

Package ‘autoRasch’

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Title Semi-Automated Rasch Analysis

Description Performs Rasch analysis (semi-)automatically, which has been shown to be comparable with the standard Rasch analysis (Feri Wijayanto et al. (2021) <[doi:10.1111/bmsp.12218](https://doi.org/10.1111/bmsp.12218)>, Feri Wijayanto et al. (2022) <[doi:10.3758/s13428-022-01947-9](https://doi.org/10.3758/s13428-022-01947-9)>, Feri Wijayanto et al. (2022) <[doi:10.1177/01466216221125178](https://doi.org/10.1177/01466216221125178)>).

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 autoRasch

autoRasch: A package for semi-automatic Rasch analysis

Description

This package helps user to do Rasch analysis (semi-)automatically which is comparable to the standard Rasch analysis using common statistics.

autoRaschOptions	<i>autoRasch Optimization Parameters Setting</i>
------------------	--

Description

Returns and updates the default settings used by the functions in **autoRasch** package.

Usage

```
autoRaschOptions(x = NULL)
```

Arguments

x	A name of single parameter setting that is wanted to be shown. NULL means returns all parameters.
---	---

Details

cd_control lists the parameters used to control the coordinate descent optimization procedure. The paramaters are:

- `init.step` Initial value of the delta parameters updating step. The default is 1.
- `scale.down` A constant value to scale down the updating step. The default is 0.5.
- `maxit.cd.higher` Maximum iteration in the higher level coordinate descent. The default is 500.
- `maxit.cd.lower` Maximum iteration for every coordinate optimization in the lower level coordinate descent. The default is 500.
- `abs.tol` The convergence tolerance. The algorithm stops if it is unable to reduce the negative log likelihood value by the given tolerance. The default is $1e-12$.
- `max.dif.par` The convergence tolerance. The algorithm stops if it is unable to update all of the parameters' value by the given tolerance. The default is $1e-8$.

Value

<code>fixed_par</code>	A vector of names of the parameter types that are set to be fixed. It means that these parameters are not going to be estimated.
<code>fixed_theta</code>	A vector of theta values when theta are listed in the <code>fixed_par</code> . If it is not set, it will be set to zero.
<code>fixed_beta</code>	A vector of beta values when beta are listed in the <code>fixed_par</code> . If it is not set, it will be set to zero.
<code>fixed_gamma</code>	A vector of gamma (natural logarithm of discrimination parameters, $\alpha = \exp(\gamma)$) values when gamma are listed in the <code>fixed_par</code> . If it is not set, it will be set to zero.
<code>fixed_delta</code>	A vector of delta values when delta are listed in the <code>fixed_par</code> . If it is not set, it will be set to zero.

isPenalized_theta	It is a logical parameter whether, in the estimation procedure, theta is penalized or not.
isPenalized_gamma	It is a logical parameter whether, in the estimation procedure, gamma is penalized or not.
isPenalized_delta	It is a logical parameter whether, in the estimation procedure, delta is penalized or not.
groups_map	A matrix $n \times f$ to map the subject into DIF groups, where n is number of subjects and f is number of focal groups.
optz_method	Options of the optimization method used. The default is <code>optim</code> which implies on applying the PJMLE which is implemented using <code>optim()</code> . When it is set to <code>mixed</code> means that it applies the coordinate descent.
optim_control	A list of setting parameters of the <code>optim()</code> . For complete settings can be seen in <code>stats::optim()</code> .
lambda_theta	The regularization parameter to the theta. The default value is 0.05
lambda_in	The regularization parameter to the gamma in the included itemset. The default value is 50.
lambda_out	The regularization parameter to the gamma in the excluded itemset. The default value is 1.
lambda_delta	The regularization parameter to the delta. The default value is 10.
randomized	A logical parameter whether the initial values of the estimated parameters are randomized or not.
random.init.th	A threshold value to limit the range of the initial values. The default value is $1e-2$, means that the initial values range between $[-0.01, 0.01]$
isHessian	A logical parameter whether, in the estimation procedure, need to return the Hessian matrix or not. The default value is <code>TRUE</code> , which means the Hessian matrix will be computed.
cd_control	A list of coordinate descent optimization setting.
mode	An option setting to use "DIF" or "DSF" mode.
isTraced	A logical value whether the progress need to be tracked or not.

Examples

```
### To show the default values
autoRaschOptions()
autoRaschOptions(x = "isHessian")

### To change the default values
adj_setting <- autoRaschOptions()
adj_setting$isHessian <- TRUE
pcm_res <- pcm(shortDIF, setting = adj_setting)
```

check.unidim	<i>Unidimensionality Check</i>
--------------	--------------------------------

Description

This function checks the unidimensionality status using the confirmatory factor analysis.

Usage

```
check.unidim(x, is.polychor = TRUE)
```

Arguments

x	The dataset of responses.
is.polychor	A boolean parameter to set whether the dataset is categorical or not.

Value

A list of the CFA output and the some of the goodness-of-fit indices (i.e., cfi, tli, rmsea, and srmr)

checkRel	<i>Compute Reliability and Standard Error</i>
----------	---

Description

This function computes the reliability index, separation and the standard error of the models estimation.

Usage

```
checkRel(obj)

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

Arguments

obj	Object that resulted from any models estimation, e.g., pcm, gpcm, pcmdif, and gpcmdif.
object	The object of class 'seprel'.
...	Further arguments to be passed.

Details

Person reliability index

Value

A list of two objects, the reliability and the standard error.

reliability

- PRI Person reliability index.
- PSR Person separation reliability.
- IRI Item reliability index.
- ISR Item separation reliability.

stdError

- var_err_pers A matrix of variance error of the estimation.
- std_err_pers A matrix of standard error of the estimation.
- rmsse_pers Root mean square of the standard error per person.
- var_err_item A matrix of variance error of the estimation.
- std_err_item A matrix of standard error of the estimation.
- rmsse_item Root mean square of the standard error per person.
- hessian_theta Hessian matrix of theta parameter.
- hessian_beta Hessian matrix of beta parameter.

Examples

```
pcmObject <- pcm(shortDIF)
rel <- checkRel(pcmObject)
summary(rel)
```

compute_score	<i>Compute the In-plus-out-of-questionnaire log likelihood (with DIF) (IPOQ-LL(-DIF))</i>
---------------	---

Description

compute_score computes the the IPOQ-LL/IPOQ-LL-DIF score of an instrument (included set) of the given initial survey. While compute_scores computes the IPOQ-LL/IPOQ-LL-DIF score of many (more than one) instruments (included sets) of the given initial survey simultaneously.

Usage

```

compute_score(
  X,
  incl_set,
  type = c("ipoqll", "ipoqlldif"),
  groups_map = c(),
  init_par_iq = c(),
  init_par_oq = c(),
  setting_par_iq = c(),
  setting_par_oq = c(),
  method = c("fast", "novel")
)

compute_scores(
  X,
  incl_sets,
  type = c("ipoqll", "ipoqlldif"),
  step_direct = c("fixed", "forward", "backward"),
  groups_map = c(),
  init_par_iq = c(),
  init_par_oq = c(),
  setting_par_iq = c(),
  setting_par_oq = c(),
  cores = NULL,
  method = c("fast", "novel"),
  timeLimit = 3600
)

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

```

Arguments

<code>X</code>	A matrix or data.frame of the observed responses (ordinal or binary response).
<code>incl_set</code>	A vector of the items (columns) number in the data.frame <code>X</code> that are included in the included set.
<code>type</code>	The type of the score. <code>ipoqll</code> if we ignore the presence of the DIF and <code>ipoqlldif</code> if we want to consider the DIF effect.
<code>groups_map</code>	Matrix to map the respondents to the DIF groups.
<code>init_par_iq</code>	Initial values of the parameters in the included set before the estimation begin.
<code>init_par_oq</code>	Initial values of the parameters in the excluded set before the estimation begin.
<code>setting_par_iq</code>	The coordinate descent optimisation setting of the included set. See autoRasch::autoRaschOptions() <code>cd_control</code> parameter.
<code>setting_par_oq</code>	The coordinate descent optimisation setting of the excluded set. See autoRasch::autoRaschOptions() <code>cd_control</code> parameter.

method	The implementation option of log likelihood function. fast using a c++ implementation and novel using an R implementation.
incl_sets	A matrix as a results of a rbind of incl_set.
step_direct	How will you compute the criterion score. fixed for the given itemset, forward computes all the scores of the possible combination of items if an item is added to the given set, backward computes all the scores of the possible combination of items if an item is removed to the given set.
cores	Number of cores that is used in the paralellization.
timeLimit	To limit the execution time of scores' computation.
object	The object from the class score. The result of the score computation.
...	further argument passed or from other method.

Value

compute_score will return a vector which contains in-questionnaire log likelihood (IQ-LL(-DIF)), out-of-questionnaire log likelihood(OQ-LL(-DIF)), IPOQ-LL(-DIF), included set's items' number in the given initial survey, the estimated theta parameters, the estimated items' parameters in the included set, and the estimated items' parameters in the excluded set, sequentially.

compute_scores will return a matrix as a result of the rbind operation of the compute_score's result.

Examples

```
ipoqll_score <- compute_score(shortDIF,incl_set = c(1:3),type = "ipoqll")
summary(ipoqll_score)

## Not run:
ipoqll_scores <- compute_scores(shortDIF,incl_set = rbind(c(1:3),c(2:4)),
                                type = "ipoqll", cores = 2)
View(ipoqll_scores)

## End(Not run)
```

correl02_multidim	<i>Multidimensional polytomous data set with 0.2 correlation</i>
-------------------	--

Description

Multidimensional polytomous data set with 0.2 correlation

Usage

```
data(correl02_multidim)
```

Format

An object of class data.frame with 301 rows and 12 columns.

correl03_multidim	<i>Multidimensional polytomous data set with 0.3 correlation</i>
-------------------	--

Description

Multidimensional polytomous data set with 0.3 correlation

Usage

```
data(correl03_multidim)
```

Format

An object of class `data.frame` with 301 rows and 12 columns.

correl04_multidim	<i>Multidimensional polytomous data set with 0.4 Correlation</i>
-------------------	--

Description

Multidimensional polytomous data set with 0.4 Correlation

Usage

```
data(correl04_multidim)
```

Format

An object of class `data.frame` with 301 rows and 12 columns.

correl05_multidim	<i>Multidimensional polytomous data set with 0.5 Correlation</i>
-------------------	--

Description

Multidimensional polytomous data set with 0.5 Correlation

Usage

```
data(correl05_multidim)
```

Format

An object of class `data.frame` with 301 rows and 12 columns.

correl06_multidim	<i>Multidimensional polytomous data set with 0.6 Correlation</i>
-------------------	--

Description

Multidimensional polytomous data set with 0.6 Correlation

Usage

```
data(correl06_multidim)
```

Format

An object of class `data.frame` with 301 rows and 12 columns.

createGroup	<i>Create Mapping Matrix of DIF Groups</i>
-------------	--

Description

This function automatically create a mapping matrix based on the existing DIF inducing covariates.

Usage

```
createGroup(backInfo, idxUsed = NULL, contMethod = c("mean", "median"))
```

Arguments

backInfo	A matrix of person background information (e.g., gender, country, age, etc);
idxUsed	The column number of backInfo that is used for creating the mapping matrix.
contMethod	The method of how to handle a continuous variable (e.g., mean, median). This parameter is passing a function used to split the variable into binary. The default is mean.

Value

A binary matrix that maps respondents to the groups that the respondents belongs to.

dataset

*The Simulated Dataset***Description**

The artificial datasets used for simulation on various cases. The datasets consist of:

- inhomogenous_rasch_dataset
- inhomogenous_dataset
- uncorrel_rasch_multidim
- uncorrel_multidim
- correl02_multidim
- correl03_multidim
- correl04_multidim
- correl05_multidim
- correl06_multidim
- withinItem_multidim
- testlets_dataset

Details

inhomogenous_rasch_dataset is an artificial dataset of dichotomous responses which simulates three subscales with different predictability level (discrimination parameters). This dataset is generated by

```
inhomogenous_rasch_dataset <- generate_data(responseType = "discriminate", ncat = 2,
alpha = c(0.04, 0.045, 0.05, 0.055, 0.06, 0.065, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45, 2.6, 2.65, 2.7, 2.75, 2.8, 2.85, 2.9
```

inhomogenous_dataset is an artificial dataset which simulates three subscales with different predictability level (discrimination parameters). This dataset is generated by

```
inhomogenous_dataset <- generate_data(responseType = "discriminate", alpha = c(0.04, 0.045, 0.05, 0.055, 0.
```

uncorrel_rasch_multidim is an artificial dataset of dichotomous responses which simulates three uncorrelated subscales from different dimensions. This dataset is generated by

```
uncorrel_rasch_multidim <- generate_data(responseType = "multidim.nocorrel", ncat =
2)
```

uncorrel_multidim is an artificial dataset which simulates three uncorrelated subscales from different dimensions. This dataset is generated by

```
uncorrel_multidim <- generate_data(responseType = "multidim.nocorrel")
```

correl02_multidim is an artificial dataset which simulates two subscales from different dimensions that having correlation of 0.2. This dataset is generated by

```
correl02_multidim <- generate_data(responseType = "multidim.withcorrel", corLevel =
0.2)
```

Similarly, `correl03_multidim`, `correl04_multidim`, `correl05_multidim`, and `correl06_multidim` are artificial datasets which consist of two correlated subscales with correlation of 0.3, 0.4, 0.5, and 0.6, respectively.

`withinItem_multidim` is an artificial dataset which consist of three subscales (dimensions) with some of items relate to more than one subscale (dimension). This dataset is generated by

```
withinItem_multidim <- generate_data(responseType = "multidim.within", ndim = 3, dim.members
= list(c(1:6,13),c(3,7:12),c(5,13:18)))
```

`testlets_dataset` is an artificial dataset which consist of two subscales with some of items relate to more than one subscale (dimension). This dataset is generated by

```
testlets_dataset <- generate_data(responseType = "testlets", ndim = 2, sdlambda = c(0,4))
```

See Also

[pcm](#), [pcm_dif](#), [gpcm](#), [gpcm_dif](#)

Examples

```
#res <- pcm(poly_inh_dset)
#res
#summary(res)

#pcmdif_res <- pcm_dif(polydif_inh_dset, groups_map = c(rep(1,245),rep(0,245)))
#fit_res <- fitStats(pcmdif_res)
#summary(fit_res)
#plot(fit_res, plotx = "gamma", ploty = "outfit")
```

dicho_inh_dset

Inhomogenous Dichotomous Data Set

Description

Data set with binary type responses containing three subsets with different discrimination values.

Usage

```
data(dicho_inh_dset)
```

Format

An object of class `data.frame` with 301 rows and 18 columns.

dicho_md_dset	<i>Uncorrelated Multidimensional Dichotomous Data Set</i>
---------------	---

Description

Data set with binary type responses containing three subsets which represent different uncorrelated dimensions.

Usage

```
data(dicho_md_dset)
```

Format

An object of class `data.frame` with 301 rows and 18 columns.

fitStats	<i>Fit statistics</i>
----------	-----------------------

Description

The goodness-of-fit statistics of Rasch analysis for items and persons. It consists of Outfit (Unweighted) Mean Square, Infit (Weighted) Mean Square, Outfit ZSTD (Standardized Unweighted Mean Square), and Outfit ZSTD (Standardized Weighted Mean Square)

Usage

```
fitStats(obj, isAlpha = TRUE)

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

itemfit(objFit)

personfit(objFit)

plot_fitStats(objFit, toPlot = c("alpha", "infit"), useName = FALSE, ...)
```

Arguments

<code>obj</code>	The object of class 'pcm' or 'pcmdif'.
<code>isAlpha</code>	Boolean value that indicates whether the discrimination parameters is needed to be estimated or not. The discrimination parameters are estimated using the corresponding models (GPCM or GPCM-DIF).
<code>object</code>	The object of class 'fit'.

...	Further arguments to be passed.
objFit	The object of class 'fit'.
toPlot	An array with length two $c(x, y)$, to choose what to plot. There are five options to plot, which are alpha, outfit, infit, outfitz, and infitz
useName	A logical statement whether the name of the variable are going to be used in the plot instead of the variable order.

Value

`fitStats()` will return a **list** which contains:

alpha A vector of estimated discrimination parameters for each items.

i.fit Item fit statistics.

- *i.outfitMSQ* A vector of Outfit mean square values for each items.
- *i.infitMSQ* A vector of Infit mean square values for each items.
- *i.outfitZ* A vector of OutfitZ values for each items.
- *i.infitZ* A vector of InfitZ values for each items.

p.fit Person fit statistics.

- *p.outfitMSQ* A vector of Outfit mean square values for each persons.
- *p.infitMSQ* A vector of Infit mean square values for each persons.
- *p.outfitZ* A vector of OutfitZ values for each persons.
- *p.infitZ* A vector of InfitZ values for each persons.

traceMat Some computed matrices in the process. Only if `isTraced = TRUE`

- *emat* The expected values matrix.
- *vmat* The variance matrix.
- *cmat* The curtosis matrix.
- *std.res* The standardized residual.

generate_data

Generate the artificial dataset

Description

This function generates simulated datasets with different attributes

Usage

```
generate_data(
  responseType = "multidim.nocorrel",
  theta = c(-3, 3),
  sdtheta = 6,
  ntheta = 301,
  beta = c(-2.5, 2.5),
  sdbeta = 4,
  nitem = 6,
  alpha = c(1),
  sdlambda = 1,
  ncat = 5,
  thGap = 0.8,
  ndim = 3,
  randtype = "uniform",
  corLevel = 0,
  dim.members = c(),
  seed = NULL
)
```

Arguments

responseType	The type of the dataset. The types include multidim.nocorrel, multidim.withcorrel, discriminate, multidim.within, and testlets.
theta	A vector of the ability parameters range value, c(min.theta,max.theta). It applies when the randtype = "uniform".
sdtheta	Standard deviation which is used to generate theta values using <code>stats::rnorm()</code> with n = ntheta, mean = 0, and sd = sdtheta.It applies when the randtype = "normal".
ntheta	The number of the observations.
beta	A vector of the item difficulty parameters range value, c(min.beta,max.beta). It applies when the randtype = "uniform".
sdbeta	Standard deviation which is used to generate item location values using <code>stats::rnorm()</code> with n = nitem, mean = 0, and sd = sdbeta.It applies when the randtype = "normal".
nitem	The number of the items in each subgroup.
alpha	A vector of the discrimination parameters apply to each items.
sdlambda	A vector of the standard deviation to simulate the testlet (local dependency) effect. The effect is added using <code>stats::rnorm()</code> with n = ntheta, mean = 0, and sd = sdlambda
ncat	The number of the response categories
thGap	The difference between adjacent threshold.
ndim	The number of subgroups (dimensions/testlets) created.
randtype	The randomize type. This includes uniform and normal.
corLevel	The correlation between the two dimensions.
dim.members	The list of item members in each dimension.
seed	Integer seed for reproducibility.

Value

The generated dataset as a `data.frame`.

Examples

```
# 1. Multidimensional Polytomous Dataset with 0.2 Correlation
# Generate multidimensional dataset which having correlation of 0.2 between the dimensions
correl02_multidim <- generate_data(
  responseType = "multidim.withcorrel", corLevel = 0.2, seed = 2021
)

# 2. Within-item Multidimensional Polytomous Dataset
# Generate multidimensional dataset with some items relate to more than one
# dimension.
withinItem_multidim <- generate_data(
  responseType = "multidim.within", ndim = 3,
  dim.members = list(c(1:6,13),c(3,7:12),c(5,13:18)), seed = 2021
)

# 3. Multi-testlets Polytomous Dataset
# Generate dataset which consist of two bundle items with different level of
# local dependency effect.
testlets_dataset <- generate_data(
  responseType = "testlets", ndim = 2, sdlambda = c(0,4), seed = 2021
)

# 4a. Inhomogenous Dichotomous Dataset
# Generate dataset with binary type responses containing three subsets
# with different discrimination values.

dicho_inh_dset <- generate_data(
  responseType = "discriminate", ncat = 2, seed = 2021,
  alpha = c(0.04,0.045,0.05,0.055,0.06,0.065,0.2,0.25,0.3,0.35,0.4,0.45,
    2.6,2.65,2.7,2.75,2.8,2.85)
)

# 4b. Inhomogenous Polytomous Dataset
# Generate dataset with polytomous responses (five categories) containing
# three subsets with different discrimination values.

poly_inh_dset <- generate_data(
  responseType = "discriminate", ncat = 5, seed = 2021,
  alpha = c(0.04,0.045,0.05,0.055,0.06,0.065,0.2,0.25,0.3,0.35,0.4,0.45,
    2.6,2.65,2.7,2.75,2.8,2.85)
)

# 4c. Shorter Inhomogenous Polytomous Dataset
short_poly_data <- generate_data(
  alpha = c(0.02,0.5,2), nitem = 3, ndim = 3, ncat = 5,
  theta = c(-6,6), beta = c(-4,4), ntheta = 151, seed = 2021
)
```



```

# 4d. Short Dataset containing DIF items
# Generate dataset with polytomous responses (five categories) containing
# three subsets with different discrimination values and two DIF-items.
seed <- c(54748,96765)
difset_short1 <- generate_data(responseType = "discriminate", ncat = 3,
                              ntheta = 50, nitem = 3, ndim = 1,
                              seed = seed[1], alpha = c(2))
difset_short2 <- generate_data(responseType = "discriminate", ncat = 3,
                              ntheta = 50, nitem = 2, ndim = 1,
                              seed = seed[2], alpha = c(0.8),
                              beta = c(-2.5,2.5))
shortDIF <- cbind(rbind(difset_short1,difset_short1),
                  c(difset_short2[,1],difset_short2[,2]))

# 5a. Uncorrelated Multidimensional Dichotomous Dataset
# Generate dataset with binary type responses containing three subsets which
# represent different uncorrelated dimensions.
dicho_md_dset <- generate_data(
  responseType = "multidim.nocorrel", ncat = 2, seed = 2021
)

# 5b. Uncorrelated Multidimensional Polytomous Dataset
# Generate dataset with polytomous responses (five categories) containing
# three subsets which represent different uncorrelated dimensions.
poly_md_dset <- generate_data(
  responseType = "multidim.nocorrel", ncat = 5, seed = 2021
)

```

generic_model

Estimation of the generic form of the models

Description

This function computes the parameter estimates of the generic form of the models by using penalized JML estimation. It allows users to adjust the default settings of the estimation.

Usage

```
generic_model(X, init_par = c(), setting = c())
```

Arguments

X	Input dataset as matrix or data frame with ordinal responses (starting from 0); rows represent individuals, column represent items.
init_par	Initial values of the estimated parameters.
setting	Parameter settings which are listed in autoRaschOptions() .

Details

In the discrimination parameters estimation, instead of estimating the discrimination parameters, we are estimating the natural logarithm of the parameters to avoid negative values, $\alpha = \exp(\gamma)$.

Value

X	The dataset that is used for estimation.
name	The name of each items in the dataset.
mt_vek	A vector of the highest response category as many as the number of items.
loglik	The log likelihood of the estimation.
objtype	Type of the model that is used.
delta	A vector of the DIF parameters of each items on each groups.
gamma	A vector of the natural logarithm of discrimination parameters of each items.
beta	A vector of the difficulty parameter of each items' categories (thresholds).
theta	A vector of the ability parameters of each individuals.

gpcm

Estimation of The Generalized Partial Credit Model

Description

This function computes the parameter estimates of a generalized partial credit model for polytomous responses by using penalized JML estimation. Inputting a dichotomous responses to this model, will automatically transforms the GPCM to the 2-PL model.

Usage

```
gpcm(X, init_par = c(), setting = c(), method = c("fast", "novel"))

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

## S3 method for class 'gpcm'
print(x, ...)
```

Arguments

X	Input dataset as matrix or data frame with ordinal responses (starting from 0); rows represent individuals, columns represent items.
init_par	a vector of initial values of the estimated parameters.
setting	a list of the optimization control setting parameters. See autoRaschOptions() .
method	The implementation option of log likelihood function. fast using a c++ implementation and novel using an R implementation.
object	The object of class 'gpcm'.
...	Further arguments to be passed.
x	The object of class 'gpcm'.

Details

In the discrimination parameters estimation, instead of estimating the discrimination parameters (α), we are estimating its natural logarithm to avoid negative values, $\alpha = \exp(\gamma)$.

Value

X	The dataset that is used for estimation.
mt_vek	A vector of the highest response given to items.
itemName	The vector of names of items (columns) in the dataset.
loglik	The log likelihood of the estimation.
hessian	The hessian matrix. Only when the isHessian = TRUE.
gamma	A vector of the natural logarithm of discrimination parameters of each items.
beta	A vector of the difficulty parameter of each items' categories (thresholds).
theta	A vector of the ability parameters of each individuals.

References

Muraki, E. (1992). A generalized partial credit model: Application of an EM algorithm. *Applied Psychological Measurement*, 16(2). <https://doi.org/10.1177/014662169201600206>

See Also

[pcm](#), [gpcm](#)

Examples

```
gpcm_res <- gpcm(short_poly_data)
summary(gpcm_res, par = "alpha")
```

gpcm_dif

Estimation of The Generalized Partial Credit Model with DIF

Description

This function computes the parameter estimates of a generalized partial credit model with DIF for polytomous responses by using penalized JML estimation.

Usage

```

gpcm_dif(
  X,
  init_par = c(),
  groups_map = c(),
  setting = c(),
  method = c("fast", "novel")
)

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

## S3 method for class 'gpcmdif'
print(x, ...)

```

Arguments

<code>X</code>	A matrix or data frame as an input with ordinal responses (starting from 0); rows represent individuals, columns represent items.
<code>init_par</code>	a vector of initial values of the estimated parameters.
<code>groups_map</code>	Binary matrix. Respondents membership to DIF groups; rows represent individuals, column represent group partitions.
<code>setting</code>	a list of the optimization control setting parameters. See autoRaschOptions()
<code>method</code>	The implementation option of log likelihood function. <code>fast</code> using a c++ implementation and <code>novel</code> using an R implementation.
<code>object</code>	The object of class 'gpcmdif'.
<code>...</code>	Further arguments to be passed.
<code>x</code>	The object of class 'gpcmdif'.

Details

In the discrimination parameters estimation, instead of estimating the discrimination parameters, we are estimating the natural logarithm of the parameters to avoid negative values, $\alpha = \exp(\gamma)$.

Value

<code>X</code>	The dataset that is used for estimation.
<code>mt_vek</code>	A vector of the highest responses given to items.
<code>itemName</code>	The vector of names of items (columns) in the dataset.
<code>loglik</code>	The log likelihood of the estimation.
<code>hessian</code>	The hessian matrix. Only when the <code>isHessian = TRUE</code> .
<code>delta</code>	A vector of the DIF parameters of each items on each groups.
<code>gamma</code>	A vector of the natural logarithm of discrimination parameters of each items.
<code>beta</code>	A vector of the difficulty parameter of each items' categories (thresholds).
<code>theta</code>	A vector of the ability parameters of each individuals.

See Also

[pcm](#), [pcm_dif](#), [gpcm](#), [gpcm_dif](#)

Examples

```
## Not run:
gpcmdif_res <- gpcm_dif(shortDIF, groups_map = c(rep(1,50),rep(0,50)))
summary(gpcmdif_res, par="delta")

## End(Not run)
```

pcm

Estimation of The Partial Credit Model (PCM)

Description

This function computes the parameter estimates of a partial credit model for dichotomous and polytomous responses by using penalized joint maximum likelihood estimation (PJMLE). Inputting a dichotomous responses to this model, will automatically transforms the PCM to the Rasch model.

`fitStats` compute the fit statistics (e.g., Outfit and Infit) of the PCM model estimation (items and persons).

Usage

```
pcm(X, init_par = c(), setting = c(), method = c("fast", "novel"))

## S3 method for class 'pcm'
fitStats(obj, isAlpha = TRUE)

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

## S3 method for class 'pcm'
print(x, ...)
```

Arguments

<code>X</code>	Input dataset as matrix or data frame with ordinal responses (starting from 0); rows represent individuals, columns represent items.
<code>init_par</code>	a vector of initial values of the estimated parameters.
<code>setting</code>	a list of the optimization control setting parameters. See autoRaschOptions() .
<code>method</code>	The implementation option of log likelihood function. <code>fast</code> using a c++ implementation and <code>novel</code> using an R implementation.
<code>obj</code>	The object of class 'pcm'.

isAlpha	Boolean value that indicates whether the discrimination parameters is needed to be estimated or not. The discrimination parameters are estimated using the corresponding models (GPCM or GPCM-DIF).
object	The object of class 'pcm'.
...	Further arguments to be passed.
x	The object of class 'pcm'.

Value

`pcm()` will return a **list** which contains:

X	The dataset that is used for estimation.
mt_vek	A vector of the highest response given to items.
itemName	The vector of names of items (columns) in the dataset.
loglik	The log likelihood of the estimation.
hessian	The hessian matrix. Only when the <code>isHessian = TRUE</code> .
beta	A vector of the difficulty parameter of each categories of items (thresholds).
theta	A vector of the ability parameters of each individuals.

`fitStats()` will return a **list** which contains:

alpha	A vector of estimated discrimination parameters for each items.
-------	---

i.fit Item fit statistics.

- *i.outfitMSQ* A vector of Outfit mean square values for each items.
- *i.infitMSQ* A vector of Infit mean square values for each items.
- *i.outfitZ* A vector of OutfitZ values for each items.
- *i.infitZ* A vector of InfitZ values for each items.

p.fit Person fit statistics.

- *p.outfitMSQ* A vector of Outfit mean square values for each persons.
- *p.infitMSQ* A vector of Infit mean square values for each persons.
- *p.outfitZ* A vector of OutfitZ values for each persons.
- *p.infitZ* A vector of InfitZ values for each persons.

traceMat Some computed matrices in the process.

- *emat* The expected values matrix.
- *vmat* The variance matrix.
- *cmat* The curtosis matrix.
- *std.res* The standardized residual.

References

- Wright, B. D., & Masters, G. N. (1982). Rating Scale Analysis. Chicago: MESA Press.
- Masters, G. N. (1982). A rasch model for partial credit scoring. *Psychometrika*, 47(2), 149–174. <https://doi.org/10.1007/BF02296272>.
- Wright, B. D., & Masters, G. N. (1990). Computation of outfit and infit statistics. *Rasch Measurement Transactions*, 3(4), 84–85. Retrieved from <https://www.rasch.org/rmt/rmt34e.htm>

See Also

[pcm](#), [gpcm](#)

Examples

```
pcm_res <- pcm(shortDIF)
summary(pcm_res)

#To summarize only for beta parameters
summary(pcm_res, par="beta")
fit_res <- fitStats(pcm_res)
itemfit(fit_res)
personfit(fit_res)
plot_fitStats(fit_res, toPlot = c("alpha", "outfit"), useName = TRUE)
```

pcm_dif

Estimation of The Partial Credit Model with DIF

Description

This function computes the parameter estimates of a partial credit model with DIF for dichotomous and polytomous responses by implementing the coordinate descent.

`fitStats` compute the fit statistics (i.e., Outfit and Infit) of the PCM-DIF model estimation (items and persons).

Usage

```
pcm_dif(
  X,
  init_par = c(),
  groups_map = c(),
  setting = c(),
  method = c("fast", "novel")
)

## S3 method for class 'pcmdif'
fitStats(obj, isAlpha = TRUE)
```

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

## S3 method for class 'pcmdif'
print(x, ...)
```

Arguments

X	A matrix or data frame as an input with ordinal responses (starting from 0); rows represent individuals, columns represent items.
init_par	a vector of initial values of the estimated parameters.
groups_map	Binary matrix. Respondents membership to DIF groups; rows represent individuals, column represent group partitions.
setting	a list of the optimization control setting parameters. See autoRaschOptions()
method	The implementation option of log likelihood function. fast using a c++ implementation and novel using an R implementation.
obj	The object of class 'pcmdif'.
isAlpha	Boolean value that indicates whether the discrimination parameters is needed to be estimated or not. The discrimination parameters are estimated using the corresponding models (GPCM or GPCM-DIF).
object	The object of class 'pcmdif'.
...	Further arguments to be passed.
x	The object of class 'pcmdif'.

Value

`pcm_dif()` will return a [list](#) which contains:

X	The dataset that is used for estimation.
mt_vek	A vector of the highest response given to items.
itemName	The vector of names of items (columns) in the dataset.
loglik	The log likelihood of the estimation.
hessian	The hessian matrix. Only when the <code>isHessian = TRUE</code> .
beta	A vector of the difficulty parameter of each categories of items (thresholds).
theta	A vector of the ability parameters of each individuals.

`fitStats()` will return a [list](#) which contains:

alpha	A vector of estimated discrimination parameters for each items.
-------	---

i.fit Item fit statistics.

- `i.outfitMSQ` A vector of Outfit mean square values for each items.
- `i.infitMSQ` A vector of Infit mean square values for each items.

- `i.outfitZ` A vector of OutfitZ values for each items.
- `i.infitZ` A vector of InfitZ values for each items.

`p.fit` Person fit statistics.

- `p.outfitMSQ` A vector of Outfit mean square values for each persons.
- `p.infitMSQ` A vector of Infit mean square values for each persons.
- `p.outfitZ` A vector of OutfitZ values for each persons.
- `p.infitZ` A vector of InfitZ values for each persons.

`traceMat` Some computed matrices in the process.

- `emat` The expected values matrix.
- `vmat` The variance matrix.
- `cmat` The curtosis matrix.
- `std.res` The standardized residual.

See Also

[pcm](#), [pcm_dif](#), [gpcm](#), [gpcm_dif](#)

Examples

```
## Not run:
pcmdif_res <- pcm_dif(shortDIF, groups_map = c(rep(1,50),rep(0,50)))
fit_res <- fitStats(pcmdif_res)
itemfit(fit_res)
personfit(fit_res)
plot_fitStats(fit_res, toPlot = c("alpha","outfit"), useName = FALSE)

## End(Not run)
```

plot_EVC

Plot The Expected Value Curves

Description

This function plots the curve(s) of the estimated ability parameters against its expected responses.

Usage

```
plot_EVC(
  obj = c(),
  itemno = 5,
  xlab = NULL,
  ylab = NULL,
  xlim = c(-10, 10),
  col = c("green4", "darkorange2", "red2"),
  lty = c(1, 1, 1),
  ...
)
```

Arguments

obj	The object of class 'pcm'.
itemno	A number of the item that is wanted to be plot.
xlab	a title for the x axis.
ylab	a title for the y axis.
xlim	the x limits (x1, x2) of the plot. Note that $x1 > x2$ is allowed and leads to a 'reversed axis'. The default value, NULL, indicates that the range of the finite values to be plotted should be used; see plot.default()
col	a vector of plotting colors
lty	a vector of line types.
...	Further arguments to be passed.

Value

There are no values to return. Instead, it plots expected values from the model.

Examples

```
res <- pcm(short_poly_data)
plot_EVC(res, itemno = 4)
```

plot_ICC

Plot The Item Characteristic Curves

Description

This function plots the curve(s) of the estimated ability parameters against the probabilities of responses.

Usage

```
plot_ICC(
  obj,
  itemno = 5,
  xlab = NULL,
  ylab = NULL,
  xlim = c(-10, 10),
  col = c("green4", "darkorange2", "red2"),
  lty = c(1, 1, 1),
  main = NULL,
  ...
)
```

Arguments

obj	The object of class 'pcm'.
itemno	A number of the item that is wanted to be plot.
xlab	a title for the x axis.
ylab	a title for the y axis.
xlim	the x limits (x1, x2) of the plot. Note that $x1 > x2$ is allowed and leads to a 'reversed axis'. The default value, NULL, indicates that the range of the finite values to be plotted should be used; see plot.default()
col	a vector of plotting colors
lty	a vector of line types.
main	String. Plot title.
...	Further arguments to be passed.

Value

There are no values to return. Instead, it plots the curve of item characteristics from the model.

Examples

```
res <- pcm(short_poly_data)
plot_ICC(res, itemno = 4)
```

plot_PImap

Plot The Person-Item Map

Description

This function maps the distribution of the persons' abilities and the items difficulties along the latent continuum.

Usage

```
plot_PImap(
  obj,
  main = NULL,
  xlab = NULL,
  cex = NULL,
  cex.lab = NULL,
  cex.axis = NULL,
  cex.main = NULL,
  lwd = NULL,
  v = NULL,
  th_dif = 1e-05
)
```

Arguments

obj	The object of class 'pcm'.
main	main title of the plot; see plot.default() .
xlab	Label for the x-axis; see plot.default() .
cex	A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default; see par() .
cex.lab	The magnification to be used for x and y labels relative to the current setting of cex; see par() .
cex.axis	The magnification to be used for axis annotation relative to the current setting of cex; see par() .
cex.main	The magnification to be used for main titles relative to the current setting of cex; see par() .
lwd	The line width, a positive number, defaulting to 1; see par() .
v	Variable names used
th_dif	The threshold at which a DIF effect is still considered a DIF.

Value

There are no values to return. Instead, it shows a graphical map of the estimated ability and the estimated difficulty on the same scale.

Examples

```
## Not run:
groupsMap <- matrix(c(rep(1,50),rep(0,50)),ncol = 1, dimnames = list(c(1:100),c("V1")))
pcmdif_res <- pcm_dif(shortDIF, groups_map = groupsMap)
plot_PImap(pcmdif_res)

## End(Not run)
```

polydif_inh_dset	<i>The Inhomogenous Polytomous Dataset containing DIF items</i>
------------------	---

Description

The artificial data set of a polytomous responses (five categories) which contains three subsets with different discrimination values and two DIF-items.

Usage

```
data(polydif_inh_dset)
```

Format

An object of class `data.frame` with 490 rows and 20 columns.

poly_inh_dset	<i>The Inhomogenous Polytomous Dataset</i>
---------------	--

Description

The artificial dataset of a polytomous responses (five categories) which contains three subsets with different discrimination values. To reproduce this dataset:

```
poly_inh_dset <- generate_data(responseType = "discriminate", ncat = 5, alpha = c(0.04, 0.045, 0.05, 0.055,
```

will lead to similar but not the same dataset, due to the randomization.

Usage

```
data(poly_inh_dset)
```

Format

An object of class `data.frame` with 301 rows and 18 columns.

poly_md_dset	<i>Uncorrelated Multidimensional Polytomous Data Set</i>
--------------	--

Description

Data set with polytomous responses (five categories) containing three subsets which represent different uncorrelated dimensions.

Usage

```
data(poly_md_dset)
```

Format

An object of class `data.frame` with 301 rows and 18 columns.

residCor	<i>Residual Correlation</i>
----------	-----------------------------

Description

Compute the correlation of the standardized residual to check the local dependency status

Usage

```
residCor(objFit)

corResid(objFit)

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

Arguments

<code>objFit</code>	object of class "fit", the output of <code>fitStats()</code> .
<code>object</code>	The object of class 'ld'.
<code>...</code>	Further arguments to be passed.

Value

<code>ld_correl</code>	Correlation matrix of the standradized residual.
<code>ld_mean</code>	The mean of the correlation.
<code>ld_lowertri</code>	The lower triangle of the correlation matrix.

shortDIF

A Shorter Polytomous Dataset with DIF

Description

The artificial dataset of a polytomous responses (three categories) which contains three non-DIF items and a DIF item.

Usage

```
data(shortDIF)
```

Format

An object of class `data.frame` with 100 rows and 4 columns.

short_poly_data

A Shorter Inhomogenous Polytomous Dataset

Description

The artificial dataset of a polytomous responses (three categories) which contains three subsets with different discrimination values. To reproduce this dataset:

```
short_poly_data <- generate_data(alpha = c(0.02, 0.5, 2), nitem = 3, ndim = 3, ncat = 5, theta = c(-6, 6), beta = c(-4, 4), ntheta = 151)
```

will lead to similar but not the same dataset, due to the randomization.

Usage

```
data(short_poly_data)
```

Format

An object of class `data.frame` with 151 rows and 9 columns.

stepwise_search	<i>Stepwise Selection Search</i>
-----------------	----------------------------------

Description

To search itemset that give maximum value of the criterion

Usage

```
stepwise_search(
  X,
  criterion = c("ipoqll", "ipoqlldif"),
  incl_set = c(),
  groups_map = c(),
  cores = NULL,
  isContinued = FALSE,
  prevData = c(),
  fileOutput = FALSE,
  tempFile = "temp_stepSearch.RData",
  isConvert = FALSE,
  setting_par_iq = c(),
  setting_par_oq = c(),
  method = c("fast", "novel"),
  isTraced = FALSE
)

backward_search(
  X,
  criterion = c("ipoqll", "ipoqlldif"),
  incl_set = c(),
  groups_map = c(),
  cores = NULL,
  isContinued = FALSE,
  prevData = c(),
  isConvert = FALSE,
  setting_par_iq = c(),
  fileOutput = FALSE,
  setting_par_oq = c(),
  method = c("fast", "novel"),
  tempFile = "temp_backSearch.RData",
  isTraced = FALSE
)

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

## S3 method for class 'search'
```



```
print(x, ...)

plot_search(obj, remOrdered = TRUE, locateMax = TRUE, ...)
```

Arguments

<code>x</code>	A matrix or data.frame of the observed responses (ordinal or binary response).
<code>criterion</code>	The criterion that should be used. The default is ipoql.
<code>incl_set</code>	A vector of initial items in the included set to start the search. The default is to start with full items.
<code>groups_map</code>	A matrix or vector to map the subject to the DIFs groups.
<code>cores</code>	An integer value of number of cores should be used for computation. The default is 2.
<code>isContinued</code>	A logical value whether this search is continuing another unfinished search.
<code>prevData</code>	The filename of the temporary .RData file of the unfinished search.
<code>fileOutput</code>	The filename if it is wished to save the output results in file (.RData and .csv) and FALSE if not.
<code>tempFile</code>	The filename of the temporary file to track the search progress. The default is "temp_stepSearch.RData" which also automatically produces "temp_stepSearch.csv".
<code>isConvert</code>	A logical value whether it is wanted to recompute the score of the search results using IPOQ-LL-DIF criterion.
<code>setting_par_iq</code>	a list of the optimization control setting parameters for the included set. See setting parameter in autoRaschOptions() .
<code>setting_par_oq</code>	a list of the optimization control setting parameters for the included set. See setting parameter in autoRaschOptions() .
<code>method</code>	The implementation option of log likelihood function. fast using a c++ implementation and novel using an R implementation.
<code>isTraced</code>	A logical value whether the progress need to be tracked or not.
<code>object</code>	The object of class 'search'.
<code>...</code>	Further arguments to be passed.
<code>x</code>	The object of class 'search'.
<code>obj</code>	An object of class "search".
<code>remOrdered</code>	A logical statement whether show the order of the items removal or not.
<code>locateMax</code>	A logical statement whether the location of the maximum score is needed to be marked or not.

Details

To search the itemset that give the maximum score.

Value

Matrix of the highest scores (IQ-LL, OQ-LL, and IPOQ-LL) for every number of items in the included set in the set along with the corresponding itemset.

Examples

```
## Not run:
search_res <- backward_search(shortDIF, criterion = "ipoql1", incl_set = c(1:4), cores = 2)
plot_search(search_res, type="1")

## End(Not run)
```

testlets_dataset	<i>Multi-testlets Polytomous Data Set</i>
------------------	---

Description

Generate data set which consist of two bundle items with different level of local dependency effect.

Usage

```
data(testlets_dataset)
```

Format

An object of class `data.frame` with 301 rows and 12 columns.

withinItem_multidim	<i>Within-item Multidimensional Polytomous Data Set</i>
---------------------	---

Description

Generate multidimensional dataset with some items relate to more than one dimension.

Usage

```
data(withinItem_multidim)
```

Format

An object of class `data.frame` with 301 rows and 18 columns.

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