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Description The purpose of this package is to factor out logic and math common to Item Factor Analysis fitting, diagnostics, and analysis. It is envisioned as core support code suitable for more specialized IRT packages to build upon. Complete access to optimized C functions are made available with R_RegisterCCallable().
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Description

Factor out logic and math common to Item Factor Analysis fitting, diagnostics, and analysis. It is envisioned as core support code suitable for more specialized IFA packages to build upon.
Details

This package provides optimized, low-level functions to map parameters to response probabilities for dichotomous (1PL, 2PL and 3PL) \texttt{rpf.drm} and polytomous (graded response \texttt{rpf.grm}, partial credit/generalized partial credit (via the nominal model), and nominal \texttt{rpf.nrm} items.

Item model parameters are passed around as a numeric vector. A 1D matrix is also acceptable. Regardless of model, parameters are always ordered as follows: discrimination/slope ("a"), difficulty/intercept ("b"), and pseudo guessing/upper-bound ("g"/"u"). If person ability ranges from negative to positive then probabilities are output from incorrect to correct. That is, a low ability person (e.g., ability = -2) will be more likely to get an item incorrect than correct. For example, a dichotomous model that returns [.25, .75] indicates a probability of .25 for incorrect and .75 for correct. A polytomous model will have the most incorrect probability at index 1 and the most correct probability at the maximum index.

All models are always in the logistic metric. To obtain normal ogive discrimination parameters, divide slope parameters by \texttt{rpf.give}. Item models are estimated in slope-intercept form. Input/output matrices arranged in the way most convenient for low-level processing in C. The maximum absolute logit is 35 because \( f(x) := 1-\exp(x) \) loses accuracy around \( f(-35) \) and equals 1 at \( f(-38) \) due to the limited accuracy of double precision floating point.

This package could also accrete functions to support plotting (but not the actual plot functions).

References


See Also

See \texttt{rpf.rparam} to create item parameters.

---

\texttt{as.IFAgroup} \hspace{1cm} \textit{Convert an OpenMx MxModel object into an IFA group}

Description

When "\texttt{minItemsPerScore}" is passed, EAP scores will be computed from the data and stored. Scores are required for some diagnostic tests. See discussion of "\texttt{minItemsPerScore}" in \texttt{EAPscores}.

Usage

\begin{verbatim}
as.IFAgroup(mxModel, data = NULL, container = NULL, ..., 
minItemsPerScore = NULL)
\end{verbatim}
bestToOmit

Arguments

mxModel         MxModel object
data            observed data (otherwise the data will be taken from the mxModel)
container       an MxModel in which to search for the latent distribution matrices
...             Not used. Forces remaining arguments to be specified by name.
minItemsPerScore minimum number of items required to compute a score (also see description)

Value

a groups with item parameters and latent distribution

See Also

ifaTools

---

bestToOmit Identify the columns with most missing data

Description

If a reference column is given then only rows that are not missing on the reference column are considered. Otherwise all rows are considered.

Usage

bestToOmit(grp, omit, ref = NULL)

Arguments

grp            an IFA group
omit           the maximum number of items to omit
ref            the reference column (optional)
Computes local dependence indices for all pairs of items

Description

Item Factor Analysis makes two assumptions: (1) that the latent distribution is reasonably approximated by the multivariate Normal and (2) that items are conditionally independent. This test examines the second assumption. The presence of locally dependent items can inflate the precision of estimates causing a test to seem more accurate than it really is.

Usage

\[
\text{ChenThissen1997(grp, ... , data = NULL, inames = NULL, qwidth = 6, qpoints = 49, method = "pearson", twotier = TRUE, parallel = TRUE)}
\]

Arguments

- `grp`: a list with the spec, param, mean, and cov describing the group
- `...`: Not used. Forces remaining arguments to be specified by name.
- `data`: data
- `inames`: a subset of items to examine
- `qwidth`: quadrature width
- `qpoints`: number of equally spaced quadrature points
- `method`: method to use to calculate P values. The default is the Pearson X^2 statistic. Use "lr" for the similar likelihood ratio statistic.
- `twotier`: whether to enable the two-tier optimization
- `parallel`: whether to take advantage of multiple CPUs (default TRUE)

Details

Statically significant entries suggest that the item pair has local dependence. Since \( \log(0.01) = -4.6 \), an absolute magnitude of 5 is a reasonable cut-off. Positive entries indicate that the two item residuals are more correlated than expected. These items may share an unaccounted for latent dimension. Consider a redesign of the items or the use of testlets for scoring. Negative entries indicate that the two item residuals are less correlated than expected.

Value

A list with raw, pval and detail. The pval matrix is a lower triangular matrix of log P values with the sign determined by relative association between the observed and expected tables (see `ordinal.gamma`
References


See Also

ifaTools

---

Class rpf.1dim

The base class for 1 dimensional response probability functions.

Description

The base class for 1 dimensional response probability functions.

---

Class rpf.1dim.drm

Unidimensional dichotomous item models (1PL, 2PL, and 3PL).

Description

Unidimensional dichotomous item models (1PL, 2PL, and 3PL).

---

Class rpf.1dim.graded

The base class for 1 dimensional graded response probability functions.

Description

This class contains methods common to both the generalized partial credit model and the graded response model.

---

Class rpf.1dim.grm

The unidimensional graded response item model.

Description

The unidimensional graded response item model.
Class rpf.mdim.graded

---

**Class rpf.1dim.lmp**  
*Unidimensional logistic function of a monotonic polynomial.*

**Description**

Unidimensional logistic function of a monotonic polynomial.

---

**Class rpf.base**  
*The base class for response probability functions.*

**Description**

Item specifications should not be modified after creation.

---

**Class rpf.mdim**  
*The base class for multi-dimensional response probability functions.*

**Description**

The base class for multi-dimensional response probability functions.

---

**Class rpf.mdim.drm**  
*Multidimensional dichotomous item models (M1PL, M2PL, and M3PL).*

**Description**

Multidimensional dichotomous item models (M1PL, M2PL, and M3PL).

---

**Class rpf.mdim.graded**  
*The base class for multi-dimensional graded response probability functions.*

**Description**

This class contains methods common to both the generalized partial credit model and the graded response model.
Class rpf.mdim.grm

The multidimensional graded response item model.

Description

The multidimensional graded response item model.

Class rpf.mdim.mcm

The multiple-choice response item model (both unidimensional and multidimensional models have the same parameterization).

Description

The multiple-choice response item model (both unidimensional and multidimensional models have the same parameterization).

Class rpf.mdim.nrm

The nominal response item model (both unidimensional and multidimensional models have the same parameterization).

Description

The nominal response item model (both unidimensional and multidimensional models have the same parameterization).

collapseCategoricalCells

Collapse small sample size categorical frequency counts

Description

Collapse small sample size categorical frequency counts

Usage

collapseCategoricalCells(observed, expected, minExpected = 1)
Arguments

observed the observed frequency table
expected the expected frequency table
minExpected the minimum expected cell frequency

Pearson’s $X^2$ test requires some minimum frequency per cell to avoid an inflated false positive rate. This function will merge cells with the lowest frequency counts until all the counts are above the minimum threshold. Cells that have been merged are filled with NAs. The resulting tables and number of merged cells is returned.

Examples

O = matrix(c(7,31,42,20,0), 1,5)
E = matrix(c(3,39,50,8,0), 1,5)
collapseCategoricalCells(O,E,9)

compressDataFrame Compress a data frame into unique rows and frequencies

Description

Compress a data frame into unique rows and frequency counts.

Usage

compressDataFrame(tabdata, freqColName = "freq", .asNumeric = FALSE)

Arguments

tabdata An object of class data.frame
freqColName Column name to contain the frequencies
.asNumeric logical. Whether to cast the frequencies to the numeric type

Value

Returns a compressed data frame

Examples

df <- as.data.frame(matrix(c(sample.int(2, 30, replace=TRUE)), 10, 3))
compressDataFrame(df)
**crosstabTest**

*Monte-Carlo test for cross-tabulation tables*

**Description**

This is for developers.

**Usage**

```r
crosstabTest(ob, ex, trials)
```

**Arguments**

- `ob`  observed table
- `ex`  expected table
- `trials` number of Monte-Carlo trials

---

**EAPscores**

*Compute EAP scores*

**Description**

If you have missing data then you must specify `minItemsPerScore`. This option will set scores to NA when there are too few items to make an accurate score estimate. If you are using the scores as point estimates without considering the standard error then you should set `minItemsPerScore` as high as you can tolerate. This will increase the amount of missing data but scores will be more accurate. If you are carefully considering the standard errors of the scores then you can set `minItemsPerScore` to 1. This will mimic the behavior of most other IFA software wherein scores are estimated if there is at least 1 non-NA item for the score. However, it may make more sense to set `minItemsPerScore` to 0. When set to 0, all NA rows are scored to the prior distribution.

**Usage**

```r
EAPscores(grp, ..., naAction = NULL, compressed = FALSE)
```

**Arguments**

- `grp`  a list with spec, param, data, and `minItemsPerScore`
- `...`  Not used. Forces remaining arguments to be specified by name.
- `naAction`  deprecated, will be removed in the next release
- `compressed`  output one score per observed data row even when `weightColumn` is set (default `FALSE`)
Examples

```r
spec <- list()
spec[1:3] <- list(rpf.grm(outcomes=3))
param <- sapply(spec, rpf.rparam)
data <- rpf.sample(5, spec, param)
colnames(param) <- colnames(data)
grp <- list(spec=spec, param=param, data=data, minItemsPerScore=1L)
EAPscores(grp)
```

---

**expandDataFrame**

*Expand summary table of patterns and frequencies*

**Description**

Expand a summary table of unique response patterns to a full sized data-set.

**Usage**

```r
expandDataFrame(tabdata, freqName = NULL)
```

**Arguments**

- `tabdata`: An object of class `data.frame` with the unique response patterns and the number of frequencies
- `freqName`: Column name containing the frequencies

**Value**

Returns a data frame with all the response patterns

**Author(s)**

Based on code by Phil Chalmers <philip.chalmers@gmail.com>

**Examples**

```r
data(LSAT7)
expandDataFrame(LSAT7, freqName="freq")
```
fromFactorLoading  
*Convert factor loadings to response function slopes*

**Description**

Convert factor loadings to response function slopes

**Usage**

```r
fromFactorLoading(loading, ogive = rpf.ogive)
```

**Arguments**

- `loading`: a matrix with items in the rows and factors in the columns
- `ogive`: the ogive constant (default rpf.ogive)

**Value**

a slope matrix with items in the columns and factors in the rows

---

fromFactorThreshold  
*Convert factor thresholds to response function intercepts*

**Description**

Convert factor thresholds to response function intercepts

**Usage**

```r
fromFactorThreshold(threshold, loading, ogive = rpf.ogive)
```

**Arguments**

- `threshold`: a matrix with items in the columns and thresholds in the rows
- `loading`: a matrix with items in the rows and factors in the columns
- `ogive`: the ogive constant (default rpf.ogive)

**Value**

an item intercept matrix with items in the columns and intercepts in the rows
itemOutcomeBySumScore  Produce an item outcome by observed sum-score table

Description

Produce an item outcome by observed sum-score table

Usage

itemOutcomeBySumScore(grp, mask, interest)

Arguments

grp  a list with spec, param, and data
mask  a vector of logicals indicating which items to include
interest  index or name of the item of interest

Examples

set.seed(1)
spec <- list()
spec[1:3] <- rpf.grm(outcomes=3)
param <- sapply(spec, rpf.rparam)
data <- rpf.sample(5, spec, param)
colnames(param) <- colnames(data)
grp <- list(spec=spec, param=param, data=data)
itemOutcomeBySumScore(grp, c(FALSE,TRUE,TRUE), 1L)

kct  Knox Cube Test dataset

Description

These data from Wright & Stone (1979, p. 31) were fit with Winsteps 3.73 using a 1PL model (slope fixed to 1).

References


Examples

data(kct)
logit

Transform from [0,1] to the reals

Description
The logit function is a standard transformation from [0,1] (such as a probability) to the real number line. This function is exactly the same as qlogis.

Usage
logit(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)

Arguments
- p: a number between 0 and 1
- location: see qlogis
- scale: see qlogis
- lower.tail: see qlogis
- log.p: see qlogis

See Also
qlogis, plogis

Examples
logit(.5)  # 0
logit(.25) # -1.098
logit(0)  # -Inf

LSAT6

Description of LSAT6 data

Description
Data from Thissen (1982); contains 5 dichotomously scored items obtained from the Law School Admissions Test, section 6.

Author(s)
Phil Chalmers <rphilip.chalmers@gmail.com>

References
Examples

data(LSAT6)

LSAT7  Description of LSAT7 data

Description

Data from Bock & Lieberman (1970); contains 5 dichotomously scored items obtained from the Law School Admissions Test, section 7.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

data(LSAT7)

multinomialFit  Multinomial fit test

Description

For degrees of freedom, we use the number of observed statistics (incorrect) instead of the number of possible response patterns (correct) (see Bock, Gibbons, & Muraki, 1998, p. 265). This is not a huge problem because this test is becomes poorly calibrated when the multinomial table is sparse. For more accurate p-values, you can conduct a Monte-Carlo simulation study (see examples).

Usage

`multinomialFit(grp, independenceGrp, ..., method = "lr", log = TRUE, .twotier = TRUE)`

Arguments

- `grp`: a list with the spec, param, mean, and cov describing the group
- `independenceGrp`: a list with the spec, param, mean, and cov describing the independence group
- `...`: Not used. Forces remaining arguments to be specified by name.
- `method`: `lr` (default) or `pearson`
- `log`: whether to report p-value in log units
- `.twotier`: whether to use the two-tier optimization (default `TRUE`)
Details

Rows with missing data are ignored.

The full information test is described in Bartholomew & Tzamourani (1999, Section 3).
For CFI and TLI, you must provide an independence model.

References


Examples

```r
# Create an example IFA group
grp <- list(spec=list(list()))
grp$spec[1:10] <- rpf.grm()
grp$param <- sapply(grp$spec, rpf.rparam)
colnames(grp$param) <- paste("i", 1:10, sep="")
grp$mean <- 0
grp$cov <- diag(1)
grp$uniqueFree <- sum(grp$param != 0)
grp$data <- rpf.sample(1000, grp=grp)

# Monte-Carlo simulation study
mcReps <- 3 # increase this to 10,000 or so
stat <- rep(NA, mcReps)
for (rx in 1:mcReps) {
  t1 <- grp
t1$data <- rpf.sample(grp=grp)
  stat[rx] <- multinomialFit(t1)$statistic
}
sum(multinomialFit(grp)$statistic > stat)/mcReps # better p-value
```

observedSumScore

Describes the observed sum-score

Usage

```
observedSumScore(grp, ..., mask, summary = TRUE)
```
omitMostMissing

Arguments

- **grp**: a list with spec, param, and data
- **mask**: a vector of logicals indicating which items to include
- **summary**: whether to return a summary (default) or per-row scores

Examples

```r
spec <- list()
spec[1:3] <- rpf.grm(outcomes=3)
param <- sapply(spec, rpf.rparam)
data <- rpf.sample(5, spec, param)
colnames(param) <- colnames(data)
grp <- list(spec=spec, param=param, data=data)
observedSumScore(grp)
```

Description

Omit items with the most missing data

Usage

```r
omitMostMissing(grp, omit)
```

Arguments

- **grp**: an IFA group
- **omit**: the maximum number of items to omit
orderCompletely

Order a data.frame by missingness and all columns

Description

Completely order all rows in a data.frame.

Usage

orderCompletely(observed)

Arguments

observed         a data.frame holding ordered factors in every column

Value

the sorted order of the rows

Examples

df <- as.data.frame(matrix(c(sample.int(2, 30, replace=TRUE)), 10, 3))
mask <- matrix(c(sample.int(3, 30, replace=TRUE)), 10, 3) == 1
df[mask] <- NA
df[orderCompletely(df),]

---

ordinal.gamma

Compute the ordinal gamma association statistic

Description

Compute the ordinal gamma association statistic

Usage

ordinal.gamma(mat)

Arguments

mat         a cross tabulation matrix

References

Examples

# Example data from Agresti (1990, p. 21)
jobsat <- matrix(c(20, 22, 13, 7, 24, 38, 28, 18, 80, 104, 81, 54, 82, 125, 113, 92), nrow=4, ncol=4)
ordinal.gamma(jobsat)

ptw2011.gof.test Compute the P value that the observed and expected tables come from the same distribution

Description

This test is an alternative to Pearson’s X^2 goodness-of-fit test. In contrast to Pearson’s X^2, no ad hoc cell collapsing is needed to avoid an inflated false positive rate in situations of sparse cell frequencies. The statistic rapidly converges to the Monte-Carlo estimate as the number of draws increases.

Usage

ptw2011.gof.test( observed, expected)

Arguments

observed observed matrix
expected expected matrix

Value

The P value indicating whether the two tables come from the same distribution. For example, a significant result (P < alpha level) rejects the hypothesis that the two matrices are from the same distribution.

References


Examples

draws <- 17
observed <- matrix(c(.294, .176, .118, .411), nrow=2) * draws
expected <- matrix(c(.235, .235, .176, .353), nrow=2) * draws
ptw2011.gof.test(observed, expected) # not significant
read.flexmirt  

Read a flexMIRT PRM file

Description

Load the item parameters from a flexMIRT PRM file.

Usage

read.flexmirt(fname)

Arguments

fname  file name

Value

a list of groups each with item parameters and the latent distribution

rpf.1dim.fit  

Calculate item and person Rasch fit statistics

Description

Note: These statistics are only appropriate if all discrimination parameters are fixed equal and items are conditionally independent (see ChenThissen1997). A best effort is made to cope with missing data.

Usage

rpf.1dim.fit(spec, params, responses, scores, margin, group = NULL, wh.exact = TRUE)

Arguments

spec  list of item models
params  matrix of item parameters, 1 per column
responses  persons in rows and items in columns
scores  model derived person scores
margin  for people 1, for items 2
group  spec, params, data, and scores can be provided in a list instead of as arguments
wh.exact  whether to use the exact Wilson-Hilferty transformation
Details

Exact distributional properties of these statistics are unknown (Masters & Wright, 1997, p. 112). For details on the calculation, refer to Wright & Masters (1982, p. 100).

The Wilson-Hilferty transformation is biased for less than 25 items. Consider wh.exact=FALSE for less than 25 items.

References


Examples

data(kct)
responses <- kct.people[,paste("V",2:19, sep="")]
rownames(responses) <- kct.people$NAME
colnames(responses) <- kct.items$NAME
scores <- kct.people$MEASURE
params <- cbind(1, kct.items$MEASURE, logit(0), logit(1))
rownames(params) <- kct.items$NAME
items<-list()
items[1:18] <- rpf.drm()
params[,2] <- -params[,2]
rpf.1dim.fit(items, t(params), responses, scores, 2, wh.exact=TRUE)

\[
\text{rpf.1dim.moment} \quad \text{Calculate cell central moments}
\]

Description

Popular central moments include 2 (variance) and 4 (kurtosis).

Usage

\[
\text{rpf.1dim.moment(spec, params, scores, m)}
\]

Arguments

- **spec**: list of item models
- **params**: data frame of item parameters, 1 per row
- **scores**: model derived person scores
- **m**: which moment
**Value**

moment matrix

---

**rpf.1dim.residual** *Calculate residuals*

**Description**

Calculate residuals

**Usage**

```r
rpf.1dim.residual(spec, params, responses, scores)
```

**Arguments**

- **spec**
  - list of item models
- **params**
  - data frame of item parameters, 1 per row
- **responses**
  - persons in rows and items in columns
- **scores**
  - model derived person scores

**Value**

residuals

---

**rpf.1dim.stdresidual** *Calculate standardized residuals*

**Description**

Calculate standardized residuals

**Usage**

```r
rpf.1dim.stdresidual(spec, params, responses, scores)
```

**Arguments**

- **spec**
  - list of item models
- **params**
  - data frame of item parameters, 1 per row
- **responses**
  - persons in rows and items in columns
- **scores**
  - model derived person scores

**Value**

standardized residuals
Item parameter derivatives

Description
Evaluate the partial derivatives of the log likelihood with respect to each parameter at `where` with `weight`.

Usage
```
rfp.dLL(m, param, where, weight)
```

Arguments
- `m`: item model
- `param`: item parameters
- `where`: location in the latent space
- `weight`: per outcome weights (typically derived by observation)

Details
It is not easy to write an example for this function. To evaluate the derivative, you need to sum the derivatives across a quadrature. You also need response outcome weights at each quadrature point. It is not anticipated that this function will be often used in R code. It’s mainly to expose a C-level function for occasional debugging.

Value
first and second order partial derivatives of the log likelihood evaluated at `where`. For p parameters, the first p values are the first derivative and the next p(p+1)/2 columns are the lower triangle of the second derivative.

See Also
The numDeriv package.
Create a dichotomous response model

**Description**

For slope vector \( a \), intercept \( c \), pseudo-guessing parameter \( g \), upper bound \( u \), and latent ability vector \( \theta \), the response probability function is

\[
P(\text{pick} = 0 | a, c, g, u, \theta) = 1 - P(\text{pick} = 1 | a, c, g, u, \theta)
\]

\[
P(\text{pick} = 1 | a, c, g, u, \theta) = \frac{g + (u - g)}{1 + \exp(-(a\theta + c))}
\]

**Usage**

`rpf.drm(factors = 1, multidimensional = TRUE, poor = FALSE)`

**Arguments**

- `factors` the number of factors
- `multidimensional` whether to use a multidimensional model. Defaults to `TRUE`.
- `poor` if `TRUE`, use the traditional parameterization of the 1d model instead of the slope-intercept parameterization

**Details**

The pseudo-guessing and upper bound parameter are specified in logit units (see `logit`).

For discussion on the choice of priors see Cai, Yang, and Hansen (2011, p. 246).

**Value**

an item model

**References**


**Examples**

```r
spec <- rpf.drm()
rpf.prob(spec, rpf.rparam(spec), 0)
```
**rpf.dTheta**  
*Item derivatives with respect to the location in the latent space*

**Description**

Evaluate the partial derivatives of the response probability with respect to ability. See rpf.info for an application.

**Usage**

```r
rpf.dTheta(m, param, where, dir)
```

**Arguments**

- `m` item model
- `param` item parameters
- `where` location in the latent distribution
- `dir` if more than 1 factor, a basis vector]

**rpf.grm**  
*Create a graded response model*

**Description**

For outcomes k in 0 to K, slope vector a, intercept vector c, and latent ability vector theta, the response probability function is

\[
P(\text{pick} = 0|a, c, \theta) = 1 - P(\text{pick} = 1|a, c_1, \theta)
\]

\[
P(\text{pick} = k|a, c, \theta) = \frac{1}{1 + \exp(-(a\theta + c_k))} - \frac{1}{1 + \exp(-(a\theta + c_{k+1}))}
\]

\[
P(\text{pick} = K|a, c, \theta) = \frac{1}{1 + \exp(-(a\theta + c_K))}
\]

**Usage**

```r
rpf.grm(outcomes = 2, factors = 1, multidimensional = TRUE)
```

**Arguments**

- `outcomes` The number of choices available
- `factors` the number of factors
- `multidimensional` whether to use a multidimensional model. Defaults to TRUE.
The graded response model was designed for an item with a series of dependent parts where a higher score implies that easier parts of the item were surmounted. If there is any chance your polytomous item has independent parts then consider `rpf.nrm`. If your categories cannot cross then the graded response model provides a little more information than the nominal model. Stronger a priori assumptions offer provide more power at the cost of flexibility.

Value

an item model

Examples

```r
spec <- rpf.grm()
rpf.prob(spec, rpf.rparam(spec), 0)
```

---

**rpf.id_of**

Convert an rpf item model name to an ID

Description

This is an internal function and should not be used.

Usage

`rpf.id_of(name)`

Arguments

- **name**: name of the item model (string)

Value

the integer ID assigned to the given model
Map an item model, item parameters, and person trait score into a information vector

Usage

```r
rpf.info(ii, ii.p, where, basis = 1)
```

Arguments

- `ii`: an item model
- `ii.p`: item parameters
- `where`: the location in the latent distribution
- `basis`: if more than 1 factor, a positive basis vector

Value

Fisher information

References


Examples

```r
i1 <- rpf.drm()
i1.p <- c(.6,.1,.1,.95)
theta <- seq(0,3,.05)
plot(theta, rpf.info(i1, i1.p, t(theta)), type="l")
```

Create logistic function of a monotonic polynomial (LMP) model

Description

This model is a dichotomous response model originally proposed by Liang (2007) and is implemented using the parameterization by Falk & Cai (in press).

Usage

```r
rpf.lmp(k = 0, multidimensional = FALSE)
```
Arguments

- **k**: a non-negative integer that controls the order of the polynomial (2k+1) with a default of k=0 (1st order polynomial = 2PL).

- **multidimensional**: whether to use a multidimensional model. Defaults to FALSE. The multidimensional version is not yet available.

Details

The LMP model replaces the linear predictor part of the two-parameter logistic function with a monotonic polynomial, \( m(\theta, \omega, \xi, \alpha, \tau) \),

\[
P(\text{pick} = 1|\omega, \xi, \alpha, \tau, \theta) = \frac{1}{1 + \exp(- (\xi + m(\theta, \omega, \xi, \alpha, \tau)))}
\]

where \( \alpha \) and \( \tau \) are vectors of length \( k \).

The order of the polynomial is always odd and is controlled by the user specified non-negative integer, \( k \). The model contains 2+2*\( k \) parameters and are used as input to the rpf.prob function in the following order: \( \omega \) - the natural log of the slope of the item model when \( k=0 \), \( \xi \) - the intercept, \( \alpha \) and \( \tau \) - two parameters that control bends in the polynomial. These latter parameters are repeated in the same order for models with \( k>1 \). For example, a \( k=2 \) polynomial with have an item parameter vector of: \( \omega, \xi, \alpha_1, \tau_1, \alpha_2, \tau_2 \).

See Falk & Cai (in press) for more details as to how the polynomial is constructed. In general, the polynomial looks like the following, but coefficients, \( b \), are not directly estimated, but are a function of the item parameters.

\[
m(\theta) = \xi + b_1 \theta + b_2 \theta^2 + \ldots + b_{2k+1} \theta^{2k+1}
\]

At the lowest order polynomial (\( k=0 \)) the model reduces to the two-parameter logistic (2PL) model. However, parameterization of the slope parameter, \( \omega \), is currently different than the 2PL (i.e., slope = \( \exp(\omega) \)). This parameterization ensures that the response function is always monotonically increasing without requiring constrained optimization.

Please note that the functions implementing this item model may eventually be replaced or subsumed by an alternative item model. That is, backwards compatibility will not necessarily be guaranteed and this item model should be considered experimental until further notice.

For example, Falk & Cai present a polytomous item model derived from the generalized partial credit model that also uses a monotonic polynomial as the linear predictor, referred to as a GPC-MP item model. Since the GPC-MP reduces to the LMP when the number of categories is 2, this is a potential candidate for replacing the LMP item model. An alternative may include the retention of a dichotomous response model, but with a lower (and upper) asymptote that further reduces to the three-parameter logistic (or four-parameter logistic) item model when \( k=0 \). Finally, future versions may reparameterize \( \omega \), or allow the option to release constraints on monotonicity. For instance, releasing constraints on \( \omega \) may be desirable in cases where the user wishes to have the option of a monotonically decreasing response function. Further releasing constraints on \( \tau \) would allow nonmonotonicity and would be equivalent to replacing the linear predictor with a polynomial.
Value

an item model

References


Examples

```r
spec <- rpf.lmp(1) # 3rd order polynomial	heta<-seq(-3,3,.1)
p<-rpf.prob(spec, c(-11,37,24,-21),theta)

spec <- rpf.lmp(2) # 5th order polynomial
p<-rpf.prob(spec, c(.69,.71,-.5,-8.48,.52,-3.32),theta)
```

**rpf.logprob**

*Map an item model, item parameters, and person trait score into a probability vector*

Description

Note that in general, exp(rpf.logprob(..)) != rpf.prob(..) because the range of logits is much wider than the range of probabilities due to limitations of floating point numerical precision.

Usage

```r
rpf.logprob(m, param, theta)
```

Arguments

- **m**: an item model
- **param**: item parameters
- **theta**: the trait score(s)

Value

a vector of probabilities. For dichotomous items, probabilities are returned in the order incorrect, correct. Although redundant, both incorrect and correct probabilities are returned in the dichotomous case for API consistency with polytomous item models.
Examples

```r
i1 <- rpf.drm()
i1.p <- rpf.rparam(i1)
rpf.logprob(i1, c(i1.p), -1)  # low trait score
rpf.logprob(i1, c(i1.p), c(0,1))  # average and high trait score
```

Description

WARNING: This model is mostly not implemented.

Usage

```r
rpf.mcm(outcomes = 2, numChoices = 5, factors = 1)
```

Arguments

- `outcomes`: the number of possible outcomes
- `numChoices`: the number of choices available
- `factors`: the number of factors

Details

This function instantiates a multiple-choice response model.

Value

an item model

Author(s)

Jonathan Weeks <weeksjp@gmail.com>
Find the point where an item provides mean maximum information

**Description**

This is a point estimate of the mean difficulty of items that do not offer easily interpretable parameters such as the Generalized PCM. Since the information curve may not be unimodal, this function integrates across the latent space.

**Usage**

```
rfp.mean.info(spec, param, grain = 0.1)
```

**Arguments**

- `spec`: list of item specs
- `param`: list or matrix of item parameters
- `grain`: the step size for numerical integration (optional)

**Details**

**WARNING:** This function is experimental and may disappear.

---

Find the point where an item provides mean maximum information

**Description**

**WARNING:** This function is experimental and may disappear.

**Usage**

```
rfp.mean.info1(spec, iparam, grain = 0.1)
```

**Arguments**

- `spec`: an item spec
- `iparam`: an item parameter vector
- `grain`: the step size for numerical integration (optional)
rpf.modify

Create a similar item specification with the given number of factors

**Description**

Create a similar item specification with the given number of factors

**Usage**

rpf.modify(m, factors)

**Arguments**

- `m`: item model
- `factors`: the number of factors/dimensions

**Examples**

```r
s1 <- rpf.grm(factors=3)
rpf.rparam(s1)
s2 <- rpf.modify(s1, 1)
rpf.rparam(s2)
```

rpf.nrm

Create a nominal response model

**Description**

This function instantiates a nominal response model.

**Usage**

rpf.nrm(outcomes = 3, factors = 1, T.a = "trend", T.c = "trend")

**Arguments**

- `outcomes`: The number of choices available
- `factors`: the number of factors
- `T.a`: the T matrix for slope parameters
- `T.c`: the T matrix for intercept parameters
Details

The transformation matrices $T_a$ and $T_c$ are chosen by the analyst and not estimated. The $T$ matrices must be invertible square matrices of size outcomes-1. As a shortcut, either $T$ matrix can be specified as "trend" for a Fourier basis or as "id" for an identity basis. The response probability function is

$$a = T_a \alpha$$

$$c = T_c \gamma$$

$$P(pick = k|s, a_k, c_k, \theta) = C \frac{1}{1 + \exp(-(s\theta a_k + c_k))}$$

where $a_k$ and $c_k$ are the result of multiplying two vectors of free parameters $\alpha$ and $\gamma$ by fixed matrices $T_a$ and $T_c$, respectively; $a_0$ and $c_0$ are fixed to 0 for identification; and $C$ is a normalizing factor to ensure that $\sum_k P(pick = k) = 1$.

Value

an item model

References


Examples

```r
spec <- rpf.nrm()
rpf.prob(spec, rpf.nrparam(spec), 0)
# typical parameterization for the Generalized Partial Credit Model
gpcm <- function(outcomes) rpf.nrm(outcomes, T.c=lower.tri(diag(outcomes-1),TRUE) * -1)
spec <- gpcm(4)
rpf.prob(spec, rpf.nrparam(spec), 0)
```

<table>
<thead>
<tr>
<th>rpf.numParam</th>
<th>Length of the item parameter vector</th>
</tr>
</thead>
</table>

Description

Length of the item parameter vector

Usage

`rpf.numParam(m)`

Arguments

- `m` item model
rpf.numSpec

Examples

rpf.numParam(rpf.grm(outcomes=3))
rpf.numParam(rpf.nrm(outcomes=3))

rpf.numSpec

**Length of the item model vector**

Description

Length of the item model vector

Usage

rpf.numSpec(m)

Arguments

m item model

Examples

rpf.numSpec(rpf.grm(outcomes=3))
rpf.numSpec(rpf.nrm(outcomes=3))

rpf.ogive

**The ogive constant**

Description

The ogive constant can be multiplied by the discrimination parameter to obtain a response curve very similar to the Normal cumulative distribution function (Haley, 1952; Molenaar, 1974). Recently, Savalei (2006) proposed a new constant of 1.749 based on Kullback-Leibler information.

Usage

rpf.ogive

Format

An object of class numeric of length 1.

Details

In recent years, the logistic has grown in favor, and therefore, this package does not offer any special support for this transformation (Baker & Kim, 2004, pp. 14-18).
References


---

**rpf.paramInfo**

*Retrieve a description of the given parameter*

---

**Description**

Retrieve a description of the given parameter

**Usage**

```
rpf.paramInfo(m, num = NULL)
```

**Arguments**

- `m` item model
- `num` vector of parameters (defaults to all)

**Value**

a list containing the type, upper bound, and lower bound

**Examples**

```
rpf.paramInfo(rpf.drm())
```
**rpf.prob**

*Map an item model, item parameters, and person trait score into a probability vector*

**Description**

Map an item model, item parameters, and person trait score into a probability vector.

**Usage**

```r
c(rpf.prob(m, param, theta))
```

**Arguments**

- `m`: an item model
- `param`: item parameters
- `theta`: the trait score(s)

**Value**

A vector of probabilities. For dichotomous items, probabilities are returned in the order incorrect, correct. Although redundant, both incorrect and correct probabilities are returned in the dichotomous case for API consistency with polytomous item models.

**Examples**

```r
i1 <- rpf.drm()
i1.p <- rpf.rparam(i1)
rpf.prob(i1, c(i1.p), -1)  # low trait score
rpf.prob(i1, c(i1.p), c(0,1))  # average and high trait score
```

---

**rpf.rescale**

*Rescale item parameters*

**Description**

Adjust item parameters for changes in mean and covariance of the latent distribution.

**Usage**

```r
c(rpf.rescale(m, param, mean, cov))
```
**Arguments**

- `m` item model
- `param` item parameters
- `mean` vector of means
- `cov` covariance matrix

**Examples**

```r
spec <- rpf.grm()
p1 <- rpf.rparam(spec)
testPoint <- rnorm(1)
move <- rnorm(1)
cov <- as.matrix(rlnorm(1))
Icov <- solve(cov)
padj <- rpf.rescale(spec, p1, move, cov)
pr1 <- rpf.prob(spec, padj, (testPoint-move) %*% Icov)
pr2 <- rpf.prob(spec, p1, testPoint)
abs(pr1 - pr2) < 1e9
```

---

**rpf.rparam**

*Generates item parameters*

**Description**

This function generates random item parameters. The version argument is available if you are writing a test that depends on reproducible random parameters (using `set.seed`).

**Usage**

```r
rpf.rparam(m, version = 2L)
```

**Arguments**

- `m` an item model
- `version` the version of random parameters

**Value**

- item parameters

**Examples**

```r
i1 <- rpf.drm()
rpf.rparam(i1)
```
**rpf.sample**  
*Randomly sample response patterns given a list of items*

**Description**

Returns a random sample of response patterns given a list of item models and parameters. If `grp` is given then `theta`, `items`, `params`, `mean`, and `cov` can be omitted.

**Usage**

```r
rpf.sample(theta, items, params, ..., prefix = "i", mean = NULL,  
cov = NULL, mcar = 0, grp = NULL)
```

**Arguments**

- `theta`  
either a vector (for 1 dimension) or a matrix (for >1 dimension) of person abilities or the number of response patterns to generate randomly

- `items`  
a list of item models

- `params`  
a list or matrix of item parameters. If omitted, random item parameters are generated for each item model.

- `...`  
Not used. Forces remaining arguments to be specified by name.

- `prefix`  
Column names are taken from `param` or `items`. If no column names are available, some will be generated using the given prefix.

- `mean`  
mean vector of latent distribution (optional)

- `cov`  
covariance matrix of latent distribution (optional)

- `mcar`  
proportion of generated data to set to NA (missing completely at random)

- `grp`  
a list with `spec`, `param`, `mean`, and `cov`

**Value**

Returns a data frame of response patterns

**See Also**

`sample`

**Examples**

```r
# 1 dimensional items
i1 <- rpf.drm()
i1.p <- rpf.rparam(i1)
i2 <- rpf.nrm(outcomes=3)
i2.p <- rpf.rparam(i2)
rpf.sample(5, list(i1,i2), list(i1.p, i2.p))
```
**Description**

These data are from Wright & Masters (1982, p. 18).

**Details**

All items were fit to a 3 category Partial Credit Model (PCM) using Ministep 3.75.0.

**References**


**Examples**

data(science)

---

**SitemFit**

*Compute the S fit statistic for a set of items*

**Description**

Runs `SitemFit1` for every item and accumulates the results.

**Usage**

```r
SitemFit(grp, ..., method = "pearson", log = TRUE, qwidth = 6, qpoints = 49L, alt = FALSE, omit = 0L, .twotier = TRUE, .parallel = TRUE)
```

**Arguments**

- **grp**
  - a list with spec, param, mean, cov, data, and the free variable pattern
- **...**
  - Not used. Forces remaining arguments to be specified by name.
- **method**
  - whether to use a pearson or rms test
- **log**
  - whether to return pvalues in log units
- **qwidth**
  - the positive width of the quadrature in Z units
- **qpoints**
  - the number of quadrature points
- **alt**
  - whether to include the item of interest in the denominator
- **omit**
  - number of items to omit (a single number) or a list of the length the number of items
- **.twotier**
  - whether to enable the two-tier optimization
- **.parallel**
  - whether to take advantage of multiple CPUs (default TRUE)
**SitemFit1**

Value

a list of output from SitemFit1

Examples

```r
gp <- list(spec=list())
gp$spec[1:20] <- list(rpf.grm())
gp$param <- sapply(gp$spec, rpf.rparam)
colnames(gp$param) <- paste("i", 1:20, sep="")
gp$mean <- 0
gp$cov <- diag(1)
gp$free <- gp$param != 0
gp$data <- rpf.sample(500, grp=gp)
SitemFit(grp)
```

---

**SitemFit1**

*Compute the S fit statistic for 1 item*

Description

Implements the Kang & Chen (2007) polytomous extension to S statistic of Orlando & Thissen (2000). Rows with missing data are ignored, but see the omit option.

Usage

```r
SitemFit1(grp, item, free = 0, ..., method = "pearson", log = TRUE,
qwidth = 6, qpoints = 49L, alt = FALSE, omit = 0L,
.twotier = TRUE)
```

Arguments

- **grp**
  a list with spec, param, mean, cov, and data
- **item**
  the item of interest
- **free**
  the number of free parameters involved in estimating the item (to adjust the df)
- **...**
  Not used. Forces remaining arguments to be specified by name.
- **method**
  whether to use a pearson or rms test
- **log**
  whether to return pvalues in log units
- **qwidth**
  the positive width of the quadrature in Z units
- **qpoints**
  the number of quadrature points
- **alt**
  whether to include the item of interest in the denominator
- **omit**
  number of items to omit or a character vector with the names of the items to omit when calculating the observed and expected sum-score tables
- **.twotier**
  whether to enable the two-tier optimization
Details

This statistic is good at finding a small number of misfitting items among a large number of well fitting items. However, be aware that misfitting items can cause other items to misfit.

Observed tables cannot be computed when data is missing. Therefore, you can optionally omit items with the greatest number of responses missing relative to the item of interest.

Pearson is slightly more powerful than RMS in most cases I examined.

Setting alt to TRUE causes the tables to match published articles. However, the default setting of FALSE probably provides slightly more power when there are less than 10 items.

The name of the test, "S", probably stands for sum-score.

References


---

**stripData**

Strip data and scores from an IFA group

**Description**

In addition, the weightColumn is reset to NULL.

**Usage**

`stripData(grp)`

**Arguments**

- **grp**
  - an IFA group

---

**sumScoreEAP**

Compute the sum-score EAP table

**Description**

Observed tables cannot be computed when data is missing. Therefore, you can optionally omit items with the greatest number of responses missing when conducting the distribution test.

**Usage**

`sumScoreEAP(grp, ..., qwidth = 6, qpoints = 49L, .twotier = TRUE)`
Arguments

- **grp**: a list with spec, param, mean, and cov
- **...**: Not used. Forces remaining arguments to be specified by name.
- **qwidth**: positive width of quadrature in Z units
- **qpoints**: number of quadrature points
- **.twotier**: whether to enable the two-tier optimization

Details

When two-tier covariance structure is detected, EAP scores are only reported for primary factors. It is possible to compute EAP scores for specific factors, but it is not clear why this would be useful because they are conditional on the specific factor sum scores. Moreover, the algorithm to compute them efficiently has not been published yet (as of Jun 2014).

Examples

```r
# see Thissen, Pommerich, Billeaud, & Williams (1995, Table 2)
spec <- list()
spec[1:3] <- rpf.grm(outcomes=4)

param <- matrix(c(1.87, .65, 1.97, 3.14,
                   2.66, .12, 1.57, 2.69,
                   1.24, .08, 2.03, 4.3), nrow=4)
# fix parameterization
param <- apply(param, 2, function(p) c(p[1], p[2:4] * -p[1]))

grp <- list(spec=spec, mean=0, cov=matrix(1,1,1), param=param)
sumScoreEAP(grp)
```

---

**sumScoreEAPTest**

Conduct the sum-score EAP distribution test

Description

Conduct the sum-score EAP distribution test

Usage

```r
sumScoreEAPTest(grp, ..., qwidth = 6, qpoints = 49L, .twotier = TRUE)
```

Arguments

- **grp**: a list with spec, param, mean, and cov
- **...**: Not used. Forces remaining arguments to be specified by name.
- **qwidth**: positive width of quadrature in Z units
- **qpoints**: number of quadrature points
- **.twotier**: whether to enable the two-tier optimization
References

Li, Z., & Cai, L. (2012, July). Summed score likelihood based indices for testing latent variable
distribution fit in Item Response Theory. Paper presented at the annual International Meeting of the
Psychometric Society, Lincoln, NE. Retrieved from http://www.cse.ucla.edu/downloads/files/SD2-
final-4.pdf

---

tabulateRows  
*Tabulate data.frame rows*

**Description**

Like `tabulate` but entire rows are the unit of tabulation. The data.frame is not sorted, but must be
sorted already.

**Usage**

```
tabulateRows(observed)
```

**Arguments**

- `observed`: a sorted data.frame holding ordered factors in every column

**See Also**

`orderCompletely`

**Examples**

```
df <- as.data.frame(matrix(c(sample.int(2, 30, replace=TRUE)), 10, 3))
df <- df[orderCompletely(df),]
tabulateRows(df)
```

---

toFactorLoading  
*Convert response function slopes to factor loadings*

**Description**

All slopes are divided by the ogive constant. Then the following transformation is applied to the
slope matrix.

**Usage**

```
toFactorLoading(slope, ogive = rpf.ogive)
```
toFactorThreshold

Arguments

- slope: a matrix with items in the columns and slopes in the rows
- ogive: the ogive constant (default rpf.ogive)

Details

\[
\text{slope} \left[ 1 + \text{rowSums}(\text{slope}^2) \right]^2
\]

Value

a factor loading matrix with items in the rows and factors in the columns

See Also

rpf.ogive

Description

Convert response function intercepts to factor thresholds

Usage

toFactorThreshold(intercept, slope, ogive = rpf.ogive)

Arguments

- intercept: a matrix with items in the columns and intercepts in the rows
- slope: a matrix with items in the columns and slopes in the rows
- ogive: the ogive constant (default rpf.ogive)

Value

a factor threshold matrix with items in the columns and factor thresholds in the rows
write.flexmirt

Write a flexMIRT PRM file

Description

Formats item parameters in the way that flexMIRT expects to read them. Use `read.flexmirt` to see what shape the groups parameter of this function should take.

Usage

```r
write.flexmirt(groups, file = NULL, fileEncoding = "")
```

Arguments

- **groups**: a list of groups each with items and latent parameters
- **file**: the destination file name
- **fileEncoding**: how to encode the text file (optional)

Details

NOTE: Support for the graded response model may not be complete.
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