(unlist(myEx1SysData$gCommandHistory))

## End(Not run)
createConQuestProject

Description
creates a standard folder structure to work with 'ACER ConQuest' Projects.

Usage
createConQuestProject(prefix = getwd(), ...)

Arguments
prefix          a valid file path where to create project folders.
...             optional params, including "setDebug"

Value
Boolean TRUE.

Examples
## Not run:
createConQuestProject()
## End(Not run)

DecompressSys

Description
Internal function to decompress an 'ACER ConQuest' system file that has been compressed using zlib.

Usage
DecompressSys(myFile)

Arguments
myFile        An connection to a compressed 'ACER ConQuest' system file created by the put command in 'ACER ConQuest'.

Value
A connection to an uncompressed system file in the users temp dir.
**fisherTrnsfrm**

**See Also**

conquestr::ConQuestSys()

---

**fisherTrnsfrm**  **fisherTrnsfrm**

**Description**

Helper function to apply Fisher’s transformation to a correlation matrix.

**Usage**

fisherTrnsfrm(myCorMat)

**Arguments**

myCorMat  A correlation matrix.

**Value**

A correlation matrix with Fisher’s transform applied to values -1 > x > 1.

---

**fmtCqItanal**  **fmtCqItanal**

**Description**

helper function to produce nicely formatted summary tables from a ConQuest Itanal.

**Usage**

fmtCqItanal(
    cqItanal,
    itemNumber = "all",
    ptBisFlag = 0,
    textColHighlight = "red",
    valueDecPlace = 2
)

**Arguments**

cqItanal  An ACER ConQuest itanal list object returned by function getCqItanal.
itemNumber  a vector of generalised item numbers to format.
ptBisFlag  Something.
textColHighlight  Something.
valueDecPlace  Something.
Values

A list

Examples

```r
myEx1Sys <- ConQuestSys()
myEx1Sys_itanal <- getCqItanal(myEx1Sys)
myItanalSummary <- fmtCqItanal(myEx1Sys_itanal)
print(myItanalSummary[[1]])
```

Description

Generates a list of item parameter matrices for use in function like `conquestr::genResponses` and `conquestr::informationWrightMap`

Usage

```r
genItems(n, scores = NULL, deltadots, taus = NULL, discrims = 1)
```

Arguments

- `n` How many items?
- `scores` When NULL it is assumed that all items have integer scoring, increasing for each category k, and beginning from 0. Otherwise a list where the elements are, in order:
  - a string naming a distribution function (for example `runif`, `rnorm`) to generate random deviates from (the scores).
  - a list of parameters to pass to the distribution function (for example, for `runif`, a list of length 2 defining "min" and "max"). This list is assumed to be in order to be directly passed into the function.
  - a boolean indicating whether the scores should be forced to be increasing across the response categories.
  - optionally a vector of item numbers to apply scores too. If not provided it is assumed that all items will be scored.
- `deltadots` A list where the elements are, in order:
  - a string naming a distribution function (for example `runif`, `rnorm`) to generate random deviates from (the delta dots).
  - a list of parameters to pass to the distribution function (for example, for `runif`, a list of length 2 defining "min" and "max"). This list is assumed to be in order to be directly passed into the function.
- `taus` When NULL all items are assumed to be dichotomies. Otherwise a list where the elements are, in order:
• a string naming a distribution function (for example `runif`, `rnorm`) to generate random deviates from (the taus). Or the string "manual" to indicate that a user-defined list of the tau parameters will be provided.

• a list of parameters to pass to the distribution function (for example, for `runif`, a list of length 2 defining "min" and "max"). This list is assumed to be in order to be directly passed into the function. If the first element in `taus` is "manual" this should be a list of taus to be used this must be of the correct dimensions - for example, if there are 2 polytomous items being generated, each with 3 response categories (k), then the list should be of length 2: 2 * (k-2) = 2 * (3-2) = 2 taus. This is because there are k-1 taus per item, and the last tau is always constrained to be the negative sum of the rest for identification purposes.

• a Boolean indicating whether the taus should be forced to be increasing across the response category boundaries (that is, enforce that no item exhibits disordered thresholds).

• optionally a vector of item numbers to produce taus for. If not provided it is assumed that all items are polytomous.

• optionally a vector of response categories to apply to each item. For example if the user indicates that 5 items are polytomous, then a vector of length 5 where the first elements describes the count of response categories for the first polytomous item, the second element describes the count of response categories for the second polytomous item, and so on.

`discrims` When NULL all items are assumed to have constant discrimination equal to 1. Otherwise a list where the elements are, in order:

• a string naming a distribution function (for example `runif`, `rnorm`) to generate random deviates from (the discriminations). Or the string "manual" to indicate that a user-defined list of the discrimination parameters will be provided.

• a list of parameters to pass to the distribution function (for example, for `runif`, a list of length 2 defining "min" and "max"). This list is assumed to be in order to be directly passed into the function.

• a Boolean indicating whether the discriminations are constant within items or whether each response category within an item will have its own score should be forced to be increasing across the response category boundaries (that is, this can be one way of specifying the Bock Nominal model).

• optionally a vector of items to apply a unique discrimination to. Otherwise it is assumed that all items have unique discriminations.

**Value**

A list of item matrices.

**See Also**

`simplef()`, `genResponses()`, `browseVignettes("conquestr")`
Examples

```r
myItem <- matrix(c(0, 0, 0, 0, 1, 1, 0, 1), ncol = 4, byrow = TRUE)
myItems <- list(myItem, myItem)
myItems[[2]][2, 2] <- -1 # make the second item delta equal to -1
myResponses <- gen Responses(abilities = rnorm(100), itemParams = myItems)
```

Description

Generates response vectors for \( n \) cases to \( i \) items given known item parameters, person abilities, and (optionally) other inputs.

Usage

```r
genResponses(
  abilities,
  groups = NULL,
  itemParams,
  BMatrix = 1,
  mcarP = 0,
  perturbR = NULL
)
```

Arguments

- **abilities** A person by latent-dimension matrix of abilities. One column per dimension.
- **groups** A vector of factors of the same length as `abilities` that allocates each case to a group. Used in `perturbR`. Defaults to NULL such that all cases are in the one group.
- **itemParams** A list of item parameters of the structure used in `simplef` (a matrix of \( k \) categories by four (category score, delta dot, tau, discrimination)). See `conquestr::makeItemList` for a helper to generate this list.
- **BMatrix** A simplified B-matrix mapping dimensions (columns) to items (rows). Or the integer "1" if items are dichotomous and ability is uni-dimensional.
- **mcarP** A double indicating the proportion of missing data under the MCAR assumption.
- **perturbR** A list of lists, where each element of the list refers to one item and contains a list of elements describing how responses to that item should be perturbed to model misfit. Each element of the list should contain, in order:
  - item number (int). Which item in `itemParams` is affected,
  - type of perturbation (string) to apply. One of
    - "discrimination" - increases or decreases the discrimination of the item at a location specified by the user.
- "shift" - increases or decreases the location of the item as to create a uniform shift in the CCC.
- ...more to come,

- scoring perturbation factor (double). When the type is "discrimination", this defines the scale that the discrimination is increased or decreased. For example, if the item has discrimination of 1, and the perturbation factor is 1.2, the resulting probabilities will be calculated assuming the discrimination is $1 \times 1.2 = 1.2$. Note that if the value given here is 1, then this kind of perturbation is the same as "shift". When the type is "shift" this value is always ignored.

- pivot point (double). When the type is "discrimination", this defines the location around which the perturbation is applied relative to the delta dot. That is, when the type is "discrimination" and the "perturbation factor" is > 1, probabilities above the pivot point will be overestimated (generated responses will higher than expectation) and probabilities below the pivot point will be underestimated (generated responses will lower than expectation). When the pivot point is 0, this calculation happens at the item location parameter (e.g., at the category boundary). When the type is "shift", this is the value added to the item location (delta dot) as to create a uniform shift (DIF) for the group.

- group (string). The group found in groups that should be perturbed. note that if groups is not used in call to genResponses' than this value is ignored and all cases' responses are perturbed.

Value

A matrix, n cases by i items, of scored item responses.

See Also

simplef(), browseVignettes("conquest")

Examples

myItem <- matrix(c(0, 0, 0, 0, 1, 1, 0, 1), ncol = 4, byrow = TRUE)
myItems <- list(myItem, myItem)
myItems[[2]][2, 2] <- -1 # make the second item delta equal to -1
myResponses <- genResponses(abilities = rnorm(100), itemParams = myItems)

getcqChain

getcqChain

Description

creates a data frame representation of the estimation chain from an MCMC model. The burn is discarded and only the unskipped iterations in MCMC chain are retained.
getCqData

Usage
getCqChain(myCqs)

Arguments
myCqs A system file.

Value
A data frame.

Examples
## Not run:
getCqChain(ConQuestSys())
## End(Not run)

Description
Get data objects from an R object of class ConQuestSys. This function returns person IDs, response
data, case estimates, regression and weight data. Each data type is stored as a data frame, and each
data frame is a named element of a list.

1. PID,
2. Responses,
3. Estimates,
4. Regression.

Usage
getcqData(mySys)

Arguments
mySys An R object of class ConQuestSys, returned by the function conquestr::ConQuestSys

Value
A List of data frames.

See Also
conquestr::ConQuestSys()
getCqDataDf

Examples

mySys <- ConQuestSys()
myData <- getCqData(mySys)

getCqDataDf <- getCqData(myData)

Description

Takes a list object returned by conquestr::getCqData and coerces it to a wide data frame. This can sometimes cause issues in complex data, for example where there are multiple response vectors for each case (for example a many-facets model). This is because it is assumed that the data can be reduced to a matrix of $gNCases \times m\ variables$ (where $m$ is the number of id, item, estimate and regression variables in the analysis). For more complex data, the user should use the outputs of conquestr::getCqData to manually merge together a data frame.

Usage

getCqDataDf(cqData)

Arguments

cqData An R object of class list, returned by the function conquestr::getCqData

Value

A data frame containing R data frames based on the list objects in the ConQuest system file that has been read in.

See Also

conquestr::ConQuestSys()
conquestr::getCqData

Examples

mySys <- ConQuestSys()
myData <- getCqData(mySys)
myDataDf <- getCqDataDf(myData)
**getCqFit**

### Description

creates a data frame representation of the fit of parameters in the item response model.

### Usage

```r
getcqFit(myCqs)
```

### Arguments

- `myCqs`: A system file.

### Value

A data frame.

### Examples

```r
## Not run:
getcqFit(ConQuestSys())
## End(Not run)
```

---

**getCqHist**

### Description

creates a data frame representation of the iteration history for all parameters.

### Usage

```r
getcqHist(myCqs)
```

### Arguments

- `myCqs`: A system file.

### Value

A data frame.
getCqItanal

Examples

```r
## Not run:
c getCqHist(ConQuestSys())

## End(Not run)
```

getcqItanal
getcqItanal

description

helper function to return list of lists, each list relates to one generalised item from an ACER ConQuest itanal output. Each list contains: (1) item-total and item-rest correlations ....

Usage

```r
getcqItanal(sysFile, matrixPrefix = '', isDebug = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sysFile</td>
<td>An ACER ConQuest system file.</td>
</tr>
<tr>
<td>matrixPrefix</td>
<td>to define which itanal to process</td>
</tr>
<tr>
<td>isDebug</td>
<td>report debug output</td>
</tr>
</tbody>
</table>

Value

A list.

Examples

```r
myItanal <-getCqItanal()
print(myItanal[[1]])
```

getcqItanalFacility
getcqItanalFacility

Description

returns an item facility for each item in itanal object created by ACER ConQuest. For a dichotomously scored Rasch-like item, facility is the percent correct. For a polytomously scored item, or with estimated scores, facility is given by: the sum of the number of cases in each response category, multiplied by the score for that category divided by the sum of all cases responding to the items times the maximum score for the item.
**Usage**

```r
getcqItanalFacility(itan)
```

**Arguments**

- `itan` A list of class "cqItanal" created by `conquestr::getcqItanal()`

**Value**

A list.

**Examples**

```r
mySys <- ConQuestSys()
myItan <- getcqItanal(mySys)
getcqItanalFacility(myItan)
```

**Description**

returns an itanal as a data frame in summary format: one row per generalised item with:

- item label
- valid N
- facility (see `conquestr::getcqItanalFacility`)
- item-rest correlation
- item-total correlation
- fit (infit/weighted MNSQ) if available
- item locations (deltas)

**Usage**

```r
getcqItanalSummary(itan)
```

**Arguments**

- `itan` A list of class "cqItanal" created by `conquestr::getcqItanal()`

**Value**

A data frame.

**Examples**

```r
mySys <- ConQuestSys()
myItan <- getcqItanal(mySys)
getcqItanalSummary(myItan)
```
**getCqRespModel**

Description

produces a table of model parameter estimates, errors, fits, and scaled 2PL estimates if available.

Usage

`getCqRespModel(sysFile)`

Arguments

- `sysFile` An ACER ConQuest system file read into R using `conquestr::ConQuestSys`

Value

A List of data frames. Each data frame is a term in the response model

Examples

```r
## Not run:
myShowRespMod <- getCqRespModel(conquestr::ConQuestSys())
## End(Not run)
```

**getCqTerms**

Description

creates a data frame representation of the terms of the model statement, including interactions.

Usage

`getCqTerms(myCqs)`

Arguments

- `myCqs` A system file.

Value

A data frame.
## Description

Creates a data frame representation of the variables in the model statement. Note that steps are not variables.

### Usage

```r
gCqVars(myCqs)
```

### Arguments

- `myCqs` A system file.

### Value

A data frame.

## Description

Returns a list of length gNDims. Each element of the list contains a vector of the gins on this dim.

### Usage

```r
ginsOnDims(sysFile)
```

### Arguments

- `sysFile` An ACER ConQuest system file read into R using `conquestr::ConQuestSys()`
Value

a list

Examples

## Not run:
myResult <- ginsOnDims(conquestr::ConQuestSys())

## End(Not run)

informationWrightMap

Description

Plots test information function, relative to ability density, and item locations.

Usage

informationWrightMap(
  myItems,  # A list of matrices describing item parameters.
  myAbilities,  # A vector of person abilities on one dimension.
  type = "empirical",  # A character string. Should the test information be calculated empirically ("empirical" - default) or analytically using moments of distribution ("approx").
  minTheta = NA,  # The smallest value of ability PDF to plot.
  maxTheta = NA,  # The largest value of ability PDF to plot.
  stepTheta = NA,  # The increment to iterate over the ability PDF. Defaults to 0.01.
  scaleInfo = 1,  # A scaling factor to apply to the plot of test information. Because ability distribution is a PDF with area one, and a test information function has area L, this can make the plot more interpretable. Defaults to 1.
  plotItemPoints = "deltadots"  # A character string indicating what item points should be plotted along the x-axis. Similar to the histogram of item locations plotted on a Wrightmap. Can be "none", "deltadots", "thresholds".
)
Description

Calculates an index representing the product of a test information function and an ability distribution.

Usage

infoWI(myItems, myAbilities, type = "empirical")

Arguments

myItems A vector of item deltas.
myAbilities A vector of person abilities.
type A character String. Should the test information be calculated empirically ("empirical" - default) or analytically using moments of distribution ("approx").

Value

A double.

Examples

infoWIOut <- infoWI(runif(10, -2, 3), rnorm(1000, 0, 1))
itemInfoAtTheta

Description

Calculates item information at a value of theta given a set of item parameters for one item.

Usage

itemInfoAtTheta(myItem, theta)

Arguments

myItem A matrix of item parameters of the structure used in simplef
theta A number.

Examples

anItem <- matrix(c(0,0,0,1,1,1,0,1), nrow = 2, byrow = TRUE)
itemInfoAtTheta(anItem, 0)

itemInfoOverTheta

Description

Calculates item information over a rage of theta given a set of item parameters. Returns a data frame with item information at a discrete set of values of theta. This is useful for plotting item information functions.

Note this function is redundant - use testInfoOverTheta and pass a single item as a list.

Usage

itemInfoOverTheta(myItem, minTheta = -6, maxTheta = 6, stepTheta = 0.1)

Arguments

myItem A matrix of item parameters of the structure used in simplef
minTheta The smallest value of ability PDF to calculate info and to plot. Defaults to -6.
maxTheta The largest value of ability PDF to calculate info and to plot. Defaults to 6.
stepTheta The increment to iterate over the ability PDF. Defaults to 0.01.

Examples

anItem <- matrix(c(0,0,0,1,1,1,0,1), nrow = 2, byrow = TRUE)
itemInfoOverTheta(anItem)
itemListToThresholds

Description

Takes a list of item parameter matrices and returns a data frame containing Thurstonian Thresholds (gammas) for all items. Thurstonian thresholds are the location on the trait/scale at which the cumulative probability of being in category k, or any higher category equals some probability (usually 0.5, the default). Thurstonian thresholds are considered a way of describing the difficulty of polytomously scored items and are usually the value used in visualisations like Wright maps. Thurstonian thresholds can only be calculated for items where response categories are scored such that each category can be placed in an order increasing scores (e.g., no ties as per the Ordered Partition model).

Usage

itemListToThresholds(
  myItems,
  threshP = 0.5,
  minTheta = -20,
  maxTheta = 20,
  convC = 1e-05
)

Arguments

- myItems: A list of item parameter matrices of the structure used in simple (a matrix of k categories by four (category score, delta dot, tau, discrimination)).
- threshP: The probability at which the thresholds are calculated (defaults to the usual value of 0.5).
- minTheta: The lower-bound starting value of the split-half search used to find the threshold for the category.
- maxTheta: The upper-bound starting value of the split-half search used to find the threshold for the category.
- convC: The convergence criteria used to determine when the threshold has been found. The difference between threshP and the cumulative probability of the category and any higher category at the current value of theta (the current proposed value of threshold being tested).

Value

A data frame including 4 columns:

- id, an integer index reflecting which item this is, in the same order as myItems
- itemid, a string with the names from the items in myItems (NA if item list is not named)
- step, which step does this threshold belong?
- location, the value of the threshold
Examples

```r
myItem <- matrix(
  c(
    0, -0.58 , 0 , 1, # delta+tau thurst thresh (gamma)
    1, -0.58 , 0.776 , 1, # 0.196 -1.14
    2, -0.58 , -0.697 , 1, # -1.277 -0.93
    3, -0.58 , -0.629 , 1, # -1.209 -0.64
    4, -0.58 , 0.55 , 1 # -0.03 0.25
  ), ncol =4, byrow=TRUE
)
itemListToThresholds(list(myItem))
```

Description

creates a list of item matrices. Each matrix represent one item's set of item parameters. The structure of the matrix is the same as used in `conquestr::simplef` (a matrix of k categories by four (category score, delta dot, tau, discrimination)).

Usage

```r
makeItemList(scores = NULL, deltaDot, tau = NULL, discrim = 1)
```

Arguments

scores a data frame or matrix containing category scores for each item. If NULL, it is assumed increasing integer scoring starting at 0 is used for all items (that is, the first category is scored 0, the second category is scored 1, the kth category is scored k-1).

If a data frame, column labels should be "id", "itemid", "step", "score". If a matrix, the column order should be: "id", a unique item ID for each item matched with values in deltaDot; "itemid", item labels for each item (or NA); "step", an indicator of which step/item category this score represents and "score" the value for the scoring parameter associated with this category. There must be one score for each category (i.e. 2 for dichotomies and one for each of k categories for polytomies).

If a data frame, or a matrix:

- "id" is an integer
- "itemid" is a character string
- "step" is an integer
- "score" is numeric

The original category scores (i.e., increasing integer scoring) is preserved in the rownames of the matrix.
**deltaDot**

A data frame or matrix of delta dots (average item location/difficulty for each item).

If a data frame, column labels should be: "id", "itemid", "delta". "itemid" should be populated with an item label or be missing for all values. If a matrix, column order should be: "id", a unique item ID for each row; "itemid", item labels for each item (or NA); "delta", a delta dot.

If a data frame, or a matrix:

- "id" is an integer
- "itemid" is a character string
- "delta" is numeric

---

**tau**

NULL if all items are dichotomies. A data frame or matrix of taus for polytomous items. Only polytomous items should be in this file. If an item ID in deltaDot is not in tau it is assumed that the item is dichotomous. The tau parameters represent the deviation from the delta dot to give the item parameters for adjacent category boundaries (e.g., $\delta_1 = \delta + \tau_1$ is the boundary between $k_1$ and $k_2$, $\delta_2 = \delta + \tau_2$ is the category boundary between $k_1$ and $k_2$).

Where a polytomous item has $k$ categories, there should be $k-2$ rows for that item in tau. For example, a 3-category item has categories $k_1$, $k_2$, and $k_3$. There will be one value in tau for this item. The value in tau represents the first category boundary. (e.g., between $k_1$ and $k_2$). The last (second in this case) category boundary is constrained to be the negative sum of the other tau values within this item (and is therefore not required in the file).

If a data frame, column labels should be "id", "itemid", "step", "tau". If a matrix, the column order should be: "id", a unique item ID for each item matched with values in deltaDot; "itemid", item labels for each item (or NA); "step", an indicator of which step/item category this threshold represents (minimum value should be 1 and maximum value should be $k-1$); "tau" the value for the tau parameter associated with this step.

If a data frame, or a matrix:

- "id" is an integer
- "itemid" is a character string
- "step" is an integer
- "tau" is numeric

---

**discrim**

A double, a data frame, or a matrix of item (or category) discrimination parameters. When a double is provided, the value is applied to all discrimination parameters. The default is 1. Setting the value to 1.7 is one approach to re-scale to the normal ogive metric. Otherwise a data frame or matrix defining the discrimination parameter for each response category. If a data frame, column labels should be "id", "itemid", "step", "discrim". If step is NA and there is only one entry for an item "itemid", the discrimination is assumed to be constant for all response categories with the item. This is the case for names models like the GPCM and 2PL models, and can be a short hand way of defining the discrimination without specifying all categories. When discrimination varies across scoring categories, the bock-nominal model is implied. In the case of discrimination varying across scoring categories, all categories must be defined.
If a data frame, or a matrix:
  • "id" is an integer
  • "itemid" is a character string
  • "step" is an integer
  • "discrim" is numeric

Value

a list.

Examples

```r
nItems <- 10
myItemsDeltaDot <- data.frame(
  id= seq(nItems),
  itemid= NA,
  delta = runif (nItems, -4, 1) # nItems items in range -4,1
)
myItemsList <- conquestr::makeItemList(deltaDot = myItemsDeltaDot)
```

Description

Creates a plot of an item characteristic curve (by response category). For a dichotomous item, this will yield a single curve, for polytomous items this will produce a curve for each response category. Note this is not for use with rout files. See the generic function plotRout for plotting rout files.

Usage

```r
plotCCC(
  item, abilities, responses, weights = NULL, groups = NULL,
  range = c(-6, 6), by = 0.1, linetype = "bins", bins = 10,
  plotZero
)
```
plotCqHist

Arguments

item
A matrix of item parameters for a single item. Matrix should be of the form used in simplef

abilities
A vector of doubles estimated person abilities.

responses
A vector of integers giving the observed person responses to this item.

weights
A vector of doubles of sampling weights.

groups
A factor vector indicating groups.

range
Lower and upper bounds to plot over (defaults to c(-6, 6)).

by
A double. The increment to the sequence along range used to plot the model lines.

linetype
A string. Should the empirical lines be based on "bins", or "regression". Defaults to "bins"

bins
If linetype is "bins", how many bins should be used to chunk the empirical lines? defaults to 10. Ignored otherwise.

plotZero
Should the zero category be plotted? Defaults to FALSE when item is dichotomous and TRUE otherwise.

Value

A ggplot2 object.

Examples

myRout <- ConQuestRout()
myPlot <- plotRout(myRout)
## Not run:
# if you run the above example you will have an ICC plot in the object 'myPlot'.
plot(myPlot)

## End(Not run)

Description

generates a plot from a history object. Use getCqHist to create a history object from an 'ACER ConQuest' system file.
plotCqHist

Usage

plotCqHist(
  myHist,
  centre = TRUE,
  params = c("all"),
  legend = FALSE,
  plotProblems = NULL
)

Arguments

myHist      an R object created by the getCqHist function.
centre      a Boolean representing whether the iteration history should be mean centred (within parameter). This is helpful for plots that include all parameters to ensure the Y axis is sensible. Consider, for example, the readability of a plot with raw values of the Likelihood and item parameters on it.
params      A string of which params to plot. Must be one or more of "all", "Likelihood", "Beta", Variance", "Xsi", "Tau". Note the match when using "Beta", Variance", "Xsi", "Tau" is by regular expression, so "Xsi1" will plot item location parameter 1, 10-19, 100-199 and so on.
legend      Should a legend be plotted?
plotProblems an optional list defining which potential problem parameters to plot.
  • Iters: The first element of the list is an integer defining how many of the final iterations to consider (e.g., identify parameters that are moving the most over the final 20 iterations). if NA, the default is to consider the last 10% of iterations.
  • Magnitude: The second element of the list is number indicating the magnitude of change over the last n iterations. if NA, and Type is "relative", defaults to 30 times the largest change at the final iteration. if NA, and Type is "absolute", defaults to 0.05 logits.
  • Type: The third element of the list is a string, either "relative" or "absolute":
    – "relative" indicates that Magnitude is the multiple of the change between the final iteration and the second-to-last iteration that indicates a potential problem.
    – "absolute" indicates that Magnitude refers to change between the the final iteration and the value in Iters that indicates a potential problem.

Value

A ggplot2 object.

Examples

```r
## Not run:
myHistPlot <- plotCqHist(getCqHist(ConQuestSys()))
## End(Not run)
```
plotDif

Description

Creates a plot (ggplot2 object) of item parameter estimates common to two system files (e.g., a DIF analysis).

Usage

plotDif(mySysToItemDifDf, myScale = "centred", mySuffixes)

Arguments

mySysToItemDifDf
An R object of class data frame returned from conquestr::sysToItemDifDf

myScale
A string specifying if the item parameter estimates displayed should be "centred" (default), "scaled" (z scores), or "none" (raw).

mySuffixes
a vector of strings specifying the names for the two groups being analysed, e.g., if the two system files are an analysis of boys and girls, the vector may be c("_male", "_female").

Value

A ggplot2 object.

See Also

conquestr::sysToItemDifDf()

Examples

mySys1 <- ConQuestSys()
mySys2 <- ConQuestSys()
mySysList <- list(mySys1, mySys2)
myDifDf <- sysToItemDifDf(mySysList, mySuffixes = c("_male", "_female"), myDims = "all")
myDifPlot <- plotDif (myDifDf, myScale = "centred", mySuffixes = c("_male", "_female"))
## Not run:
# if you run the above example you will have the plot in the object `myDifPlot`.
plot(myDifPlot)
## End(Not run)
plotItemMap

Description

Creates a plot (ggplot2 object) of item parameter estimates and abilities on latent trait. Note this
is not for use with rout files. See the method method plotRout.itemMap to the generic function
plotRout

Usage

plotItemMap(mySys, myDims = "D1", ginLabs = "short", abilityType = "PV", ...)

Arguments

mySys An 'ACER ConQuest' system file object created using the conquestr::ConQuestSys
function.

myDims A string specifying which specific dimensions should be included. The default
is "D1". Specific dimensions are specified by the label "D1" for dimensions 1
etc.

ginLabs A string specifying whether short or long gin labels should be used. Default to
"short".

abilityType What kind of person ability estimate should be used? Defaults to plausible val-
ues. Alternatively WLE, MLE, EAP.

... Optional arguments, mostly for debugging, e.g., setDebug = TRUE will print
temporary data frames.

Value

A ggplot2 object.

Examples

mySys1 <- ConQuestSys()
myItemMap <- plotItemMap(mySys1)
## Not run:
# if you run the above example you will have the plot in the object `myItemMap`
plot(myItemMap)
## End(Not run)
Description

Creates a plot of a model implied category characteristic curve. Note this is not for use with rout files. See the generic function plotRout for plotting rout files.

Usage

plotModelCCC(item, range = c(-6, 6), by = 0.1, plotZero)

Arguments

- item: Item parameters for a single item.
- range: Lower and upper bounds to plot over (defaults to c(-6, 6)).
- by: Increment to the sequence along “range”.
- plotZero: Should the zero category be plotted? Defaults to FALSE when item is dichotomous and TRUE otherwise.

Value

A ggplot2 object.

Examples

myItem <- matrix(
  c(
    0, 0, 0, 1,
    1, 1, 0, 1
  ),
  ncol = 4, byrow=TRUE
)
myPlot <- plotModelCCC(myItem)

Description

Creates a plot of an item- or test- expected score curve. If ability estimates are provided, both empirical and model curves are produced. Can optionally handle weights and groups as required. Note this is not for use with rout files. See the generic function plotRout for plotting rout files.
Usage

```
plotModelExp(
  items,
  range = c(-6, 6),
  by = 0.1,
  bins = NULL,
  abilities = NULL,
  weights = NULL,
  group = NULL,
  scale = FALSE
)
```

Arguments

- `items`: a list of one or more matrices of item parameters. Used in producing model-implied curves.
- `range`: Lower and upper bounds to plot over (defaults to c(-6, 6). Used in producing model-implied curves. For empirical curves a range is chosen given the min and max values in abilities.
- `by`: Increment to calculate expectation along range. Used in producing model-implied curves.
- `bins`: A double. Optional. How many equally sized bins should abilities be broken up into? Used in producing empirical curves. If not provided and abilities are provided, a suitable value is chosen given the length of abilities.
- `group`: A vector of type factor. Optional.
- `scale`: A Boolean. Whether plot should be scaled such that the Y-axis ranges from 0 to 1.

Value

A ggplot2 object.

Examples

```
myItem <- matrix(
  c(
    0, 0, 0, 1,
    1, 1, 0, 1
  ),
  ncol = 4, byrow=TRUE
)
myPlot <- plotModelExp(list(myItem))
```
plotRout

Description

generates a plot from an 'ACER ConQuest' Rout file. use ConQuestRout to read in an Rout file created by a plot command in 'ACER ConQuest'.

Usage

plotRout(myRout, ...)

## S3 method for class 'TestInfo'
plotRout(myRout, ...)

## S3 method for class 'InformationWithLatentDist'
plotRout(myRout, ...)

## S3 method for class 'ICC'
plotRout(myRout, ...)

## S3 method for class 'MCC'
plotRout(myRout, ...)

## S3 method for class 'TCC'
plotRout(myRout, ...)

## Default S3 method:
plotRout(myRout, ...)

Arguments

myRout an R object created by the ConQuestRout function.

... additional arguments passed into plotting functions

Value

A ggplot2 object.

Examples

myRout <- ConQuestRout()
myPlot <- plotRout(myRout)
## to see why we import this, see https://ggplot2.tidyverse.org/articles/ggplot2-in-packages.html
**Description**

Applies the law of total variance (EVEs law) to calculate the mean and variance of a set of PVs for one dimension.

**Usage**

`pvMeanVar(myData)`

**Arguments**

- `myData`: A matrix of PVs for one dimension: m PVs by n cases.

**Value**

A list containing the mean and variance of the PVs.

---

**Description**

Helper function to apply correction to correlation matrix. When working with standardised residuals, the expectation of the correlations is `-1/(L-1)` rather than 0. See DOI: 10.1177/0013164410379322

**Usage**

`q3ExpCorrect(myCorMat)`

**Arguments**

- `myCorMat`: A correlation matrix.

**Value**

A correlation matrix with the Q3 statistic correction applied.
ReadSys

Description
Internal function to read an 'ACER ConQuest' system file. Called by conquestr::ConQuestSys.

Usage
ReadSys(myFile, isMini)

Arguments
myFile: An connection to an 'ACER ConQuest' system file created by the put command in 'ACER ConQuest'. If the file is compressed, and uncompressed temporary file is created.
isMini: A boolean, set to TRUE if the system file is a mini system file created by 'ACER ConQuest' command put with option "mini = yes".

Value
A list containing the data objects created by 'ACER ConQuest'.

See Also
conquestr::ConQuestSys()

ReadSysMini

Description
Internal function to read an 'ACER ConQuest' system file. Called by conquestr::ConQuestSys.

Usage
ReadSysMini(myFile, Dimensions, N, NPlausibles, isDebug)

Arguments
myFile: An 'ACER ConQuest' mini system file created by the put command in 'ACER ConQuest' with the option "mini = yes". The put command must use the option compressed = no.
Dimensions: .
N: .
NPlausibles: .
isDebug: .
recodeResps

Value
A list containing the data objects created by 'ACER ConQuest'.

See Also
conquestr::ConQuestSys()

recodeResps recodeResps

Description
Recode raw item responses for analyses.

Usage
recodeResps(data, recodeMap, varLabel, rawLabel, recodeLabel)

Arguments

data Raw data, a data frame.
recodeMap A data frame which contains the raw responses and corresponding recoded responses for each of the items in long form.
varLabel A variable name in recodeMap that identifies the item label.
rawLabel A variable name in recodeMap that identifies the raw item responses to be recoded.
recodeLabel A variable name in recodeMap that identifies the new values to recode to.

Value
a data frame with raw data recoded according to recodeMap.

replaceInDataFrame iterate through a data frame and use replaceInVector

Description
iterate through a data frame and use replaceInVector

Usage
replaceInDataFrame(d, r, x)
Arguments

- \( d \): A DataFrame.
- \( r \): A double - the value to be replaced if it is \(< -1e300 \).
- \( x \): A double - the value to replace \( r \) with.

replaceInVector: replace a very large negative number with something - usually NA_REAL

Description

replace a very large negative number with something - usually NA_REAL

Usage

replaceInVector(\( v, r, x \))

Arguments

- \( v \): A NumericVector.
- \( r \): A double - the value to be replaced if it is \(< -1e300 \).
- \( x \): A double - the value to replace \( r \) with.

searchConQuestSys: searchConQuestSys

Description

Search for object names within a ConQuest System file object.

Usage

searchConQuestSys(searchString, mySys, value = TRUE, ignore.case = TRUE)

Arguments

- \( searchString \): A string to search within the names of mySys.
- \( mySys \): An 'ACER ConQuest' system file object created using the conquestr::ConQuestSys function.
- \( value \): Should searchConQuestSys return the name of the object or its index.
- \( ignore.case \): Should searchConQuestSys ignore the case of the search term.

Value

a string including object names matching the search term
steigerStat

Description

Function to calculate the Steiger statistic. The Steiger statistic is a test of independence of the standardised residuals \(((O-E)/\sqrt{Var(E)}))\), where \(Var(E) = p(x)/(1-p(x))\).

Usage

```r
steigerStat(myDat, q3Adj = TRUE, fisher = TRUE, dfAdj = FALSE, tpm)
```

Arguments

- **myDat**: A data frame or matrix containing standardised residuals.
- **q3Adj**: A bool indicating whether the Q3 correction should be applied.
- **fisher**: A bool indicating whether the Fisher Transform should be applied.
- **dfAdj**: A bool indicating whether the df should be adjusted for sample size, L, and targeting. If dfAdj is TRUE, then you must pass in the optional argument tpm (test-person match).
- **tpm**: A number indicating the test-person match, where 0 indicates that mean item difficulty is equal to mean person ability, and -1 indicates that mean item difficulty is 1 logit below mean person ability.

Value

A list of class "steigerStat" with the Steiger Statistic, correlation matrix, and chi square test.

summariseCqChain

Description

takes a data frame created by getCqChain and returns a list reporting the mean and variance for each parameter.

Usage

```r
summariseCqChain(myChain)
```

Arguments

- **myChain**: A data frame returned from getCqChain.
sysFileOk

Description
checks

Usage
sysFileOk(sysFile, defaultSys)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sysFile</td>
<td>An ACER ConQuest system file read into R using conquestr::ConQuestSys</td>
</tr>
<tr>
<td>defaultSys</td>
<td>A Boolean indicating if sysFile is the default system file created by an empty call to conquestr::ConQuestSys</td>
</tr>
</tbody>
</table>

Examples

```r
## Not run:
sysFileOkResult <- sysFileOk(conquestr::ConQuestSys())
## End(Not run)
```

sysToBMatrixDf

Description
Read an R object of class ConQuestSys and create a labelled representation of the B matrix (scoring matrix). This maps item response categories to items and dimensions. Returns long data frame, where items are duplicated if they are in many dimensions.

Usage
sysToBMatrixDf(sysToBMatrixDf)

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mySys</td>
<td>An ACER ConQuest system file read into R using conquestr::ConQuestSys</td>
</tr>
<tr>
<td>applyLabels</td>
<td>A Boolean indicating if sysFile is the default system file created by an empty call to conquestr::ConQuestSys</td>
</tr>
</tbody>
</table>

Examples

```r
## Not run:
sysToBMatrixDfResult <- sysToBMatrixDf(conquestr::ConQuestSys())
## End(Not run)
```
**sysToItemDifDf**

**Arguments**

<table>
<thead>
<tr>
<th>mySys</th>
<th>An R object of class ConQuestSys, returned by the function conquestr::ConQuestSys</th>
</tr>
</thead>
<tbody>
<tr>
<td>applyLabels</td>
<td>A bool indicating whether labels (e.g., dimension labels) should be appended.</td>
</tr>
</tbody>
</table>

**Value**

A data frame containing the labelled B matrix.

**Examples**

```r
myBMatrix <- sysToBMatrixDf(ConQuestSys())
## Not run:
# if you run the above example you will have the B Matrix from the example system file.
str(myBMatrix)
## End(Not run)
```

**Description**

Creates a data frame that includes the common item parameter estimates from two (or more) system files (e.g., a DIF analysis).

**Usage**

```r
sysToItemDifDf(listOfSysFiles, mySuffixes, myDims = "all")
```

**Arguments**

<table>
<thead>
<tr>
<th>listOfSysFiles</th>
<th>A list of system files returned from conquestr::ConQuestSys</th>
</tr>
</thead>
<tbody>
<tr>
<td>mySuffixes</td>
<td>A vector of strings specifying the names for the two groups being analysed, e.g., if the two system files are an analysis of boys and girls, the vector may be c(&quot;_male&quot;, &quot;_female&quot;).</td>
</tr>
<tr>
<td>myDims</td>
<td>A string specifying if all or specific dimensions should be included. The default is &quot;all&quot;. Specific dimensions are specified by the label &quot;D1&quot; for dimensions 1 etc.</td>
</tr>
</tbody>
</table>

**Value**

A data frame object.

**See Also**

conquestr::plotDif ()
testInfoAtTheta

Description

Calculates test information at a value of theta given a list of matrices of item parameters for one or more items.

Usage

testInfoAtTheta(myItems, theta)

Arguments

myItems A list of matrices of item parameters of the structure used in simplef
theta a number.

Examples

anItem <- matrix(c(0,0,0,1,1,1,0,1), nrow = 2, byrow = TRUE)
testInfoAtTheta(list(anItem), 0)

testInfoOverTheta

Description

Calculates test information over a range of theta given a list of matrices of item parameters for one or more items. Returns a data frame with item information at a discrete set of values of theta. This is useful for plotting test information functions.

Usage

testInfoOverTheta(myItems, minTheta = -6, maxTheta = 6, stepTheta = 0.1)

Arguments

myItems a list of item parameters of the structure used in simplef
minTheta The smallest value of ability PDF to calculate info and to plot. Defaults to -6.
maxTheta The largest value of ability PDF to calculate info and to plot. Defaults to 6.
stepTheta The increment to iterate over the ability PDF. Defaults to 0.01.

Examples

anItem <- matrix(c(0,0,0,1,1,1,0,1), nrow = 2, byrow = TRUE)
testInfoOverTheta(list(anItem))
Description

Generates Thurstonian Thresholds (sometimes called *gammas*) to an item. Thurstonian thresholds are the location on the trait/scale at which the cumulative probability of being in category $k$, or any higher category equals some probability (usually 0.5, the default). Thurstonian thresholds are considered a way of describing the difficulty of polytomously scored items and are usually the value used in visualisations like Wright maps. Thurstonian thresholds can only be calculated for items where response categories are scored such that each category can be placed in an order increasing scores (e.g., no ties as per the Ordered Partition model).

Usage

```r
thrstThrsh(myItem, threshP = 0.5, minTheta = -20, maxTheta = 20, convC = 1e-05)
```

Arguments

- **myItem**: A matrix of parameters for a single item of the structure used in `simplef` (a matrix of $k$ categories by four (category score, delta dot, tau, discrimination)).
- **threshP**: The probability at which the threshold is calculated (defaults to the usual value of 0.5).
- **minTheta**: The lower-bound starting value of the split-half search used to find the threshold for the category.
- **maxTheta**: The upper-bound starting value of the split-half search used to find the threshold for the category.
- **convC**: The convergence criteria used to determine when the threshold has been found. The difference between `threshP` and the cumulative probability of the category and any higher category at the current value of theta (the current threshold being tested).

Value

A $k-1$ by 1 matrix with Thurstonian thresholds for this item. Values are NA when the threshold cannot be calculated.

Examples

```r
myItem <- matrix(c(  
  0, -0.58 , 0 , 1, # delta+tau thurst thresh (gamma)  
  1, -0.58 , 0.776, 1,  # 0.196 -1.14  
  2, -0.58 , -0.697, 1,  # -1.277 -0.93  
  3, -0.58 , -0.629, 1,  # -1.209 -0.64  
  4, -0.58 , 0.55 , 1 # -0.03 0.25  
), ncol =4, byrow=TRUE)
```

transformPvs

Description

Helper function to Transform PVs onto a new metric (e.g., PISA Mean = 500, SD = 100). Uses the method described in the PISA 2012 technical manual.

Usage

transformPvs(data, mT = 0, sdT = 1, weights = 1)

Arguments

data A data frame or matrix that contains the PVs
mT The desired mean of the PVs
sdT The desired sd of the PVs
weights a vector of weights, the same length as data[1] used to calculate the mean and SD across the PVs

Value

a List of transformed PVs with as many elements as PVs were listed in 'x'.

writeImportXsi

Description

Writes a fixed width text file in the format required for the ACER ConQuest command and argument import anchor_xsi. Can also be used for initial values, though caution should be used with the interpretation of the argument lconstraint which should relate to the model of interest ACER ConQuest Currently only works with implicit variables. Explicit variables may be added in the future.

Usage

writeImportXsi(items, bmatix = 1L, lconstraint = "none", file)
**Arguments**

- **items**: a list of item matrices
- **bmatrix**: either the integer 1L for a unidimensional model, or a matrix, items by dimensions with 1L representing that the item in on this dimension, and a 0 otherwise.
- **lconstraint**: the identification constraint in use, one of "none", "items", or "cases".
- **file**: a path and filename to write file to disk. # @return invisibly returns path of file written to disk

**See Also**

- `simplef()`, `genResponses()`, `browseVignettes("conquestr")`

**Examples**

```r
myItem <- matrix(c(0, 0, 0, 0, 1, 1, 0, 1), ncol = 4, byrow = TRUE)
myItems <- list(myItem, myItem)
myItems[[2]][2] <- -1 # make the second item delta equal to -1
myResponses <- genResponses(abilities = rnorm(100), itemParams = myItems)
```
Index

checkItemRespValid, 3
checkVars, 4
cnvrtItemParam, 4
ConQuestCall, 5
ConQuestRout, 6
ConQuestSys, 7
createConQuestProject, 8
DecompressSys, 8
fisherTrnsfrm, 9
fmtCqItanal, 9
genItems, 10
genResponses, 12
genResponses(), 11, 45
getCqChain, 13
getCqData, 14
getCqDataDf, 15
getCqFit, 16
getCqHist, 16
getCqItanal, 17
getCqItanalFacility, 17
getCqItanalSummary, 18
getCqRespModel, 19
getCqTerms, 19
getCqVars, 20
 GinsOnDims, 20
informationWrightMap, 21
 infoWI, 22
itemInfoAtTheta, 23
itemInfoOverTheta, 23
itemListToThresholds, 24
makeItemList, 25
plotCCC, 27
plotCqHist, 28
plotDif, 30
plotItemMap, 31
plotModelCCC, 32
plotModelExp, 32
plotRout, 34
pvMeanVar, 35
q3ExpCorrect, 35
ReadSys, 36
ReadSysMini, 36
recodeResps, 37
replaceInDataFrame, 37
replaceInVector, 38
searchConQuestSys, 38
simplef(), 11, 13, 45
steigerStat, 39
summariseCqChain, 39
sysFileOk, 40
sysToMatrixDf, 40
sysToItemDifDf, 41
testInfoAtTheta, 42
testInfoOverTheta, 42
 thrstThrsh, 43
transformPvs, 44
writeImportXsi, 44