# Package 'GDINA'

January 20, 2022

Type Package

Version 2.8.8

**Encoding UTF-8** 

Title The Generalized DINA Model Framework

Date 2022-01-19 **Description** A set of psychometric tools for cognitive diagnosis modeling based on the generalized deterministic inputs, noisy and gate (G-DINA) model by de la Torre (2011) <DOI:10.1007/s11336-011-9207-7> and its extensions, including the sequential G-DINA model by Ma and de la Torre (2016) < DOI:10.1111/bmsp.12070 > for polytomous responses, and the polytomous G-DINA model by Chen and de la Torre < DOI:10.1177/0146621613479818 > for polytomous attributes. Joint attribute distribution can be independent, saturated, higher-order, loglinear smoothed or structured. Q-matrix validation, item and model fit statistics, model comparison at test and item level and differential item functioning can also be conducted. A graphical user interface is also provided. For tutorials, please check Ma and de la Torre (2020) < DOI:10.18637/jss.v093.i14 >, Ma and de la Torre (2019) < DOI:10.1111/emip.1 3-030-05584-4\_29> and de la Torre and Akbay (2019). License GPL-3 LazyData TRUE **Depends** R (>= 3.1.0) **Imports** alabama, graphics, ggplot2, MASS, numDeriv, Rcpp (>= 0.12.1), Rsolnp, stats, shiny, shinydashboard, utils Suggests CDM, Matrix, testthat, poLCA, stringr, knitr, rmarkdown LinkingTo Rcpp, RcppArmadillo URL https://github.com/Wenchao-Ma/GDINA, https://wenchao-ma.github.io/GDINA/ BugReports https://github.com/Wenchao-Ma/GDINA/issues RoxygenNote 7.1.2

Collate 'CA.R' 'CR.R' 'DTM.R' 'ExportedFuncs.R' 'GDINA.R' 'GDI.R'

'GDINA-package.R' 'GMSCDM.R' 'HO.R' 'ILCA.R' 'M2.R' 'MCmodel.R'

'Mstep.R' 'Mstep_DTM.R' 'MultipleGroup_Estimation.R'
'RcppExports.R' 'SingleGroup_Estimation.R' 'anova.GDINA.R'
'autoGDINA.R' 'bootSE.R' 'coef.R' 'dif.R' 'ecpe.R' 'simGDINA.R'
'itemfit.R' 'modelcomp.R' 'extract.R' 'frac20.R'
'itemparm.GDINA.R' 'monocheck.R' 'personparm.GDINA.R'
'plotIRF.GDINA.R' 's3GDINA.R' 'print.GDINA.R' 'score.R'
'sim10GDINA.R' 'sim10MCDINA.R' 'sim10MCDINA2.R'
'sim20seqGDINA.R' 'sim21seqDINA.R' 'sim30DINA.R' 'sim30GDINA.R'
'sim30pGDINA.R' 'startGDINA.R' 'structuralparm.R'
'summary.GDINA.R' 'utils.R' 'zzz.R'
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**Date/Publication** 2022-01-20 20:32:41 UTC

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## **Description**

For conducting CDM analysis within the G-DINA model framework

# **Details**

This package (Ma & de la Torre, 2020a) provides a framework for a series of cognitively diagnostic analyses for dichotomous and polytomous responses.

Various cognitive diagnosis models (CDMs) can be calibrated using the GDINA function, including the G-DINA model (de la Torre, 2011), the deterministic inputs, noisy and gate (DINA; de la Torre, 2009; Junker & Sijtsma, 2001) model, the deterministic inputs, noisy or gate (DINO; Templin & Henson, 2006) model, the reduced reparametrized unified model (R-RUM; Hartz, 2002), the additive CDM (A-CDM; de la Torre, 2011), and the linear logistic model (LLM; Maris, 1999), the multiple-strategy DINA model (de la Torre, & Douglas, 2008) and models defined by users under the G-DINA framework using different link functions and design matrices (de la Torre, 2011). Note that the LLM is also called compensatory RUM and the RRUM is equivalent to the generalized NIDA model.

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For ordinal and nominal responses, the sequential G-DINA model (Ma, & de la Torre, 2016) can be fitted and most of the aforementioned CDMs can be used as the processing functions (Ma, & de la Torre, 2016) at the category level. Different CDMs can be assigned to different items within a single assessment. Item parameters are estimated using the MMLE/EM algorithm. Details about the estimation algorithm can be found in Ma and de la Torre (2020). The joint attribute distribution can be modeled using an independent model, a higher-order IRT model (de la Torre, & Douglas, 2004), a loglinear model (Xu & von Davier, 2008), a saturated model or a hierarchical structures (e.g., linear, divergent). Monotonicity constraints for item/category success probabilities can also be specified.

In addition, to handle multiple strategies, generalized multiple-strategy CDMs for dichotomous response (Ma & Guo, 2019) can be fitted using GMSCDM function and diagnostic tree model (Ma, 2019) can also be estimated using DTM function for polytomous responses. Note that these functions are experimental, and are expected to be further extended in the future. Other diagnostic approaches include the multiple-choice model (de la Torre, 2009) and an iterative latent class analysis (ILCA; Jiang, 2019).

Various Q-matrix validation methods (de la Torre, & Chiu, 2016; de la Torre & Ma, 2016; Ma & de la Torre, 2020b; Najera, Sorrel, & Abad, 2019; see Qval), model-data fit statistics (Chen, de la Torre, & Zhang, 2013; Hansen, Cai, Monroe, & Li, 2016; Liu, Tian, & Xin, 2016; Ma, 2020; see modelfit and itemfit), model comparison at test and item level (de la Torre, 2011; de la Torre, & Lee, 2013; Ma, Iaconangelo, & de la Torre, 2016; Ma & de la Torre, 2019; Sorrel, Abad, Olea, de la Torre, & Barrada, 2017; Sorrel, de la Torre, Abad, & Olea, 2017; see modelcomp), and differential item functioning (Hou, de la Torre, & Nandakumar, 2014; Ma, Terzi, Lee, & de la Torre, 2017; see dif) can also be conducted.

To use the graphical user interface, check startGDINA.

## Author(s)

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#### See Also

**CDM** for estimating G-DINA model and a set of other CDMs; **ACTCD** and **NPCD** for nonparametric CDMs; **dina** for DINA model in Bayesian framework

att.structure

Generate hierarchical attribute structures

## **Description**

This function can be used to generate hierarchical attributes structures, and to provide prior joint attribute distribution with hierarchical structures.

# Usage

```
att.structure(hierarchy.list = NULL, K, Q, att.prob = "uniform")
```

#### **Arguments**

hierarchy.list a list specifying the hierarchical structure between attributes. Each element in this list specifies a DIRECT prerequisite relation between two or more attributes. See example for more information.

K the number of attributes involved in the assessment

Q Q-matrix

\*\*

att.prob How are the probabilities for latent classes simulated? It can be "random" or "uniform".

## Value

att.str reduced latent classes under the specified hierarchical structure impossible.latentclass impossible latent classes under the specified hierarchical structure att.prob probabilities for all latent classes; 0 for impossible latent classes

#### Author(s)

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## See Also

GDINA, autoGDINA

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## **Examples**

```
## Not run:
##################
# Leighton et al. (2004, p.210)
####################
# linear structure A1->A2->A3->A4->A5->A6
K <- 6
linear=list(c(1,2),c(2,3),c(3,4),c(4,5),c(5,6))
att.structure(linear,K)
# convergent structure A1->A2->A3->A5->A6;A1->A2->A4->A5->A6
K <- 6
converg <- list(c(1,2),c(2,3),c(2,4),
              c(3,4,5), #this is how to show that either A3 or A4 is a prerequisite to A5
               c(5,6)
att.structure(converg,K)
# convergent structure [the difference between this one and the previous one is that
                        A3 and A4 are both needed in order to master A5]
K <- 6
converg2 <- list(c(1,2),c(2,3),c(2,4),
               c(3,5), #this is how to specify that both A3 and A4 are needed for A5 \,
               c(4,5), #this is how to specify that both A3 and A4 are needed for A5
               c(5,6))
att.structure(converg2,K)
# divergent structure A1->A2->A3;A1->A4->A5;A1->A4->A6
diverg <- list(c(1,2),
               c(2,3),
               c(1,4),
               c(4,5),
               c(4,6))
att.structure(diverg,K)
# unstructured A1->A2;A1->A3;A1->A4;A1->A5;A1->A6
unstru \leftarrow list(c(1,2),c(1,3),c(1,4),c(1,5),c(1,6))
att.structure(unstru,K)
## See Example 4 and 5 in GDINA function
## End(Not run)
```

attributepattern

Generate all possible attribute patterns

## **Description**

This function generates all possible attribute patterns. The Q-matrix needs to be specified for polytomous attributes.

# Usage

```
attributepattern(K, Q)
```

## **Arguments**

```
K number of attributes
```

Q — Q-matrix; required when Q-matrix is polytomous

#### Value

A  $2^K \times K$  matrix consisting of attribute profiles for  $2^K$  latent classes

## Author(s)

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#### **Examples**

```
attributepattern(3)

q <- matrix(scan(text = "0 1 2 1 0 1 1 2 0"),ncol = 3)
q
attributepattern(Q=q)

q <- matrix(scan(text = "0 1 1 1 0 1 1 1 0"),ncol = 3)
q
attributepattern(K=ncol(q),Q=q)</pre>
```

autoGDINA

Q-matrix validation, model selection and calibration in one run

# **Description**

autoGDINA conducts a series of CDM analyses within the G-DINA framework. Particularly, the GDINA model is fitted to the data first using the GDINA function; then, the Q-matrix is validated using the function Qval. Based on the suggested Q-matrix, the data is fitted by the G-DINA model again, followed by an item level model selection via the Wald test using modelcomp. Lastly, the selected models are calibrated based on the suggested Q-matrix using the GDINA function. The Q-matrix validation and item-level model selection can be disabled by the users. Possible reduced CDMs for Wald test include the DINA model, the DINO model, A-CDM, LLM and RRUM. See Details for the rules of item-level model selection.

## Usage

```
autoGDINA(
   dat,
   Q,
   modelselection = TRUE,
   modelselectionrule = "simpler",
   alpha.level = 0.05,
   modelselection.args = list(),
   Qvalid = TRUE,
   Qvalid.args = list(),
   GDINA1.args = list(),
   GDINA2.args = list(),
   CDM.args = list()
)

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

## **Arguments**

dat

A required  $N \times J$  matrix or data.frame consisting of the responses of N individuals to J items. Missing values need to be coded as NA.

0

A required matrix; The number of rows occupied by a single-strategy dichotomous item is 1, by a polytomous item is the number of nonzero categories, and by a mutiple-strategy dichotomous item is the number of strategies. The number of column is equal to the number of attributes if all items are single-strategy dichotomous items, but the number of attributes + 2 if any items are polytomous or have multiple strategies. For a polytomous item, the first column represents the item number and the second column indicates the nonzero category number. For a multiple-strategy dichotomous item, the first column represents the item number and the second column indicates the strategy number. For binary attributes, 1 denotes the attributes are measured by the items and 0 means the attributes are not measured. For polytomous attributes, non-zero elements indicate which level of attributes are needed (see Chen, & de la Torre, 2013). See Examples.

modelselection logical; conducting model selection or not? modelselectionrule

how to conducted model selection? Possible options include simpler, largestp and DS. See Details.

alpha.level nominal level for the Wald test. The default is 0.05.

modelselection.args

arguments passed to modelcomp

Qvalid logical; validate Q-matrix or not? TRUE is the default.

Qvalid.args arguments passed to Qval

GDINA1.args arguments passed to GDINA function for initial G-DINA calibration arguments passed to GDINA function for the second G-DINA calibration

CDM. args arguments passed to GDINA function for final calibration

object GDINA object for various S3 methods

... additional arguments

#### **Details**

After the Wald statistics for each reduced CDM were calculated for each item, the reduced models with p values less than the pre-specified alpha level were rejected. If all reduced models were rejected for an item, the G-DINA model was used as the best model; if at least one reduced model was retained, three different rules can be implemented for selecting the best model:

When modelselectionrule is simpler:

If (a) the DINA or DINO model was one of the retained models, then the DINA or DINO model with the larger p value was selected as the best model; but if (b) both DINA and DINO were rejected, the reduced model with the largest p value was selected as the best model for this item. Note that when the p-values of several reduced models were greater than 0.05, the DINA and DINO models were preferred over the A-CDM, LLM, and R-RUM because of their simplicity. This procedure is originally proposed by Ma, Iaconangelo, and de la Torre (2016).

When modelselectionrule is largestp:

The reduced model with the largest p-values is selected as the most appropriate model.

When modelselectionrule is DS:

The reduced model with non-significant p-values but the smallest dissimilarity index is selected as the most appropriate model. Dissimilarity index can be viewed as an effect size measure, which quatifies how dis-similar the reduced model is from the G-DINA model (See Ma, Iaconangelo, and de la Torre, 2016 for details).

#### Value

a list consisting of the following elements:

GDINA1.obj initial GDINA calibration of class GDINA

GDINA2.obj second GDINA calibration of class GDINA

Qval.obj Q validation object of class Qval

Wald.obj model comparison object of class model comp

CDM.obj Final CDM calibration of class GDINA

## Methods (by generic)

• summary: print summary information

## Note

Returned GDINA1.obj, GDINA2.obj and CDM.obj are objects of class GDINA, and all S3 methods suitable for GDINA objects can be applied. See GDINA and extract. Similarly, returned Qval.obj and Wald.obj are objects of class Qval and modelcomp.

## Author(s)

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#### References

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Ma, W., Iaconangelo, C., & de la Torre, J. (2016). Model similarity, model selection and attribute classification. *Applied Psychological Measurement*, 40, 200-217.

#### See Also

GDINA, modelcomp, Qval

```
## Not run:
# simulated responses
Q <- sim10GDINA$simQ
dat <- sim10GDINA$simdat</pre>
#misspecified Q
misQ \leftarrow Q
misQ[10,] <- c(0,1,0)
out1 <- autoGDINA(dat,misQ,modelselectionrule="largestp")</pre>
summary(out1)
AIC(out1$CDM.obj)
# simulated responses
Q <- sim30GDINA$simQ
dat <- sim30GDINA$simdat
#misspecified Q
mis0 <- 0
misQ[1,] \leftarrow c(1,1,0,1,0)
auto <- autoGDINA(dat,misQ,Qvalid = TRUE, Qvalid.args = list(method = "wald"),</pre>
                   modelselectionrule="simpler")
auto
summary(auto)
AIC(auto$CDM.obj)
#using the other selection rule
out11 <- autoGDINA(dat,misQ,modelselectionrule="simpler",</pre>
                    modelselection.args = list(models = c("DINO", "DINA")))
out11
summary(out11)
# disable model selection function
out12 <- autoGDINA(dat,misQ,modelselection=FALSE)</pre>
out12
```

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```
# Disable Q-matrix validation
out3 <- autoGDINA(dat = dat, Q = misQ, Qvalid = FALSE)
out3
summary(out3)
## End(Not run)</pre>
```

bdiagMatrix

Create a block diagonal matrix

# Description

Create a block diagonal matrix

# Usage

```
bdiagMatrix(mlist, fill = 0)
```

# Arguments

mlist a list of matrices

fill value to fill the non-diagnoal elements

# Value

a block diagonal matrix

## See Also

bdiag in Matrix

```
m1 <- bdiagMatrix(list(matrix(1:4, 2), diag(3)))
m2 <- bdiagMatrix(list(matrix(1:4, 2), diag(3)),fill = NA)</pre>
```

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bootSE	Calculating standard errors and variance-covariance matrix using bootstrap methods

# **Description**

This function conducts nonparametric and parametric bootstrap to calculate standard errors of model parameters. Parametric bootstrap is only applicable to single group models.

## **Usage**

```
bootSE(GDINA.obj, bootsample = 50, type = "nonparametric", randomseed = 12345)
```

## **Arguments**

GDINA.obj an object of class GDINA

bootsample the number of bootstrap samples

type type of bootstrap method. Can be parametric or nonparametric

randomseed random seed for resampling

#### Value

itemparm.se standard errors for item probability of success in list format delta.se standard errors for delta parameters in list format lambda.se standard errors for structural parameters of joint attribute distribution boot.est resample estimates

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#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

```
## Not run:
# For illustration, only 5 resamples are run
# results are definitely not reliable

dat <- sim30GDINA$simdat
Q <- sim30GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA",att.dist = "higher.order")
boot.fit <- bootSE(fit,bootsample = 5,randomseed=123)
boot.fit$delta.se</pre>
```

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```
boot.fit$lambda.se
## End(Not run)
```

CA

Calculate classification accuracy

## **Description**

This function calculate test-, pattern- and attribute-level classification accuracy indices based on GDINA estimates from the GDINA function using approaches in Iaconangelo (2017) and Wang, Song, Chen, Meng, and Ding (2015). It is only applicable for dichotomous attributes.

# Usage

```
CA(GDINA.obj, what = "MAP")
```

## **Arguments**

GDINA.obj estimated GDINA object returned from GDINA what what attribute estimates are used? Default is "MAP".

# Value

a list with elements

tau estimated test-level classification accuracy, see Iaconangelo (2017, Eq 2.2)

tau\_l estimated pattern-level classification accuracy, see Iaconangelo (2017, p. 13)

tau k estimated attribute-level classification accuracy, see Wang, et al (2015, p. 461 Eq 6)

CCM Conditional classification matrix, see Iaconangelo (2017, p. 13)

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

# References

Iaconangelo, C.(2017). Uses of Classification Error Probabilities in the Three-Step Approach to Estimating Cognitive Diagnosis Models. (Unpublished doctoral dissertation). New Brunswick, NJ: Rutgers University.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Wang, W., Song, L., Chen, P., Meng, Y., & Ding, S. (2015). Attribute-Level and Pattern-Level Classification Consistency and Accuracy Indices for Cognitive Diagnostic Assessment. *Journal of Educational Measurement*, 52, 457-476.

cjoint 15

# **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
fit
CA(fit)
## End(Not run)</pre>
```

cjoint

Combine R Objects by Columns

# Description

Combine a sequence of vector, matrix or data-frame arguments by columns. Vector is treated as a column matrix.

# Usage

```
cjoint(..., fill = NA)
```

# **Arguments**

... vectors or matrices

fill a scalar used when these objects have different number of rows.

## Value

a data frame

# See Also

cbind

```
cjoint(2,c(1,2,3,4),matrix(1:6,2,3))

cjoint(v1 = 2, v2 = c(3,2), v3 = matrix(1:6,3,2),

v4 = data.frame(c(3,4,5,6,7),rep("x",5)),fill = 99)
```

16 ClassRate

ClassRate

Classification Rate Evaluation

## **Description**

This function evaluates the classification rates for two sets of attribute profiles

# Usage

```
ClassRate(att1, att2)
```

## **Arguments**

att1 a matrix or data frame of attribute profiles att2 a matrix or data frame of attribute profiles

#### Value

a list with the following components:

PCA the proportion of correctly classified attributes (i.e., attribute level classification rate)

**PCV** a vector giving the proportions of correctly classified attribute vectors (i.e., vector level classification rate). The fist element is the proportion of at least one attribute in the vector are correctly identified; the second element is the proportion of at least two attributes in the vector are correctly identified; and so forth. The last element is the proportion of all elements in the vector are correctly identified.

# Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

```
## Not run:
N <- 2000
# model does not matter if item parameter is probability of success
Q <- sim30GDINA$simQ
J <- nrow(Q)
gs <- matrix(0.1,J,2)

set.seed(12345)
sim <- simGDINA(N,Q,gs.parm = gs)
GDINA.est <- GDINA(sim$dat,Q)</pre>
```

designmatrix 17

```
CR <- ClassRate(sim$attribute,personparm(GDINA.est))
CR
## End(Not run)</pre>
```

designmatrix

Generate design matrix

# **Description**

This function generates the design matrix for an item

# Usage

```
designmatrix(Kj = NULL, model = "GDINA", Qj = NULL)
```

# Arguments

Kj	Required except for the MS-DINA model; The number of attributes required for item j
model	the model associated with the design matrix; It can be "GDINA", "DINA", "DINO", "ACDM" or "MSDINA". The default is "GDINA". Note that models "LLM" and "RRUM" have the same design matrix as the ACDM.
Qj	the Q-matrix for item j; This is required for "MSDINA" model; The number of rows is equal to the number of strategies and the number of columns is equal to the number of attributes.

# Value

```
a design matrix (Mj). See de la Torre (2011) for details.
```

# References

de la Torre, J. (2011). The generalized DINA model framework. Psychometrika, 76, 179-199.

18 dif

dif

Differential item functioning for cognitive diagnosis models

# Description

This function is used to detect differential item functioning using the Wald test (Hou, de la Torre, & Nandakumar, 2014; Ma, Terzi, & de la Torre, 2021) and the likelihood ratio test (Ma, Terzi, & de la Torre, 2021). The forward anchor item search procedure developed in Ma, Terzi, and de la Torre (2021) was implemented. Note that it can only detect DIF for two groups currently.

# Usage

```
dif(
  dat,
  Q,
  group,
  model = "GDINA",
  method = "wald",
  anchor.items = NULL,
  dif.items = "all",
  p.adjust.methods = "holm",
  approx = FALSE,
  SE.type = 2,
  FS.args = list(on = FALSE, alpha.level = 0.05, maxit = 10, verbose = FALSE),
  ...
)

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

#### **Arguments**

dat	item responses from two groups; missing data need to be coded as NA
Q	Q-matrix specifying the association between items and attributes
group	a factor or a vector indicating the group each individual belongs to. Its length must be equal to the number of individuals.
model	model for each item.
method	DIF detection method; It can be "wald" for Hou, de la Torre, and Nandakumar's (2014) Wald test method, and "LR" for likelihood ratio test (Ma, Terzi, Lee,& de la Torre, 2017).
anchor.items	which items will be used as anchors? Default is NULL, which means none of the items are used as anchors. For LR method, it can also be an integer vector giving the item numbers for anchors or "all", which means all items are treated as anchor items.

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dif.items which items are subject to DIF detection? Default is "all". It can also be an integer vector giving the item numbers.

p.adjust.methods

adjusted p-values for multiple hypothesis tests. This is conducted using p.adjust function in **stats**, and therefore all adjustment methods supported by p.adjust can be used, including "holm", "hochberg", "hommel", "bonferroni", "BH" and "BY". See p.adjust for more details. "holm" is the default.

approx Whether an approximated LR test is implemented? If TRUE, parameters of items except the studied one will not be re-estimated.

SE. type Type of standard error estimation methods for the Wald test.

FS. args arguments for the forward anchor item search procedure developed in Ma, Terzi, and de la Torre (2021). A list with the following elements:

- on logical; TRUE if activate the forward anchor item search procedure.
   Default = FALSE.
- alpha.level nominal level for Wald or LR test. Default = .05.
- maxit maximum number of iterations allowed. Default = 10.
- verbose logical; print information for each iteration or not? Default = FALSE.

arguments passed to GDINA function for model calibration

object dif object for S3 method

#### Value

A data frame giving the Wald statistics and associated p-values.

#### Methods (by generic)

• summary: print summary information

# Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu> Jimmy de la Torre, The University of Hong Kong

#### References

Hou, L., de la Torre, J., & Nandakumar, R. (2014). Differential item functioning assessment in cognitive diagnostic modeling: Application of the Wald test to investigate DIF in the DINA model. *Journal of Educational Measurement*, *51*, 98-125.

Ma, W., Terzi, R., & de la Torre, J. (2021). Detecting differential item functioning using multiple-group cognitive diagnosis models. *Applied Psychological Measurement*.

#### See Also

GDINA

20 DTM

## **Examples**

```
## Not run:
set.seed(123456)
N <- 3000
Q <- sim30GDINA$simQ
gs <- matrix(.2,ncol = 2, nrow = nrow(Q))
# By default, individuals are simulated from uniform distribution
# and deltas are simulated randomly
sim1 <- simGDINA(N,Q,gs.parm = gs,model="DINA")</pre>
sim2 <- simGDINA(N,Q,gs.parm = gs,model=c(rep("DINA",nrow(Q)-1),"DINO"))</pre>
dat <- rbind(extract(sim1,"dat"),extract(sim2,"dat"))</pre>
gr <- rep(c("G1","G2"),each=N)</pre>
# DIF using Wald test
dif.wald <- dif(dat, Q, group=gr, method = "Wald")</pre>
dif.wald
# DIF using LR test
dif.LR <- dif(dat, Q, group=gr, method="LR")</pre>
# DIF using Wald test + forward search algorithm
dif.wald.FS <- dif(dat, Q, group=gr, method = "Wald", FS.args = list(on = TRUE, verbose = TRUE))</pre>
dif.wald.FS
# DIF using LR test + forward search algorithm
dif.LR.FS <- dif(dat, Q, group=gr, method = "LR", FS.args = list(on = TRUE, verbose = TRUE))
dif.LR.FS
## End(Not run)
```

DTM

Experimental function for diagnostic multiple-strategy CDMs

# **Description**

This function estimates the diagnostic tree model (Ma, 2018) for polytomous responses with multiple strategies. It is an experimental function, and will be further optimized.

# Usage

```
DTM(
   dat,
   Qc,
   delta = NULL,
   Tmatrix = NULL,
   conv.crit = 0.001,
   conv.type = "pr",
   maxitr = 1000
)
```

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# **Arguments**

dat	A required $N \times J$ data matrix of N examinees to J items. Missing values are currently not allowed.
Qc	A required $J \times K + 2$ category and attribute association matrix, where J represents the number of items or nonzero categories and K represents the number of attributes. Entry 1 indicates that the attribute is measured by the item, and 0 otherwise. The first column gives the item number, which must be numeric and match the number of column in the data. The second column indicates the category number.
delta	initial item parameters
Tmatrix	The mapping matrix showing the relation between the OBSERVED responses (rows) and the PSEDUO items (columns); The first column gives the observed responses.
conv.crit	The convergence criterion for max absolute change in item parameters.
conv.type	convergence criteria; Can be pr,LL and delta, indicating category response function, log-likelihood and delta parameters,respectively.
maxitr	The maximum iterations allowed.

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

## References

Ma, W. (2018). A Diagnostic Tree Model for Polytomous Responses with Multiple Strategies. *British Journal of Mathematical and Statistical Psychology*.

#### See Also

GDINA for MS-DINA model and single strategy CDMs, and GMSCDM for generalized multiple strategies CDMs for dichotomous response data

```
## Not run:
K=5
g=0.2
item.no <- rep(1:6,each=4)
# the first node has three response categories: 0, 1 and 2
node.no <- rep(c(1,1,2,3),6)
Q1 <- matrix(0,length(item.no),K)
Q2 <- cbind(7:(7+K-1),rep(1,K),diag(K))
for(j in 1:length(item.no)) {
    Q1[j,sample(1:K,sample(3,1))] <- 1
}
Qc <- rbind(cbind(item.no,node.no,Q1),Q2)
Tmatrix.set <- list(cbind(c(0,1,2,3,3),c(0,1,2,1,2),c(NA,0,NA,1,NA),c(NA,NA,0,NA,1)),
cbind(c(0,1,2,3,4),c(0,1,2,1,2),c(NA,0,NA,1,NA),c(NA,NA,0,NA,1)),</pre>
```

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```
cbind(c(0,1),c(0,1)))
Tmatrix <- Tmatrix.set[c(1,1,1,1,1,1,rep(3,K))]
sim <- simDTM(N=2000,Qc=Qc,gs.parm=matrix(0.2,nrow(Qc),2),Tmatrix=Tmatrix)
est <- DTM(dat=sim$dat,Qc=Qc,Tmatrix = Tmatrix)
## End(Not run)</pre>
```

ecpe

Examination for the Certificate of Proficiency in English (ECPE) data

## Description

Examination for the Certificate of Proficiency in English (ECPE) data (the grammar section) has been used in Henson and Templin (2007), Templin and Hoffman (2013), Feng, Habing, and Huebner (2014), and Templin and Bradshaw (2014), among others.

## Usage

ecpe

#### **Format**

A list of responses and Q-matrix with components:

```
dat Responses of 2922 examinees to 28 items. Q The 28\times3 Q-matrix.
```

#### **Details**

The data consists of responses of 2922 examinees to 28 items involving 3 attributes. Attribute 1 is morphosyntactic rules, Attribute 2 is cohesive rules and Attribute 3 is lexical rules.

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

## References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Feng, Y., Habing, B. T., & Huebner, A. (2014). Parameter estimation of the reduced RUM using the EM algorithm. *Applied Psychological Measurement*, *38*, 137-150.

Henson, R. A., & Templin, J. (2007, April). Large-scale language assessment using cognitive diagnosis models. Paper presented at the annual meeting of the National Council for Measurement in Education in Chicago, Illinois.

Templin, J., & Bradshaw, L. (2014). Hierarchical diagnostic classification models: A family of models for estimating and testing attribute hierarchies. *Psychometrika*, 79, 317-339.

Templin, J., & Hoffman, L. (2013). Obtaining diagnostic classification model estimates using Mplus. *Educational Measurement: Issues and Practice*, 32, 37-50.

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## **Examples**

```
## Not run:
mod1 <- GDINA(ecpe$dat,ecpe$Q)</pre>
mod1
summary(mod1)
mod2 <- GDINA(ecpe$dat,ecpe$Q,model="RRUM")</pre>
mod2
anova(mod1, mod2)
# You may compare the following results with Feng, Habing, and Huebner (2014)
coef(mod2,"rrum")
# G-DINA with hierarchical structure
# see Templin & Bradshaw, 2014
ast <- att.structure(list(c(3,2),c(2,1)),K=3)
est.gdina2 <- GDINA(ecpe$dat,ecpe$Q,model = "GDINA",</pre>
                   control = list(conv.crit = 1e-6),
                   att.str = list(c(3,2),c(2,1))
# see Table 7 in Templin & Bradshaw, 2014
summary(est.gdina2)
## End(Not run)
```

extract

extract elements from objects of various classes

#### **Description**

A generic function to extract elements from objects of class GDINA, itemfit, modelcomp, Qval or simGDINA. This page gives the elements that can be extracted from the class GDINA. To see what can be extracted from itemfit, modelcomp, and Qval, go to the corresponding function help page.

Objects which can be extracted from GDINA objects include:

## AIC AIC

**att.prior** attribute prior weights for calculating marginalized likelihood in the last EM iteration **attributepattern** all attribute patterns involved in the current calibration

**BIC** BIC

**CAIC** Consistent AIC

catprob.cov covariance matrix of item probability parameter estimates; Need to specify SE.type
catprob.parm item parameter estimates

**catprob.se** standard error of item probability parameter estimates; Need to specify SE. type **convergence** TRUE if the calibration is converged.

dat raw data

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**del.ind** deleted observation number

delta.cov covariance matrix of delta parameter estimates; Need to specify SE. type

delta.parm delta parameter estimates

delta.se standard error of delta parameter estimates; Need to specify SE. type

designmatrix A list of design matrices for each item/category

deviance deviance, or negative two times observed marginal log likelihood

discrim GDINA discrimination index

expectedCorrect expected # of examinees in each latent group answering item correctly

expectedTotal expected # of examinees in each latent group

higher.order higher-order model specifications

LCprob.parm success probabilities for all latent classes

logLik observed marginal log likelihood

linkfunc link functions for each item

initial.catprob initial item category probability parameters

**natt** number of attributes

ncat number of categories

ngroup number of groups

nitem number of items

nitr number of EM iterations

**nobs** number of observations, or sample size

nLC number of latent classes

prevalence of each attribute

posterior.prob posterior weights for each latent class

reduced.LG Reduced latent group for each item

SABIC Sample size Adusted BIC

sequential is a sequential model fitted?

# Usage

```
extract(object, what, ...)
```

## **Arguments**

objects from class GDINA, itemfit, modelcomp, Qval or simGDINA

what what to extract

.. additional arguments

frac20 25

## **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
extract(fit, "discrim")
extract(fit, "designmatrix")
## End(Not run)</pre>
```

frac20

Tatsuoka's fraction subtraction data

# **Description**

Fraction Subtraction data (Tatsuoka, 2002) consists of responses of 536 examinees to 20 items measuring 8 attributes.

# Usage

frac20

#### **Format**

A list of responses and Q-matrix with components:

```
dat responses of 536 examinees to 20 items 
 Q The 20 \times 8 Q-matrix
```

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Tatsuoka, C. (2002). Data analytic methods for latent partially ordered classification models. *Journal of the Royal Statistical Society, Series C, Applied Statistics*, *51*, 337-350.

## **Examples**

```
## Not run:
mod1 <- GDINA(frac20$dat,frac20$Q,model="DINA")
mod1
summary(mod1)
# Higher order model
mod2 <- GDINA(frac20$dat,frac20$Q,model="DINA",att.dist="higher.order")
mod2
anova(mod1,mod2)
## End(Not run)</pre>
```

**GDINA** 

CDM calibration under the G-DINA model framework

## **Description**

GDINA calibrates the generalized deterministic inputs, noisy and gate (G-DINA; de la Torre, 2011) model for dichotomous responses, and its extension, the sequential G-DINA model (Ma, & de la Torre, 2016a; Ma, 2017) for ordinal and nominal responses. By setting appropriate constraints, the deterministic inputs, noisy and gate (DINA; de la Torre, 2009; Junker & Sijtsma, 2001) model, the deterministic inputs, noisy or gate (DINO; Templin & Henson, 2006) model, the reduced reparametrized unified model (R-RUM; Hartz, 2002), the additive CDM (A-CDM; de la Torre, 2011), the linear logistic model (LLM; Maris, 1999), and the multiple-strategy DINA model (MS-DINA; de la Torre & Douglas, 2008; Huo & de la Torre, 2014) can also be calibrated. Note that the LLM is equivalent to the C-RUM (Hartz, 2002), a special case of the GDM (von Davier, 2008), and that the R-RUM is also known as a special case of the generalized NIDA model (de la Torre, 2011).

In addition, users are allowed to specify design matrix and link function for each item, and distinct models may be used in a single test for different items. The attributes can be either dichotomous or polytomous (Chen & de la Torre, 2013). Joint attribute distribution may be modelled using independent or saturated model, structured model, higher-order model (de la Torre & Douglas, 2004), or loglinear model (Xu & von Davier, 2008). Marginal maximum likelihood method with Expectation-Maximization (MMLE/EM) alogrithm is used for item parameter estimation.

To compare two or more GDINA objects, use method anova.

To calculate structural parameters for item and joint attribute distributions, use method coef.

To calculate lower-order incidental (person) parameters use method personparm. To extract other components returned, use extract. To plot item/category response function, use plot. To check whether monotonicity is violated, use monocheck. To conduct analysis in graphical user interface, use startGDINA.

#### Usage

```
GDINA(
  dat,
  Q,
  model = "GDINA",
```

```
sequential = FALSE,
  att.dist = "saturated",
  mono.constraint = FALSE,
  group = NULL,
  linkfunc = NULL,
  design.matrix = NULL,
  latent.var = "att",
  att.prior = NULL,
  att.str = NULL,
  verbose = 1,
  higher.order = list(),
  loglinear = 2,
  catprob.parm = NULL,
  control = list(),
  item.names = NULL,
  solver = NULL,
  nloptr.args = list(),
  auglag.args = list(),
  solnp.args = list(),
)
## S3 method for class 'GDINA'
anova(object, ...)
## S3 method for class 'GDINA'
coef(
 object,
 what = c("catprob", "delta", "gs", "itemprob", "LCprob", "rrum", "lambda"),
 withSE = FALSE,
  SE.type = 2,
 digits = 4,
)
## S3 method for class 'GDINA'
extract(object, what, SE.type = 2, ...)
## S3 method for class 'GDINA'
personparm(object, what = c("EAP", "MAP", "MLE", "mp", "HO"), digits = 4, ...)
## S3 method for class 'GDINA'
logLik(object, ...)
## S3 method for class 'GDINA'
deviance(object, ...)
## S3 method for class 'GDINA'
```

```
nobs(object, ...)
## S3 method for class 'GDINA'
vcov(object, ...)
## S3 method for class 'GDINA'
npar(object, ...)
## S3 method for class 'GDINA'
indlogLik(object, ...)
## S3 method for class 'GDINA'
indlogPost(object, ...)
## S3 method for class 'GDINA'
summary(object, ...)
```

#### **Arguments**

dat

A required  $N \times J$  matrix or data.frame consisting of the responses of N individuals to J items. Missing values need to be coded as NA.

Q

A required matrix; The number of rows occupied by a single-strategy dichotomous item is 1, by a polytomous item is the number of nonzero categories, and by a mutiple-strategy dichotomous item is the number of strategies. The number of column is equal to the number of attributes if all items are single-strategy dichotomous items, but the number of attributes + 2 if any items are polytomous or have multiple strategies. For a polytomous item, the first column represents the item number and the second column indicates the nonzero category number. For a multiple-strategy dichotomous item, the first column represents the item number and the second column indicates the strategy number. For binary attributes, 1 denotes the attributes are measured by the items and 0 means the attributes are not measured. For polytomous attributes, non-zero elements indicate which level of attributes are needed (see Chen, & de la Torre, 2013). See Examples.

model

A vector for each item or nonzero category, or a scalar which will be used for all items or nonzero categories to specify the CDMs fitted. The possible options include "GDINA", "DINA", "DINO", "ACDM", "LLM", "RRUM", "MSDINA" and "UDF". Note that model can also be "logitGDINA" and "logGDINA", indicating the saturated G-DINA model in logit and log link functions. They are equivalent to the identity link saturated G-DINA model. The logit G-DINA model is identical to the log-linear CDM. When "UDF", indicating user defined function, is specified for any item, arguments design.matrix and linkfunc need to be defined.

sequential

logical; TRUE if the sequential model is fitted for polytomous responses.

att.dist

How is the joint attribute distribution estimated? It can be (1) saturated, which is the default, indicating that the proportion parameter for each permissible latent class is estimated separately; (2) higher order, indicating that a higherorder joint attribute distribution is assumed (higher-order model can be specified in higher.order argument); (3) fixed, indicating that the weights speci-

fied in att.prior argument are fixed in the estimation process. If att.prior is not specified, a uniform joint attribute distribution is employed initially; (4) independent, indicating that all attributes are assumed to be independent; and (5) loglinear, indicating a loglinear model is employed. If different groups have different joint attribute distributions, specify att.dist as a character vector with the same number of elements as the number of groups. However, if a higher-order model is used for any group, it must be used for all groups.

mono.constraint

logical; TRUE indicates that  $P(\alpha_1) <= P(\alpha_2)$  if for all k,  $\alpha_{1k} < \alpha_{2k}$ . Can be a vector for each item or nonzero category or a scalar which will be used for all items to specify whether monotonicity constraint should be added.

a factor or a vector indicating the group each individual belongs to. Its length must be equal to the number of individuals.

a vector of link functions for each item/category; It can be "identity", "log" or "logit". Only applicable when, for some items, model="UDF".

a list of design matrices; Its length must be equal to the number of items (or nonzero categories for sequential models). If CDM for item j is specified as "UDF" in argument model, the corresponding design matrix must be provided; otherwise, the design matrix can be NULL, which will be generated automatically.

A string indicating the nature of the latent variables. It is "att" (by default) if the latent variables are attributes, and "bugs" if the latent variables are misconceptions. When "bugs" is specified, only the DINA, DINO or G-DINA model can be specified in model argument (Kuo, Chen, Yang & Mok, 2016).

A vector of length  $2^K$  for single group model, or a matrix of dimension  $2^K \times$  no. of groups to specify attribute prior distribution for  $2^K$  latent classes for all groups under a multiple group model. Only applicable for dichotomous attributes. The sum of all elements does not have to be equal to 1; however, it will be normalized so that the sum is equal to 1 before calibration. The label for each latent class can be obtained by calling attributepattern(K). See examples for more info.

Specify attribute structures. NULL, by default, means there is no structure. Attribute structure needs be specified as a list - which will be internally handled by att.structure function. See examples. It can also be a matrix giving all permissible attribute profiles.

How to print calibration information after each EM iteration? Can be 0, 1 or 2, indicating to print no information, information for current iteration, or information for all iterations.

A list specifying the higher-order joint attribute distribution with the following components:

• model - a character indicating the IRT model for higher-order joint attribute

model - a character indicating the IRT model for higher-order joint attribute distribution. Can be "2PL", "1PL" or "Rasch", representing two parameter logistic IRT model, one parameter logistic IRT model and Rasch model, respectively. For "1PL" model, a common slope parameter is estimated. "Rasch" is the default model when att.dist = "higher.order". Note that slope-intercept form is used for parameterizing the higher-order IRT model (see Details).

group

linkfunc

design.matrix

latent.var

att.prior

att.str

verbose

higher.order

- nquad a scalar specifying the number of integral nodes. Default = 25.
- SlopeRange a vector of length two specifying the range of slope parameters. Default = [0.1, 5].
- InterceptRange a vector of length two specifying the range of intercept parameters. Default = [-4, 4].
- SlopePrior a vector of length two specifying the mean and variance of log(slope) parameters, which are assumed normally distributed. Default: mean = 0 and sd = 0.25.
- InterceptPrior a vector of length two specifying the mean and variance of intercept parameters, which are assumed normally distributed. Default: mean = 0 and sd = 1.
- Prior logical; indicating whether prior distributions should be imposed to slope and intercept parameters. Default is FALSE.

loglinear

the order of loglinear smooth for attribute space. It can be either 1 or 2 indicating the loglinear model with main effect only and with main effect and first-order interaction.

catprob.parm

A list of initial success probability parameters for each nonzero category.

control

A list of control parameters with elements:

- maxitr A vector for each item or nonzero category, or a scalar which will be used for all items or nonzero categories to specify the maximum number of EM cycles allowed. Default = 2000.
- conv.crit The convergence criterion. Default = 0.0001.
- conv.type How is the convergence criterion evaluated? A vector with possible elements: "ip", indicating the maximum absolute change in item success probabilities, "mp", representing the maximum absolute change in mixing proportion parameters, "delta", indicating the maximum absolute change in delta parameters, neg2LL indicating the absolute change in negative two times loglikeihood, or neg2LL indicating the relative absolute change in negative two times loglikeihood (i.e., the absolute change divided by -2LL of the previous iteration). Multiple criteria can be specified. If so, all criteria need to be met. Default = c("ip", "mp").
- nstarts how many sets of starting values? Default = 3.
- lower.p A vector for each item or nonzero category, or a scalar which will be used for all items or nonzero categories to specify the lower bound for success probabilities. Default = .0001.
- upper.p A vector for each item or nonzero category, or a scalar which will be used for all items or nonzero categories to specify the upper bound for success probabilities. Default = .9999.
- lower.prior The lower bound for mixing proportion parameters (latent class sizes). Default = .Machine\$double.eps.
- randomseed Random seed for generating initial item parameters. Default = 123456.
- smallNcorrection A numeric vector with two elements specifying the corrections applied when the expected number of individuals in some latent groups are too small. If the expected no. of examinees is less than

the second element, the first element and two times the first element will be added to the numerator and denominator of the closed-form solution of probabilities of success. Only applicable for the G-DINA, DINA and DINO model estimation without monotonic constraints.

• MstepMessage Integer; Larger number prints more information from Mstep optimizer. Default = 1.

item.names

A vector giving the item names. By default, items are named as "Item 1", "Item 2", etc.

solver

A string indicating which solver should be used in M-step. By default, the solver is automatically chosen according to the models specified. Possible options include slsqp, nloptr, solnp and auglag.

nloptr.args

a list of control parameters to be passed to opts argument of nloptr function.

auglag.args

a list of control parameters to be passed to the alabama::auglag() function. It can contain two elements: control.outer and control.optim. See auglag.

solnp.args

a list of control parameters to be passed to control argument of solnp function.

. . .

additional arguments

object

GDINA object for various S3 methods

what

argument for various S3 methods; For calculating structural parameters using coef, what can be

- itemprob item success probabilities of each reduced attribute pattern.
- catprob category success probabilities of each reduced attribute pattern; the same as itemprob for dichtomous response data.
- LCprob item success probabilities of each attribute pattern.
- gs guessing and slip parameters of each item/category.
- delta delta parameters of each item/category, see G-DINA formula in details.
- rrum RRUM parameters when items are estimated using RRUM.
- lambda structural parameters for joint attribute distribution.

For calculating incidental parameters using personparm, what can be

- EAP EAP estimates of attribute pattern.
- MAP MAP estimates of attribute pattern.
- MLE MLE estimates of attribute pattern.
- mp marginal mastery probabilities.
- HO EAP estimates of higher-order ability if a higher-order is fitted.

withSE

argument for method coef; estimate standard errors or not?

SE.type

type of standard errors. For now, SEs are calculated based on outper-product of gradient. It can be 1 based on item-wise information, 2 based on incomplete information and 3 based on complete information.

digits

How many decimal places in each number? The default is 4.

#### Value

GDINA returns an object of class GDINA. Methods for GDINA objects include extract for extracting various components, coef for extracting structural parameters, personparm for calculating incidental (person) parameters, summary for summary information. AIC, BIC,logLik, deviance and npar can also be used to calculate AIC, BIC, observed log-likelihood, deviance and number of parameters.

#### Methods (by generic)

- anova: Model comparison using likelihood ratio test
- coef: extract structural parameter estimates
- extract: extract various elements of GDINA estimates
- personparm: calculate person attribute patterns and higher-order ability
- logLik: calculate log-likelihood
- deviance: calculate deviance
- · nobs: calculate number of observations
- vcov: calculate covariance-matrix for delta parameters
- npar: calculate the number of parameters
- indlogLik: extract log-likelihood for each individual
- indlogPost: extract log posterior for each individual
- summary: print summary information

# The G-DINA model

The generalized DINA model (G-DINA; de la Torre, 2011) is an extension of the DINA model. Unlike the DINA model, which collaspes all latent classes into two latent groups for each item, if item j requires  $K_j^*$  attributes, the G-DINA model collapses  $2^K$  latent classes into  $2^{K_j^*}$  latent groups with unique success probabilities on item j, where  $K_j^* = \sum_{k=1}^K q_{jk}$ .

Let  $\alpha_{lj}^*$  be the reduced attribute pattern consisting of the columns of the attributes required by item j, where  $l=1,\ldots,2^{K_j^*}$ . For example, if only the first and the last attributes are required,  $\alpha_{lj}^*=(\alpha_{l1},\alpha_{lK})$ . For notational convenience, the first  $K_j^*$  attributes can be assumed to be the required attributes for item j as in de la Torre (2011). The probability of success  $P(X_j=1|\alpha_{lj}^*)$  is denoted by  $P(\alpha_{lj}^*)$ . To model this probability of success, different link functions as in the generalized linear models are used in the G-DINA model. The item response function of the G-DINA model using the identity link can be written as

$$f[P(\alpha_{lj}^*)] = \delta_{j0} + \sum_{k=1}^{K_j^*} \delta_{jk} \alpha_{lk} + \sum_{k'=k+1}^{K_j^*} \sum_{k=1}^{K_j^*-1} \delta_{jkk'} \alpha_{lk} \alpha_{lk'} + \dots + \delta_{j12\dots K_j^*} \prod_{k=1}^{K_j^*} \alpha_{lk},$$

or in matrix form,

$$f[\mathbf{P}_j] = \mathbf{M}_j \delta_j,$$

where  $\delta_{j0}$  is the intercept for item j,  $\delta_{jk}$  is the main effect due to  $\alpha_{lk}$ ,  $\delta_{jkk'}$  is the interaction effect due to  $\alpha_{lk}$  and  $\alpha_{lk'}$ ,  $\delta_{j12...K_j^*}$  is the interaction effect due to  $\alpha_{l1}, \cdots, \alpha_{lK_j^*}$ . The log and logit links can also be employed.

#### Other CDMs as special cases

Several widely used CDMs can be obtained by setting appropriate constraints to the G-DINA model. This section introduces the parameterization of different CDMs within the G-DINA model framework very breifly. Readers interested in this please refer to de la Torre(2011) for details.

DINA model In DINA model, each item has two item parameters - guessing (g) and slip (s). In traditional parameterization of the DINA model, a latent variable  $\eta$  for person i and item j is defined as

$$\eta_{ij} = \prod_{k=1}^{K} \alpha_{ik}^{q_{jk}}$$

Briefly speaking, if individual i master all attributes required by item j,  $\eta_{ij}=1$ ; otherwise,  $\eta_{ij}=0$ . Item response function of the DINA model can be written by

$$P(X_{ij} = 1 | \eta_{ij}) = (1 - s_j)^{\eta_{ij}} g_j^{1 - \eta_{ij}}$$

To obtain the DINA model from the G-DINA model, all terms in identity link G-DINA model except  $\delta_0$  and  $\delta_{12...K_i^*}$  need to be fixed to zero, that is,

$$P(\alpha_{lj}^*) = \delta_{j0} + \delta_{j12...K_j^*} \prod_{k=1}^{K_j^*} \alpha_{lk}$$

In this parameterization,  $\delta_{j0}=g_j$  and  $\delta_{j0}+\delta_{j12\cdots K_j^*}=1-s_j$ . DINO model The DINO model can be given by

$$P(\alpha_{lj}^*) = \delta_{j0} + \delta_{j1} I(\alpha_{lj}^* \neq \mathbf{0})$$

where  $I(\cdot)$  is an indicator variable. The DINO model is also a constrained identity link G-DINA model. As shown by de la Torre (2011), the appropriate constraint is

$$\delta_{jk} = -\delta_{jk'k''} = \dots = (-1)^{K_j^* + 1} \delta_{j12\dots K_j^*},$$

for 
$$k = 1, \dots, K_i^*, k' = 1, \dots, K_i^* - 1$$
, and  $k'' > k', \dots, K_i^*$ .

Additive models with different link functions The A-CDM, LLM and R-RUM can be obtained by setting all interactions to be zero in identity, logit and log link G-DINA model, respectively. Specifically, the A-CDM can be formulated as

$$P(\alpha_{lj}^*) = \delta_{j0} + \sum_{k=1}^{K_j^*} \delta_{jk} \alpha_{lk}.$$

The item response function for LLM can be given by

$$logit[P(\alpha_{lj}^*)] = \delta_{j0} + \sum_{k=1}^{K_j^*} \delta_{jk} \alpha_{lk},$$

and lastly, the RRUM, can be written as

$$log[P(\alpha_{lj}^*)] = \delta_{j0} + \sum_{k=1}^{K_j^*} \delta_{jk} \alpha_{lk}.$$

It should be noted that the LLM is equivalent to the compensatory RUM, which is subsumed by the GDM, and that the RRUM is a special case of the generalized noisy inputs, deterministic "And" gate model (G-NIDA).

#### Joint Attribute Distribution

The joint attribute distribution can be modeled using various methods. This section mainly focuses on the so-called higher-order approach, which was originally proposed by de la Torre and Douglas (2004) for the DINA model. It has been extended in this package for all condensation rules. Particularly, three IRT models are available for the higher-order attribute structure: Rasch model (Rasch), one parameter logistic model (1PL) and two parameter logistic model (2PL). For the Rasch model, the probability of mastering attribute k for individual i is defined as

$$P(\alpha_k = 1 | \theta_i, \lambda_{0k}) = \frac{exp(\theta_i + \lambda_{0k})}{1 + exp(\theta_i + \lambda_{0k})}$$

For the 1PL model, the probability of mastering attribute k for individual i is defined as

$$P(\alpha_k = 1 | \theta_i, \lambda_{0k}, \lambda_1) = \frac{exp(\lambda_1 \theta_i + \lambda_{0k})}{1 + exp(\lambda_1 \theta_i + \lambda_{0k})}$$

For the 2PL model, the probability of mastering attribute k for individual i is defined as

$$P(\alpha_k = 1 | \theta_i, \lambda_{0k}, \lambda_{1k}) = \frac{exp(\lambda_{1k}\theta_i + \lambda_{0k})}{1 + exp(\lambda_{1k}\theta_i + \lambda_{0k})}$$

where  $\theta_i$  is the ability of examinee i.  $\lambda_{0k}$  and  $\lambda_{1k}$  are the intercept and slope parameters for attribute k, respectively. In the Rasch model,  $\lambda_{1k} = 1 \forall k$ ; whereas in the 1PL model, a common slope parameter  $\lambda_1$  is estimated. The probability of joint attributes can be written as

$$P(\alpha|\theta_i, \lambda) = \prod_k P(\alpha_k|\theta_i, \lambda)$$

.

# **Model Estimation**

The MMLE/EM algorithm is implemented in this package. For G-DINA, DINA and DINO models, closed-form solutions exist. See de la Torre (2009) and de la Torre (2011) for details. For ACDM, LLM and RRUM, closed-form solutions do not exist, and therefore some general optimization techniques are adopted in M-step (Ma, Iaconangelo & de la Torre, 2016). The selection of optimization techniques mainly depends on whether some specific constraints need to be added.

The sequential G-DINA model is a special case of the diagnostic tree model (DTM; Ma, 2019) and estimated using the mapping matrix accordingly (See Tutz, 1997; Ma, 2019).

# The Number of Parameters

For dichotomous response models: Assume a test measures K attributes and item j requires  $K_j^*$  attributes: The DINA and DINO model has 2 item parameters for each item; if item j is ACDM, LLM or RRUM, it has  $K_j^*+1$  item parameters; if it is G-DINA model, it has  $2^{K_j^*}$  item parameters. Apart from item parameters, the parameters involved in the estimation of joint attribute distribution need to be estimated as well. When using the saturated attribute structure, there are  $2^K-1$  parameters for joint attribute distribution estimation; when using a higher-order attribute structure, there are K, K+1, and K+1, and K+1 parameters for the Rasch model, 1PL model and 2PL model, respectively. For polytomous response data using the sequential G-DINA model, the number of item parameters are counted at category level.

#### Note

anova function does NOT check whether models compared are nested or not.

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## See Also

See autoGDINA for Q-matrix validation, item-level model comparison and model calibration in one run; See modelfit and itemfit for model and item fit analysis, Qval for Q-matrix validation, modelcomp for item level model comparison and simGDINA for data simulation. GMSCDM for a series of multiple strategy CDMs for dichotomous data, and DTM for diagnostic tree model for multiple strategies in polytomous response data Also see gdina in CDM package for the G-DINA model estimation.

```
## Not run:
#
       Example 1.
#
    GDINA, DINA, DINO
   ACDM, LLM and RRUM
# estimation and comparison
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
#----#
mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")</pre>
mod1
# summary information
summary(mod1)
AIC(mod1) #AIC
BIC(mod1) #BIC
logLik(mod1) #log-likelihood value
```

```
deviance(mod1) # deviance: -2 log-likelihood
npar(mod1) # number of parameters
head(indlogLik(mod1)) # individual log-likelihood
head(indlogPost(mod1)) # individual log-posterior
# structural parameters
# see ?coef
coef(mod1) # item probabilities of success for each latent group
coef(mod1, withSE = TRUE) # item probabilities of success & standard errors
coef(mod1, what = "delta") # delta parameters
coef(mod1, what = "delta",withSE=TRUE) # delta parameters
coef(mod1, what = "gs") # guessing and slip parameters
coef(mod1, what = "gs", with SE = TRUE) \# guessing and slip parameters \& standard errors
# person parameters
# see ?personparm
personparm(mod1) # EAP estimates of attribute profiles
personparm(mod1, what = "MAP") # MAP estimates of attribute profiles
personparm(mod1, what = "MLE") # MLE estimates of attribute profiles
#plot item response functions for item 10
plot(mod1, item = 10)
plot(mod1,item = 10,withSE = TRUE) # with error bars
#plot mastery probability for individuals 1, 20 and 50
plot(mod1, what = "mp", person = c(1, 20, 50))
# Use extract function to extract more components
# See ?extract
# -----#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod2 <- GDINA(dat = dat, Q = Q, model = "DINA")</pre>
coef(mod2, what = "gs") # guess and slip parameters
coef(mod2, what = "gs", withSE = TRUE) # guess and slip parameters and standard errors
# Model comparison at the test level via likelihood ratio test
anova(mod1,mod2)
# -----#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod3 <- GDINA(dat = dat, Q = Q, model = "DINO")</pre>
#slip and guessing
coef(mod3, what = "gs") # guess and slip parameters
coef(mod3, what = "gs",withSE = TRUE) # guess and slip parameters + standard errors
# Model comparison at test level via likelihood ratio test
anova(mod1, mod2, mod3)
```

```
# -----#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod4 <- GDINA(dat = dat, Q = Q, model = "ACDM")</pre>
# -----#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod4b <- GDINA(dat = dat, Q = Q, model = "LLM")</pre>
# -----#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod4c <- GDINA(dat = dat, Q = Q, model = "RRUM")</pre>
mod4c
# --- Different CDMs for different items --- #
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
models <- c(rep("GDINA",3),"LLM","DINA","DINO","ACDM","RRUM","LLM","RRUM")</pre>
mod5 <- GDINA(dat = dat, Q = Q, model = models)</pre>
anova(mod1, mod2, mod3, mod4, mod4b, mod4c, mod5)
Example 2.
        Model estimations
# With monotonocity constraints
                                #
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
# for item 10 only
mod11 <- GDINA(dat = dat, Q = Q, model = "GDINA",mono.constraint = c(rep(FALSE,9),TRUE))</pre>
mod11a <- GDINA(dat = dat, Q = Q, model = "DINA",mono.constraint = TRUE)</pre>
mod11a
mod11b <- GDINA(dat = dat, Q = Q, model = "ACDM", mono.constraint = TRUE)</pre>
mod11c <- GDINA(dat = dat, Q = Q, model = "LLM", mono.constraint = TRUE)</pre>
mod11c
mod11d <- GDINA(dat = dat, Q = Q, model = "RRUM", mono.constraint = TRUE)</pre>
mod11d
coef(mod11d,"delta")
coef(mod11d,"rrum")
#
          Example 3a.
#
        Model estimations
# With Higher-order att structure #
```

```
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
# --- Higher order G-DINA model ---#
mod12 <- GDINA(dat = dat, Q = Q, model = "DINA",</pre>
             att.dist="higher.order",higher.order=list(nquad=31,model = "2PL"))
personparm(mod12,"HO") # higher-order ability
# structural parameters
# first column is slope and the second column is intercept
coef(mod12,"lambda")
# --- Higher order DINA model ---#
mod22 <- GDINA(dat = dat, Q = Q, model = "DINA", att.dist="higher.order",</pre>
             higher.order=list(model = "2PL",Prior=TRUE))
#
           Example 3b.
#
        Model estimations
#
   With log-linear att structure #
# --- DINA model with loglinear smoothed attribute space ---#
dat <- sim10GDINA$simdat</pre>
0 <- sim10GDINA$sim0</pre>
mod23 <- GDINA(dat = dat, Q = Q, model = "DINA",att.dist="loglinear",loglinear=1)</pre>
coef(mod23,"lambda") # intercept and three main effects
Example 3c.
        Model estimations
# With independent att structure #
# --- GDINA model with independent attribute space ---#
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod33 <- GDINA(dat = dat, Q = Q, att.dist="independent")</pre>
coef(mod33,"lambda") # mastery probability for each attribute
#
          Example 4.
#
        Model estimations
    With fixed att structure
# --- User-specified attribute priors ----#
# prior distribution is fixed during calibration
# Assume each of 000,100,010 and 001 has probability of 0.1
# and each of 110, 101,011 and 111 has probability of 0.15
# Note that the sum is equal to 1
prior < c(0.1,0.1,0.1,0.1,0.15,0.15,0.15,0.15)
# fit GDINA model with fixed prior dist.
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
```

```
modp1 <- GDINA(dat = dat, Q = Q, att.prior = prior, att.dist = "fixed")</pre>
extract(modp1, what = "att.prior")
Example 5a.
                                 #
#
            G-DINA
                                 #
# with hierarchical att structure #
# --- User-specified attribute structure ----#
Q <- sim30GDINA$simQ
K \leftarrow ncol(Q)
# divergent structure A1->A2->A3;A1->A4->A5
diverg <- list(c(1,2),
              c(2,3),
              c(1,4),
              c(4,5))
struc <- att.structure(diverg,K)</pre>
set.seed(123)
# data simulation
N <- 1000
true.lc <- sample(c(1:2^K),N,replace=TRUE,prob=struc$att.prob)
table(true.lc) #check the sample
true.att <- attributepattern(K)[true.lc,]</pre>
gs <- matrix(rep(0.1,2*nrow(Q)),ncol=2)</pre>
# data simulation
simD <- simGDINA(N,Q,gs.parm = gs, model = "GDINA",attribute = true.att)</pre>
dat <- extract(simD, "dat")</pre>
modp1 <- GDINA(dat = dat, Q = Q, att.str = diverg, att.dist = "saturated")</pre>
modp1
coef(modp1,"lambda")
Example 5b.
   Reduced model (e.g., ACDM)
# with hierarchical att structure #
# --- User-specified attribute structure ----#
Q <- sim30GDINA$simQ
K <- ncol(0)
# linear structure A1->A2->A3->A4->A5
linear <- list(c(1,2),
              c(2,3),
              c(3,4),
              c(4,5))
struc <- att.structure(linear,K)</pre>
set.seed(123)
# data simulation
N <- 1000
true.lc <- sample(c(1:2^K),N,replace=TRUE,prob=struc$att.prob)
table(true.lc) #check the sample
```

```
true.att <- attributepattern(K)[true.lc,]</pre>
gs <- matrix(rep(0.1,2*nrow(Q)),ncol=2)</pre>
# data simulation
simD <- simGDINA(N,Q,gs.parm = gs, model = "ACDM",attribute = true.att)</pre>
dat <- extract(simD, "dat")</pre>
modp1 <- GDINA(dat = dat, Q = Q, model = "ACDM",</pre>
             att.str = linear, att.dist = "saturated")
coef(modp1)
coef(modp1,"lambda")
#
          Example 6.
# Specify initial values for item
# parameters
# check initials to see the format for initial item parameters
initials <- sim10GDINA$simItempar</pre>
dat <- sim10GDINA$simdat</pre>
0 <- sim10GDINA$sim0</pre>
mod.initial <- GDINA(dat,Q,catprob.parm = initials)</pre>
# compare initial item parameters
Map(rbind, initials,extract(mod.initial,"initial.catprob"))
Example 7a.
# Fix item and structure parameters#
# Estimate person attribute profile#
# check initials to see the format for initial item parameters
initials <- sim10GDINA$simItempar</pre>
prior < c(0.1,0.1,0.1,0.1,0.15,0.15,0.15,0.15)
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
mod.ini <- GDINA(dat,Q,catprob.parm = initials,att.prior = prior,</pre>
                att.dist = "fixed",control=list(maxitr = 0))
personparm(mod.ini)
# compare item parameters
Map(rbind, initials,coef(mod.ini))
#
          Example 7b.
 Fix parameters for some items #
# Estimate person attribute profile#
# check initials to see the format for initial item parameters
initials <- sim10GDINA$simItempar</pre>
prior \leftarrow c(0.1,0.1,0.1,0.1,0.15,0.15,0.15,0.15)
```

```
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
# fix parameters of the first 5 items; do not fix mixing proportion parameters
mod.ini <- GDINA(dat,Q,catprob.parm = initials,</pre>
                att.dist = "saturated",control=list(maxitr = c(rep(0,5),rep(2000,5))))
personparm(mod.ini)
# compare item parameters
Map(rbind, initials,coef(mod.ini))
#
          Example 8.
#
       polytomous attribute
#
         model estimation
    see Chen, de la Torre 2013
# --- polytomous attribute G-DINA model --- #
dat <- sim30pGDINA$simdat</pre>
Q <- sim30pGDINA$simQ
#polytomous G-DINA model
pout <- GDINA(dat,Q)</pre>
# ---- polymous DINA model -----#
pout2 <- GDINA(dat,Q,model="DINA")</pre>
anova(pout,pout2)
Example 9.
#
       Sequential G-DINA model
                               #
#
    see Ma, & de la Torre 2016
                               #
# --- polytomous attribute G-DINA model --- #
dat <- sim20seqGDINA$simdat</pre>
Q <- sim20seqGDINA$simQ
    Item Cat A1 A2 A3 A4 A5
#
      1 1 1 0 0 0 0
#
          2 0
               1
                  0
             0
               0
          1
                  1
      2
          2 0 0 0
                     1
      3
          1 0 0 0 0 1
      3 2 1 0 0 0 0
#
       4
         1 0 0 0 0 1
#sequential G-DINA model
sGDINA <- GDINA(dat,Q,sequential = TRUE)</pre>
sDINA <- GDINA(dat,Q,sequential = TRUE,model = "DINA")</pre>
anova(sGDINA,sDINA)
coef(sDINA) # processing function
coef(sDINA,"itemprob") # success probabilities for each item
```

```
coef(sDINA,"LCprob") # success probabilities for each category for all latent classes
Example 10a.
    Multiple-Group G-DINA model
Q <- sim10GDINA$simQ
K <- ncol(0)
# parameter simulation
# Group 1 - female
N1 <- 3000
gs1 <- matrix(rep(0.1,2*nrow(Q)),ncol=2)</pre>
# Group 2 - male
N2 <- 3000
gs2 <- matrix(rep(0.2,2*nrow(Q)),ncol=2)</pre>
# data simulation for each group
sim1 <- simGDINA(N1,Q,gs.parm = gs1,model = "DINA",att.dist = "higher.order",</pre>
                higher.order.parm = list(theta = rnorm(N1),
                lambda = data.frame(a=rep(1.5,K),b=seq(-1,1,length.out=K))))
sim2 <- simGDINA(N2,Q,gs.parm = gs2,model = "DINO",att.dist = "higher.order",</pre>
                higher.order.parm = list(theta = rnorm(N2),
                lambda = data.frame(a=rep(1,K),b=seq(-2,2,length.out=K))))
# combine data - all items have the same item parameters
dat <- rbind(extract(sim1, "dat"), extract(sim2, "dat"))</pre>
gr <- rep(c(1,2),c(3000,3000))
# Fit G-DINA model
mg.est <- GDINA(dat = dat,Q = Q,group = gr)</pre>
summary(mg.est)
extract(mg.est, "posterior.prob")
coef(mg.est,"lambda")
Example 10b.
    Multiple-Group G-DINA model
Q <- sim30GDINA$simQ
K <- ncol(0)
# parameter simulation
N1 <- 3000
gs1 <- matrix(rep(0.1,2*nrow(Q)),ncol=2)</pre>
N2 <- 3000
gs2 <- matrix(rep(0.2,2*nrow(Q)),ncol=2)</pre>
# data simulation for each group
# two groups have different theta distributions
sim1 <- simGDINA(N1,Q,gs.parm = gs1,model = "DINA",att.dist = "higher.order",</pre>
                higher.order.parm = list(theta = rnorm(N1),
                lambda = data.frame(a=rep(1,K),b=seq(-2,2,length.out=K))))
```

```
sim2 <- simGDINA(N2,Q,gs.parm = gs2,model = "DINO",att.dist = "higher.order",</pre>
                higher.order.parm = list(theta = rnorm(N2,1,1),
                lambda = data.frame(a=rep(1,K),b=seq(-2,2,length.out=K))))
# combine data - different groups have distinct item parameters
# see ?bdiagMatrix
dat <- bdiagMatrix(list(extract(sim1,"dat"),extract(sim2,"dat")),fill=NA)</pre>
Q \leftarrow rbind(Q,Q)
gr \leftarrow rep(c(1,2),c(3000,3000))
mg.est <- GDINA(dat = dat,Q = Q,group = gr)</pre>
# Fit G-DINA model
mg.est <- GDINA(dat = dat,Q = Q,group = gr,att.dist="higher.order",</pre>
higher.order=list(model = "Rasch"))
summary(mg.est)
coef(mg.est,"lambda")
personparm(mg.est)
personparm(mg.est,"HO")
extract(mg.est, "posterior.prob")
Example 11.
#
#
           Bug DINO model
set.seed(123)
Q <- sim10GDINA$simQ # 1 represents misconceptions/bugs
ip <- list(</pre>
c(0.8, 0.2),
c(0.7, 0.1),
c(0.9, 0.2),
c(0.9,0.1,0.1,0.1),
c(0.9,0.1,0.1,0.1),
c(0.9, 0.1, 0.1, 0.1),
c(0.9,0.1,0.1,0.1),
c(0.9,0.1,0.1,0.1),
c(0.9,0.1,0.1,0.1),
c(0.9,0.1,0.1,0.1,0.1,0.1,0.1,0.1))
sim <- simGDINA(N=1000,Q=Q,catprob.parm = ip,model = "DINO")</pre>
dat <- extract(sim, "dat")</pre>
# use latent.var to specify a bug model
est <- GDINA(dat=dat,Q=Q,latent.var="bugs",model="DINO")</pre>
coef(est)
#
           Example 12.
                                  #
           Bug DINA model
set.seed(123)
Q <- sim10GDINA$simQ # 1 represents misconceptions/bugs
ip <- list(</pre>
c(0.8, 0.2),
```

```
c(0.7, 0.1),
c(0.9, 0.2),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.1),
c(0.9,0.9,0.9,0.9,0.9,0.9,0.9,0.1))
sim <- simGDINA(N=1000,Q=Q,catprob.parm = ip,model="DINA")</pre>
dat <- extract(sim, "dat")</pre>
# use latent.var to specify a bug model
est <- GDINA(dat=dat,Q=Q,latent.var="bugs",model="DINA")</pre>
coef(est)
#
           Example 13a.
     user specified design matrix #
#
        LCDM (logit G-DINA)
dat <- sim30GDINA$simdat</pre>
Q <- sim30GDINA$simQ
# LCDM
lcdm <- GDINA(dat = dat, Q = Q, model = "logitGDINA", control=list(conv.type="neg2LL"))</pre>
#Another way is to find design matrix for each item first => must be a list
D <- lapply(rowSums(Q),designmatrix,model="GDINA")</pre>
# for comparison, use change in -2LL as convergence criterion
# LCDM
lcdm2 <- GDINA(dat = dat, Q = Q, model = "UDF", design.matrix = D,</pre>
linkfunc = "logit", control=list(conv.type="neg2LL"),solver="slsqp")
# identity link GDINA
iGDINA <- GDINA(dat = dat, Q = Q, model = "GDINA",</pre>
control=list(conv.type="neg2LL"),solver="slsqp")
# compare all three models => identical
anova(lcdm,lcdm2,iGDINA)
#
           Example 13b.
#
     user specified design matrix #
            RRUM
dat <- sim30GDINA$simdat</pre>
Q <- sim30GDINA$simQ
# specify design matrix for each item => must be a list
# D can be defined by the user
D <- lapply(rowSums(Q),designmatrix,model="ACDM")</pre>
```

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```
# for comparison, use change in -2LL as convergence criterion
logACDM <- GDINA(dat = dat, Q = Q, model = "UDF", design.matrix = D,</pre>
linkfunc = "log", control=list(conv.type="neg2LL"),solver="slsqp")
# identity link GDINA
RRUM <- GDINA(dat = dat, Q = Q, model = "RRUM",
             control=list(conv.type="neg2LL"),solver="slsqp")
# compare two models => identical
anova(logACDM,RRUM)
Example 14.
     Multiple-strategy DINA model #
Q \leftarrow matrix(c(1,1,1,1,0,
1,2,0,1,1,
2,1,1,0,0,
3,1,0,1,0,
4,1,0,0,1,
5,1,1,0,0,
5,2,0,0,1),ncol = 5,byrow = TRUE)
d <- list(</pre>
 item1=c(0.2,0.7),
 item2=c(0.1,0.6),
 item3=c(0.2,0.6),
 item4=c(0.2,0.7),
 item5=c(0.1,0.8))
 set.seed(12345)
sim <- simGDINA(N=1000,Q = Q, delta.parm = d,
              model = c("MSDINA", "MSDINA", "DINA",
                        "DINA", "DINA", "MSDINA", "MSDINA"))
# simulated data
dat <- extract(sim, what = "dat")</pre>
# estimation
# MSDINA need to be specified for each strategy
est <- GDINA(dat,Q,model = c("MSDINA","MSDINA","DINA",</pre>
                             "DINA", "DINA", "MSDINA", "MSDINA"))
coef(est, "delta")
## End(Not run)
```

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### **Description**

An (experimental) function for calibrating the multiple-strategy CDMs for dichotomous response data (Ma & Guo, 2019)

#### Usage

```
GMSCDM(
  dat,
  msQ,
  model = "ACDM",
  s = 1,
  att.prior = NULL,
  delta = NULL,
  control = list()
)
```

### **Arguments**

dat A required binary item response matrix

msQ A multiple-strategy Q-matrix; the first column gives item numbers and the sec-

ond column gives the strategy number. See examples.

model CDM used; can be "DINA", "DINO", "ACDM", "LLM", and "RRUM", representing the

GMS-DINA, GMS-DINO, GMS-ACDM, GMS-LLM and GMS-RRUM in Ma & Guo (2019), respectively. It can also be "rDINA" and "rDINO", representing restricted GMS-DINA and GMS-DINO models where delta\_jm1 are equal for all strategies. Note that only a single model can be used for the whole test.

s strategy selection parameter. It is equal to 1 by default.

att.prior mixing proportion parameters.
delta delta parameters in list format.
control a list of control arguments

## Value

an object of class GMSCDM with the following components:

IRF A matrix of success probabilities for each latent class on each item (IRF)

**delta** A list of delta parameters

attribute A list of estimated attribute profiles including EAP, MLE and MAP estimates.

testfit A list of test fit statistics including deviance, number of parameters, AIC and BIC

**sIRF** strategy-specific item response function

**pimc** Probability of adopting each strategy on each item for each latent class

sprv Strategy pravelence

### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

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### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Ma, W., & Guo, W. (2019). Cognitive Diagnosis Models for Multiple Strategies. *British Journal of Mathematical and Statistical Psychology*.

### See Also

GDINA for MS-DINA model and single strategy CDMs, and DTM for diagnostic tree model for multiple strategies in polytomous response data

```
## Not run:
###################
# data simulation
####################
set.seed(123)
msQ <- matrix(</pre>
c(1,1,0,1,
1,2,1,0,
2,1,1,0,
3,1,0,1,
4,1,1,1,
5,1,1,1),6,4,byrow = T
# J \times L - 00,10,01,11
LC.prob <- matrix(c(</pre>
0.2,0.7727,0.5889,0.8125,
0.1,0.9,0.1,0.9,
0.1,0.1,0.8,0.8,
0.2,0.5,0.4,0.7,
0.2,0.4,0.7,0.9),5,4,byrow=TRUE)
N <- 10000
att <- sample(1:4,N,replace=TRUE)</pre>
dat <- 1*(t(LC.prob[,att])>matrix(runif(N*5),N,5))
est <- GMSCDM(dat,msQ)</pre>
# item response function
est$IRF
# strategy specific IRF
est$sIRF
#####################################
# Example 14 from GDINA function
####################################
```

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```
Q \leftarrow matrix(c(1,1,1,1,0,
1,2,0,1,1,
2,1,1,0,0,
3,1,0,1,0,
4,1,0,0,1,
5,1,1,0,0,
5,2,0,0,1),ncol = 5,byrow = TRUE)
d <- list(</pre>
  item1=c(0.2,0.7),
  item2=c(0.1,0.6),
  item3=c(0.2,0.6),
  item4=c(0.2,0.7),
  item5=c(0.1,0.8))
  set.seed(123)
sim <- simGDINA(N=1000,Q = Q, delta.parm = d,
               model = c("MSDINA", "MSDINA", "DINA",
                           "DINA", "DINA", "MSDINA", "MSDINA"))
# simulated data
dat <- extract(sim,what = "dat")</pre>
# estimation
# MSDINA need to be specified for each strategy
est <- GDINA(dat,Q,model = c("MSDINA","MSDINA","DINA",</pre>
                               "DINA", "DINA", "MSDINA", "MSDINA"),
              control = list(conv.type = "neg2LL",conv.crit = .01))
# Approximate the MS-DINA model using GMS DINA model
est2 <- GMSCDM(dat, Q, model = "rDINA", s = 10,</pre>
               control = list(conv.type = "neg2LL",conv.crit = .01))
## End(Not run)
```

ILCA

Iterative latent-class analysis

### **Description**

This function implements an iterative latent class analysis (ILCA; Jiang, 2019) approach to estimating attributes for cognitive diagnosis.

### Usage

```
ILCA(dat, Q, seed.num = 5)
```

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## **Arguments**

dat A required binary item response matrix.

Q A required binary item and attribute association matrix.

seed.num seed number; Default = 5.

### Value

Estimated attribute profiles.

## Author(s)

Zhehan Jiang, The University of Alabama

### References

Jiang, Z. (2019). Using the iterative latent-class analysis approach to improve attribute accuracy in diagnostic classification models. *Behavior research methods*, 1-10.

## **Examples**

```
## Not run:
ILCA(sim10GDINA$simdat, sim10GDINA$simQ)
## End(Not run)
```

indlog Lik

Extract log-likelihood for each individual

## Description

Extract individual log-likelihood.

### Usage

```
indlogLik(object, ...)
```

# Arguments

object GDINA object

... additional arguments

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# Examples

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ

fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
iL <- indlogLik(fit)
iL[1:6,]
## End(Not run)</pre>
```

indlogPost

Extract log posterior for each individual

# Description

Extract individual log posterior.

## Usage

```
indlogPost(object, ...)
```

## **Arguments**

```
object GDINA object
... additional arguments
```

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
iP <- indlogPost(fit)
iP[1:6,]
## End(Not run)</pre>
```

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itemfit

Item fit statistics

### **Description**

Calculate item fit statistics (Chen, de la Torre, & Zhang, 2013) and draw heatmap plot for item pairs

### Usage

```
itemfit(
  GDINA.obj,
  person.sim = "post",
  p.adjust.methods = "holm",
  cor.use = "pairwise.complete.obs",
  digits = 4,
  N.resampling = NULL,
  randomseed = 123456
)

## S3 method for class 'itemfit'
  extract(object, what, ...)

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

#### **Arguments**

GDINA.obj An estimated model object of class GDINA

person.sim Simulate expected responses from the posterior or based on EAP, MAP and

MLE estimates.

p.adjust.methods

p-values for the proportion correct, transformed correlation, and log-odds ratio can be adjusted for multiple comparisons at test and item level. This is conducted using p.adjust function in **stats**, and therefore all adjustment methods supported by p.adjust can be used, including "holm", "hochberg", "hommel", "bonferroni", "BH" and "BY". See p.adjust for more details. "holm" is the

defaul

cor.use how to deal with missing values when calculating correlations? This argument

will be passed to use when calling stats::cor.

digits How many decimal places in each number? The default is 4.

N. resampling the sample size of resampling. By default, it is the maximum of 1e+5 and ten

times of current sample size.

randomseed random seed; This is used to make sure the results are replicable. The default

random seed is 123456.

object objects of class itemfit for various S3 methods

itemfit 53

what argument for S3 method extract indicating what to extract; It can be "p" for proportion correct statistics, "r" for transformed correlations, logOR for log odds ratios and "maxitemfit" for maximum statistics for each item.
... additional arguments

#### Value

an object of class itemfit consisting of several elements that can be extracted using method extract. Components that can be extracted include:

p the proportion correct statistics, adjusted and unadjusted p values for each item

r the transformed correlations, adjusted and unadjusted p values for each item pair

logOR the log odds ratios, adjusted and unadjusted p values for each item pair

**maxitemfit** the maximum proportion correct, transformed correlation, and log-odds ratio for each item with associated item-level adjusted p-values

#### **Methods (by generic)**

- extract: extract various elements from itemfit objects
- summary: print summary information

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu> Jimmy de la Torre, The University of Hong Kong

#### References

Chen, J., de la Torre, J., & Zhang, Z. (2013). Relative and Absolute Fit Evaluation in Cognitive Diagnosis Modeling. *Journal of Educational Measurement*, 50, 123-140.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ

mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")
mod1
itmfit <- itemfit(mod1)

# Print "test-level" item fit statistics
# p-values are adjusted for multiple comparisons
# for proportion correct, there are J comparisons
# for log odds ratio and transformed correlation,
# there are J*(J-1)/2 comparisons</pre>
```

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```
itmfit

# The following gives maximum item fit statistics for
# each item with item level p-value adjustment
# For each item, there are J-1 comparisons for each of
# log odds ratio and transformed correlation
summary(itmfit)

# use extract to extract various components
extract(itmfit,"r")

mod2 <- GDINA(dat,Q,model="DINA")
itmfit2 <- itemfit(mod2)
#misfit heatmap
plot(itmfit2)
itmfit2

## End(Not run)</pre>
```

itemparm

extract item parameters (deprecated)

### **Description**

This function has been deprecated; use coef instead.

### Usage

```
itemparm(
  object,
  what = c("catprob", "gs", "delta", "rrum", "itemprob", "LCprob"),
  withSE = FALSE,
  SE.type = 2,
  digits = 4,
  ...
)

## S3 method for class 'GDINA'
itemparm(
  object,
  what = c("catprob", "gs", "delta", "rrum", "itemprob", "LCprob"),
  withSE = FALSE,
  SE.type = 2,
  digits = 4,
  ...
)
```

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## **Arguments**

object	estimated GDINA object returned from GDINA
what	what to show.
withSE	show standard errors or not?
SE.type	Type of standard errors.
digits	how many decimal places for the ouput?
• • •	additional arguments

### References

Philipp, M., Strobl, C., de la Torre, J., & Zeileis, A.(2017). On the estimation of standard errors in cognitive diagnosis models. *Journal of Educational and Behavioral Statistics*, 43, 88-115.

## **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
# deprecated
itemparm(fit)
coef(fit)
## End(Not run)</pre>
```

LC2LG

Transformation between latent classes and latent groups

## Description

This function gives the equivalent latent classes which have the same category success probabilities for each category or item.

### Usage

```
LC2LG(Q, sequential = FALSE, att.str = NULL)
```

### **Arguments**

Q	A required $J \times K$ binary Q-matrix. J represents test length and K represents the number of attributes of this test. Entry 1 at row j and column k represents the $k^{th}$ attribute is measured by item $j$ , and 0 means item $j$ does not measure attribute $k$ .
sequential	logical; whether the Q-matrix is a Qc-matrix for sequential models?

att.str attribute structure. See GDINA for details.

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#### Value

An item or category by latent class matrix. In the G-DINA model, if item j measures Kj attributes,  $2^K$  latent classes can be combined into  $2^{Kj}$  latent groups. This matrix gives which latent group each of  $2^K$  latent classes belongs to for each item.

### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu> Jimmy de la Torre, The University of Hong Kong

#### **Examples**

```
attributepattern(3)
q <- matrix(scan(text = "0 1 0 1 0 1 1 1 0"),ncol = 3)
q
LC2LG(Q = q)</pre>
```

MCmode1

Multiple-choice models

### **Description**

This function estimates the multiple-choice DINA model (de la Torre, 2009).

### Usage

```
MCmodel(
  dat,
  Qc,
  model = "MCDINA",
  key = NULL,
  conv.crit = 0.001,
  maxitr = 2000,
  conv.type = "pr"
)
```

### **Arguments**

dat

A required  $N \times J$  data matrix of N examinees to J items. Values must be 1, 2,... representing nominal categories. Missing values are currently not allowed.

Qс

A required category and attribute association matrix. The first column gives the item number, which must be numeric (i.e., 1,2,...) and match the number of column in the data. The second column indicates the coded category of each item. The number in the second column must match with the number in the data, but if a category is not coded, it should not be included in the Q-matrix. Entry

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1 indicates that the attribute is measured by the category, and 0 otherwise. Note that the MC-DINA model assumes that the category with the largest number of 1s is the key and that the coded distractors should allow to assign examinees

uniquely.

model MCDINA only currently. Other MC models may be incorporated.

key a numeric vector giving the key of each item. See Examples. NULL by default

indicating the coded category requiring the largest number of 1s is the key.

conv.crit The convergence criterion for max absolute change in conv.type for two con-

secutive iterations.

maxitr The maximum iterations allowed.

conv. type convergence criteria; Can be pr or LL, indicating category response function, or

-2 times log-likelihood, respectively.

### Value

an object of class MCmodel with the following components:

**prob.parm** A list of success probabilities for each reduced latent class on each item (IRF)

prob.se A list of standard errors of item parameters

attribute A list of estimated attribute profiles including EAP, MLE and MAP estimates.

testfit A list of test fit statistics including deviance, number of parameters, AIC and BIC

**R** expected # of individuals in each latent group choosing each option

**lik** posterior probability

itr Total # of iterations

### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

De La Torre, J. (2009). A cognitive diagnosis model for cognitively based multiple-choice options. *Applied Psychological Measurement*, *33*, 163–183.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

#### See Also

GDINA for G-DINA model

```
## Not run:
  # check the format of the data
  # Entry 0 is not allowed
  head(sim10MCDINA$simdat)
```

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```
# check the format of the Q-matrix
# Take item 1 as an example:
# category 2 has a q-vector (1,0,0)
# category 1 has a q-vector (0,1,0)
# category 4 has a q-vector (1,1,0)
# category 3 is not included in the Q-matrix because it is not coded
# the order of the coded categories in the Q-matrix doesn't matter
sim10MCDINA$simQ
      Item coded cat A1 A2 A3
#
              2 1 0 0
#
        1
#
                   1 0 1 0
#
         1
                   4 1 1 0
#...
est <- MCmodel(sim10MCDINA$simdat,sim10MCDINA$simQ)</pre>
est
est$testfit
# Distractors involving more attributes
# some distractors may involve attributes that are not invovled by the key option
# this is not allowed by the "original" MC-DINA (de la Torre, 2009) but is allowed
# in the current implementation
# Users need to specify the key for each item to appropriate handle such an issue
# Note item 1 below: category 1 is the key (as indicated in the key argument below)
# The distractor (category 4) involves an attribute not included by the key option
Qc <- matrix(c(1,1,1,1,0,
               1,2,0,1,0,
               1,3,1,0,0,
              1,4,1,0,1,
               2,1,1,0,0,
               2,3,1,1,0,
               2,2,1,1,1,
               3,4,1,1,1,
               3,2,1,1,0,
               3,3,0,1,1,
               4,1,0,1,1,
               4,2,0,0,1,
               5,1,1,0,0,
               6,3,0,1,0,
               7,2,0,0,1,
               8,4,1,0,0,
               9,1,0,1,0,
               10, 4,0,0,1), ncol = 5, byrow = TRUE)
est2 <- MCmodel(sim10MCDINA2$simdat,Qc, key = c(1,2,4,1,1,3,2,4,1,4))
est2
est2$prob.parm
```

```
est2$testfit
est2$attribute
## End(Not run)
```

modelcomp

Item-level model comparison using Wald, LR or LM tests

### **Description**

This function evaluates whether the saturated G-DINA model can be replaced by reduced CDMs without significant loss in model data fit for each item using the Wald test, likelihood ratio (LR) test or Lagrange multiplier (LM) test. For Wald test, see de la Torre (2011), de la Torre and Lee (2013), Ma, Iaconangelo and de la Torre (2016) and Ma & de la Torre (2018) for details. For LR test and a two-step LR approximation procedure, see Sorrel, de la Torre, Abad, and Olea (2017), Ma (2017) and Ma & de la Torre (2019). For LM test, which is only applicable for DINA, DINO and ACDM, see Sorrel, Abad, Olea, de la Torre, and Barrada (2017). This function also calculates the dissimilarity between the reduced models and the G-DINA model, which can be viewed as a measure of effect size (Ma, Iaconangelo & de la Torre, 2016).

### Usage

```
modelcomp(
  GDINA.obj = NULL,
 method = "Wald",
  items = "all",
  p.adjust.methods = "holm",
 models = c("DINA", "DINO", "ACDM", "LLM", "RRUM"),
  decision.args = list(rule = "simpler", alpha.level = 0.05, adjusted = FALSE),
 DS = FALSE,
 Wald.args = list(SE.type = 2, varcov = NULL),
 LR.args = list(LR.approx = FALSE),
 LM.args = list(reducedMDINA = NULL, reducedMDINO = NULL, reducedMACDM = NULL, SE.type
    = 2)
)
## S3 method for class 'modelcomp'
extract(
  object,
 what = c("stats", "pvalues", "adj.pvalues", "df", "DS", "selected.model"),
  digits = 4,
)
## S3 method for class 'modelcomp'
summary(object, ...)
```

### **Arguments**

GDINA. obj An estimated model object of class GDINA

method method for item level model comparison; can be wald, LR or LM.

items a vector of items to specify the items for model comparsion

p.adjust.methods

adjusted p-values for multiple hypothesis tests. This is conducted using p.adjust function in **stats**, and therefore all adjustment methods supported by p.adjust can be used, including "holm", "hochberg", "hommel", "bonferroni", "BH" and "BY". See p.adjust for more details. "holm" is the default, indicating the

Holm method.

models a vector specifying which reduced CDMs are possible reduced CDMs for each

item. The default is "DINA", "DINO", "ACDM", "LLM", and "RRUM".

decision.args a list of options for determining the most appropriate models including (1) rule

can be either "simpler" or "largestp". See details; (2) alpha.level for the nominal level of decision; and (3) adjusted can be either TRUE or FALSE indicating whether the decision is based on p value (adjusted = FALSE) or adjusted

p values.

DS whether dissimilarity index should be calculated? FALSE is the default.

Wald.args a list of options for Wald test including (1) SE. type giving the type of covariance

matrix for the Wald test; by default, it uses outer product of gradient based on incomplete information matrix; (2) varcov for user specified variance-covariance matrix. If supplied, it must be a list, giving the variance covariance matrix of success probability for each item or category. The default is NULL, in which case, the estimated variance-covariance matrix from the GDINA function is used.

LR. args a list of options for LR test including for now only LR. approx, which is either

TRUE or FALSE, indicating whether a two-step LR approximation is implemented

or not.

LM. args a list of options for LM test including reducedMDINA, reducedMDINO, and reducedMACDM

for DINA, DINO and ACDM estimates from the GDINA function; SE. type spec-

ifies the type of covariance matrix.

object of class modelcomp for various S3 methods

what argument for S3 method extract indicating what to extract; It can be "wald" for

wald statistics, "wald.p" for associated p-values, "df" for degrees of freedom,

and "DS" for dissimilarity between G-DINA and other CDMs.

digits How many decimal places in each number? The default is 4.

... additional arguments

#### **Details**

After the test statistics for each reduced CDM were calculated for each item, the reduced models with p values less than the pre-specified alpha level were rejected. If all reduced models were rejected for an item, the G-DINA model was used as the best model; if at least one reduced model was retained, two different rules can be implemented for selecting the best model specified in argument decision.args:

(1) when rule="simpler", which is the default,

If (a) the DINA or DINO model was one of the retained models, then the DINA or DINO model with the larger p value was selected as the best model; but if (b) both DINA and DINO were rejected, the reduced model with the largest p value was selected as the best model for this item. Note that when the p-values of several reduced models were greater than 0.05, the DINA and DINO models were preferred over the A-CDM, LLM, and R-RUM because of their simplicity. This procedure is originally proposed by Ma, Iaconangelo, and de la Torre (2016).

(2) When rule="largestp":

The reduced model with the largest p-values is selected as the most appropriate model.

#### Value

an object of class modelcomp. Elements that can be extracted using extract method include

stats Wald or LR statistics

**pvalues** p-values associated with the test statistics

adj.pvalues adjusted p-values

df degrees of freedom

DS dissimilarity between G-DINA and other CDMs

### Methods (by generic)

- extract: extract various elements from modelcomp objects
- summary: print summary information

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu> Miguel A. Sorrel, Universidad Autonoma de Madrid Jimmy de la Torre, The University of Hong Kong

#### References

de la Torre, J., & Lee, Y. S. (2013). Evaluating the wald test for item-level comparison of saturated and reduced models in cognitive diagnosis. *Journal of Educational Measurement*, 50, 355-373.

Ma, W., Iaconangelo, C., & de la Torre, J. (2016). Model similarity, model selection and attribute classification. *Applied Psychological Measurement*, 40, 200-217.

Ma, W. (2017). A Sequential Cognitive Diagnosis Model for Graded Response: Model Development, Q-Matrix Validation, and Model Comparison. Unpublished doctoral dissertation. New Brunswick, NJ: Rutgers University.

Ma, W., & de la Torre, J. (2019). Category-Level Model Selection for the Sequential G-DINA Model. *Journal of Educational and Behavioral Statistics*. 44, 61-82.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Sorrel, M. A., Abad, F. J., Olea, J., de la Torre, J., & Barrada, J. R. (2017). Inferential Item-Fit Evaluation in Cognitive Diagnosis Modeling. *Applied Psychological Measurement*, 41, 614-631.

Sorrel, M. A., de la Torre, J., Abad, F. J., & Olea, J. (2017). Two-Step Likelihood Ratio Test for Item-Level Model Comparison in Cognitive Diagnosis Models. *Methodology*, *13*, 39-47.

### See Also

```
GDINA, autoGDINA
```

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
# --- GDINA model ---#
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")</pre>
####################
# Wald test
####################
w <- modelcomp(fit)</pre>
# wald statistics
extract(w, "stats")
#p values
extract(w, "pvalues")
# selected models
extract(w, "selected.model")
# LR and Two-step LR test
lr <- modelcomp(fit,method = "LR")</pre>
lr
TwostepLR <- modelcomp(fit,items =c(6:10),method = "LR",LR.args = list(LR.approx = TRUE))</pre>
TwostepLR
#############################
# LM test
dina <- GDINA(dat = dat, Q = Q, model = "DINA")</pre>
dino <- GDINA(dat = dat, Q = Q, model = "DINO")</pre>
acdm <- GDINA(dat = dat, Q = Q, model = "ACDM")</pre>
lm <- modelcomp(method = "LM",LM.args=list(reducedMDINA = dina,</pre>
reducedMDINO = dino, reducedMACDM = acdm))
1m
```

modelfit 63

## End(Not run)

modelfit

Model fit statistics

#### **Description**

Calculate various absolute model-data fit statistics

#### Usage

```
modelfit(GDINA.obj, CI = 0.9, ItemOnly = FALSE)
```

#### **Arguments**

GDINA.obj An estimated model object of class GDINA

CI numeric value from 0 to 1 indicating the range of the confidence interval for

RMSEA. Default returns the 90% interval.

ItemOnly should joint attribute distribution parameters be considered? Default = FALSE.

See Ma (2019).

#### Details

Various model-data fit statistics including M2 statistic for G-DINA model with dichotmous responses (Liu, Tian, & Xin, 2016; Hansen, Cai, Monroe, & Li, 2016) and for sequential G-DINA model with graded responses (Ma, 2020). It also calculates SRMSR and RMSEA2.

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Hansen, M., Cai, L., Monroe, S., & Li, Z. (2016). Limited-information goodness-of-fit testing of diagnostic classification item response models. *British Journal of Mathematical and Statistical Psychology*. 69, 225–252.

Liu, Y., Tian, W., & Xin, T. (2016). An Application of M2 Statistic to Evaluate the Fit of Cognitive Diagnostic Models. *Journal of Educational and Behavioral Statistics*, 41, 3-26.

Ma, W. (2020). Evaluating the fit of sequential G-DINA model using limited-information measures. *Applied Psychological Measurement*, 44, 167-181.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

Maydeu-Olivares, A. (2013). Goodness-of-Fit Assessment of Item Response Theory Models. *Measurement*, 11, 71-101.

64 monocheck

### **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
mod1 <- GDINA(dat = dat, Q = Q, model = "DINA")
modelfit(mod1)
## End(Not run)</pre>
```

monocheck

This function checks if monotonicity is violated

## **Description**

If mastering an additional attribute lead to a lower probabilities of success, the monotonicity is violated.

## Usage

```
monocheck(object, strict = FALSE)
```

## **Arguments**

object of class GDINA

strict whether a strict monotonicity is checked?

### Value

a logical vector for each item or category indicating whether the monotonicity is violated (TRUE) or not (FALSE)

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ

mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")
check <- monocheck(mod1)
check
mod2 <- GDINA(dat = dat, Q = Q, model = "GDINA", mono.constraint = check)
check2 <- monocheck(mod2)
check2
## End(Not run)</pre>
```

npar 65

npar

Calculate the number of parameters

## Description

Calculate the number of parameters for GDINA estimates. Returned the total number of parameters, the number of item parameters and the number parameters of joint attribute distribution.

### Usage

```
npar(object, ...)
```

### **Arguments**

```
object GDINA object
... additional arguments
```

### **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ

fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
npar(fit)
## End(Not run)</pre>
```

personparm

calculate person (incidental) parameters

### **Description**

Function to calculate various person attribute parameters, including "EAP", "MAP", and "MLE", for EAP, MAP and MLE estimates of attribute patterns (see Huebner & Wang, 2011), "mp" for marginal mastery probabilities, and "HO" for higher-order ability estimates if a higher-order model is fitted. See GDINA for examples.

### Usage

```
personparm(object, what = c("EAP", "MAP", "MLE", "mp", "HO"), digits = 4, ...)
```

plot.GDINA

## **Arguments**

object estimated GDINA object returned from GDINA

what what to extract; It can be "EAP", "MAP", and "MLE", for EAP, MAP and MLE
estimates of attribute patterns, and "mp" for marginal mastery probabilities, and
"HO" for higher-order ability estimates if a higher-order model is fitted.

digits number of decimal places.
... additional arguments

### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu> Jimmy de la Torre, The University of Hong Kong

#### References

Huebner, A., & Wang, C. (2011). A note on comparing examinee classification methods for cognitive diagnosis models. *Educational and Psychological Measurement*, 71, 407-419.

### **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
# EAP
head(personparm(fit))
# MAP
head(personparm(fit, what = "MAP"))
## End(Not run)</pre>
```

plot.GDINA

Create plots for GDINA estimates

### **Description**

Create various plots for GDINA estimates

## Usage

```
## S3 method for class 'GDINA'
plot(
    x,
    what = "IRF",
    item = "all",
    withSE = FALSE,
```

plot.itemfit 67

```
SE.type = 2,
person = 1,
att.names = NULL,
...
)
```

### **Arguments**

Х model object of class GDINA type of plot. Can be "IRF" for item/category response function plot, or "mp" for what mastery probabilities for individuals. A scalar or vector specifying the item(s) for IRF plots. item withSE logical; Add error bar (estimate - SE, estimate + SE) to the IRF plots? How is SE estimated. By default, it's based on OPG using incomplete informa-SE.type A scalar or vector specifying the number of individuals for mastery plots. person Optional; a vector for attribute names. att.names additional arguments

#### See Also

GDINA, autoGDINA

## Examples

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")
#plot item response functions for item 10
plot(mod1, item = 10)
plot(mod1, what = "IRF", item = 10,withSE = TRUE)

# plot mastery probabilities for individuals 4 and 10
plot(mod1, what = "mp", person = c(4,10))
plot(mod1, what = "mp", person = c(4,10,15),
att.names = c("addition", "subtraction", "multiplication"))
## End(Not run)</pre>
```

plot.itemfit

Item fit plots

### **Description**

Create plots of bivariate heatmap for item fit

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### Usage

```
## S3 method for class 'itemfit'
plot(x, type = "all", adjusted = TRUE, ...)
```

### **Arguments**

```
x model object of class itemfittype type of heatmap plotadjusted logical; plot adjusted or unadjusted p-values?additional arguments
```

#### See Also

```
GDINA, itemfit
```

### **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ

fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
ift <- itemfit(fit)
# plot the adjusted p values for log odds or transformed correlation
plot(ift)
# plot unadjusted p values for log odds
plot(ift,adjusted = FALSE, type = "logOR")
## End(Not run)</pre>
```

plot.Qval

Mesa plot for Q-matrix validation

### **Description**

The mesa plot was first proposed by de la Torre and Ma (2016) for graphically illustrating the best q-vector(s) for each item. The q-vector on the edge of the mesa is likely to be the best q-vector.

## Usage

```
## $3 method for class 'Qval'
plot(
    x,
    item,
    type = "best",
    no.qvector = 10,
    data.label = TRUE,
```

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```
eps = "auto",
  original.q.label = FALSE,
  auto.ylim = TRUE,
  ...
)
```

# Arguments ×

item a vector specifying which item(s) the plots are drawn for type types of the plot. It can be "best" or "all". If "best", for all q-vectors requiring the same number of attributes, only the one with the largest PVAF is plotted, which means  $K_j$  q-vectors are plotted; If "all", all q-vectors will be plotted. no qvector the number of q vectors that need to be plotted when type="all". The default is 10, which means the 10 q vectors with the largest PVAFs are plotted. data.label logical; To show data label or not?

eps the cutoff for PVAF. If not NULL, it must be a value between 0 and 1. A horizontal

line will be drawn accordingly.

model object of class Qvalidation

original.q.label

logical; print the label showing the original q-vector or not?

auto.ylim logical; create y range automatically or not?
... additional arguments passed to plot function

#### References

de la Torre, J., & Ma, W. (2016, August). Cognitive diagnosis modeling: A general framework approach and its implementation in R. A Short Course at the Fourth Conference on Statistical Methods in Psychometrics, Columbia University, New York.

#### See Also

```
Qval, autoGDINA
```

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
Q[1,] <- c(0,1,0)
mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")
out <- Qval(mod1,eps = 0.9)
item <- c(1,2,10)
plot(out,item=item,data.label=FALSE,type="all")
plot(out,item=10,type="best",eps=0.95)
plot(out,item=10,type="all",no.qvector=6)
## End(Not run)</pre>
```

70 Qval

Qval

Q-matrix validation

#### Description

Q-matrix validation for the (sequential) G-DINA model based on PVAF (de la Torre & Chiu, 2016; Najera, Sorrel, & Abad, 2019; Najera et al., 2020), stepwise Wald test (Ma & de la Torre, 2020) or mesa plot (de la Torre & Ma, 2016). All these methods are suitable for dichotomous and ordinal response data. If too many modifications are suggested based on the default PVAF method, you are suggested to try the stepwise Wald test method, iterative procedures or predicted cutoffs. You should always check the mesa plots for further examination.

### Usage

```
Qval(
  GDINA.obj,
  method = "PVAF",
  iter = "none",
  eps = 0.95,
  digits = 4,
  wald.args = list(),
  iter.args = list(empty.att = FALSE, max.iter = 150, verbose = FALSE)
)

## S3 method for class 'Qval'
  extract(object, what = c("sug.Q", "varsigma", "PVAF", "eps", "Q"), ...)

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

### **Arguments**

GDINA.obi an estimated model object of class GDINA which Q-matrix validation method is used? Can be either "PVAF" or "wald". method iter implement the method iteratively? Can be "none" for non-iterative validation (by default), "test", "test.att", or "item" (Najera et al., 2020). cutoff value for PVAF from 0 to 1. Default = 0.95. Note that it can also be -1, eps indicating the predicted cutoff based on Najera, Sorrel, and Abad (2019). how many decimal places in each number? The default is 4. digits wald.args a list of arguments for the stepwise Wald test method. **SE.type** type of covariance matrix for the Wald test alpha.level alpha level for the wald test

**GDI** it can be 0, 1 or 2; 0 means GDI is not used to choose the attribute - when more than one attributes are significant, the one with the largest p-value will be selected; GDI=1 means the attribute with the largest GDI will be selected; GDI=2 means the q-vector with the largest GDI will be selected.

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verbose print detailed information or not?

stepwise TRUE for stepwise approach and FALSE for forward approach

iter.args a list of arguments for the iterative implementation.

empty.att can a Q-matrix with an empty attribute (i.e., measured by no items)

be provided? Default is FALSE

max.iter maximum number of iterations. Default is 150

verbose print information after each iteration? Default is FALSE

object Qval objects for S3 methods

what argument for S3 method extract indicating what to extract; It can be "sug.Q"

for suggested Q-matrix, "Q" for original Q-matrix, "varsigma" for varsigma

index, and "PVAF" for PVAF.

... additional arguments

#### Value

An object of class Qval. Elements that can be extracted using extract method include:

sug.Q suggested Q-matrix

Q original Q-matrix

varsigma varsigma index

**PVAF** PVAF

### Methods (by generic)

• extract: extract various elements from Qval objects

• summary: print summary information

### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>, Miguel A. Sorrel, Universidad Autónoma de Madrid, Jimmy de la Torre, The University of Hong Kong

#### References

de la Torre, J. & Chiu, C-Y. (2016). A General Method of Empirical Q-matrix Validation. *Psychometrika*, 81, 253-273.

de la Torre, J., & Ma, W. (2016, August). Cognitive diagnosis modeling: A general framework approach and its implementation in R. A Short Course at the Fourth Conference on Statistical Methods in Psychometrics, Columbia University, New York.

Ma, W., & de la Torre, J. (2020). An empirical Q-matrix validation method for the sequential G-DINA model. *British Journal of Mathematical and Statistical Psychology*, 73, 142-163.

Najera, P., Sorrel, M. A., & Abad, F.J. (2019). Reconsidering cutoff points in the general method of empirical Q-matrix validation. *Educational and Psychological Measurement*, 79, 727-753.

Najera, P., Sorrel, M. A., de la Torre, J., & Abad, F. J. (2020). Improving robustness in Q-matrix validation using an iterative and dynamic procedure. *Applied Psychological Measurement*.

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### See Also

**GDINA** 

```
## Not run:
# Binary response
dat <- sim10GDINA$simdat</pre>
Q <- sim10GDINA$simQ
Q[10,] \leftarrow c(0,1,0)
# Fit the G-DINA model
mod1 <- GDINA(dat = dat, Q = Q, model = "GDINA")</pre>
# Q-validation using de la Torre and Chiu's method
pvaf <- Qval(mod1,method = "PVAF",eps = 0.95)</pre>
extract(pvaf, what = "PVAF")
#See also:
extract(pvaf,what = "varsigma")
extract(pvaf,what = "sug.Q")
# Draw mesa plots using the function plot
plot(pvaf,item=10)
#The stepwise Wald test
stepwise <- Qval(mod1,method = "wald")</pre>
stepwise
extract(stepwise, what = "PVAF")
#See also:
extract(stepwise,what = "varsigma")
extract(stepwise, what = "sug.Q")
\#Set\ eps = -1\ to\ determine\ the\ cutoff\ empirically
pvaf2 <- Qval(mod1,method = "PVAF",eps = -1)</pre>
pvaf2
#Iterative procedure (test-attribute level)
pvaf3 <- Qval(mod1, method = "PVAF", eps = -1,</pre>
             iter = "test.att", iter.args = list(verbose = 1))
pvaf3
# Ordinal response
```

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```
seq.est <- GDINA(sim20seqGDINA$simdat,sim20seqGDINA$simQ, sequential = TRUE)
stepwise <- Qval(seq.est, method = "wald")
## End(Not run)</pre>
```

rowMatch

Count the frequency of a row vector in a data frame

## **Description**

Count the frequency of a row vector in a data frame

#### Usage

```
rowMatch(df, vec = NULL)
```

## **Arguments**

df a data frame or matrix vec the vector for matching

#### Value

count the number of vector vec in the data frame row.no row numbers of the vector vec in the data frame

## **Examples**

```
\label{eq:df} \begin{array}{ll} df <- \mbox{ data.frame(V1=c(1L,2L),V2=LETTERS[1:3],V3=rep(1,12))} \\ rowMatch(df,c(2,"B",1)) \end{array}
```

score

Score function

#### **Description**

Calculate score function for each dichotomous item or each nonzero category for polytomous items Only applicable to saturated model of joint attribute distribution

#### Usage

```
score(object, parm = "delta")
```

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#### **Arguments**

object an object of class GDINA

parm Either delta or prob indicating score function for delta parameters and success

probabily parameters

#### Value

a list where elements give the score functions for each item or category

## **Examples**

```
## Not run:
dat <- sim10GDINA$simdat
Q <- sim10GDINA$simQ
fit <- GDINA(dat = dat, Q = Q, model = "GDINA")
score(fit)
## End(Not run)</pre>
```

sim10GDINA

Simulated data (10 items, G-DINA model)

## **Description**

Simulated data, Q-matrix and item parameters for a 10-item test with 3 attributes.

#### Usage

sim10GDINA

#### Format

A list with components:

```
simdat simulated responses of 1000 examinees
simQ artificial Q-matrix
simItempar artificial item parameters (probability of success for each latent group)
```

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

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sim10MCDINA

Simulated data (10 items, MC-DINA model)

## Description

Simulated data, Q-matrix and item parameters for a 10-item test measuring 3 attributes.

#### Usage

sim10MCDINA

## **Format**

A list with components:

simdat simulated responses of 3000 examinees simQ artificial Q-matrix

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

sim10MCDINA2

Simulated data (10 items, MC-DINA model)

## **Description**

Simulated data, Q-matrix and item parameters for a 10-item test measuring 5 attributes.

## Usage

sim10MCDINA2

#### **Format**

A list with components:

simdat simulated responses of 3000 examinees simQ artificial Q-matrix

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## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

sim20seqGDINA

Simulated data (20 items, sequential G-DINA model)

## Description

Simulated data, Qc-matrix and item parameters for a 20-item test measuring 5 attributes.

#### Usage

sim20seqGDINA

## **Format**

A list with components:

simulated polytomous responses of 2000 examinees

simQ artificial Qc-matrix

simItempar artificial item parameters (category level probability of success for each latent group)

#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

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sim21seqDINA

Simulated data (21 items, sequential DINA model)

#### **Description**

Simulated data, and Qc-matrix for a 21-item test measuring 5 attributes.

## Usage

sim21seqDINA

#### **Format**

A list with components:

simdat simulated responses of 2000 examinees simQ artificial Qc-matrix

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

sim30DINA

Simulated data (30 items, DINA model)

## **Description**

Simulated data, Q-matrix and item parameters for a 30-item test measuring 5 attributes.

## Usage

sim30DINA

## **Format**

A list with components:

simdat simulated responses of 1000 examinees simQ artificial Q-matrix

simItempar artificial item parameters (probability of success for each latent group)

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#### Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

sim30GDINA

Simulated data (30 items, G-DINA model)

## Description

Simulated data, Q-matrix and item parameters for a 30-item test measuring 5 attributes.

#### Usage

sim30GDINA

## **Format**

A list with components:

```
simdat simulated responses of 1000 examinees  \\ \text{simQ artificial } 30 \times 5 \text{ Q-matrix} \\ \\ \text{simItempar artificial item parameters(probability of success for each latent group)}
```

#### Author(s)

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#### References

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

sim30pGDINA 79

sim30pGDINA	Simulated data (30 items, polytomous G-DINA model)	
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## Description

Simulated data, Q-matrix and item parameters for a 30-item test measuring 5 attributes.

## Usage

```
sim30pGDINA
```

#### **Format**

A list with components:

```
simulated responses of 3000 examinees
```

simQ artificial Q-matrix

simItempar artificial item parameters(probability of success for each latent group)

simDTM	Simulating data for diagnostic tree model	

## Description

Data generation for diagnostic tree model

## Usage

```
simDTM(N, Qc, gs.parm, Tmatrix, red.delta = NULL, att.gr = NULL)
```

## Arguments

N	sample size
Qc	Association matrix between attributes (column) and PSEUDO items (row); The first column is item number and the second column is the pseudo item number for each item. If a pseudo item has more than one nonzero categories, more than one rows are needed.
gs.parm	the same as the gs.parm in simGDINA function in the GDINA package. It is a list with the same number of elements as the number of rows in the Qc matrix
Tmatrix	mapping matrix showing the relation between the OBSERVED responses (rows) and the PSEDUO items (columns); The first column gives the observed responses.
red.delta	reduced delta parameters using logit link function
att.gr	attribute group indicator

#### **Examples**

```
## Not run:
K=5
g = 0.2
item.no <- rep(1:6,each=4)
# the first node has three response categories: 0, 1 and 2
node.no <- rep(c(1,1,2,3),6)
Q1 <- matrix(0,length(item.no),K)
Q2 \leftarrow cbind(7:(7+K-1), rep(1,K), diag(K))
for(j in 1:length(item.no)) {
  Q1[j, sample(1:K, sample(3,1))] <- 1
Qc <- rbind(cbind(item.no,node.no,Q1),Q2)</pre>
Tmatrix.set \leftarrow list(cbind(c(0,1,2,3,3),c(0,1,2,1,2),c(NA,0,NA,1,NA),c(NA,NA,0,NA,1)),
cbind(c(0,1,2,3,4),c(0,1,2,1,2),c(NA,0,NA,1,NA),c(NA,NA,0,NA,1)),
cbind(c(0,1),c(0,1)))
Tmatrix <- Tmatrix.set[c(1,1,1,1,1,1,rep(3,K))]</pre>
sim <- simDTM(N=2000,Qc=Qc,gs.parm=matrix(0.2,nrow(Qc),2),Tmatrix=Tmatrix)</pre>
est <- DTM(dat=sim$dat,Qc=Qc,Tmatrix = Tmatrix)</pre>
## End(Not run)
```

simGDINA

Data simulation based on the G-DINA models

#### **Description**

Simulate responses based on the G-DINA model (de la Torre, 2011) and sequential G-DINA model (Ma & de la Torre, 2016), or CDMs subsumed by them, including the DINA model, DINO model, ACDM, LLM and R-RUM. Attributes can be simulated from uniform, higher-order or multivariate normal distributions, or be supplied by users. See Examples and Details for how item parameter specifications. See the help page of GDINA for model parameterizations.

#### Usage

```
simGDINA(
    N,
    Q,
    gs.parm = NULL,
    delta.parm = NULL,
    catprob.parm = NULL,
    model = "GDINA",
    sequential = FALSE,
    gs.args = list(type = "random", mono.constraint = TRUE),
    delta.args = list(design.matrix = NULL, linkfunc = NULL),
    attribute = NULL,
    att.dist = "uniform",
    item.names = NULL,
```

## **Arguments**

Q

N Sample size.

A required matrix; The number of rows occupied by a single-strategy dichotomous item is 1, by a polytomous item is the number of nonzero categories, and by a mutiple-strategy dichotomous item is the number of strategies. The number of column is equal to the number of attributes if all items are single-strategy dichotomous items, but the number of attributes + 2 if any items are polytomous or have multiple strategies. For a polytomous item, the first column represents the item number and the second column indicates the nonzero category number. For a multiple-strategy dichotomous item, the first column represents the item number and the second column indicates the strategy number. For binary attributes, 1 denotes the attributes are measured by the items and 0 means the attributes are not measured. For polytomous attributes, non-zero elements indicate which level of attributes are needed. See Examples.

gs.parm

A matrix or data frame for guessing and slip parameters. The number of rows occupied by a dichotomous item is 1, and by a polytomous item is the number of nonzero categories. The number of columns must be 2, where the first column represents the guessing parameters (or P(0)), and the second column represents slip parameters (or 1-P(1)). This may need to be used in conjunction with the argument gs.args.

delta.parm

A list of delta parameters of each latent group for each item or category. This may need to be used in conjunction with the argument delta.args.

catprob.parm

A list of success probabilities of each latent group for each non-zero category of each item. See Examples and Details for more information.

mode1

A character vector for each item or nonzero category, or a scalar which will be used for all items or nonzero categories to specify the CDMs. The possible options include "GDINA", "DINA", "DINO", "ACDM", "LLM", "RRUM", "MSDINA" and "UDF". When "UDF", indicating user defined function, is specified for any item, delta.parm must be specified, as well as options design.matrix and linkfunc in argument delta.args.

sequential

logical; TRUE if the sequential model is used for polytomous responses simulation, and FALSE if there is no polytomously scored items.

gs.args

a list of options when gs.parm is specified. It consists of two components:

- type How are the delta parameters for ACDM, LLM, RRUM generated? It can be either "random" or "equal". "random" means the delta parameters are simulated randomly, while "equal" means that each required attribute contributes equally to the probability of success (P), logit(P) or log(P) for ACDM, LLM and RRUM, respectively. See Details for more information.
- mono.constraint A vector for each item/category or a scalar which will be used for all items/categories to specify whether monotonicity constraints should be satisfied if the generating model is the G-DINA model. Note that this is applicable only for the G-DINA model when gs.parm is used. For ACDM, LLM and RRUM, monotonicity constraints are always satisfied and therefore this argument is ignored.

delta.args

a list of options when delta.parm is specified. It consists of two components:

- linkfunc a vector of link functions for each item/category; It can be "identity", "log" or "logit". Only necessary when, for some items, model="UDF".
- design.matrix a list of design matrices; Its length must be equal to the number of items (or nonzero categories for sequential models). If CDM for item j is specified as "UDF" in argument model, the corresponding design matrix must be provided; otherwise, the design matrix can be NULL, which will be generated automatically.

attribute

optional user-specified person attributes. It is a  $N \times K$  matrix or data frame. If this is not supplied, attributes are simulated from a distribution specified in att.dist.

att.dist

A string indicating the distribution for attribute simulation. It can be "uniform", "higher.order", "mvnorm" or "categorical" for uniform, higher-order, multivariate normal and categorical distributions, respectively. The default is the uniform distribution. To specify structural parameters for the higher-order and multivariate normal distributions, see higher.order.parm and mvnorm.parm, respectively. To specify the probabilities for the categorical distribution, use att.prior argument.

item.names

A vector giving the name of items or categories. If it is NULL (default), items are named as "Item 1", "Item 2", etc.

higher.order.parm

A list specifying parameters for higher-order distribution for attributes if att.dist=higher.order. Particularly, theta is a vector of length N representing the higher-order ability for each examinee. and lambda is a  $K \times 2$  matrix. Column 1 gives the slopes for the higher-order model and column 2 gives the intercepts. See GDINA for the formulations of the higher-order models.

mvnorm.parm

a list of parameters for multivariate normal attribute distribution. mean is a vector of length K specifying the mean of multivariate normal distribution; and sigma is a positive-definite symmetric matrix specifying the variance-covariance matrix. cutoffs is a vector giving the cutoff for each attribute. See Examples.

att.prior

probability for each attribute pattern. Order is the same as that returned from attributepattern(Q = Q). This is only applicable when att.dist="categorical".

digits

How many decimal places in each number? The default is 4.

object of class simGDINA for method extract

what argument for S3 method extract indicating what to extract

... additional arguments

#### **Details**

Item parameter specifications in simGDINA:

Item parameters can be specified in one of three different ways.

The first and probably the easiest way is to specify the guessing and slip parameters for each item or nonzero category using gs.parm, which is a matrix or data frame for  $P(\alpha_{lj}^*=0)$  and  $1-P(\alpha_{lj}^*=1)$  for all items for dichotomous items and  $S(\alpha_{ljh}^*=0)$  and  $1-S(\alpha_{ljh}^*=1)$  for all nonzero categories for polytomous items. Note that  $1-P(\alpha_{lj}^*=0)-P(\alpha_{lj}^*=1)$  or  $1-S(\alpha_{lj}^*=0)-S(\alpha_{lj}^*=1)$  must be greater than 0. For generating ACDM, LLM, and RRUM, delta parameters are generated randomly if type="random", or in a way that each required attribute contributes equally, as in Ma, Iaconangelo, & de la Torre (2016) if type="equal". For ACDM, LLM and RRUM, generated delta parameters are always positive, which implies that monotonicity constraints are always satisfied. If the generating model is the G-DINA model, mono.constraint can be used to specify whether monotonicity constraints should be satisfied.

The second way of simulating responses is to specify success probabilities (i.e.,  $P(\alpha_{lj}^*)$  or  $S(\alpha_{ljh}^*)$ ) for each nonzero category of each item directly using the argument catprob.parm. If an item or category requires  $K_j^*$  attributes,  $2^{K_j^*}$  success probabilities need to be provided. catprob.parm must be a list, where each element gives the success probabilities for nonzero category of each item. Note that success probabilities cannot be negative or greater than one.

The third way is to specify delta parameters for data simulation. For DINA and DINO model, each nonzero category requires two delta parameters. For ACDM, LLM and RRUM, if a nonzero category requires  $K_j^*$  attributes,  $K_j^*+1$  delta parameters need to be specified. For the G-DINA model, a nonzero category requiring  $K_j^*$  attributes has  $2^{K_j^*}$  delta parameters. It should be noted that specifying delta parameters needs to ascertain the derived success probabilities are within the [0,1] interval.

Please note that you need to specify item parameters in ONLY one of these three ways. If gs.parm is specified, it will be used regardless of the inputs in catprob.parm and delta.parm. If gs.parm is not specified, simGDINA will check if delta.parm is specified; if yes, it will be used for data generation. if both gs.parm and delta.parm are not specified, catprob.parm is used for data generation.

## Value

an object of class simGDINA. Elements that can be extracted using method extract include:

dat simulated item response matrix

**Q** Q-matrix

**attribute** A  $N \times K$  matrix for inviduals' attribute patterns

catprob.parm a list of non-zero category success probabilities for each latent group

**delta.parm** a list of delta parameters

higher.order.parm Higher-order parameters

**mvnorm.parm** multivariate normal distribution parameters

**LCprob.parm** A matrix of item/category success probabilities for each latent class

#### Author(s)

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#### References

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Maris, E. (1999). Estimating multiple classification latent class models. *Psychometrika*, 64, 187-212.

Templin, J. L., & Henson, R. A. (2006). Measurement of psychological disorders using cognitive diagnosis models. *Psychological Methods*, 11, 287-305.

## **Examples**

```
# and other CDMs, change model argument accordingly
sim <- simGDINA(N,Q,gs.parm = gs,model = "DINA")</pre>
# True item success probabilities
extract(sim,what = "catprob.parm")
# True delta parameters
extract(sim,what = "delta.parm")
# simulated data
extract(sim,what = "dat")
# simulated attributes
extract(sim,what = "attribute")
Example 2
            Data simulation (RRUM)
                                             #
N <- 500
Q <- sim30GDINA$simQ
J <- nrow(Q)</pre>
gs <- data.frame(guess=rep(0.2,J),slip=rep(0.2,J))</pre>
# Simulated RRUM
# deltas except delta0 for each item will be simulated
# randomly subject to the constraints of RRUM
sim <- simGDINA(N,Q,gs.parm = gs,model = "RRUM")</pre>
# simulated data
extract(sim,what = "dat")
# simulated attributes
extract(sim,what = "attribute")
Example 3
            Data simulation (LLM)
N <- 500
Q <- sim30GDINA$simQ
J \leftarrow nrow(Q)
gs <- data.frame(guess=rep(0.1,J),slip=rep(0.1,J))</pre>
# Simulated LLM
# By specifying type="equal", each required attribute is
# assumed to contribute to logit(P) equally
sim <- simGDINA(N,Q,gs.parm = gs,model = "LLM",gs.args = list (type="equal"))</pre>
#check below for what the equal contribution means
extract(sim, what = "delta.parm")
# simulated data
extract(sim, what = "dat")
```

```
# simulated attributes
extract(sim,what = "attribute")
#
                 Example 4
                                              #
#
         Data simulation (all CDMs)
                                              #
set.seed(12345)
N <- 500
Q <- sim10GDINA$simQ
J \leftarrow nrow(Q)
gs <- data.frame(guess=rep(0.1,J),slip=rep(0.1,J))</pre>
# Simulated different CDMs for different items
models <- c("GDINA","DINO","DINA","ACDM","LLM","RRUM","GDINA","LLM","RRUM","DINA")</pre>
sim <- simGDINA(N,Q,gs.parm = gs,model = models,gs.args = list(type="random"))</pre>
# simulated data
extract(sim, what = "dat")
# simulated attributes
extract(sim,what = "attribute")
#
                 Example 5
                                              #
#
         Data simulation (all CDMs)
                                              #
# using probability of success in list format
# success probabilities for each item need to be provided in list format as follows:
# if item j requires Kj attributes, 2^Kj success probabilities
# need to be specified
# e.g., item 1 only requires 1 attribute
# therefore P(0) and P(1) should be specified;
# similarly, item 10 requires 3 attributes,
# P(000),P(100),P(010)...,P(111) should be specified;
# the latent class represented by each element can be obtained
# by calling attributepattern(Kj)
itemparm.list <- list(item1=c(0.2,0.9),
                  item2=c(0.1,0.8),
                  item3=c(0.1,0.9),
                  item4=c(0.1,0.3,0.5,0.9),
                  item5=c(0.1,0.1,0.1,0.8),
                  item6=c(0.2,0.9,0.9,0.9),
                  item7=c(0.1,0.45,0.45,0.8),
                  item8=c(0.1,0.28,0.28,0.8),
                  item9=c(0.1,0.4,0.4,0.8),
                  item10=c(0.1,0.2,0.3,0.4,0.4,0.5,0.7,0.9))
set.seed(12345)
N <- 500
Q <- sim10GDINA$simQ
# When simulating data using catprob.parm argument,
```

```
# it is not necessary to specify model and type
sim <- simGDINA(N,Q,catprob.parm = itemparm.list)</pre>
Example 6
#
          Data simulation (all CDMs)
                                          #
     using delta parameters in list format
delta.list <- list(c(0.2,0.7),
                c(0.1, 0.7),
                c(0.1, 0.8),
                c(0.1, 0.7),
                c(0.1, 0.8),
                c(0.2,0.3,0.2,0.1),
                c(0.1,0.35,0.35),
                c(-1.386294, 0.9808293, 1.791759),
                c(-1.609438, 0.6931472, 0.6),
                c(0.1,0.1,0.2,0.3,0.0,0.0,0.1,0.1))
model <- c("GDINA", "GDINA", "GDINA", "DINA", "DINO", "GDINA", "ACDM", "LLM", "RRUM", "GDINA")
N <- 500
Q <- sim10GDINA$simQ
# When simulating using delta.parm argument, model needs to be
# specified
sim <- simGDINA(N,Q,delta.parm = delta.list, model = model)</pre>
Example 7
     Data simulation (higher order DINA model)
Q <- sim30GDINA$simQ
gs <- matrix(0.1,nrow(Q),2)</pre>
N <- 500
set.seed(12345)
theta <- rnorm(N)
K <- ncol(Q)
lambda <- data.frame(a=rep(1,K),b=seq(-2,2,length.out=K))</pre>
sim <- simGDINA(N,Q,gs.parm = gs, model="DINA", att.dist = "higher.order",</pre>
              higher.order.parm = list(theta = theta,lambda = lambda))
#
                Example 8
     Data simulation (higher-order CDMs)
Q <- sim30GDINA$simQ
gs <- matrix(0.1,nrow(Q),2)</pre>
models <- c(rep("GDINA",5),</pre>
          rep("DINO",5),
```

```
rep("DINA",5),
           rep("ACDM",5),
           rep("LLM",5),
           rep("RRUM",5))
N <- 500
set.seed(12345)
theta <- rnorm(N)
K \leftarrow ncol(Q)
lambda <- data.frame(a=runif(K,0.7,1.3),b=seq(-2,2,length.out=K))
sim <- simGDINA(N,Q,gs.parm = gs, model=models, att.dist = "higher.order",</pre>
               higher.order.parm = list(theta = theta,lambda = lambda))
#
                  Example 9
#
      Data simulation (higher-order model)
# using the multivariate normal threshold model
# See Chiu et al., (2009)
N <- 500
Q <- sim10GDINA$simQ
K \leftarrow ncol(Q)
gs \leftarrow matrix(0.1,nrow(Q),2)
cutoffs <- qnorm(c(1:K)/(K+1))
m \leftarrow rep(0,K)
vcov <- matrix(0.5,K,K)</pre>
diag(vcov) <- 1</pre>
simMV <- simGDINA(N,Q,gs.parm = gs, att.dist = "mvnorm",</pre>
               mvnorm.parm=list(mean = m, sigma = vcov,cutoffs = cutoffs))
Example 10
        Simulation using
#
      user-specified att structure#
# --- User-specified attribute structure ----#
Q <- sim30GDINA$simQ
K \leftarrow ncol(Q)
# divergent structure A1->A2->A3;A1->A4->A5;A1->A4->A6
diverg <- list(c(1,2),
              c(2,3),
              c(1,4),
              c(4,5))
struc <- att.structure(diverg,K)</pre>
# data simulation
N <- 1000
# data simulation
gs \leftarrow matrix(0.1, nrow(Q), 2)
```

```
simD <- simGDINA(N,Q,gs.parm = gs,</pre>
                model = "DINA",att.dist = "categorical",att.prior = struc$att.prob)
Example 11
               Data simulation
                                             #
# (GDINA with monotonicity constraints)
set.seed(12345)
N <- 500
Q <- sim30GDINA$simQ
J \leftarrow nrow(Q)
gs <- data.frame(guess=rep(0.1,J),slip=rep(0.1,J))</pre>
# Simulated different CDMs for different items
\verb|sim <- simGDINA(N,Q,gs.parm = gs,model = "GDINA",gs.args=list(mono.constraint=TRUE)||
# True item success probabilities
extract(sim, what = "catprob.parm")
# True delta parameters
extract(sim,what = "delta.parm")
# simulated data
extract(sim, what = "dat")
# simulated attributes
extract(sim,what = "attribute")
#
                 Example 12
               Data simulation
# (Sequential G-DINA model - polytomous responses) #
set.seed(12345)
N <- 2000
# restricted Qc matrix
Qc <- sim20seqGDINA$simQ
#total number of categories
J <- nrow(Qc)</pre>
gs <- data.frame(guess=rep(0.1,J),slip=rep(0.1,J))</pre>
# simulate sequential DINA model
simseq <- simGDINA(N, Qc, sequential = TRUE, gs.parm = gs, model = "GDINA")</pre>
# True item success probabilities
extract(simseq,what = "catprob.parm")
# True delta parameters
extract(simseq,what = "delta.parm")
```

```
# simulated data
extract(simseq,what = "dat")
# simulated attributes
extract(simseq,what = "attribute")
Example 13
#
        DINA model Attribute generated using
           categorical distribution
#
Q <- sim10GDINA$simQ
gs <- matrix(0.1,nrow(Q),2)</pre>
N <- 5000
set.seed(12345)
prior \leftarrow c(0.1,0.2,0,0,0.2,0,0,0.5)
sim <- simGDINA(N,Q,gs.parm = gs, model="DINA", att.dist = "categorical",att.prior = prior)</pre>
# check latent class sizes
table(sim$att.group)/N
Example 14
                MS-DINA model
Q \leftarrow matrix(c(1,1,1,1,0,
1,2,0,1,1,
2,1,1,0,0,
3,1,0,1,0,
4,1,0,0,1,
5,1,1,0,0,
5,2,0,0,1),ncol = 5,byrow = TRUE)
d <- list(</pre>
 item1=c(0.2,0.7),
 item2=c(0.1,0.6),
 item3=c(0.2,0.6),
 item4=c(0.2,0.7),
 item5=c(0.1,0.8))
 set.seed(12345)
sim <- simGDINA(N=1000,Q = Q, delta.parm = d,
            model = c("MSDINA", "MSDINA", "DINA", "DINA", "DINA", "MSDINA", "MSDINA"))
# simulated data
extract(sim,what = "dat")
# simulated attributes
extract(sim,what = "attribute")
```

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```
## End(Not run)
```

startGDINA

Graphical user interface of the GDINA function

## **Description**

An interactive Shiny application for running GDINA function. See Ma and de la Torre (2019) and de la Torre and Akbay (2019) for tutorials.

## Usage

startGDINA()

## Author(s)

Wenchao Ma, The University of Alabama, <wenchao.ma@ua.edu>

## References

de la Torre, J & Akbay, L. (2019). Implementation of Cognitive Diagnosis Modeling using the GDINA R Package. *Eurasian Journal of Educational Research*, 80, 171-192.

Ma, W., & de la Torre, J. (2019). Digital Module 05: Diagnostic measurement-The G-DINA framework. *Educational Measurement: Issues and Practice*, *39*, 114-115.

Ma, W., & de la Torre, J. (2020). GDINA: An R Package for Cognitive Diagnosis Modeling. *Journal of Statistical Software*, 93(14), 1-26.

## **Examples**

```
## Not run:
library(shiny)
library(shinydashboard)
startGDINA()
## End(Not run)
```

92 unrestrQ

unique\_only

Unique values in a vector

## Description

Unique values in a vector

## Usage

```
unique_only(vec)
```

## Arguments

vec

a vector

## Value

sorted unique values

## See Also

unique

## **Examples**

```
vec <- c(4,2,3,5,4,4,4)
unique_only(vec)
# see the difference from unique
unique(vec)

vec <- letters[1:5]
unique_only(vec)</pre>
```

unrestrQ

Generate unrestricted Qc matrix from an restricted Qc matrix

## Description

Generate unrestricted Qc matrix from an restricted Qc matrix

## Usage

```
unrestrQ(Qc)
```

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# Arguments

Qc an restricted Qc matrix

## Value

an unrestricted Qc matrix

# Examples

```
Qc <- sim21seqDINA$simQc
Qc
unrestrQ(Qc)</pre>
```

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