Package ‘mirt’

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Description Analysis of dichotomous and polytomous response data using unidimensional and multidimensional latent trait models under the Item Response Theory paradigm (Chalmers (2012) <doi:10.18637/jss.v048.i06>). Exploratory and confirmatory models can be estimated with quadrature (EM) or stochastic (MHRM) methods. Confirmatory bi-factor and two-tier analyses are available for modeling item testlets. Multiple group analysis and mixed effects designs also are available for detecting differential item and test functioning as well as modeling item and person covariates. Finally, latent class models such as the DINA, DINO, multidimensional latent class, and several other discrete latent variable models, including mixture and zero-inflated response models, are supported.

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mirt-package

Full information maximum likelihood estimation of IRT models.

Description

Full information maximum likelihood estimation of multidimensional IRT models

Details

Analysis of dichotomous and polytomous response data using unidimensional and multidimensional latent trait models under the Item Response Theory paradigm. Exploratory and confirmatory models can be estimated with quadrature (EM) or stochastic (MHRM) methods. Confirmatory bi-factor and two-tier analyses are available for modeling item testlets. Multiple group analysis and mixed effects designs also are available for detecting differential item and test functioning as well as modeling item and person covariates. Finally, latent class models such as the DINA, DINO, multidimensional latent class, and several other discrete variable models are supported.

Users interested in the most recent version of this package can visit https://github.com/philchalmers/mirt and follow the instructions for installing the package from source. Questions regarding the package can be sent to the mirt-package Google Group, located at https://groups.google.com/forum/#!forum/mirt-package. User contributed files, workshop files, and evaluated help files are also available on the package wiki (https://github.com/philchalmers/mirt/wiki).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


anova-method

Compare nested models with likelihood-based statistics

Description

Compare nested models using likelihood ratio test (X2), Akaike Information Criterion (AIC), sample size adjusted AIC (AICc), Bayesian Information Criterion (BIC), Sample-Size Adjusted BIC (SABIC), and Hannan-Quinn (HQ) Criterion.
Usage

```r
## S4 method for signature 'SingleGroupClass'
anova(object, object2, bounded = FALSE, mix = 0.5, verbose = TRUE)
```

Arguments

- `object`: an object of class `SingleGroupClass`, `MultipleGroupClass`, or `MixedClass`
- `object2`: a second model estimated from any of the mirt package estimation methods
- `bounded`: logical; are the two models comparing a bounded parameter (e.g., comparing a single 2PL and 3PL model with 1 df)? If `TRUE` then a 50:50 mix of chi-squared distributions is used to obtain the p-value
- `mix`: proportion of chi-squared mixtures. Default is 0.5
- `verbose`: logical; print additional information to console?

Value

a `data.frame/mirt_df` object

References


Examples

```r
## Not run:
x <- mirt(Science, 1)
x2 <- mirt(Science, 2)
anova(x, x2)

# in isolation
anova(x)

# bounded parameter
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)
mod2 <- mirt(dat, 1, itemtype = c(rep('2PL', 4), '3PL'))
anova(mod, mod2) #unbounded test
anova(mod, mod2, bounded = TRUE) #bounded

# priors
model <- 'F = 1-5
PRIOR = (5, g, norm, -1, 1)'
mod1b <- mirt(dat, model, itemtype = c(rep('2PL', 4), '3PL'))
anova(mod1b)

model2 <- 'F = 1-5
PRIOR = (1-5, g, norm, -1, 1)'
mod2b <- mirt(dat, model2, itemtype = '3PL')
```
areainfo

Function to calculate the area under a selection of information curves

Description

Compute the area within test or item information over a definite integral range.

Usage

areainfo(
  x,
  theta_lim,
  which.items = 1:extract.mirt(x, "nitems"),
  group = NULL,
  ...
)

Arguments

x an object of class 'SingleGroupClass', or an object of class 'MultipleGroupClass' if a suitable group input were supplied
theta_lim range of integration to be computed
which.items an integer vector indicating which items to include in the expected information function. Default uses all possible items
group group argument to pass to extract.group function. Required when the input object is a multiple-group model
...
... additional arguments passed to integrate

Value

a data.frame with the lower and upper integration range, the information area within the range (Info), the information area over the range -10 to 10 (Total.Info), proportion of total information given the integration range (Info.Proportion), and the number of items included (nitems)

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

Examples

dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)

areainfo(mod, c(-2,0), which.items = 1) #item 1
## Not run:
areainfo(mod, c(-2,0), which.items = 1:3) #items 1 to 3
areainfo(mod, c(-2,0)) # all items (total test information)

# plot the area
area <- areainfo(mod, c(-2,0))
Theta <- matrix(seq(-3,3, length.out=1000))
info <- testinfo(mod, Theta)
plot(info ~ Theta, type = 'l')
pick <- Theta >= -2 & Theta <=0
polygon(c(-2, Theta[pick], 0), c(0, info[pick], 0), col='lightblue')
text(x = 2, y = 0.5, labels = paste("Total Information: ", round(area$TotalInfo, 3),

"Information in (-2, 0): ", round(area$Info, 3),
paste("", round(100 * area$Proportion, 2), ",%", sep = "")), cex = 1.2)

## End(Not run)

averageMI

**Collapse values from multiple imputation draws**

Description

This function computes updated parameter and standard error estimates using multiple imputation methodology. Given a set of parameter estimates and their associated standard errors the function returns the weighted average of the overall between and within variability due to the multiple imputations according to Rubin’s (1987) methodology.

Usage

```r
averageMI(par, SEpar, as.data.frame = TRUE)
```

Arguments

- `par`: a list containing parameter estimates which were computed the imputed datasets
- `SEpar`: a list containing standard errors associated with `par`
- `as.data.frame`: logical; return a data.frame instead of a list? Default is TRUE

Value

returns a list or data.frame containing the updated averaged parameter estimates, standard errors, and t-values with the associated degrees of freedom and two tailed p-values
Author(s)
Phil Chalmers <rphilip.chalmers@gmail.com>

References

Examples

```r
## Not run:
# simulate data
set.seed(1234)
N <- 1000

# covariates
X1 <- rnorm(N); X2 <- rnorm(N)
covdata <- data.frame(X1, X2)
Theta <- matrix(0.5 * X1 + -1 * X2 + rnorm(N, sd = 0.5))

# items and response data
a <- matrix(1, 20); d <- matrix(rnorm(20))
dat <- simdata(a, d, 1000, itemtype = '2PL', Theta=Theta)
mod1 <- mirt(dat, 1, 'Rasch', covdata=covdata, formula = ~ X1 + X2)
coef(mod1, simplify=TRUE)

# draw plausible values for secondary analyses
pv <- fscores(mod1, plausible.draws = 10)
pvmods <- lapply(pv, function(x, covdata) lm(x ~ covdata$X1 + covdata$X2),
                   covdata=covdata)

# compute Rubin's multiple imputation average
so <- lapply(pvmods, summary)
par <- lapply(so, function(x) x$coefficients[, 'Estimate'])
SEpar <- lapply(so, function(x) x$coefficients[, 'Std. Error'])
averageMI(par, SEpar)

## End(Not run)
```
bfactor

Description

bfactor fits a confirmatory maximum likelihood two-tier/bifactor/testlet model to dichotomous and polytomous data under the item response theory paradigm. The IRT models are fit using a dimensional reduction EM algorithm so that regardless of the number of specific factors estimated the model only uses the number of factors in the second-tier structure plus 1. For the bifactor model the maximum number of dimensions is only 2 since the second-tier only consists of a ubiquitous unidimensional factor. See mirt for appropriate methods to be used on the objects returned from the estimation.

Usage

bfactor(
  data,
  model,
  model2 = paste0("G = 1-", ncol(data)),
  group = NULL,
  quadpts = NULL,
  invariance = "",
  ...
)

Arguments

data a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA

model a numeric vector specifying which factor loads on which item. For example, if for a 4 item test with two specific factors, the first specific factor loads on the first two items and the second specific factor on the last two, then the vector is c(1,1,2,2). For items that should only load on the second-tier factors (have no specific component) NA values may be used as place-holders. These numbers will be translated into a format suitable for mirt.model(), combined with the definition in model2, with the letter 'S' added to the respective factor number

model2 a two-tier model specification object defined by mirt.model() or a string to be passed to mirt.model. By default the model will fit a unidimensional model in the second-tier, and therefore be equivalent to the bifactor model

group a factor variable indicating group membership used for multiple group analyses

quadpts number of quadrature nodes to use after accounting for the reduced number of dimensions. Scheme is the same as the one used in mirt, however it is in regards to the reduced dimensions (e.g., a bifactor model has 2 dimensions to be integrated)

invariance see multipleGroup for details, however, the specific factor variances and means will be constrained according to the dimensional reduction algorithm

... additional arguments to be passed to the estimation engine. See mirt for more details and examples
bfactor follows the item factor analysis strategy explicated by Gibbons and Hedeker (1992), Gibbons et al. (2007), and Cai (2010). Nested models may be compared via an approximate chi-squared difference test or by a reduction in AIC or BIC (accessible via `anova`). See `mirt` for more details regarding the IRT estimation approach used in this package.

The two-tier model has a specific block diagonal covariance structure between the primary and secondary latent traits. Namely, the secondary latent traits are assumed to be orthogonal to all traits and have a fixed variance of 1, while the primary traits can be organized to vary and covary with other primary traits in the model.

\[
\Sigma_{\text{two-tier}} = \begin{pmatrix} G & 0 \\ 0 & \text{diag}(S) \end{pmatrix}
\]

The bifactor model is a special case of the two-tier model when \( G \) above is a 1x1 matrix, and therefore only 1 primary factor is being modeled. Evaluation of the numerical integrals for the two-tier model requires only \( ncol(G) + 1 \) dimensions for integration since the \( S \) second order (or 'specific') factors require only 1 integration grid due to the dimension reduction technique.

Note: for multiple group two-tier analyses only the second-tier means and variances should be freed since the specific factors are not treated independently due to the dimension reduction technique.

Value

function returns an object of class SingleGroupClass (SingleGroupClass-class) or MultipleGroupClass (MultipleGroupClass-class).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

mirt
Examples

## Not run:
###load SAT12 and compute bifactor model with 3 specific factors
data(SAT12)
data <- key2binary(SAT12,
    key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
specific <- c(2,3,2,3,2,1,2,1,1,1,3,1,2,1,1,3,3,1,1,3,3,1,3,1,2,3,1,2)
mod1 <- bfactor(data, specific)
summary(mod1)
itemplot(mod1, 18, drop.zeros = TRUE) #drop the zero slopes to allow plotting

###Try with fixed guessing parameters added
guess <- rep(.1,32)
mod2 <- bfactor(data, specific, guess = guess)
coef(mod2)
anova(mod1, mod2)

## don't estimate specific factor for item 32
specific[32] <- NA
mod3 <- bfactor(data, specific)
anova(mod1, mod3)

# same, but declared manually (not run)
#sv <- mod2values(mod1)
#sv$value[220] <- 0 #parameter 220 is the 32 items specific slope
#sv$est[220] <- FALSE
#mod3 <- bfactor(data, specific, pars = sv) #with excellent starting values

#########
# mixed itemtype example

#simulate data
a <- matrix(c(
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA
),ncol=3,byrow=TRUE)
d <- matrix(c(
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5,
    1,NA,0.5),ncol=3,byrow=TRUE)
d <- matrix(c(
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA,
    1,0.5,NA
),ncol=3,byrow=TRUE)

```r
# simulate data
set.seed(1234)
a <- matrix(0, 12, 4)
a[,1] <- rlnorm(12, .2, .3)
ind <- 1
for(i in 1:3){
a[ind:(ind+3),i+1] <- a[ind:(ind+3),1]
ind <- ind+4
}
print(a)
d <- rnorm(12, 0, .5)
sigma <- diag(c(1, .5, 1, .5))
dataset <- simdata(a,d,2000,itemtype=rep('2PL', 12),sigma=sigma)

# estimate by applying constraints and freeing the latent variances
specific <- c(rep(1,4),rep(2,4), rep(3,4))
model <- "G = 1-12
CONSTRATN = (1, a1, a2), (2, a1, a2), (3, a1, a2), (4, a1, a2),
(5, a1, a3), (6, a1, a3), (7, a1, a3), (8, a1, a3),
(9, a1, a4), (10, a1, a4), (11, a1, a4), (12, a1, a4)
COV = S1*S1, S2*S2, S3*S3"

simmod <- bfactor(dataset, specific, model)
coef(simmod, simplify=TRUE)
```
# Two-tier model

# simulate data
set.seed(1234)
a <- matrix(c(
  0,1,0.5,NA,NA,
  0,1,0.5,NA,NA,
  0,1,0.5,NA,NA,
  0,1,0.5,NA,NA,
  0,1,0.5,NA,NA,
  0,1,NA,0.5,NA,
  0,1,NA,0.5,NA,
  0,1,NA,0.5,NA,
  1,0,NA,0.5,NA,
  1,0,NA,0.5,NA,
  1,0,NA,0.5,NA,
  1,0,NA,NA,0.5,
  1,0,NA,NA,0.5,
  1,0,NA,NA,0.5,
  1,0,NA,NA,0.5),ncol=5,byrow=TRUE)
d <- matrix(rnorm(16))
items <- rep("\'Var\n2PL\'", 16)
sigma <- diag(5)
sigma[1,2] <- sigma[2,1] <- .4
dataset <- simdata(a,d,2000,itemtype=items,sigma=sigma)

specific <- c(rep(1,5),rep(2,6),rep(3,5))
model <- 'G1 = 1-8
G2 = 9-16
COV = G1*G2'

# quadpts dropped for faster estimation, but not as precise
simmod <- bfactor(dataset, specific, model, quadpts = 9, TOL = 1e-3)
coef(simmod, simplify=TRUE)
summary(simmod)
itemfit(simmod, QMC=TRUE)
M2(simmod, QMC=TRUE)
residuals(simmod, QMC=TRUE)

## End(Not run)
**Description**

A 3-item tabulated data set extracted from Table 3 in Chapter Two.

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
## Not run:
dat <- expand.table(Bock1997)
head(dat)
mod <- mirt(dat, 1, 'nominal')

# reproduce table 3 in Bock (1997)
fs <- round(fscores(mod, verbose = FALSE, full.scores = FALSE)[,c('F1','SE_F1')],2)
fttd <- residuals(mod, type = 'exp')
table <- data.frame(fttd[,ncol(fttd)], fs)
table

mod <- mirt(dat, 1, 'nominal')
coef(mod)

## End(Not run)
```

---

**boot.LR**  
*Parametric bootstrap likelihood-ratio test*

**Description**

Given two fitted models, compute a parametric bootstrap test to determine whether the less restrictive models fits significantly better than the more restricted model. Note that this hypothesis test also works when prior parameter distributions are included for either model. Function can be run in parallel after using a suitable `mirtCluster` definition.

**Usage**

`boot.LR(mod, mod2, R = 1000)`
Arguments

mod          an estimated model object
mod2         an estimated model object
\( R \)       number of parametric bootstraps to use.

Value

a p-value evaluating whether the more restrictive model fits significantly worse than the less restrictive model

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
#standard
dat <- expand.table(LSAT7)
mod1 <- mirt(dat, 1)
mod2 <- mirt(dat, 1, '3PL')

# standard LR test
anova(mod1, mod2)

# bootstrap LR test (run in parallel to save time)
mirtCluster()
boot.LR(mod1, mod2, R=200)

## End(Not run)
```

Description

Given an internal mirt object estimate the bootstrapped standard errors. It may be beneficial to run the computations using multi-core architecture (e.g., the parallel package). Parameters are organized from the freely estimated values in \texttt{mod2values(x)} (equality constraints will also be returned in the bootstrapped estimates).
Usage

boot.mirt(x, R = 100, technical = NULL, ...)

Arguments

x an estimated model object
R number of draws to use (passed to the boot() function)
technical technical arguments passed to estimation engine. See mirt for details
... additional arguments to be passed on to boot(...) and estimation engine

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

## Not run:
#standard
mod <- mirt(Science, 1)
booted <- boot.mirt(mod, R=20)
plot(booted)
booted

#run in parallel using snow back-end using all available cores
mod <- mirt(Science, 1)
booted <- boot.mirt(mod, parallel = 'snow', ncpus = parallel::detectCores())
booted

## End(Not run)

---

**coef-method**

Extract raw coefs from model object

Description

Return a list (or data.frame) of raw item and group level coefficients. Note that while the output to the console is rounded to three digits, the returned list of objects is not. Hence, elements from cfs <-coef(mod); cfs[[1]] will contain the unrounded results (useful for simulations).
Usage

## S4 method for signature 'SingleGroupClass'
coef(
  object,
  CI = 0.95,
  printSE = FALSE,
  rotate = "none",
  Target = NULL,
  IRTpars = FALSE,
  rawug = FALSE,
  as.data.frame = FALSE,
  simplify = FALSE,
  unique = FALSE,
  verbose = TRUE,
  ...
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an object of class SingleGroupClass, MultipleGroupClass, or MixedClass</td>
</tr>
<tr>
<td>CI</td>
<td>the amount of converged used to compute confidence intervals; default is 95 percent confidence intervals</td>
</tr>
<tr>
<td>printSE</td>
<td>logical; print the standard errors instead of the confidence intervals? When IRTpars = TRUE then the delta method will be used to compute the associated standard errors from mirt's default slope-intercept form</td>
</tr>
<tr>
<td>rotate</td>
<td>see summary method for details. The default rotation is 'none'</td>
</tr>
<tr>
<td>Target</td>
<td>a dummy variable matrix indicting a target rotation pattern</td>
</tr>
<tr>
<td>IRTpars</td>
<td>logical; convert slope intercept parameters into traditional IRT parameters? Only applicable to unidimensional models. If a suitable ACOV estimate was computed in the fitted model, and printSE = FALSE, then suitable CIs will be included based on the delta method (where applicable)</td>
</tr>
<tr>
<td>rawug</td>
<td>logical; return the untransformed internal g and u parameters? If FALSE, g and u's are converted with the original format along with delta standard errors</td>
</tr>
<tr>
<td>as.data.frame</td>
<td>logical; convert list output to a data.frame instead?</td>
</tr>
<tr>
<td>simplify</td>
<td>logical; if all items have the same parameter names (indicating they are of the same class) then they are collapsed to a matrix, and a list of length 2 is returned containing a matrix of item parameters and group-level estimates</td>
</tr>
<tr>
<td>unique</td>
<td>return the vector of uniquely estimated parameters</td>
</tr>
<tr>
<td>verbose</td>
<td>logical; allow information to be printed to the console?</td>
</tr>
<tr>
<td>...</td>
<td>additional arguments to be passed</td>
</tr>
</tbody>
</table>

References

createGroup

Create a user defined group-level object with correct generic functions

Description

Initializes the proper S4 class and methods necessary for mirt functions to use in estimation for defining customized group-level functions. To use the defined objects pass to the mirt(..., customGroup = OBJECT) command, and ensure that the class parameters are properly labeled.

Usage

createGroup(
  par,
  est,
  den,
  nfact,
  standardize = FALSE,
  gr = NULL,
  hss = NULL,
  gen = NULL,
  lbound = NULL,
  ...
)

Examples

## Not run:
dat <- expand.table(LSAT7)
x <- mirt(dat, 1)
coef(x)
coef(x, IRTpars = TRUE)
coef(x, simplify = TRUE)

#with computed information matrix
x <- mirt(dat, 1, SE = TRUE)
coef(x)
coef(x, printSE = TRUE)
coef(x, as.data.frame = TRUE)

#two factors
x2 <- mirt(Science, 2)
coef(x2)
coef(x2, rotate = 'varimax')

## End(Not run)
ubound = NULL,
       derivType = "Richardson"
)

Arguments

par    a named vector of the starting values for the parameters
est    a logical vector indicating which parameters should be freely estimated by de-
den    the probability density function given the Theta/ability values. First input con-
tains a vector of all the defined parameters and the second input must be a matrix
called Theta. Function also must return a numeric vector object corresponding
to the associated densities for each row in the Theta input
nfact  number of factors required for the model. E.g., for unidimensional models with
       only one dimension of integration nfact = 1
standardize logical; use standardization of the quadrature table method proposed by Woods
       and Thissen (2006)? If TRUE, the logical elements named 'MEAN_1' and 'COV_11'
can be included in the parameter vector, and when these values are set to FALSE
       in the est input the E-table will be standardized to these fixed values (e.g., par
       <-c(a1=1,d=0,MEAN_1=0,COV_11=1) with est <-c(TRUE,TRUE,FALSE,FALSE)
       will standardize the E-table to have a 0 mean and unit variance)
gr     gradient function (vector of first derivatives) of the log-likelihood used in esti-
mation. The function must be of the form gr(x,Theta), where x is the object
defined by createGroup() and Theta is a matrix of latent trait parameters
hss    Hessian function (matrix of second derivatives) of the log-likelihood used in
       estimation. If not specified a numeric approximation will be used. The input is
       identical to the gr argument
gen    a function used when GenRandomPars = TRUE is passed to the estimation func-
tion to generate random starting values. Function must be of the form function(object)
       ... and must return a vector with properties equivalent to the par object. If
       NULL, parameters will remain at the defined starting values by default
lbound optional vector indicating the lower bounds of the parameters. If not specified
       then the bounds will be set to -Inf
ubound optional vector indicating the lower bounds of the parameters. If not specified
       then the bounds will be set to Inf
derivType if the gr or hss terms are not specified this type will be used to obtain them
       numerically. Default is 'Richardson'

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

roment. Journal of Statistical Software, 48(6), 1-29. doi: 10.18637/jss.v048.i06
createItem

Examples

# normal density example, N(mu, sigma^2)
den <- function(obj, Theta) dnorm(Theta, obj@par[1], sqrt(obj@par[2]))
par <- c(mu = 0, sigma2 = .5)
est <- c(FALSE, TRUE)
lbound <- c(-Inf, 0)
grp <- createGroup(par, est, den, nfact = 1, lbound=lbound)
dat <- expand.table(LSAT6)
mod <- mirt(dat, 1, 'Rasch')
modcustom <- mirt(dat, 1, 'Rasch', customGroup=grp)
coef(mod)
coef(modcustom)

createItem

Create a user defined item with correct generic functions

Description

Initializes the proper S4 class and methods necessary for mirt functions to use in estimation. To use the defined objects pass to the mirt(...,customItems = list()) command, and ensure that the classes are properly labeled and unique in the list. Additionally, the input mirt(...,customItemsData = list()) can also be included to specify additional item-level information to better recycle custom-item definitions (e.g., for supplying varying Q-matricies), where the list input must have the same length as the number of items. For further examples regarding how this function can be used for fitting unfolding-type models see Liu and Chalmers (2018).

Usage

createItem(
  name,
  par,
  est,
  P,
  gr = NULL,
  hss = NULL,
  gen = NULL,
  lbound = NULL,
  ubound = NULL,
  derivType = "Richardson",
  derivType.hss = "Richardson",
  bytecompile = TRUE
)
createItem

Arguments

name  a character indicating the item class name to be defined
par   a named vector of the starting values for the parameters
est   a logical vector indicating which parameters should be freely estimated by default
P     the probability trace function for all categories (first column is category 1, second category two, etc). First input contains a vector of all the item parameters, the second input must be a matrix called Theta, the third input must be the number of categories called ncat, and (optionally) a fourth argument termed itemdata may be included containing further users specification information. The last optional input is to be utilized within the estimation functions such as mirt via the list input customItemsData to more naturally recycle custom-item definitions. Therefore, these inputs must be of the form
function(par,Theta,ncat){...}
or
function(par,Theta,ncat,itemdata){...}
to be valid; however, the names of the arguments is not relevant.
Finally, this function must return a matrix object of category probabilities, where the columns represent each respective category

gr    gradient function (vector of first derivatives) of the log-likelihood used in estimation. The function must be of the form gr(x,Theta), where x is the object defined by createItem() and Theta is a matrix of latent trait parameters. Tabulated (EM) or raw (MHRM) data are located in the x@dat slot, and are used to form the complete data log-likelihood. If not specified a numeric approximation will be used

hss   Hessian function (matrix of second derivatives) of the log-likelihood used in estimation. If not specified a numeric approximation will be used (required for the MH-RM algorithm only). The input is identical to the gr argument

gen  a function used when GenRandomPars = TRUE is passed to the estimation function to generate random starting values. Function must be of the form function(object) ... and must return a vector with properties equivalent to the par object. If NULL, parameters will remain at the defined starting values by default

lbound optional vector indicating the lower bounds of the parameters. If not specified then the bounds will be set to -Inf

ubound optional vector indicating the lower bounds of the parameters. If not specified then the bounds will be set to Inf

derivType if the gr term is not specified this type will be used to obtain the gradient numerically or symbolically. Default is the 'Richardson' extrapolation method; see numerical_deriv for details and other options. If 'symbolic' is supplied then the gradient will be computed using a symbolical approach (potentially the most accurate method, though may fail depending on how the P function was defined)
derivType.hss if the hss term is not specified this type will be used to obtain the Hessian numerically. Default is the 'Richardson' extrapolation method; see numerical_deriv
for details and other options. If 'symbolic' is supplied then the Hessian will be computed using a symbolical approach (potentially the most accurate method, though may fail depending on how the P function was defined)

bytecompile logical; where applicable, byte compile the functions provided? Default is TRUE to provide

Details

The summary() function will not return proper standardized loadings since the function is not sure how to handle them (no slopes could be defined at all!). Instead loadings of .001 are filled in as place-holders.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
name <- 'old2PL'
par <- c(a = .5, b = -2)
est <- c(TRUE, TRUE)
P.old2PL <- function(par,Theta, ncat){
a <- par[1]
b <- par[2]
P1 <- 1 / (1 + exp(-1*a*(Theta - b)))
cbind(1-P1, P1)
}
x <- createItem(name, par=par, est=est, P=P.old2PL)
#So, let's estimate it!
dat <- expand.table(LSAT7)
sv <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x), pars = 'values')
tail(sv) #looks good
mod <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x))
coef(mod)
mod2 <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x), method = 'MHRM')
coef(mod2)
```

# same definition as above, but using symbolic derivative computations
# (can be more accurate/stable)
xs <- createItem(name, par=par, est=est, P=P.old2PL, derivType = 'symbolic')
mod <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=xs))
coef(mod, simplify=TRUE)

# several secondary functions supported
M2(mod, calcNull=FALSE)
itemfit(mod)
fscores(mod, full.scores=FALSE)
plot(mod)

# fit the same model, but specify gradient function explicitly (use of a browser() may be helpful)
gr <- function(x, Theta){
  # browser()
  a <- x@par[1]
  b <- x@par[2]
  P <- probtrace(x, Theta)
  PQ <- apply(P, 1, prod)
  r_P <- x@dat / P
  grad <- numeric(2)
  grad[2] <- sum(-a * PQ * (r_P[,2] - r_P[,1]))
  grad[1] <- sum((Theta - b) * PQ * (r_P[,2] - r_P[,1]))
  # check with internal numerical form to be safe
  # numericalderiv(mirt:::EML, x@par[x@est], obj=x, Theta=Theta)
  grad
}
x <- createItem(name, par=par, est=est, P=P.old2PL, gr=gr)
mod <- mirt(dat, 1, c(rep('2PL',4), 'old2PL'), customItems=list(old2PL=x))
coef(mod, simplify=TRUE)

### non-linear
name <- 'nonlin'
par <- c(a1 = .5, a2 = .1, d = 0)
est <- c(TRUE, TRUE, TRUE)
P.nonlin <- function(par,Theta, ncat=2){
  a1 <- par[1]
  a2 <- par[2]
  d <- par[3]
  P1 <- 1 / (1 + exp(-1*(a1*Theta + a2*Theta^2 + d)))
  cbind(1-P1, P1)
}
x2 <- createItem(name, par=par, est=est, P=P.nonlin)
mod <- mirt(dat, 1, c(rep('2PL',4), 'nonlin'), customItems=list(nonlin=x2))
coef(mod)

### nominal response model (Bock 1972 version)
Tnom.dev <- function(ncat) {
  T <- matrix(1/ncat, ncat, ncat - 1)
  diag(T[,1]) <- diag(T[,1]) - 1
  return(T)
name <- 'nom'
par <- c(alp=c(3,0,-3),gam=rep(.4,3))
est <- rep(TRUE, length(par))
P.nom <- function(par, Theta, ncat){
   alp <- par[1:(ncat-1)]
   gam <- par[ncat:length(par)]
   a <- Tnom.dev(ncat) %*% alp
   c <- Tnom.dev(ncat) %*% gam
   z <- matrix(0, nrow(Theta), ncat)
   for(i in 1:ncat)
      z[,i] <- a[i] * Theta + c[i]
   P <- exp(z) / rowSums(exp(z))
   P
}
nom1 <- createItem(name, par=par, est=est, P=P.nom)
nommod <- mirt(Science, 1, 'nom1', customItems=list(nom1=nom1))
coef(nommod)
Tnom.dev(4) %*% coef(nommod)[[1]][1:3] #a
Tnom.dev(4) %*% coef(nommod)[[1]][4:6] #d

## Not run:
dat <- expand.table(deAyala)
head(dat)
## End(Not run)

---

deAyala

**Description of deAyala data**

Mathematics data from de Ayala (2009; pg. 14); 5 item dataset in table format.

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
## Not run:
dat <- expand.table(deAyala)
head(dat)
## End(Not run)
```
DIF

Differential item functioning statistics

Description

This function runs the Wald and likelihood-ratio approaches for testing differential item functioning (DIF). This is primarily a convenience wrapper to the \texttt{multipleGroup} function for performing standard DIF procedures. Independent models can be estimated in parallel by defining a parallel object with \texttt{mirtCluster}, which will help to decrease the runtime. For best results, the baseline model should contain a set of 'anchor' items and have freely estimated hyper-parameters in the focal groups.

Usage

\begin{verbatim}
DIF(
  MGmodel,which.par,
  scheme = "add",
  items2test = 1:extract.mirt(MGmodel, "nitems"),
  seq_stat = "SABIC",
  Wald = FALSE,
  p.adjust = "none",
  return_models = FALSE,
  return_seq_model = FALSE,
  max_run = Inf,
  plotdif = FALSE,
  type = "trace",
  simplify = TRUE,
  verbose = TRUE,
  ...
)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{MGmodel} \hspace{1cm} an object returned from \texttt{multipleGroup} to be used as the reference model
\item \texttt{which.par} \hspace{1cm} a character vector containing the parameter names which will be inspected for DIF
\item \texttt{scheme} \hspace{1cm} type of DIF analysis to perform, either by adding or dropping constraints across groups. These can be:
  \item \texttt{'add'} parameters in \texttt{which.par} will be constrained each item one at a time for items that are specified in \texttt{items2test}. This is beneficial when examining DIF from a model with parameters freely estimated across groups, and when inspecting differences via the Wald test
  \item \texttt{'drop'} parameters in \texttt{which.par} will be freely estimated for items that are specified in \texttt{items2test}. This is useful when supplying an overly restrictive model and attempting to detect DIF with a slightly less restrictive model
\end{itemize}
'add_sequential' sequentially loop over the items being tested, and at the end of the loop treat DIF tests that satisfy the seq_stat criteria as invariant. The loop is then re-run on the remaining invariant items to determine if they are now displaying DIF in the less constrained model, and when no new invariant item is found the algorithm stops and returns the items that displayed DIF. Note that the DIF statistics are relative to this final, less constrained model which includes the DIF effects.

'drop_sequential' sequentially loop over the items being tested, and at the end of the loop treat items that violate the seq_stat criteria as demonstrating DIF. The loop is then re-run, leaving the items that previously demonstrated DIF as variable across groups, and the remaining test items that previously showed invariance are re-tested. The algorithm stops when no more items showing DIF are found and returns the items that displayed DIF. Note that the DIF statistics are relative to this final, less constrained model which includes the DIF effects.

**items2test** a numeric vector, or character vector containing the item names, indicating which items will be tested for DIF. In models where anchor items are known, omit them from this vector. For example, if items 1 and 2 are anchors in a 10 item test, then *items2test = 3:10* would work for testing the remaining items (important to remember when using sequential schemes).

**seq_stat** select a statistic to test for in the sequential schemes. Potential values are (in descending order of power) 'AIC', 'AICc', 'SABIC', 'HQ', and 'BIC'. If a numeric value is input that ranges between 0 and 1, the 'p' value will be tested (e.g., *seq_stat = .05* will test for the difference of p < .05 in the add scheme, or p > .05 in the drop scheme), along with the specified p.adjust input. For models fitted with prior distributions 'DIC' is also supported, though for these models the p-value approach is not.

**Wald** logical; perform Wald tests for DIF instead of likelihood ratio test?

**p.adjust** string to be passed to the p.adjust function to adjust p-values. Adjustments are located in the adj_pvals element in the returned list.

**return_models** logical; return estimated model objects for further analysis? Default is FALSE.

**return_seq_model** logical; on the last iteration of the sequential schemes, return the fitted multiple-group model containing the freely estimated parameters indicative of DIF? This is generally only useful when scheme = 'add_sequential'. Default is FALSE.

**max_run** a number indicating the maximum number of cycles to perform in sequential searches. The default is to perform search until no further DIF is found.

**plotdif** logical; create item plots for items that are displaying DIF according to the seq_stat criteria? Only available for 'add' type schemes.

**type** the type of plot argument passed to plot(). Default is 'trace', though another good option is 'infotrace'. For ease of viewing, the facet_item argument to mirt's plot() function is set to TRUE.

**simplify** logical; simplify the output by returning a data.frame object with the differences between AIC, BIC, etc, as well as the chi-squared test (X2) and associated df and p-values.
verbose logical print extra information to the console?
... additional arguments to be passed to `multipleGroup` and `plot`

**Details**

Generally, the precomputed baseline model should have been configured with two estimation properties: 1) a set of ‘anchor’ items, where the anchor items have various parameters that have been constrained to be equal across the groups, and 2) contain freely estimated latent mean and variance terms in all but one group (the so-called ‘reference’ group). These two properties help to fix the metric of the groups so that item parameter estimates do not contain latent distribution characteristics.

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**See Also**

`multipleGroup`, `DRF`

**Examples**

```r
## Not run:

# simulate data where group 2 has a smaller slopes and more extreme intercepts
set.seed(12345)
a1 <- a2 <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d1 <- d2 <- matrix(rnorm(15,0,.7),ncol=1)
a2[1:2, ] <- a1[1:2, ]/3
d1[c(1,3), ] <- d2[c(1,3), ]/4
head(data.frame(a.group1 = a1, a.group2 = a2, d.group1 = d1, d.group2 = d2))
itemtype <- rep(‘2PL’, nrow(a1))
N <- 1000
dataset1 <- simdata(a1, d1, N, itemtype)
dataset2 <- simdata(a2, d2, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep(‘D1’, N), rep(‘D2’, N))

##### no anchors, all items tested for DIF by adding item constrains one item at a time.
# define a parallel cluster (optional) to help speed up internal functions
mirtCluster()

# Information matrix with Oakes’ identity (not controlling for latent group differences)
```

# NOTE: Without properly equating the groups the following example code is not testing for DIF, # but instead reflects a combination of DIF + latent-trait distribution effects
model <- multipleGroup(dat, 1, group, SE = TRUE)

# Likelihood-ratio test for DIF (as well as model information)
DIF(model, c('a1', 'd'))
DIF(model, c('a1', 'd'), simplify = FALSE)  # return list output

# same as above, but using Wald tests with Benjamini & Hochberg adjustment
DIF(model, c('a1', 'd'), Wald = TRUE, p.adjust = 'fdr')

# equate the groups by assuming the last 5 items have no DIF
itemnames <- colnames(dat)
model <- multipleGroup(dat, 1, group, SE = TRUE,
invariance = c(itemnames[11:ncol(dat)], 'free_means', 'free_var'))

# test whether adding slopes and intercepts constraints results in DIF. Plot items showing DIF
resulta1d <- DIF(model, c('a1', 'd'), plotdif = TRUE, items2test = 1:10)
resulta1d

# test whether adding only slope constraints results in DIF for all items
DIF(model, 'a1', items2test = 1:10)

# Determine whether it's a1 or d parameter causing DIF (could be joint, however)
(als <- DIF(model, 'a1', items2test = 1:3))
(ds <- DIF(model, 'd', items2test = 1:3))

### drop down approach (freely estimating parameters across groups) when
### specifying a highly constrained model with estimated latent parameters
model_constrained <- multipleGroup(dat, 1, group,
invariance = c(colnames(dat), 'free_means', 'free_var'))
dropdown <- DIF(model_constrained, c('a1', 'd'), scheme = 'drop')
dropdown

### sequential schemes (add constraints)
### sequential searches using SABIC as the selection criteria
# starting from completely different models
stepup <- DIF(model, c('a1', 'd'), scheme = 'add_sequential',
  items2test = 1:10)
stepup

# step down procedure for highly constrained model
stepdown <- DIF(model_constrained, c('a1', 'd'), scheme = 'drop_sequential')
stepdown

# view final MG model (only useful when scheme is 'add_sequential')
updated_mod <- DIF(model, c('a1', 'd'), scheme = 'add_sequential',
  return_seq_model = TRUE)
plot(updated_mod, type = 'trace')

## End(Not run)
DiscreteClass-class  

Class "DiscreteClass"

Description

Defines the object returned from \texttt{mdirt}.

Slots

Call: function call
Data: list of data, sometimes in different forms
Options: list of estimation options
Fit: a list of fit information
Model: a list of model-based information
ParObjects: a list of the S4 objects used during estimation
OptimInfo: a list of arguments from the optimization process
Internals: a list of internal arguments for secondary computations (inspecting this object is generally not required)
vcov: a matrix represented the asymptotic covariance matrix of the parameter estimates
time: a data.frame indicating the breakdown of computation times in seconds

Methods

\texttt{print} signature(x = "DiscreteClass")
\texttt{show} signature(object = "DiscreteClass")
\texttt{anova} signature(object = "DiscreteClass")
\texttt{coef} signature(x = "DiscreteClass")
\texttt{summary} signature(object = "DiscreteClass")
\texttt{residuals} signature(object = "DiscreteClass")

Author(s)

Phil Chalmers \texttt{<rphilip.chalmers@gmail.com>}

References

draw_parameters

Description

Draws plausible parameters from a model using parametric sampling (if the information matrix was computed) or via bootstrap sampling. Primarily for use with the DRF function.

Usage

draw_parameters(
  mod,
  draws,
  method = c("parametric", "bootstrap"),
  redraws = 20,
  ...
)

Arguments

mod estimated single or multiple-group model
draws number of draws to obtain
method type of plausible values to obtain. Can be 'parametric', for the parametric sampling scheme which uses the estimated information matrix, or 'bootstrap' to obtain values from the boot function. Default is 'parametric'
redraws number of redraws to perform when the given parameteric sample does not satisfy the upper and lower parameter bounds. If a valid set cannot be found within this number of draws then an error will be thrown
...
additional arguments to be passed

Value

returns a draws x p matrix of plausible parameters, where each row corresponds to a single set

Examples

## Not run:
set.seed(1234)
n <- 40
N <- 500

# only first 5 items as anchors
model <- 'F = 1-40
    CONSTRAINTB = (1-5, a1), (1-5, d)'
a <- matrix(1, n)
d <- matrix(rnorm(n), n)
group <- c(rep('Group_1', N), rep('Group_2', N))

#------------------------------------------------------------------------------
## groups completely equal
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a, d, N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE,
  invariance=c('free_means', 'free_var'))

param_set <- draw_parameters(mod, 100)
head(param_set)

## End(Not run)

---

**DRF**

**Differential Response Functioning statistics**

**Description**

Function performs various omnibus differential item (DIF), bundle (DBF), and test (DTF) functioning procedures on an object estimated with `multipleGroup()`. The compensatory and non-compensatory statistics provided are described in Chalmers (2018), which generally can be interpreted as IRT generalizations of the SIBTEST and CSIBTEST statistics. These require the ACOV matrix to be computed in the fitted multiple-group model (otherwise, sets of plausible draws from the posterior are explicitly required).

**Usage**

```r
DRF(
  mod,
  draws = NULL,
  focal_items = 1L:extract.mirt(mod, "nitems"),
  param_set = NULL,
  CI = 0.95,
  npts = 1000,
  quadpts = NULL,
  theta_lim = c(-6, 6),
  Theta_nodes = NULL,
  plot = FALSE,
  DIF = FALSE,
  p.adjust = "none",
  par.strip.text = list(cex = 0.7),
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
  auto.key = list(space = "right", points = FALSE, lines = TRUE),
)```
Arguments

mod

a multipleGroup object which estimated only 2 groups

draws

a number indicating how many draws to take to form a suitable multiple imputation or bootstrap estimate of the expected test scores (100 or more). If boot = FALSE, requires an estimated parameter information matrix. Returns a list containing the bootstrap/imputation distribution and null hypothesis test for the sDRF statistics

focal_items

a numeric vector indicating which items to include in the DRF tests. The default uses all of the items (note that including anchors in the focal items has no effect because they are exactly equal across groups). Selecting fewer items will result in tests of 'differential bundle functioning'

param_set

an N x p matrix of parameter values drawn from the posterior (e.g., using the parametric sampling approach, bootstrap, or MCMC). If supplied, then these will be used to compute the DRF measures. Can be much more efficient to pre-compute these values if DIF, DBF, or DTF are being evaluated within the same model (especially when using the bootstrap method). See draw_parameters

CI

range of confidence interval when using draws input

npts

number of points to use for plotting. Default is 1000

quadpts

number of quadrature nodes to use when constructing DRF statistics. Default is extracted from the input model object

theta_lim

lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with quadpts and npts

Theta_nodes

an optional matrix of Theta values to be evaluated in the draws for the sDRF statistics. However, these values are not averaged across, and instead give the bootstrap confidence intervals at the respective Theta nodes. Useful when following up a large sDRF or uDRF statistic, for example, to determine where the difference between the test curves are large (while still accounting for sampling variability). Returns a matrix with observed variability

plot

logical; plot the 'sDRF' functions for the evaluated sDBF or sDTF values across the integration grid or, if DIF = TRUE, the selected items as a faceted plot of individual items? If plausible parameter sets were obtained/supplied then imputed confidence intervals will be included

DIF

logical; return a list of item-level imputation properties using the DRF statistics? These can generally be used as a DIF detection method and as a graphical display for understanding DIF within each item

p.adjust

string to be passed to the p.adjust function to adjust p-values. Adjustments are located in the adj_pvals element in the returned list. Only applicable when DIF = TRUE

par.strip.text

plotting argument passed to lattice

par.settings

plotting argument passed to lattice

auto.key

plotting argument passed to lattice

... additional arguments to be passed to lattice
Author(s)
Phil Chalmers <rphilip.chalmers@gmail.com>

References

See Also
multipleGroup.DIF

Examples

```r
## Not run:
set.seed(1234)
n <- 30
N <- 500

# only first 5 items as anchors
model <- 'F = 1-30
         CONSTRAINB = (1-5, a1), (1-5, d)'

a <- matrix(1, n)
d <- matrix(rnorm(n), n)
group <- c(rep('Group_1', N), rep('Group_2', N))

## ------------
# groups completely equal
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a, d, N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE,
invariance=c('free_means', 'free_var'))
plot(mod)
plot(mod, which.items = 6:10) #DBF
plot(mod, type = 'itemscore')
plot(mod, type = 'itemscore', which.items = 10:15)

DRF(mod)
DRF(mod, focal_items = 6:10) #DBF
DRF(mod, DIF=TRUE)
DRF(mod, DIF=TRUE, focal_items = 10:15)

DRF(mod, plot = TRUE)
DRF(mod, focal_items = 6:10, plot = TRUE) #DBF
DRF(mod, DIF=TRUE, plot = TRUE)
DRF(mod, DIF=TRUE, focal_items = 10:15, plot = TRUE)

mirtCluster()
DRF(mod, draws = 500)
```
DRF(mod, draws = 500, plot=TRUE)

# pre-draw parameter set to save computations
param_set <- draw_parameters(mod, draws = 500)
DRF(mod, focal_items = 6, param_set=param_set) #DIF
DRF(mod, DIF=TRUE, param_set=param_set) #DIF
DRF(mod, focal_items = 6:10, param_set=param_set) #DBF
DRF(mod, param_set=param_set) #DTF

DRF(mod, focal_items = 6:10, draws=500) #DBF
DRF(mod, focal_items = 10:15, draws=500) #DBF

DIFs <- DRF(mod, draws = 500, DIF=TRUE)
print(DIFs)
DRF(mod, draws = 500, DIF=TRUE, plot=TRUE)

DIFs <- DRF(mod, draws = 500, DIF=TRUE, focal_items = 6:10)
print(DIFs)
DRF(mod, draws = 500, DIF=TRUE, focal_items = 6:10, plot = TRUE)

DRF(mod, DIF=TRUE, focal_items = 6)
DRF(mod, draws=500, DIF=TRUE, focal_items = 6)

# evaluate specific values for sDRF
Theta_nodes <- matrix(seq(-6,6,length.out = 100))
sDTF <- DRF(mod, Theta_nodes=Theta_nodes)
head(sDTF)
sDTF <- DRF(mod, Theta_nodes=Theta_nodes, draws=200)
head(sDTF)

# sDIF (isolate single item)
sDIF <- DRF(mod, Theta_nodes=Theta_nodes, focal_items=6)
head(sDIF)
sDIF <- DRF(mod, Theta_nodes=Theta_nodes, focal_items = 6, draws=200)
head(sDIF)

## --------------
## random slopes and intercepts for 15 items, and latent mean difference
## (no systematic DTF should exist, but DIF will be present)
set.seed(1234)
dat1 <- simdata(a, d, N, itemtype = 'dich', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), rnorm(n-15, 0, .25)),
              d + c(numeric(15), rnorm(n-15, 0, .5)), N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod1 <- multipleGroup(dat, 1, group=group)
plot(mod1)
DRF(mod1) #does not account for group differences! Need anchors

mod2 <- multipleGroup(dat, model, group=group, SE=TRUE,
                      invariance=c('free_means', 'free_var'))
plot(mod2)
# significant DIF in multiple items....
# DIF(mod2, which.par=c('a1', 'd'), items2test=16:30)
DRF(mod2)
DRF(mod2, draws=500) # non-sig DTF due to item cancellation

## systemad differing slopes and intercepts (clear DTF)
set.seed(1234)

dat1 <- simdata(a, d, N, itemtype = 'dich', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), rnorm(n-15, 1, .25)), d + c(numeric(15), rnorm(n-15, 1, .5)), N, itemtype = 'dich')
dat <- rbind(dat1, dat2)
mod3 <- multipleGroup(dat, model, group=group, SE=TRUE, invariance=c('free_means', 'free_var'))
plot(mod3) # visable DTF happening

# DIF(mod3, c('a1', 'd'), items2test=16:30)
DRF(mod3) # unsigned bias. Signed bias indicates group 2 scores generally higher on average
DRF(mod3, draws=500)
DRF(mod3, draws=500, plot=TRUE) # multiple DRF areas along Theta

# plot the DIF
DRF(mod3, draws=500, DIF=TRUE, plot=TRUE)

# evaluate specific values for sDRF
Theta_nodes <- matrix(seq(-6, 6, length.out = 100))
sDTF <- DRF(mod3, Theta_nodes=Theta_nodes, draws=200)
head(sDTF)

# DIF
sDIF <- DRF(mod3, Theta_nodes=Theta_nodes, focal_items = 30, draws=200)
car::some(sDIF)

## multidimensional DTF

set.seed(1234)
n <- 50
N <- 1000

# only first 5 items as anchors within each dimension
model <- 'F1 = 1-25
          F2 = 26-50
          COV = F1*F2
          CONSTRAINB = (1-5, a1), (1-5, 26-30, d), (26-30, a2)'
a <- matrix(c(rep(1, 25), numeric(50), rep(1, 25)), n)
d <- matrix(rnorm(n), n)
group <- c(rep('Group_1', N), rep('Group_2', N))
Cov <- matrix(c(1, .5, .5, 1.5), 2)
Mean <- c(0, 0.5)

# groups completely equal
dat1 <- simdata(a, d, N, itemtype = 'dich', sigma = cov2cor(Cov))
dat2 <- simdata(a, d, N, itemtype = 'dich', sigma = Cov, mu = Mean)
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE,
invariance=c('free_means', 'free_var'))
coef(mod, simplify=TRUE)
plot(mod, degrees = c(45,45))
DRF(mod)

# some intercepts slightly higher in Group 2
d2 <- d
d2[c(10:15, 31:35)] <- d2[c(10:15, 31:35)] + 1
dat1 <- simdata(a, d, N, itemtype = 'dich', sigma = cov2cor(Cov))
dat2 <- simdata(a, d2, N, itemtype = 'dich', sigma = Cov, mu = Mean)
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE,
invariance=c('free_means', 'free_var'))
coef(mod, simplify=TRUE)
plot(mod, degrees = c(45,45))
DRF(mod)
DRF(mod, draws = 500)

## End(Not run)

---

**DTF**

**Differential test functioning statistics**

**Description**

Function performs various omnibus differential test functioning procedures on an object estimated with `multipleGroup()`. If the latent means/covariances are suspected to differ then the input object should contain a set of ‘anchor’ items to ensure that only differential test features are being detected rather than group differences. Returns signed (average area above and below) and unsigned (total area) statistics, with descriptives such as the percent average bias between group total scores for each statistic. If a grid of Theta values is passed, these can be evaluated as well to determine specific DTF location effects. For best results, the baseline model should contain a set of ‘anchor’ items and have freely estimated hyper-parameters in the focal groups. See `DIF` for details.

**Usage**

```r
DTF(
  mod,
  draws = NULL,
  CI = 0.95,
  npts = 1000,
  theta_lim = c(-6, 6),
  Theta_nodes = NULL,
)```

plot = "none",
auto.key = list(space = "right", points = FALSE, lines = TRUE),
...)

Arguments

mod a multipleGroup object which estimated only 2 groups
draws a number indicating how many draws to take to form a suitable multiple im-
putation estimate of the expected test scores (usually 100 or more). Returns a
list containing the imputation distribution and null hypothesis test for the sDTF
statistic
CI range of confidence interval when using draws input
npts number of points to use in the integration. Default is 1000
theta_lim lower and upper limits of the latent trait (theta) to be evaluated, and is used in
conjunction with npts
Theta_nodes an optional matrix of Theta values to be evaluated in the draws for the sDTF
statistic. However, these values are not averaged across, and instead give the
bootstrap confidence intervals at the respective Theta nodes. Useful when fol-
lowing up a large uDTF/sDTF statistic to determine where the difference be-
tween the test curves are large (while still accounting for sampling variability).
Returns a matrix with observed variability
plot a character vector indicating which plot to draw. Possible values are 'none',
'func' for the test score functions, and 'sDTF' for the evaluated sDTF values
across the integration grid. Each plot is drawn with imputed confidence en-
velopes
auto.key logical; automatically generate key in lattice plot?
... additional arguments to be passed to lattice and boot

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

ronment. *Journal of Statistical Software, 48*(6), 1-29. doi: 10.18637/jss.v048.i06

Differential Test Functioning statistics that account for sampling variability. *Educational and Psy-
chological Measurement, 76*, 114-140. doi: 10.1177/0013164415584576

See Also

multipleGroup, DIF
Examples

```r
## Not run:
set.seed(1234)
n <- 30
N <- 500

# only first 5 items as anchors
model <- 'F = 1-30
    CONSTRANBi = (1-5, a1), (1-5, d)

a <- matrix(1, n)
d <- matrix(rnorm(n), n)
group <- c(rep('Group_1', N), rep('Group_2', N))

## ------------
# groups completely equal
dat1 <- simdata(a, d, N, itemtype = '2PL')
dat2 <- simdata(a, d, N, itemtype = '2PL')
dat <- rbind(dat1, dat2)
mod <- multipleGroup(dat, model, group=group, SE=TRUE,
    invariance=c('free_means', 'free_var'))
plot(mod)

DTF(mod)
mirtCluster()
DTF(mod, draws = 1000) #95% C.I. for sDTF containing 0. uDTF is very small
DTF(mod, draws = 1000, plot='sDTF') #sDTF 95% C.I.'s across Theta always include 0

## ------------
## random slopes and intercepts for 15 items, and latent mean difference
## (no systematic DTF should exist, but DIF will be present)
set.seed(1234)
dat1 <- simdata(a, d, N, itemtype = '2PL', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), runif(n-15, -.2, .2)),
    d + c(numeric(15), runif(n-15, -.5, .5)), N, itemtype = '2PL')
dat <- rbind(dat1, dat2)
mod1 <- multipleGroup(dat, 1, group=group)
plot(mod1) #does not account for group differences! Need anchors

mod2 <- multipleGroup(dat, model, group=group, SE=TRUE,
    invariance=c('free_means', 'free_var'))
plot(mod2)

#significant DIF in multiple items....
# DIF(mod2, which.par=c('a1', 'd'), items2test=16:30)
DTF(mod2)
DTF(mod2, draws=1000) #non-sig DTF due to item cancellation

## ------------
## systematic differing slopes and intercepts (clear DTF)
dat1 <- simdata(a, d, N, itemtype = '2PL', mu=.50, sigma=matrix(1.5))
dat2 <- simdata(a + c(numeric(15), rnorm(n-15, 1, .25)),
    d + c(numeric(15), rnorm(n-15, 1, .5)),
```
empirical_ES

N, itemtype = '2PL')
dat <- rbind(dat1, dat2)
mod3 <- multipleGroup(dat, model, group=group, SE=TRUE,
invariance=c('free_means', 'free_var'))
plot(mod3) #visable DTF happening

# DIF(mod3, c('a1', 'd'), items2test=16:30)
DTF(mod3) #unsigned bias. Signed bias indicates group 2 scores generally higher on average
DTF(mod3, draws=1000)
DTF(mod3, draws=1000, plot='func')
DTF(mod3, draws=1000, plot='sDTF') #multiple DTF areas along Theta

# evaluate specific values for sDTF
Theta_nodes <- matrix(seq(-6,6,length.out = 100))
sDTF <- DTF(mod3, Theta_nodes=Theta_nodes)
head(sDTF)
sDTF <- DTF(mod3, Theta_nodes=Theta_nodes, draws=100)
head(sDTF)

## End(Not run)

---

empirical_ES

Empirical effect sizes based on latent trait estimates

Description

Computes effect size measures of differential item functioning and differential test/bundle functioning based on expected scores from Meade (2010). Item parameters from both reference and focal group are used in conjunction with focal group empirical theta estimates (and an assumed normally distributed theta) to compute expected scores.

Usage

empirical_ES(
  mod,
  Theta.focal = NULL,
  focal_items = 1L:extract.mirt(mod, "nitems"),
  DIF = TRUE,
  npts = 61,
  theta_lim = c(-6, 6),
  ref.group = 1,
  plot = FALSE,
  par.strip.text = list(cex = 0.7),
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
  ...
)
Arguments

mod

a multipleGroup object which estimated only 2 groups

Theta.focal

an optional matrix of Theta values from the focal group to be evaluated. If not supplied the default values to fscores will be used in conjunction with the ... arguments passed

focal_items

a numeric vector indicating which items to include the tests. The default uses all of the items. Selecting fewer items will result in tests of ‘differential bundle functioning’ when DIF = FALSE

DIF

logical; return a data.frame of item-level imputation properties? If FALSE, only DBF and DTF statistics will be reported

npts

number of points to use in the integration. Default is 61

theta_lim

lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with npts

ref.group

either 1 or 2 to indicate which group is considered the ‘reference’ group. Default is 1

plot

logical; plot expected scores of items/test where expected scores are computed using focal group thetas and both focal and reference group item parameters

par.strip.text

plotting argument passed to lattice

par.settings

plotting argument passed to lattice

... additional arguments to be passed to fscores and xyplot

DIF

The default DIF = TRUE produces several effect sizes indices at the item level. Signed indices allow DIF favoring the focal group at one point on the theta distribution to cancel DIF favoring the reference group at another point on the theta distribution. Unsigned indices take the absolute value before summing or averaging, thus not allowing cancellation of DIF across theta.

SIDS Signed Item Difference in the Sample. The average difference in expected scores across the focal sample using both focal and reference group item parameters.

UIDS Unsigned Item Difference in the Sample. Same as SIDS except absolute value of expected scores is taken prior to averaging across the sample.

D-Max The maximum difference in expected scores in the sample.

ESSD Expected Score Standardized Difference. Cohen’s D for difference in expected scores.

SIDN Signed Item Difference in a Normal distribution. Identical to SIDS but averaged across a normal distribution rather than the sample.

UIDN Unsigned Item Difference in a Normal distribution. Identical to UIDS but averaged across a normal distribution rather than the sample.

DBF/DTF

DIF = FALSE produces a series of test/bundle-level indices that are based on item-level indices.

STDS Signed Test Differences in the Sample. The sum of the SIDS across items.
**empirical_ES**

**UTDS** Unsigned Test Differences in the Sample. The sum of the UIDS across items.

**Stark’s DTFR** Stark’s version of STDS using a normal distribution rather than sample estimated thetas.

**UDTFR** Unsigned Expected Test Scores Differences in the Sample. The difference in observed summed scale scores expected, on average, across a hypothetical focal group with a normally distributed theta, had DF been uniform in nature for all items.

**UETSDS** Unsigned Expected Test Score Differences in the Sample. The hypothetical difference expected scale scores that would have been present if scale-level DF had been uniform across respondents (i.e., always favoring the focal group).

**UETSDN** Identical to UETSDS but computed using a normal distribution.

**Test D-Max** Maximum expected test score differences in the sample.

**ETSSD** Expected Test Score Standardized Difference. Cohen’s D for expected test scores.

**Author(s)**

Adam Meade and Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
## Not run:
#no DIF
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('2PL', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('Ref', N), rep('Focal', N))

mod <- multipleGroup(dat, 1, group = group,
    invariance = c(colnames(dat)[1:5], 'free_means', 'free_var'))
coef(mod, simplify=TRUE)

empirical_ES(mod)
empirical_ES(mod, DIF=FALSE)
empirical_ES(mod, DIF=FALSE, focal_items = 10:15)

empirical_ES(mod, plot=TRUE)
empirical_ES(mod, plot=TRUE, DIF=FALSE)
```
### empirical_plot

Function to generate empirical unidimensional item and test plots

**Description**

Given a dataset containing item responses this function will construct empirical graphics using the observed responses to each item conditioned on the total score. When individual item plots are requested then the total score will be formed without the item of interest (i.e., the total score without that item).

**Usage**

```r
empirical_plot(
  data,
  which.items = NULL,
  smooth = FALSE,
  formula = resp ~ s(TS, k = 5),
  main = NULL,
  par.strip.text = list(cex = 0.7),
  boxplot = FALSE,
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
)```

```r
# DIF
set.seed(12345)
a1 <- a2 <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d1 <- d2 <- matrix(rnorm(15,0,.7),ncol=1)
a2[10:15,] <- a2[10:15,] + rnorm(6, 0, .3)
d2[10:15,] <- d2[10:15,] + rnorm(6, 0, .3)
itemtype <- rep("dich", nrow(a1))
N <- 1000
dataset1 <- simdata(a1, d1, N, itemtype)
dataset2 <- simdata(a2, d2, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep("Ref", N), rep("Focal", N))
mod <- multipleGroup(dat, 1, group = group,
  invariance = c(colnames(dat)[1:5], 'free_means', 'free_var'))
coef(mod, simplify=TRUE)
empirical_ES(mod)
empirical_ES(mod, DIF = FALSE)
empirical_ES(mod, plot=TRUE)
empirical_ES(mod, plot=TRUE, DIF=FALSE)
```
Arguments

data a data.frame or matrix of item responses (see mirt for typical input)
which.items a numeric vector indicating which items to plot in a faceted image plot. If NULL
then a empirical test plot will be constructed instead
smooth logical; include a GAM smoother instead of the raw proportions? Default is
FALSE
formula formula used for the GAM smoother
main the main title for the plot. If NULL an internal default will be used
par.strip.text plotting argument passed to lattice
boxplot logical; use a boxplot to display the marginal total score differences instead of
scatter plots of proportions? Default is FALSE
par.settings plotting argument passed to lattice
auto.key auto.key = list(space = "right", points = FALSE, lines = TRUE),
... additional arguments to be passed to lattice and coef()

Details

Note that these types of plots should only be used for unidimensional tests with monotonically
increasing item response functions. If monotonicity should be true for all items, however, then these
plots may serve as a visual diagnostic tool so long as the majority of items are indeed monotonic.

References

ronnement. Journal of Statistical Software, 48(6), 1-29. doi: 10.18637/jss.v048.i06

See Also

itemplot, itemGAM

Examples

## Not run:
SAT12[SAT12 == 8] <- NA
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
#test plot
empirical_plot(data)
#items 1, 2 and 5
empirical_plot(data, c(1, 2, 5))
empirical_plot(data, c(1, 2, 5), smooth = TRUE)
empirical_plot(data, c(1, 2, 5), boxplot = TRUE)

# replace weird looking items with unscored versions for diagnostics
empirical_plot(data, 32)
data[,32] <- SAT12[,32]
empirical_plot(data, 32)
empirical_plot(data, 32, smooth = TRUE)

## End(Not run)

empirical_rxx

---

**Function to calculate the empirical (marginal) reliability**

**Description**

Given secondary latent trait estimates and their associated standard errors returned from `fscores`, compute the empirical reliability.

**Usage**

```r
empirical_rxx(Theta_SE)
```

**Arguments**

- `Theta_SE`: a matrix of latent trait estimates returned from `fscores` with the options `full.scores = TRUE` and `full.scores.SE = TRUE`

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**See Also**

`fscores`, `marginal_rxx`
Examples

```r
## Not run:

dat <- expand.table(deAyala)
mod <- mirt(dat, 1)
theta_se <- fscores(mod, full.scores.SE = TRUE)
empirical_rxx(theta_se)

theta_se <- fscores(mod, full.scores.SE = TRUE, method = "ML")
empirical_rxx(theta_se)

## End(Not run)
```

Description

A function for extracting the empirical estimating functions of a fitted `mirt`, `multipleGroup` or `bfactor` model. This is the derivative of the log-likelihood with respect to the parameter vector, evaluated at the observed (case-wise) data. In other words, this function returns the case-wise scores, evaluated at the fitted model parameters. Currently, models fitted via the EM or BL method are supported. For the computations, the internal Theta grid of the model is being used which was already used during the estimation of the model itself along with its matching normalized density.

Usage

```r
estfun.AllModelClass(
  x,
  weights = extract.mirt(x, "survey.weights"),
  centering = FALSE
)
```

Arguments

- `x`: a fitted model object of class `SingleGroupClass` or `MultipleGroupClass`.
- `weights`: by default, the `survey.weights` which were (optionally) specified when fitting the model are included to calculate the scores. If specified by the user, this should be a numeric vector of length equal to the total sample size. Note that if not all cases were weighted equally when fitting the model, the weights must be corrected by taking their square root if the scores are being used to compute the outer product of gradients (OPG) estimate of the variance-covariance matrix (see examples below).
- `centering`: a boolean variable that allows the centering of the case-wise scores (i.e., setting their expected values to 0). If the case-wise scores were obtained from maximum likelihood estimates, this setting does not affect the result.
Value

An n x k matrix corresponding to n observations and k parameters

Author(s)

Lennart Schneider <lennart.sch@web.de>; centering argument contributed by Rudolf Debelak (<rudolf.debelak@psychologie.uzh.ch>)

See Also

mirt, multipleGroup, bfactor

Examples

```r
## Not run:
# fit a 2PL on the LSAT7 data and get the scores
mod1 <- mirt(expand.table(LSAT7), 1, SE = TRUE, SE.type = "crossprod")
s1 <- estfun.AllModelClass(mod1)
# get the gradient
colSums(s1)
# calculate the OPG estimate of the variance-covariance matrix "by hand"
v1 <- vcov(mod1)
all.equal(crossprod(s1), chol2inv(chol(v1)), check.attributes = FALSE)

# fit a multiple group 2PL and do the same as above
group <- rep(c("G1", "G2"), 500)
mod2 <- multipleGroup(expand.table(LSAT7), 1, group, SE = TRUE,
                      SE.type = "crossprod")
s2 <- estfun.AllModelClass(mod2)
colSums(s2)
v2 <- vcov(mod2)
all.equal(crossprod(s2), chol2inv(chol(v2)), check.attributes = FALSE)

# fit a bifactor model with 2 specific factors and do the same as above
mod3 <- bfactor(expand.table(LSAT7), c(2, 2, 1, 1, 2), SE = TRUE,
                SE.type = "crossprod")
s3 <- estfun.AllModelClass(mod3)
colSums(s3)
v3 <- vcov(mod3)
all.equal(crossprod(s3), chol2inv(chol(v3)), check.attributes = FALSE)

# fit a 2PL not weighting all cases equally
survey.weights <- c(rep(2, sum(LSAT7$freq) / 2), rep(1, sum(LSAT7$freq) / 2))
survey.weights <- survey.weights / sum(survey.weights)
mod4 <- mirt(expand.table(LSAT7), 1, SE = TRUE, SE.type = "crossprod",
            survey.weights = survey.weights)
s4 <- estfun.AllModelClass(mod4,
                weights = extract.mirt(mod4, "survey.weights"))
# get the gradient
colSums(s4)
# to calculate the OPG estimate of the variance-covariance matrix "by hand",
```
expand.table

# the weights must be adjusted by taking their square root
sc4_crp <- estfun.AllModelClass(mod4,
    weights = sqrt(extract.mirt(mod4, "survey.weights")))
vc4 <- vcov(mod4)
all.equal(crossprod(sc4_crp), chol2inv(chol(vc4)), check.attributes = FALSE)

## End(Not run)

expand.table

Expand summary table of patterns and frequencies

Description
The expand.table function expands a summary table of unique response patterns to a full sized
data-set. The response frequencies must be on the rightmost column of the input data.

Usage
expand.table(tabdata, sample = FALSE)

Arguments
- tabdata: An object of class data.frame or matrix with the unique response patterns and
  the number of frequencies in the rightmost column
- sample: logical; randomly switch the rows in the expanded table? This does not change
  the expanded data, only the row locations

Value
Returns a numeric matrix with all the response patterns.

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

References

Examples

data(LSAT7)
head(LSAT7)
LSAT7full <- expand.table(LSAT7)
head(LSAT7full)
**expected.item**

*Function to calculate expected value of item*

**Description**

Given an internal mirt object extracted from an estimated model compute the expected value for an item given the ability parameter(s).

**Usage**

```r
equated.item(x, Theta, min = 0)
```

**Arguments**

- `x`: an extracted internal mirt object containing item information (see `extract.item`)
- `Theta`: a vector (unidimensional) or matrix (multidimensional) of latent trait values
- `min`: a constant value added to the expected values indicating the lowest theoretical category. Default is 0

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**See Also**

`extract.item, expected.test`

**Examples**

```r
mod <- mirt(Science, 1)
extr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-6, 6, length.out=200))
expected <- expected.item(extr.2, Theta, min(Science[,1])) #min() of first item
head(data.frame(expected, Theta=Theta))
```
expected.test

Function to calculate expected test score

Description

Given an estimated model compute the expected test score. Returns the expected values in the same form as the data used to estimate the model.

Usage

expected.test(
  x, Theta, group = NULL, mins = TRUE, individual = FALSE, which.items = NULL
)

Arguments

x an estimated mirt object
Theta a matrix of latent trait values
group a number signifying which group the item should be extracted from (applies to 'MultipleGroupClass' objects only)
mins logical; include the minimum value constants in the dataset. If FALSE, the expected values for each item are determined from the scoring 0:(ncat-1)
individual logical; return tracelines for individual items?
which.items an integer vector indicating which items to include in the expected test score. Default uses all possible items

References


See Also

dexpected.item

Examples

## Not run:
dat <- expand.table(deAyala)
model <- 'F = 1-5
CONSTRAIN = (1-5, a1)'
mod <- mirt(dat, model)

Theta <- matrix(seq(-6, 6, .01))
tscore <- expected.test(mod, Theta)
tail(cbind(Theta, tscore))

# use only first two items (i.e., a bundle)
bscore <- expected.test(mod, Theta, which.items = 1:2)
tail(cbind(Theta, bscore))

## End(Not run)

---

**extract.group**

*Extract a group from a multiple group mirt object*

**Description**

Extract a single group from an object defined by `multipleGroup`.

**Usage**

`extract.group(x, group)`

**Arguments**

- `x`: mirt model of class `MultipleGroupClass`
- `group`: a number signifying which group should be extracted

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**See Also**

`extract.item`, `extract.mirt`
Examples

```r
## Not run:
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('2PL', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
models <- 'F1 = 1-15'
mod_configural <- multipleGroup(dat, models, group = group)
group.1 <- extract.group(mod_configural, 1) #extract first group
summary(group.1)
plot(group.1)
## End(Not run)
```

---

**extract.item**

**Extract an item object from mirt objects**

**Description**

Extract the internal mirt objects from any estimated model.

**Usage**

```r
extract.item(x, item, group = NULL, drop.zeros = FALSE)
```

**Arguments**

- `x` mirt model of class 'SingleGroupClass' or 'MultipleGroupClass'
- `item` a number or character signifying which item to extract
- `group` a number signifying which group the item should be extracted from (applies to 'MultipleGroupClass' only)
- `drop.zeros` logical; drop slope values that are numerically close to zero to reduce dimensionality? Useful in objects returned from `bfactor` or other confirmatory models that contain several zero slopes

**References**

extract.mirt

See Also

extract.group, extract.mirt

Examples

```r
## Not run:
mod <- mirt(Science, 1)
extr.1 <- extract.item(mod, 1)
## End(Not run)
```

extract.mirt

Extract various elements from estimated model objects

Description

A generic function to extract the internal objects from estimated models.

Usage

```r
extract.mirt(x, what)
```

Arguments

- `x` mirt model of class 'SingleGroupClass', 'MultipleGroupClass', 'MixedClass' or 'DiscreteGroupClass'
- `what` a string indicating what to extract

Details

Objects which can be extracted from mirt objects include:

- **logLik** observed log-likelihood
- **logPrior** log term contributed by prior parameter distributions
- **G2** goodness of fit statistic
- **df** degrees of freedom
- **p** p-value for G2 statistic
- **RMSEA** root mean-square error of approximation based on G2
- **CFI** CFI fit statistic
- **TLI** TLI fit statistic
- **AIC** AIC
- **AICc** corrected AIC
- **BIC** BIC
SABIC  sample size adjusted BIC
DIC  DIC
HQ  HQ
F  unrotated standardized loadings matrix
h2  factor communality estimates
LLhistory  EM log-likelihood history
tabdata  a tabular version of the raw response data input. Frequencies are stored in freq
freq  frequencies associated with tabdata
K  an integer vector indicating the number of unique elements for each item
mins  an integer vector indicating the lowest category found in the input data
model  input model syntax
method  estimation method used
itemtype  a vector of item types for each respective item (e.g., ‘graded’, ’2PL’, etc)
itemnames  a vector of item names from the input data
factorNames  a vector of factor names from the model definition
rowID  an integer vector indicating all valid row numbers used in the model estimation (when
        all cases are used this will be 1:nrow(data)). Mostly useful when the option technical =
        list(removeEmptyRows = TRUE) was passed
data  raw input data of item responses
covdata  raw input data of data used as covariates
tabdatalong  similar to tabdata, however the responses have been transformed into dummy coded
        variables
fulldatalong  analogous to tabdatafull, but for the raw input data instead of the tabulated fre-
        quencies
exp Resp  expected probability of the unique response patterns
survey.weights  if supplied, the vector of survey weights used during estimation (NULL if missing)
converged  a logical value indicating whether the model terminated within the convergence criteria
iterations  number of iterations it took to reach the convergence criteria
nest  number of freely estimated parameters
parvec  vector containing uniquely estimated parameters
vcov  parameter covariance matrix (associated with parvec)
condnum  the condition number of the Hessian (if computed). Otherwise NA
constrain  a list of item parameter constraints to indicate which item parameters were equal during
        estimation
Prior  prior density distribution for the latent traits
key  if supplied, the data scoring key
nfact  number of latent traits/factors
nitems  number of items
extract.mirt

ngroups  number of groups

groupNames  character vector of unique group names

group  a character vector indicating the group membership

secondordertest  a logical indicating whether the model passed the second-order test based on the Hessian matrix. Indicates whether model is a potential local maximum solution

SEMconv  logical; check whether the supplemented EM information matrix converged. Will be NA if not applicable

time  estimation time, broken into different sections

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

extract.group, extract.item, mod2values

Examples

```r
## Not run:
mod <- mirt(Science, 1)

extract.mirt(mod, 'logLik')
extract.mirt(mod, 'F')

#multiple group model
gp <- rep(c('G1', 'G2'), each = nrow(Science)/2)
mod2 <- multipleGroup(Science, 1, gp)

grp1 <- extract.group(mod2, 1) #extract single group model
extract.mirt(mod2, 'parvec')
extract.mirt(grp1, 'parvec')

## End(Not run)
```
Description
Create expected values for fixed effects parameters in latent regression models.

Usage
fixef(x)

Arguments
x
an estimated model object from the mixedmirt or mirt function

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

References

See Also
mirt, mixedmirt

Examples
## Not run:
#simulate data
set.seed(1234)
N <- 1000

# covariates
X1 <- rnorm(N); X2 <- rnorm(N)
covdata <- data.frame(X1, X2)
Theta <- matrix(0.5 * X1 + -1 * X2 + rnorm(N, sd = 0.5))

#items and response data
a <- matrix(1, 20); d <- matrix(rnorm(20))
dat <- simdata(a, d, 1000, itemtype = '2PL', Theta=Theta)

#conditional model using X1 and X2 as predictors of Theta
mod1 <- mirt(dat, 1, 'Rasch', covdata=covdata, formula = ~ X1 + X2)
# latent regression fixed effects (i.e., expected values)
fe <- fixef(mod1)
head(fe)

# with mixedmirt()
mod1b <- mixedmirt(dat, covdata, 1, lr.fixed = ~ X1 + X2, fixed = ~ 0 + items)
fe2 <- fixef(mod1b)
head(fe2)

## End(Not run)

### fscores

**fscores**  
Compute factor score estimates (a.k.a, ability estimates, latent trait estimates, etc)

**Description**
Computes MAP, EAP, ML (Embretson & Reise, 2000), EAP for sum-scores (Thissen et al., 1995), or WLE (Warm, 1989) factor scores with a multivariate normal prior distribution using equally spaced quadrature. EAP scores for models with more than three factors are generally not recommended since the integration grid becomes very large, resulting in slower estimation and less precision if the quadpts are too low. Therefore, MAP scores should be used instead of EAP scores for higher dimensional models. Multiple imputation variants are possible for each estimator if a parameter information matrix was computed, which are useful if the sample size/number of items were small. As well, if the model contained latent regression predictors this information will be used in computing MAP and EAP estimates (for these models, full.scores=TRUE will always be used). Finally, plausible value imputation is also available, and will also account for latent regression predictor effects.

**Usage**

```r
fscores(
  object,  
  method = "EAP",  
  full.scores = TRUE,  
  rotate = "oblimin",  
  Target = NULL,  
  response.pattern = NULL,  
  append_response.pattern = TRUE,  
  na.rm = FALSE,  
  plausible.draws = 0,  
  plausible.type = "normal",  
  quadpts = NULL,  
  returnER = FALSE,  
  return.acov = FALSE,  
  mean = NULL,  
  ...  
)
```
cov = NULL,
verbose = TRUE,
full.scores.SE = FALSE,
theta_lim = c(-6, 6),
MI = 0,
use_dentype_estimate = FALSE,
QMC = FALSE,
custom_den = NULL,
custom_theta = NULL,
min_expected = 1,
converge_info = FALSE,
max_theta = 20,
start = NULL,
...
)

Arguments

object  a computed model object of class SingleGroupClass, MultipleGroupClass, or DiscreteClass
method  type of factor score estimation method. Can be:
  • "EAP" for the expected a-posteriori (default)
  • "MAP" for the maximum a-posteriori (i.e, Bayes modal)
  • "ML" for maximum likelihood
  • "WLE" for weighted likelihood estimation
  • "EAPsum" for the expected a-posteriori for each sum score
  • "plausible" for a single plausible value imputation for each case. This is equivalent to setting plausible.draws = 1
  • "classify" for the posteriori classification probabilities (only applicable when the input model was of class MixtureClass)
full.scores  if FALSE then a summary table with factor scores for each unique pattern is displayed. Otherwise, a matrix of factor scores for each response pattern in the data is returned (default)
rotate  prior rotation to be used when estimating the factor scores. See summary-method for details. If the object is not an exploratory model then this argument is ignored
Target
response.pattern  an optional rotation; see summary-method for details
append_response.pattern  logical; should the inputs from response.pattern also be appended to the factor score output?
na.rm  logical; remove rows with any missing values? This is generally not required due to the nature of computing factors scores, however for the "EAPsum" method this may be necessary to ensure that the sum-scores correspond to the same composite score
plausible.draws

number of plausible values to draw for future researchers to perform secondary analyses of the latent trait scores. Typically used in conjunction with latent regression predictors (see mirt for details), but can also be generated when no predictor variables were modeled. If plausible.draws is greater than 0 a list of plausible values will be returned.

plausible.type

type of plausible values to obtain. Can be either 'normal' (default) to use a normal approximation based on the ACOV matrix, or 'MH' to obtain Metropolis-Hastings samples from the posterior (silently passes object to mirt, therefore arguments like technical can be supplied to increase the number of burn-in draws and discarded samples).

quadpts

number of quadratures to use per dimension. If not specified, a suitable one will be created which decreases as the number of dimensions increases (and therefore for estimates such as EAP, will be less accurate). This is determined from the switch statement quadpts <- switch(as.character(nfact), '1'=61, '2'=31, '3'=15, '4'=9, '5'=7, 3)

returnER

logical; return empirical reliability (also known as marginal reliability) estimates as a numeric values?

return.acov

logical; return a list containing covariance matrices instead of factors scores?

impute = TRUE not supported with this option

mean

a vector for custom latent variable means. If NULL, the default for 'group' values from the computed mirt object will be used

cov

a custom matrix of the latent variable covariance matrix. If NULL, the default for 'group' values from the computed mirt object will be used

verbose

logical; print verbose output messages?

full.scores.SE

logical; when full.scores == TRUE, also return the standard errors associated with each respondent? Default is FALSE

theta_lim

lower and upper range to evaluate latent trait integral for each dimension. If omitted, a range will be generated automatically based on the number of dimensions

MI

a number indicating how many multiple imputation draws to perform. Default is 0, indicating that no MI draws will be performed

use_dens.type_estimate

logical; if the density of the latent trait was estimated in the model (e.g., via Davidian curves or empirical histograms), should this information be used to compute the latent trait estimates? Only applicable for EAP-based estimates (EAP, EAPsum, and plausible)

QMC

logical; use quasi-Monte Carlo integration? If quadpts is omitted the default number of nodes is 5000

custom_den

a function used to define the integration density (if required). The NULL default assumes that the multivariate normal distribution with the 'GroupPars' hyperparameters are used. At the minimum must be of the form:

function(Theta,...)

where Theta is a matrix of latent trait values (will be a grid of values if method == 'EAPsum' or method == 'EAP', otherwise Theta will have only 1 row). Additional arguments may included and are caught through the fscores(...) input.
fscores

The function must return a numeric vector of density weights (one for each row in Theta)

custom_theta  a matrix of custom integration nodes to use instead of the default, where each column corresponds to the respective dimension in the model

min_expected  when computing goodness of fit tests when method = 'EAPsum', this value is used to collapse across the conditioned total scores until the expected values are greater than this value. Note that this only affect the goodness of fit tests and not the returned EAP for sum scores table

converge_info  logical; include a column in the return objects containing a logical for each response pattern indicating whether a maximum value was found (not relevant non-iterative methods, such as EAP and EAPsum). Value is a reflection of the code element from nlm (e.g., 1 indicates convergence)

max_theta  the maximum/minimum value any given factor score estimate will achieve using any modal estimator method (e.g., MAP, WLE, ML)

start  a matrix of starting values to use for iterative estimation methods. Default will start at a vector of 0’s for each response pattern, or will start at the EAP estimates (unidimensional models only). Must be in the form that matches full.scores = FALSE (mostly used in the mirtCAT package)

...  additional arguments to be passed to nlm

Details

The function will return either a table with the computed scores and standard errors, the original data matrix with scores appended to the rightmost column, or the scores only. By default the latent means and covariances are determined from the estimated object, though these can be overwritten. Iterative estimation methods can be estimated in parallel to decrease estimation times if a mirtCluster object is available.

If the input object is a discrete latent class object estimated from mdirt then the returned results will be with respect to the posterior classification for each individual. The method inputs for 'DiscreteClass' objects may only be 'EAP', for posterior classification of each response pattern, or 'EAPsum' for posterior classification based on the raw sum-score. For more information on these algorithms refer to the mirtCAT package and the associated JSS paper (Chalmers, 2016).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


**See Also**

averageMI

**Examples**

```r
mod <- mirt(Science, 1)
tabscores <- fscores(mod, full.scores = FALSE)
head(tabscores)

## Not run:
fullscores <- fscores(mod)
fullscores_with_SE <- fscores(mod, full.scores.SE=TRUE)
head(fullscores)
head(fullscores_with_SE)

#change method argument to use MAP estimates
fullscores <- fscores(mod, method='MAP')
head(fullscores)

#calculate MAP for a given response vector
fscores(mod, method='MAP', response.pattern = c(1,2,3,4))
#or matrix
fscores(mod, method='MAP', response.pattern = rbind(c(1,2,3,4), c(2,2,1,3)))

# return only the scores and their SEs
fscores(mod, method='MAP', response.pattern = c(1,2,3,4),
       append_response.pattern=FALSE)

#use custom latent variable properties (diffuse prior for MAP is very close to ML)
fscores(mod, method="MAP", cov = matrix(1000), full.scores = FALSE)
fcores(mod, method='ML', full.scores = FALSE)

# EAPsum table of values based on total scores
fscores(mod, method = 'EAPsum', full.scores = FALSE)

#WLE estimation, run in parallel using available cores
mirtCluster()
head(fscores(mod, method='WLE', full.scores = FALSE))

#multiple imputation using 30 draws for EAP scores. Requires information matrix
mod <- mirt(Science, 1, SE=TRUE)
fs <- fscores(mod, MI = 30)
head(fs)
```
# plausible values for future work
pv <- fscores(mod, plausible.draws = 5)
lapply(pv, function(x) c(mean=mean(x), var=var(x), min=min(x), max=max(x)))

## define a custom_den function. EAP with a uniform prior between -3 and 3
fun <- function(Theta, ...) as.numeric(dunif(Theta, min = -3, max = 3))
head(fscores(mod, custom_den = fun))

# custom MAP prior: standard truncated normal between 5 and -2
library(msm)
# need the :: scope for parallel to see the function (not require if no mirtCluster() defined)
fun <- function(Theta, ...) msm::dtnorm(Theta, mean = 0, sd = 1, lower = -2, upper = 5)
head(fscores(mod, custom_den = fun, method = 'MAP', full.scores = FALSE))

## End(Not run)

---

**imputeMissing**  
*Imputing plausible data for missing values*

**Description**

Given an estimated model from any of mirt’s model fitting functions and an estimate of the latent trait, impute plausible missing data values. Returns the original data in a data.frame without any NA values. If a list of Theta values is supplied then a list of complete datasets is returned instead.

**Usage**

```r
imputeMissing(x, Theta, warn = TRUE, ...)
```

**Arguments**

- `x` an estimated model x from the mirt package
- `Theta` a matrix containing the estimates of the latent trait scores (e.g., via `fscores`)
- `warn` logical; print warning messages?
- `...` additional arguments to pass

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**

Examples

```r
## Not run:
dat <- expand.table(LSAT7)
(original <- mirt(dat, 1))
NAperson <- sample(1:nrow(dat), 20, replace = TRUE)
NAitem <- sample(1:ncol(dat), 20, replace = TRUE)
for(i in 1:20)
    dat[NAperson[i], NAitem[i]] <- NA
(mod <- mirt(dat, 1))
scores <- fscores(mod, method = 'MAP')

# re-estimate imputed dataset (good to do this multiple times and average over)
fulldata <- imputeMissing(mod, scores)
(fullmod <- mirt(fulldata, 1))

# with multipleGroup
set.seed(1)
group <- sample(c('group1', 'group2'), 1000, TRUE)
mod2 <- multipleGroup(dat, 1, group, TOL=1e-2)
fs <- fscores(mod2)
fulldata2 <- imputeMissing(mod2, fs)
```

## End(Not run)

---

**itemfit**

*Item fit statistics*

**Description**

Computes item-fit statistics for a variety of unidimensional and multidimensional models. Poorly fitting items should be inspected with the empirical plots/tables for unidimensional models, otherwise `itemGAM` can be used to diagnose where the functional form of the IRT model was misspecified, or models can be refit using more flexible semi-parametric response models (e.g., `itemtype = 'spline'`). If the latent trait density was approximated (e.g., Davidian curves, Empirical histograms, etc) then passing `use_dentype_estimate = TRUE` will use the internally saved quadrature and density components (where applicable). Currently, only S-X2 statistic supported for mixture IRT models. Finally, where applicable the root mean-square error of approximation (RMSEA) is reported to help gauge the magnitude of item misfit.

**Usage**

```r
itemfit(
    x,
    fit_stats = "S_X2",
    which.items = 1:extract.mirt(x, "nitems"),
    na.rm = FALSE,
    group.bins = 10,
```
itemfit

Arguments

x a computed model object of class SingleGroupClass, MultipleGroupClass, or DiscreteClass

fit_stats a character vector indicating which fit statistics should be computed. Supported inputs are:

- 'Zh' : Drasgow, Levine, & Williams (1985) Zh
- 'X2' : Bock's (1972) chi-squared method. The default inputs compute Yen's (1981) Q1 variant of the X2 statistic (i.e., uses a fixed group.bins = 10). However, Bock's group-size variable median-based method can be computed by passing group.fun = median and modifying the group.size input to the desired number of bins
- 'G2' : McKinley & Mills (1985) G2 statistic (similar method to Q1, but with the likelihood-ratio test).
- 'PV_Q1' : Chalmers and Ng's (2017) plausible-value variant of the Q1 statistic.
- 'PV_Q1*' : Chalmers and Ng's (2017) plausible-value variant of the Q1 statistic that uses parametric bootstrapping to obtain a suitable empirical distribution.
- 'X2*' : Stone's (2000) fit statistics that require parametric bootstrapping
- 'X2*_df' : Stone's (2000) fit statistics that require parametric bootstrapping to obtain scaled versions of the X2* and degrees of freedom
- 'infit' : Compute the infit and outfit statistics
Note that 'infit', 'S_X2', and 'Zh' cannot be computed when there are missing response data (i.e., will require multiple-imputation/row-removal techniques).

which.items: an integer vector indicating which items to test for fit. Default tests all possible items.

na.rm: logical; remove rows with any missing values? This is required for methods such as S-X2 because they require the "EAPsum" method from fscores.

group.bins: the number of bins to use for X2 and G2. For example, setting group.bins = 10 will compute Yen’s (1981) Q1 statistic when 'X2' is requested.

group.size: approximate size of each group to be used in calculating the $\chi^2$ statistic. The default NA disables this command and instead uses the group.bins input to try and construct equally sized bins.

group.fun: function used when 'X2' or 'G2' are computed. Determines the central tendency measure within each partitioned group. E.g., setting group.fun = median will obtain the median of each respective ability estimate in each subgroup (this is what was used by Bock, 1972).

mincell: the minimum expected cell size to be used in the S-X2 computations. Tables will be collapsed across items first if polytomous, and then across scores if necessary.

mincell.X2: the minimum expected cell size to be used in the X2 computations. Tables will be collapsed if polytomous, however if this condition can not be met then the group block will be omitted in the computations.

S_X2.tables: logical; return the tables in a list format used to compute the S-X2 stats?

pv_draws: number of plausible-value draws to obtain for PV_Q1 and PV_Q1*.

boot: number of parametric bootstrap samples to create for PV_Q1* and X2*.

boot_dfapprox: number of parametric bootstrap samples to create for the X2*_df statistic to approximate the scaling factor for X2* as well as the scaled degrees of freedom estimates.

ETrange: range of integration nodes for Stone’s X2* statistic.

ETpoints: number of integration nodes to use for Stone’s X2* statistic.

empirical.plot: a single numeric value or character of the item name indicating which item to plot (via itemplot) and overlay with the empirical $\theta$ groupings (see empirical.CI). Useful for plotting the expected bins based on the 'X2' or 'G2' method.

empirical.CI: a numeric value indicating the width of the empirical confidence interval ranging between 0 and 1 (default of 0 plots not interval). For example, a 95 interval would be plotted when empirical.CI = .95. Only applicable to dichotomous items.

empirical.table: a single numeric value or character of the item name indicating which item table of expected values should be returned. Useful for visualizing the expected bins based on the 'X2' or 'G2' method.

empirical.poly.collapse: logical; collapse polytomous item categories to for expected scoring functions for empirical plots? Default is FALSE.

method: type of factor score estimation method. See fscores for more detail.
Theta

Theta is a matrix of factor scores for each person used for statistics that require empirical estimates. If supplied, arguments typically passed to `fscores()` will be ignored and these values will be used instead. Also required when estimating statistics with missing data via imputation.

par.strip.text

par.strip.text is a plotting argument passed to `lattice`.

par.settings

par.settings is a plotting argument passed to `lattice`.

...

additional arguments to be passed to `fscores()` and `lattice`.

Author(s)

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References


See Also

`personfit`, `itemGAM`
Examples

## Not run:

P <- function(Theta){exp(Theta^2 * 1.2 - 1) / (1 + exp(Theta^2 * 1.2 - 1))}

# make some data
set.seed(1234)
a <- matrix(rlnorm(20, meanlog=0, sdlog = .1),ncol=1)
d <- matrix(rnorm(20),ncol=1)
Theta <- matrix(rnorm(2000))
items <- rep('ZPL', 20)
ps <- P(Theta)
baditem <- numeric(2000)
for(i in 1:2000)
  baditem[i] <- sample(c(0,1), 1, prob = c(1-ps[i], ps[i]))
data <- cbind(simdata(a,d, 2000, items, Theta=Theta), baditem=baditem)

x <- mirt(data, 1)
raschfit <- mirt(data, 1, itemtype='Rasch')
fit <- itemfit(x)

itemfit(x)
itemfit(x, 'X2') # just X2
itemfit(x, 'X2', method='ML') # X2 with maximum-likelihood estimates for traits
itemfit(x, c('S_X2', 'X2')) # both S_X2 and X2
itemfit(x, group.bins=15, empirical.plot=1, method='ML') # empirical item plot with 15 points
itemfit(x, group.bins=15, empirical.plot=21, method='ML')

# PV and X2* statistics (parametric bootstrap stats not run to save time)
itemfit(x, 'PV_Q1')

# mirtCluster() # improve speed of bootstrap samples by running in parallel
# itemfit(x, 'PV_Q1*')
# itemfit(x, 'X2*') # Stone's 1993 statistic
# itemfit(x, 'X2*df') # Stone's 2000 scaled statistic with df estimate

# empirical tables for X2 statistic
itemfit(x, empirical.table=1)
itemfit(x, empirical.table=21)

# infit/outfit statistics. method='ML' agrees better with eRm package
itemfit(raschfit, 'infit', method='ML') # infit and outfit stats

# same as above, but inputting ML estimates instead (saves time for re-use)
Theta <- fscores(raschfit, method='ML')
itemfit(raschfit, 'infit', Theta=Theta)
itemfit(raschfit, empirical.plot=1, Theta=Theta)
itemfit(raschfit, empirical.table=1, Theta=Theta)

# fit a new more flexible model for the mis-fitting item
itemtype <- c(rep('2PL', 20), 'spline')
x2 <- mirt(data, 1, itemtype=itemtype)
itemfit(x2)
itemplot(x2, 21)
anova(x2, x)

#------------------------------------------------------------

#similar example to Kang and Chen 2007
a <- matrix(c(.8,.4,.7, .8, .4, .7, 1, 1, 1, 1))
d <- matrix(rep(c(2.0,0.0,-1,-1.5),10), ncol=4, byrow=TRUE)
dat <- simdata(a,d,2000, itemtype = rep('graded', 10))
head(dat)

mod <- mirt(dat, 1)
itemfit(mod)
itemfit(mod, 'X2') #pretty much useless given inflated Type I error rates
itemfit(mod, empirical.plot = 1)
itemfit(mod, empirical.plot = 1, empirical.poly.collapse=TRUE)

# collapsed tables (see mincell.X2) for X2 and G2
itemfit(mod, empirical.table = 1)

mod2 <- mirt(dat, 1, 'Rasch')
itemfit(mod2, 'infit', method = 'ML')

#massive list of tables for S-X2
 tables <- itemfit(mod, S_X2.tables = TRUE)

#observed and expected total score patterns for item 1 (post collapsing)
 tables$O[[1]]
 tables$E[[1]]

# fit stats with missing data (run in parallel using all cores)
 dat[sample(1:prod(dim(dat)), 100)] <- NA
 raschfit <- mirt(dat, 1, itemtype='Rasch')

#use only valid data by removing rows with missing terms
itemfit(raschfit, c('S_X2', 'infit'), na.rm = TRUE)

# note that X2, G2, PV-Q1, and X2* do not require complete datasets
thetas <- fscores(raschfit, method = 'ML') # save scores for faster computations
itemfit(raschfit, c('X2', 'G2'), Theta=thetas)
itemfit(raschfit, empirical.plot=1, Theta=thetas)
itemfit(raschfit, empirical.table=1, Theta=thetas)

## End(Not run)
itemGAM

Parametric smoothed regression lines for item response probability functions

Description

This function uses a generalized additive model (GAM) to estimate response curves for items that do not seem to fit well in a given model. Using a stable auxiliary model, traceline functions for poorly fitting dichotomous or polytomous items can be inspected using point estimates (or plausible values) of the latent trait. Plots of the tracelines and their associated standard errors are available to help interpret the misfit. This function may also be useful when adding new items to an existing, well established set of items, especially when the parametric form of the items under investigation are unknown.

Usage

itemGAM(
  item,
  Theta,
  formula = resp ~ s(Theta, k = 10),
  CI = 0.95,
  theta_lim = c(-3, 3),
  return.models = FALSE,
  ...
)

## S3 method for class 'itemGAM'
plot(
  x,
  y = NULL,
  par.strip.text = list(cex = 0.7),
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
  auto.key = list(space = "right", points = FALSE, lines = TRUE),
  ...
)

Arguments

item         a single poorly fitting item to be investigated. Can be a vector or matrix
Theta        a list or matrix of latent trait estimates typically returned from fscores
formula      an R formula to be passed to the gam function. Default fits a spline model with 10 nodes. For multidimensional models, the traits are assigned the names 'Theta1', 'Theta2', ..., 'ThetaN'
CI            a number ranging from 0 to 1 indicating the confidence interval range. Default provides the 95 percent interval
theta_lim    range of latent trait scores to be evaluated
return.models logical; return a list of GAM models for each category? Useful when the GAMs should be inspected directly, but also when fitting multidimensional models (this is set to TRUE automatically for multidimensional models)

... additional arguments to be passed to `gam` or `lattice`
x an object of class 'itemGAM'
y a NULL value ignored by the plotting function
par.strip.text plotting argument passed to `lattice`
par.settings plotting argument passed to `lattice`
auto.key plotting argument passed to `lattice`

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

`itemfit`

Examples

```r
## Not run:
set.seed(10)
N <- 1000
J <- 30

a <- matrix(1, J)
d <- matrix(rnorm(J))
Theta <- matrix(rnorm(N, 0, 1.5))
dat <- simdata(a, d, N, itemtype = '2PL', Theta=Theta)

# make a bad item
ps <- exp(Theta^2 + Theta) / (1 + exp(Theta^2 + Theta))
item1 <- sapply(ps, function(x) sample(c(0,1), size = 1, prob = c(1-x, x)))

ps2 <- exp(2 * Theta^2 + Theta + .5 * Theta^3) / (1 + exp(2 * Theta^2 + Theta + .5 * Theta^3))
item2 <- sapply(ps2, function(x) sample(c(0,1), size = 1, prob = c(1-x, x)))

# how the actual item looks in the population
plot(Theta, ps, ylim = c(0,1))
plot(Theta, ps2, ylim = c(0,1))

baditems <- cbind(item1, item2)
newdat <- cbind(dat, baditems)
```
badmod <- mirt(newdat, 1)
itemfit(badmod) # clearly a bad fit for the last two items
mod <- mirt(dat, 1) # fit a model that does not contain the bad items
itemfit(mod)

#### Pure non-parametric way of investigating the items
library(KernSmoothIRT)
ks <- ksIRT(newdat, rep(1, ncol(newdat)), 1)
plot(ks, item=c(1,31,32))
par(ask=FALSE)

# Using point estimates from the model
Theta <- fscores(mod)
IG0 <- itemGAM(dat[,1], Theta) # good item
IG1 <- itemGAM(baditems[,1], Theta)
IG2 <- itemGAM(baditems[,2], Theta)
plot(IG0)
plot(IG1)
plot(IG2)

# same as above, but with plausible values to obtain the standard errors
set.seed(4321)
ThetaPV <- fscores(mod, plausible.draws=10)
IG0 <- itemGAM(dat[,1], ThetaPV) # good item
IG1 <- itemGAM(baditems[,1], ThetaPV)
IG2 <- itemGAM(baditems[,2], ThetaPV)
plot(IG0)
plot(IG1)
plot(IG2)

## for polytomous test items
SAT12[SAT12 == 8] <- NA
dat <- key2binary(SAT12,
     key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
dat <- dat[,32]
mod <- mirt(dat, 1)

# Kernel smoothing is very sensitive to which category is selected as 'correct'
# 5th category as correct
ks <- ksIRT(cbind(dat, SAT12[,32]), c(rep(1, 31), 5), 1)
plot(ks, items = c(1,2,32))

# 3rd category as correct
ks <- ksIRT(cbind(dat, SAT12[,32]), c(rep(1, 31), 3), 1)
plot(ks, items = c(1,2,32))

# splines approach
Theta <- fscores(mod)
IG <- itemGAM(SAT12[,32], Theta)
plot(IG)

set.seed(1423)
ThetaPV <- fscores(mod, plausible.draws=10)
iteminfo

Function to calculate item information

Description

Given an internal mirt item object extracted by using `extract.item`, compute the item information.

Usage

```
iteminfo(x, Theta, degrees = NULL, total.info = TRUE, multidim_matrix = FALSE)
```

Arguments

- **x**: an extracted internal mirt object containing item information (see `extract.item`)
- **Theta**: a vector (unidimensional) or matrix (multidimensional) of latent trait values
- **degrees**: a vector of angles in degrees that are between 0 and 90. Only applicable when the input object is multidimensional
- **total.info**: logical; return the total information curve for the item? If FALSE, information curves for each category are returned as a matrix
- **multidim_matrix**: logical; compute the information matrix for each row in Theta? If Theta contains more than 1 row then a list of matrices will be returned, otherwise if Theta has exactly one row then a matrix will be returned

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>
References


See Also

`extract.item`

Examples

```r
mod <- mirt(Science, 1)
extr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-4,4, by = .1))
info.2 <- iteminfo(extr.2, Theta)

#do something with the info?
plot(Theta, info.2, type = 'l', main = 'Item information')

## Not run:
#category information curves
cat.info <- iteminfo(extr.2, Theta, total.info = FALSE)
plot(Theta, cat.info[,1], type = 'l', ylim = c(0, max(cat.info)),
     ylab = 'info', main = 'Category information')
for(i in 2:ncol(cat.info))
  lines(Theta, cat.info[,i], col = i)

## Customized test information plot
T1 <- T2 <- 0
dat <- expand.table(LSAT7)
mod1 <- mirt(dat, 1, 'Rasch')
mod2 <- mirt(dat, 1)
for(i in 1:5){
  T1 <- T1 + iteminfo(extract.item(mod1, i), Theta)
  T2 <- T2 + iteminfo(extract.item(mod2, i), Theta)
}
plot(Theta, T2/T1, type = 'l', ylab = 'Relative Test Information', las = 1)
lines(Theta, T1/T1, col = 'red')

# multidimensional
mod <- mirt(dat, 2, TOL=1e-2)
ii <- extract.item(mod, 1)
Theta <- as.matrix(expand.grid(-4:4, -4:4))

iteminfo(ii, Theta, degrees=c(45,45)) # equal angle
iteminfo(ii, Theta, degrees=c(90,0)) # first dimension only

# information matrices
iteminfo(ii, Theta, multidim_matrix = TRUE)
iteminfo(ii, Theta[,1], drop=FALSE, multidim_matrix = TRUE)
```
itemplot

Displays item surface and information plots

Description

itemplot displays various item based IRT plots, with special options for plotting items that contain several 0 slope parameters. Supports up to three dimensional models.

Usage

itemplot(
  object,
  item,
  type = "trace",
  degrees = 45,
  CE = FALSE,
  CEalpha = 0.05,
  CEdraws = 1000,
  drop.zeros = FALSE,
  theta_lim = c(-6, 6),
  shiny = FALSE,
  rot = list(xaxis = -70, yaxis = 30, zaxis = 10),
  par.strip.text = list(cex = 0.7),
  npts = 200,
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
  auto.key = list(space = "right", points = FALSE, lines = TRUE),
  ...
)

Arguments

object a computed model object of class SingleGroupClass or MultipleGroupClass. Input may also be a list for comparing similar item types (e.g., 1PL vs 2PL)

item a single numeric value, or the item name, indicating which item to plot

type plot type to use, information ('info'), standard errors ('SE'), item trace lines ('trace'), information and standard errors ('infoSE') or information and trace lines ('infotrace'), relative efficiency lines ('RE'), expected score 'score', or information and trace line contours ('infocontour' and 'tracecontour'; not supported for MultipleGroupClass objects)

degrees the degrees argument to be used if there are two or three factors. See iteminfo for more detail. A new vector will be required for three dimensional models to override the default
CE logical; plot confidence envelope?
CEalpha area remaining in the tail for confidence envelope. Default gives 95% confidence region
CEdraws draws number of draws to use for confidence envelope
drop.zeros logical; drop slope values that are numerically close to zero to reduce dimensionality? Useful in objects returned from \texttt{bfactor} or other confirmatory models that contain several zero slopes
theta_lim lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with \texttt{npts}
shiny logical; run interactive display for item plots using the \texttt{shiny} interface. This primarily is an instructive tool for demonstrating how item response curves behave when adjusting their parameters
rot a list of rotation coordinates to be used for 3 dimensional plots
par.strip.text plotting argument passed to \texttt{lattice}
npts number of quadrature points to be used for plotting features. Larger values make plots look smoother
par.settings plotting argument passed to \texttt{lattice}
auto.key plotting argument passed to \texttt{lattice}
... additional arguments to be passed to \texttt{lattice} and \texttt{coef()}

\textbf{Author(s)}

Phil Chalmers <rphilip.chalmers@gmail.com>

\textbf{References}


\textbf{Examples}

\begin{verbatim}
## Not run:
data(LSAT7)
fulldata <- expand.table(LSAT7)
mod1 <- mirt(fulldata,1,SE=TRUE)
mod2 <- mirt(fulldata,1, itemtype = 'Rasch')
mod3 <- mirt(fulldata,2)

itemplot(mod1, 2)
itemplot(mod1, 2, CE = TRUE)
itemplot(mod1, 2, type = 'info')
itemplot(mod1, 2, type = 'info', CE = TRUE)

mods <- list(twoPL = mod1, onePL = mod2)
itemplot(mods, 1, type = 'RE')
\end{verbatim}
key2binary

Score a test by converting response patterns to binary data

Description

The key2binary function will convert response pattern data to a dichotomous format, given a response key.

Usage

key2binary(fulldata, key, score_missing = FALSE)

Arguments

fulldata an object of class data.frame, matrix, or table with the response patterns
key a vector or matrix consisting of the 'correct' response to the items. Each value/row corresponds to each column in fulldata. If the input is a matrix, multiple scoring keys can be supplied for each item. NA values are used to indicate no scoring key (or in the case of a matrix input, no additional scoring keys)
score_missing  logical; should missing data elements be returned as incorrect (i.e., 0)? If FALSE, all missing data terms will be kept as missing

Value

Returns a numeric matrix with all the response patterns in dichotomous format

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

data(SAT12)
head(SAT12)
key <- c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5)
dicho.SAT12 <- key2binary(SAT12, key)
head(dicho.SAT12)

# multiple scoring keys
key2 <- cbind(c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5), c(2,3,NA,rep(NA, 28)))
dicho.SAT12 <- key2binary(SAT12, key2)

# keys from raw character responses
resp <- as.data.frame(matrix(c("B","B","D","D","E",
"B","A","D","D","E",
"B","A","D","C","E",
"D","D","D","C","E",
"B","C","A","D","A"), ncol=5, byrow=TRUE))
key <- c("B", "D", "D", "C", "E")
d01 <- key2binary(resp, key)
head(d01)

# score/don't score missing values
resp[1,1] <- NA
d01NA <- key2binary(resp, key) # without scoring
d01NA

d01 <- key2binary(resp, key, score_missing = TRUE) # with scoring
d01
**lagrange**

*Lagrange test for freeing parameters*

**Description**

Lagrange (i.e., score) test to test whether parameters should be freed from a more constrained baseline model.

**Usage**

`lagrange(mod, parnum, SE.type = "Oakes", type = "Richardson", ...)`

**Arguments**

- `mod`: an estimated model
- `parnum`: a vector, or list of vectors, containing one or more parameter locations/sets of locations to be tested. See objects returned from `mod2values` for the locations
- `SE.type`: type of information matrix estimator to use. See `mirt` for further details
- `type`: type of numerical algorithm passed to `numerical_deriv` to obtain the gradient terms
- `...`: additional arguments to pass to `mirt`

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**See Also**

- `wald`

**Examples**

```r
## Not run:
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1, 'Rasch')
(values <- mod2values(mod))

#test all fixed slopes individually
parnum <- values$parnum[values$name == 'a1']
lagrange(mod, parnum)
```
# compare to LR test for first two slopes
mod2 <- mirt(dat, 'F = 1-5
FREE = (1, a1)', 'Rasch')
coef(mod2, simplify=TRUE)$items
anova(mod, mod2)

mod2 <- mirt(dat, 'F = 1-5
FREE = (2, a1)', 'Rasch')
coef(mod2, simplify=TRUE)$items
anova(mod, mod2)

mod2 <- mirt(dat, 'F = 1-5
FREE = (3, a1)', 'Rasch')
coef(mod2, simplify=TRUE)$items
anova(mod, mod2)

# test slopes first two slopes and last three slopes jointly
lagrange(mod, list(parnum[1:2], parnum[3:5]))

# test all 5 slopes and first + last jointly
lagrange(mod, list(parnum[1:5], parnum[c(1, 5)]))

## End(Not run)

---

**likert2int**

*Convert ordered Likert-scale responses (character or factors) to integers*

**Description**

Given a matrix or data.frame object consisting of Likert responses return an object of the same dimensions with integer values.

**Usage**

```r
likert2int(x, levels = NULL)
```

**Arguments**

- **x**
  - a matrix of character values or data.frame of character/factor vectors

- **levels**
  - a named character vector indicating which integer values should be assigned to which elements. If omitted, the order of the elements will be determined after converting each column in `x` to a factor variable

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>


References


See Also

key2binary, poly2dich

Examples

```r
## Not run:

# simulate data

dat1 <- matrix(sample(c('Disagree', 'Strongly Disagree', 'Agree',
                         'Neutral', 'Strongly Agree'), 1000*5, replace=TRUE),
               nrow=1000, ncol=5)
dat2 <- matrix(sample(c('D', 'SD', 'A', 'N', 'SA'), 1000*5, replace=TRUE),
               nrow=1000, ncol=5)
dat <- cbind(dat1, dat2)

# separately

intdat1 <- likert2int(dat1)
head(dat1)
head(intdat1)

# more useful with explicit levels

lvl1 <- c('Strongly Disagree'=1, 'Disagree'=2, 'Neutral'=3, 'Agree'=4,
          'Strongly Agree'=5)
intdat1 <- likert2int(dat1, levels = lvl1)
head(dat1)
head(intdat1)

# second data

lvl2 <- c('SD'=1, 'D'=2, 'N'=3, 'A'=4, 'SA'=5)
intdat2 <- likert2int(dat2, levels = lvl2)
head(dat2)
head(intdat2)

# full dataset (using both mapping schemes)

intdat <- likert2int(dat, levels = c(lvl1, lvl2))
head(dat)
head(intdat)

####

# data.frame as input with ordered factors

dat1 <- data.frame(dat1)
dat2 <- data.frame(dat2)
dat.old <- cbind(dat1, dat2)
```


colnames(dat.old) <- paste0('Item_', 1:10)
str(dat.old) # factors are leveled alphabetically by default

# create explicit ordering in factor variables
for(i in 1:ncol(dat1))
  levels(dat1[[i]]) <- c('Strongly Disagree', 'Disagree', 'Neutral', 'Agree', 'Strongly Agree')

for(i in 1:ncol(dat2))
  levels(dat2[[i]]) <- c('SD', 'D', 'N', 'A', 'SA')

dat <- cbind(dat1, dat2)

colnames(dat) <- colnames(dat.old)
str(dat) # note ordering

intdat <- likert2int(dat)
head(dat)
head(intdat)

## End(Not run)

---

**logLik-method**

*Extract log-likelihood*

**Description**

Extract the observed-data log-likelihood.

**Usage**

```r
## S4 method for signature 'SingleGroupClass'
logLik(object)
```

**Arguments**

- `object`: an object of class `SingleGroupClass`, `MultipleGroupClass`, or `MixedClass`

**References**


**Examples**

```r
## Not run:
x <- mirt(Science, 1)
logLik(x)
```
## Description of LSAT6 data

**Description**

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

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
# Not run:
dat <- expand.table(LSAT6)
head(dat)
model <- 'F = 1-5
  CONSTRAIN = (1-5, a1)'
(mod <- mirt(dat, model))
M2(mod)
itemfit(mod)
coef(mod, simplify=TRUE)

#equivalently, but with a different parameterization
mod2 <- mirt(dat, 1, itemtype = 'Rasch')
anova(mod, mod2) #equal
M2(mod2)
itemfit(mod2)
coef(mod2, simplify=TRUE)
sqrt(coef(mod2)$GroupPars[2]) #latent SD equal to the slope in mod
```

## End(Not run)
**LSAT7**  
*Description of LSAT7 data*

**Description**

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

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
## Not run:
dat <- expand.table(LSAT7)
head(dat)
(mod <- mirt(dat, 1))
coef(mod)

## End(Not run)
```

---

**M2**  
*Compute the M2 model fit statistic*

**Description**

Computes the M2 (Maydeu-Olivares & Joe, 2006) statistic when all data are dichotomous, the collapsed M2* statistic (collapsing over univariate and bivariate response categories; see Cai and Hansen, 2013), and the hybrid C2 statistic which only collapses only the bivariate moments (Cai and Monro, 2014). The C2 variant is mainly useful when polytomous response models do not have sufficient degrees of freedom to compute M2*. This function also computes associated fit indices that are based on fitting the null model. Supports single and multiple-group models. If the latent trait density was approximated (e.g., Davidian curves, Empirical histograms, etc) then passing `use_dentype_estimate = TRUE` will use the internally saved quadrature and density components (where applicable).
Usage

```r
M2(
  obj,
  type = "M2*",
  calcNull = TRUE,
  na.rm = FALSE,
  quadpts = NULL,
  theta_lim = c(-6, 6),
  CI = 0.9,
  residmat = FALSE,
  QMC = FALSE,
  suppress = 1,
  ...
)
```

Arguments

- **obj**: an estimated model object from the mirt package
- **type**: type of fit statistic to compute. Options are "M2", "M2*" for the univariate and bivariate collapsed version of the M2 statistic ("M2" currently limited to dichotomous response data only), and "C2" for a hybrid between M2 and M2* where only the bivariate moments are collapsed
- **calcNull**: logical; calculate statistics for the null model as well? Allows for statistics such as the limited information TLI and CFI. Only valid when items all have a suitable null model (e.g., those created via `createItem` will not)
- **na.rm**: logical; remove rows with any missing values? The M2 family of statistics requires a complete dataset in order to be well defined
- **quadpts**: number of quadrature points to use during estimation. If NULL, a suitable value will be chosen based on the rubric found in `fscores`
- **theta_lim**: lower and upper range to evaluate latent trait integral for each dimension
- **CI**: numeric value from 0 to 1 indicating the range of the confidence interval for RMSEA. Default returns the 90% interval
- **residmat**: logical; return the residual matrix used to compute the SRMSR statistic? Only the lower triangle of the residual correlation matrix will be returned (the upper triangle is filled with NA's)
- **QMC**: logical; use quasi-Monte Carlo integration? Useful for higher dimensional models. If `quadpts` not specified, 5000 nodes are used by default
- **suppress**: a numeric value indicating which parameter residual dependency combinations to flag as being too high. Absolute values for the standardized residuals greater than this value will be returned, while all values less than this value will be set to NA. Must be used in conjunction with the argument `residmat = TRUE`
- **...**: additional arguments to pass
Value

Returns a data.frame object with the M2-type statistic, along with the degrees of freedom, p-value, RMSEA (with 90% confidence interval), SRMSR for each group (if all items were ordinal), and optionally the TLI and CFI model fit statistics if calcNull = TRUE.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
dat <- as.matrix(expand.table(LSAT7))
(mod1 <- mirt(dat, 1))
M2(mod1)
M2(mod1, residmat=TRUE) #lower triangle of residual correlation matrix

#M2 with missing data present
dat[sample(1:prod(dim(dat)), 250)] <- NA
mod2 <- mirt(dat, 1)
# Compute stats by removing missing data row-wise
M2(mod2, na.rm = TRUE)

# C2 statistic (useful when polytomous IRT models have too few df)
pmod <- mirt(Science, 1)
# This fails with too few df:
# M2(pmod)
# This, however, works:
M2(pmod, type = 'C2')

## End(Not run)
```
Function to calculate the marginal reliability

### Description

Given an estimated model and a prior density function, compute the marginal reliability (Thissen and Wainer, 2001). This is only available for unidimensional tests.

### Usage

```r
marginal_rxx(mod, density = dnorm, ...)
```

### Arguments

- `mod`: an object of class 'SingleGroupClass'
- `density`: a density function to use for integration. Default assumes the latent traits are from a normal (Gaussian) distribution
- `...`: additional arguments passed to the density function

### Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

### References


### See Also

- `empirical_rxx`
- `extract.group`
- `testinfo`

### Examples

```r
dat <- expand.table(deAyala)
mod <- mirt(dat, 1)

# marginal estimate
marginal_rxx(mod)

## Not run:

# empirical estimate (assuming the same prior)
fscores(mod, returnER = TRUE)
```
# empirical rxx the alternative way, given theta scores and SEs
fs <- fscores(mod, full.scores.SE=TRUE)
head(fs)
empirical_rxx(fs)

## End(Not run)

---

**MDIFF**

*Compute multidimensional difficulty index*

**Description**

Returns a matrix containing the MDIFF values (Reckase, 2009). Only supported for items of class 'dich' and 'graded'.

**Usage**

`MDIFF(x, which.items = NULL, group = NULL)`

**Arguments**

- `x` an object of class 'SingleGroupClass', or an object of class 'MultipleGroupClass' if a suitable group input were supplied
- `which.items` a vector indicating which items to select. If NULL is used (the default) then MDISC will be computed for all items
- `group` group argument to pass to `extract.group` function. Required when the input object is a multiple-group model

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**References**


**See Also**

`extract.group, MDISC`
Examples

```r
# Not run:
mod <- mirt(Science, 2)
MDIFF(mod)

mod <- mirt(expand.table(LSAT7), 2)
MDIFF(mod)
```

## End(Not run)

mdirt

Multidimensional discrete item response theory

Description

mdirt fits a variety of item response models with discrete latent variables. These include, but are not limited to, latent class analysis, multidimensional latent class models, multidimensional discrete latent class models, DINA/DINO models, grade of measurement models, C-RUM, and so on. If response models are not defined explicitly then customized models can defined using the `createItem` function.

Usage

```r
mdirt(
  data,
  model,
  customTheta = NULL,
  structure = NULL,
  item.Q = NULL,
  nruns = 1,
  method = "EM",
  covdata = NULL,
  formula = NULL,
  itemtype = "lca",
  optimizer = "nlminb",
  return_max = TRUE,
  group = NULL,
  GenRandomPars = FALSE,
  verbose = TRUE,
  pars = NULL,
  technical = list(),
  ...
)
```
Arguments

data a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA

model number of mutually exclusive classes to fit, or alternatively a more specific mirt.model definition (which reflects the so-called Q-matrix). Note that when using a mirt.model, the order with which the syntax factors/attributes are defined are associated with the columns in the customTheta input

customTheta input passed to technical = list(customTheta = ...), but is included directly in this function for convenience. This input is most interesting for discrete latent models because it allows customized patterns of latent classes (i.e., defines the possible combinations of the latent attribute profile). The default builds the pattern customTheta = diag(model), which is the typical pattern for the traditional latent class analysis whereby class membership mutually distinct and exhaustive. See thetaComb for a quick method to generate a matrix with all possible combinations

structure an R formula allowing the profile probability patterns (i.e., the structural component of the model) to be fitted according to a log-linear model. When NULL, all profile probabilities (except one) will be estimated. Use of this input requires that the customTheta input is supplied, and that the column names in this matrix match the names found within this formula

item.Q a list of item-level Q-matrices indicating how the respective categories should be modeled by the underlying attributes. Each matrix must represent a $K_i \times A$ matrix, where $K_i$ represents the number of categories for the ith item, and $A$ is the number of attributes included in the Theta matrix; otherwise, a value of NULL will default to a matrix consisting of 1’s for each $K_i \times A$ element except for the first row, which contains only 0’s for proper identification. Incidentally, the first row of each matrix must contain only 0’s so that the first category represents the reference category for identification

nruns a numeric value indicating how many times the model should be fit to the data when using random starting values. If greater than 1, GenRandomPars is set to true by default

method estimation method. Can be 'EM' or 'BL' (see mirt for more details)
covdata a data.frame of data used for latent regression models

formula an R formula (or list of formulas) indicating how the latent traits can be regressed using external covariates in covdata. If a named list of formulas is supplied (where the names correspond to the latent trait/attribute names in model) then specific regression effects can be estimated for each factor. Supplying a single formula will estimate the regression parameters for all latent variables by default

itemtype a vector indicating the itemtype associated with each item. For discrete models this is limited to only 'lca' or items defined using a createItem definition

optimizer optimizer used for the M-step, set to 'nlminb' by default. See mirt for more details

return_max logical; when nruns > 1, return the model that has the most optimal maximum likelihood criteria? If FALSE, returns a list of all the estimated objects
group a factor variable indicating group membership used for multiple group analyses
GenRandomPars logical; use random starting values
verbose logical; turn on messages to the R console
pars used for modifying starting values; see mirt for details
technical list of lower-level inputs. See mirt for details
... additional arguments to be passed to the estimation engine. See mirt for more details and examples

Details

Posterior classification accuracy for each response pattern may be obtained via the fscores function. The summary() function will display the category probability values given the class membership, which can also be displayed graphically with plot(), while coef() displays the raw coefficient values (and their standard errors, if estimated). Finally, anova() is used to compare nested models, while M2 and itemfit may be used for model fitting purposes.

'lea' model definition

The latent class IRT model with two latent classes has the form

$$P(x = k|\theta_1, \theta_2, a1, a2) = \frac{exp(a1\theta_1 + a2\theta_2)}{\sum^K_j exp(a1\theta_1 + a2\theta_2)}$$

where the \( \theta \) values generally take on discrete points (such as 0 or 1). For proper identification, the first category slope parameters (\( a1 \) and \( a2 \)) are never freely estimated. Alternatively, supplying a different grid of \( \theta \) values will allow the estimation of similar models (multidimensional discrete models, grade of membership, etc.). See the examples below.

When the item.Q for is utilized, the above equation can be understood as

$$P(x = k|\theta_1, \theta_2, a1, a2) = \frac{exp(a1\theta_1 Q_{j1} + a2\theta_2 Q_{j2})}{\sum^K_j exp(a1\theta_1 Q_{j1} + a2\theta_2 Q_{j2})}$$

where by construction Q is a \( K_i \times A \) matrix indicating whether the category should be modeled according to the latent class structure. For the standard latent class model, the Q-matrix has as many rows as categories, as many columns as the number of classes/attributes modeled, and consist of 0's in the first row and 1's elsewhere. This of course can be over-written by passing an alternative item.Q definition for each respective item.

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References


See Also

thetaComb, fscores, mirt.model, M2, itemfit, boot.mirt, mirtCluster, wald, coef-method, summary-method, anova-method, residuals-method

Examples

#LSAT6 dataset
dat <- expand.table(LSAT6)

# fit with 2-3 latent classes
(mod2 <- mdirt(dat, 2))
## Not run:
(mod3 <- mdirt(dat, 3))
summary(mod2)
residuals(mod2)
residuals(mod2, type = 'exp')
anova(mod2, mod3)
M2(mod2)
itemfit(mod2)

# generate classification plots
plot(mod2)
plot(mod2, facet_items = FALSE)
plot(mod2, profile = TRUE)

# available for polytomous data
mod <- mdirt(Science, 2)
summary(mod)
plot(mod)
plot(mod, profile=TRUE)

# classification based on response patterns
fscores(mod2, full.scores = FALSE)

# classify individuals either with the largest posterior probability.....
fs <- fscores(mod2)
head(fs)
classes <- 1:2
class_max <- classes[apply(apply(fs, 1, max) == fs, 1, which)]
table(class_max)

# ... or by probability sampling (i.e., plausible value draws)
class_prob <- apply(fs, 1, function(x) sample(1:2, 1, prob=x))
table(class_prob)

# plausible value imputations for stochastic classification in both classes
pvs <- fscores(mod2, plausible.draws=10)
tabs <- lapply(pvs, function(x) apply(x, 2, table))
tabs[[1]]
# fit with random starting points (run in parallel to save time)
mirtCluster()
mod <- mdir(dat, 2, nruns=10)

# Grade of measurement model
# define a custom Theta grid for including a 'fuzzy' class membership
(Theta <- matrix(c(1, 0, .5, .5, 0, 1), nrow=3, ncol=2, byrow=TRUE))
(mod_gom <- mdir(dat, 2, customTheta = Theta))
summary(mod_gom)

# Multidimensional discrete latent class model
dat <- key2binary(SAT12, key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
# define Theta grid for three latent classes
(Theta <- thetaComb(0:1, 3))
(mod_discrete <- mdir(dat, 3, customTheta = Theta))
summary(mod_discrete)

# Located latent class model
model <- mirt.model('C1 = 1-32
C2 = 1-32
C3 = 1-32
CONSTRAN = (1-32, a1), (1-32, a2), (1-32, a3)'
(mod_located <- mdir(dat, model, customTheta = diag(3)))
summary(mod_located)

### DINA model example
# generate some suitable data for a two dimensional DINA application
# (first columns are intercepts)
set.seed(1)
Theta <- expand.table(matrix(c(1,0,0,0, 200,
     1,1,0,0, 200,
     1,0,1,0, 100,
     1,1,1,1, 500), 4, 5, byrow=TRUE))
a <- matrix(c(rnorm(15, -1.5, .5), rlnorm(5, .2, .3), numeric(15), rlnorm(5, .2, .3),
numeric(15), rlnorm(5, .2, .3)), 15, 4)
guess <- plogis(a[11:15,1]) # population guess
slip <- 1 - plogis(rowSums(a[11:15,])) # population slip
dat <- simdata(a, Theta=Theta, itemtype = 'lca')

# first column is the intercept, 2nd and 3rd are attributes
theta <- cbind(1, thetaComb(0:1, 2))
theta <- cbind(theta, theta[,2] * theta[,3]) #DINA interaction of main attributes
model <- mirt.model('Intercept = 1-15
A1 = 1-5
A2 = 6-10
A1A2 = 11-15

# last 5 items are DINA (first 10 are unidimensional C-RUMs)
DINA <- mdirt(dat, model, customTheta = theta)
coef(DINA, simplify=TRUE)
summary(DINA)
M2(DINA) # fits well (as it should)

cfs <- coef(DINA, simplify=TRUE)$items[11:15,]
cbind(guess, estguess = plogis(cfs[,1]))
cbind(slip, estslip = 1 - plogis(rowSums(cfs)))

### DINO model example
theta <- cbind(1, thetaComb(0:1, 2))
# define theta matrix with negative interaction term
(theta <- cbind(theta, -theta[,2] * theta[,3]))
model <- mirt.model('Intercept = 1-15
A1 = 1-5, 11-15
A2 = 6-15
Yoshi = 11-15
CONSTRAIN = (11,a2,a3,a4), (12,a2,a3,a4), (13,a2,a3,a4),
(14,a2,a3,a4), (15,a2,a3,a4)')

# last five items are DINOs (first 10 are unidimensional C-RUMs)
DINO <- mdirt(dat, model, customTheta = theta)
coef(DINO, simplify=TRUE)
summary(DINO)
M2(DINO) # doesn't fit as well, because not the generating model

### C-RUM (analogous to MIRT model)
theta <- cbind(1, thetaComb(0:1, 2))
model <- mirt.model('Intercept = 1-15
A1 = 1-5, 11-15
A2 = 6-15')

CRUM <- mdirt(dat, model, customTheta = theta)
coef(CRUM, simplify=TRUE)
summary(CRUM)

# good fit, but over-saturated (main effects for items 11-15 can be set to 0)
M2(CRUM)

#------------------
# multidimensional latent class model

dat <- key2binary(SAT12,
    key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

# 5 latent classes within 2 different sets of items
model <- mirt.model('C1 = 1-16
theta <- diag(10) # defined explicitly. Otherwise, this profile is assumed
mod <- mdirt(dat, model, customTheta = theta)
coef(mod, simplify=TRUE)
summary(mod)

# multiple group with constrained group probabilities
dat <- key2binary(SAT12,
 key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
 Theta <- diag(2)
 # the latent class parameters are technically located in the (nitems + 1) location
model <- mirt.model('A1 = 1-32
 A2 = 1-32
 CONSTRAINT = (33, c1)')
mod <- mdirt(dat, model, group = group, customTheta = Theta)
coef(mod, simplify=TRUE)
summary(mod)

# Probabilistic Guttman Model (Proctor, 1970)

# example analysis can also be found in the sirt package (see ?prob.guttman)
data(data.read, package = 'sirt')
head(data.read)

Theta <- matrix(c(1,0,0,0,
 1,1,0,0,
 1,1,1,0,
 1,1,1,1), 4, byrow=TRUE)

model <- mirt.model("INTERCEPT = 1-12
 C1 = 1,7,9,11
 C2 = 2,5,8,10,12
 C3 = 3,4,6")
mod <- mdirt(data.read, model, customTheta=Theta)
summary(mod)
MDISC

Compute multidimensional discrimination index

Description

Returns a vector containing the MDISC values for each item in the model input object (Reckase, 2009).

Usage

MDISC(x, group = NULL)

Arguments

x an object of class 'SingleGroupClass', or an object of class 'MultipleGroupClass' if a suitable group input were supplied

group group argument to pass to extract.group function. Required when the input object is a multiple-group model

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References


See Also

extract.group

Examples

## Not run:

mod <- mirt(Science, 2)
MDISC(mod)

## End(Not run)
**Description**

`mirt` fits a maximum likelihood (or maximum a posteriori) factor analysis model to any mixture of dichotomous and polytomous data under the item response theory paradigm using either Cai’s (2010) Metropolis-Hastings Robbins-Monro (MHRM) algorithm, with an EM algorithm approach outlined by Bock and Aiken (1981) using rectangular or quasi-Monte Carlo integration grids, or with the stochastic EM (i.e., the first two stages of the MH-RM algorithm). Models containing ‘explanatory’ person or item level predictors can only be included by using the `mixedmirt` function, though latent regression models can be fit using the `formula` input in this function. Tests that form a two-tier or bi-factor structure should be estimated with the `bfactor` function, which uses a dimension reduction EM algorithm for modeling item parcels. Multiple group analyses (useful for DIF and DTF testing) are also available using the `multipleGroup` function.

**Usage**

```r
mirt(
  data,
  model,
  itemtype = NULL,
  guess = 0,
  upper = 1,
  SE = FALSE,
  covdata = NULL,
  formula = NULL,
  SE.type = "Oakes",
  method = "EM",
  optimizer = NULL,
  dentype = "Gaussian",
  pars = NULL,
  constrain = NULL,
  parprior = NULL,
  calcNull = FALSE,
  draws = 5000,
  survey.weights = NULL,
  quadpts = NULL,
  TOL = NULL,
  gpcm_mats = list(),
  grsm.block = NULL,
  rsm.block = NULL,
  monopoly.k = 1L,
  key = NULL,
  large = FALSE,
  GenRandomPars = FALSE,
)```
accelerate = "Ramsay",
verbose = TRUE,
solnp_args = list(),
nloptr_args = list(),
spline_args = list(),
control = list(),
technical = list(),
...  
)

Arguments

data  a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA (to convert from an ordered factor data.frame see data.matrix)
model a string to be passed (or an object returned from) mirt.model, declaring how the IRT model is to be estimated (loadings, constraints, priors, etc). For exploratory IRT models, a single numeric value indicating the number of factors to extract is also supported
itemtype type of items to be modeled, declared as a vector for each item or a single value which will be recycled for each item. The NULL default assumes that the items follow a graded or 2PL structure, however they may be changed to the following:

- 'Rasch' - Rasch/partial credit model by constraining slopes to 1 and freely estimating the variance parameters (alternatively, can be specified by applying equality constraints to the slope parameters in 'gpcm'; Rasch, 1960)
- '2PL', '3PL', '3PLu', and '4PL' - 2-4 parameter logistic model, where 3PL estimates the lower asymptote only while 3PLu estimates the upper asymptote only (Lord and Novick, 1968; Lord, 1980)
- 'graded' - graded response model (Samejima, 1969)
- 'grsm' and 'grsmIRT' - graded ratings scale model in the slope-intercept and classical IRT parameterization. 'grsmIRT' is restricted to unidimensional models (Muraki, 1992)
- 'gpcm' and 'gpcmIRT' - generalized partial credit model in the slope-intercept and classical parameterization. 'gpcmIRT' is restricted to unidimensional models. Note that optional scoring matrices for 'gpcm' are available with the gpcm_mats input (Muraki, 1992)
- 'rsm' - Rasch rating scale model using the 'gpcmIRT' structure (unidimensional only; Andrich, 1978)
- 'nominal' - nominal response model (Bock, 1972)
- 'ideal' - dichotomous ideal point model (Maydeu-Olivares, 2006)
- 'ggum' - generalized graded unfolding model (Roberts, Donoghue, & Laughlin, 2000) and its multidimensional extension
- 'sequential' - multidimensional sequential response model (Tutz, 1990) in slope-intercept form
- 'Tutz' - same as the 'sequential' itemtype, except the slopes are fixed to 1 and the latent variance terms are freely estimated (similar to the 'Rasch' itemtype input)
• 'PC2PL' and 'PC3PL' - 2-3 parameter partially compensatory model. Note that constraining the slopes to be equal across items will reduce the model to Embretson’s (a.k.a. Whitely’s) multicomponent model (1980).
• '2PLNRM', '3PLNRM', '3PLuNRM', and '4PLNRM' - 2-4 parameter nested logistic model, where 3PLNRM estimates the lower asymptote only while 3PLuNRM estimates the upper asymptote only (Suh and Bolt, 2010)
• 'spline' - spline response model with the bs (default) or the ns function (Winsberg, Thissen, and Wainer, 1984)
• 'monopoly' - monotonic polynomial model for unidimensional tests for dichotomous and polytomous response data (Falk and Cai, 2016)

Additionally, user defined item classes can also be defined using the `createItem` function

`guess` fixed pseudo-guessing parameters. Can be entered as a single value to assign a global guessing parameter or may be entered as a numeric vector corresponding to each item

`upper` fixed upper bound parameters for 4-PL model. Can be entered as a single value to assign a global guessing parameter or may be entered as a numeric vector corresponding to each item

`SE` logical; estimate the standard errors by computing the parameter information matrix? See `SE.type` for the type of estimates available

`covdata` a data.frame of data used for latent regression models

`formula` an R formula (or list of formulas) indicating how the latent traits can be regressed using external covariates in `covdata`. If a named list of formulas is supplied (where the names correspond to the latent trait names in `model`) then specific regression effects can be estimated for each factor. Supplying a single formula will estimate the regression parameters for all latent traits by default

`SE.type` type of estimation method to use for calculating the parameter information matrix for computing standard errors and `wald` tests. Can be:

• 'Richardson', 'forward', or 'central' for the numerical Richardson, forward difference, and central difference evaluation of observed Hessian matrix

• 'crossprod' and 'Louis' for standard error computations based on the variance of the Fisher scores as well as Louis' (1982) exact computation of the observed information matrix. Note that Louis' estimates can take a long time to obtain for large sample sizes and long tests

• 'sandwich' for the sandwich covariance estimate based on the 'crossprod' and 'Oakes' estimates (see Chalmers, in press, for details)

• 'sandwich.Louis' for the sandwich covariance estimate based on the 'crossprod' and 'Louis' estimates

• 'Oakes' for Oakes' (1999) method using a central difference approximation (see Chalmers, in press, for details)

• 'SEM' for the supplemented EM (disables the `accelerate` option automatically; EM only)

• 'Fisher' for the expected information, 'complete' for information based on the complete-data Hessian used in EM algorithm
• 'MHRM' and 'FMHRM' for stochastic approximations of observed information matrix based on the Robbins-Monro filter or a fixed number of MHRM draws without the RM filter. These are the only options supported when method = 'MHRM'.

• 'numerical' to obtain the numerical estimate from a call to optim when method = 'BL'.

Note that both the 'SEM' method becomes very sensitive if the ML solution has not been reached with sufficient precision, and may be further sensitive if the history of the EM cycles is not stable/sufficient for convergence of the respective estimates. Increasing the number of iterations (increasing NCYCLES and decreasing TOL, see below) will help to improve the accuracy, and can be run in parallel if a mirtCluster object has been defined (this will be used for Oakes' method as well). Additionally, inspecting the symmetry of the ACOV matrix for convergence issues by passing technical = list(symmetric = FALSE) can be helpful to determine if a sufficient solution has been reached.

method

a character object specifying the estimation algorithm to be used. The default is 'EM', for the standard EM algorithm with fixed quadrature, 'QMCEM' for quasi-Monte Carlo EM estimation, or 'MCEM' for Monte Carlo EM estimation. The option 'MHRM' may also be passed to use the MH-RM algorithm, 'SEM' for the Stochastic EM algorithm (first two stages of the MH-RM stage using an optimizer other than a single Newton-Raphson iteration), and 'BL' for the Bock and Lieberman approach (generally not recommended for longer tests).

The 'EM' is generally effective with 1-3 factors, but methods such as the 'QMCEM', 'MCEM', 'SEM', or 'MHRM' should be used when the dimensions are 3 or more. Note that when the optimizer is stochastic the associated SE.type is automatically changed to SE.type = 'MHRM' by default to avoid the use of quadrature.

optimizer

a character indicating which numerical optimizer to use. By default, the EM algorithm will use the 'BFGS' when there are no upper and lower bounds box-constraints and 'nlminb' when there are.

Other options include the Newton-Raphson ('NR'), which can be more efficient than the 'BFGS' but not as stable for more complex IRT models (such as the nominal or nested logit models) and the related 'NR1' which is also the Newton-Raphson but consists of only 1 update that has been coupled with RM Hessian (only applicable when the MH-RM algorithm is used). The MH-RM algorithm uses the 'NR1' by default, though currently the 'BFGS', 'L-BFGS-B', and 'NR' are also supported with this method (with fewer iterations by default) to emulate stochastic EM updates. As well, the 'Nelder-Mead' and 'SANN' estimators are available, but their routine use generally is not required or recommended.

Additionally, estimation subroutines from the Rsolnp and nloptr packages are available by passing the arguments 'solnp' and 'nloptr', respectively. This should be used in conjunction with the solnp_args and nloptr_args specified below. If equality constraints were specified in the model definition only the parameter with the lowest parnum in the pars = 'values' data.frame is used in the estimation vector passed to the objective function, and group hyper-parameters are omitted. Equality an inequality functions should be of the form function(p, optim_args), where optim_args is a list of internally parameters that largely can be ignored when defining constraints (though use of browser() here may be helpful).
dentity: type of density form to use for the latent trait parameters. Current options include

- 'Gaussian' (default) assumes a multivariate Gaussian distribution with an associated mean vector and variance-covariance matrix.
- 'empiricalhist' or 'EH' estimates latent distribution using an empirical histogram described by Bock and Aitkin (1981). Only applicable for unidimensional models estimated with the EM algorithm. For this option, the number of cycles, TOL, and quadpts are adjusted to accommodate for less precision during estimation (namely: TOL = 3e-5, NCYCLES = 2000, quadpts = 121).
- 'empiricalhist_Woods' or 'EHW' estimates latent distribution using an empirical histogram described by Bock and Aitkin (1981), with the same specifications as \texttt{dentity = 'empiricalhist'}, but with the extrapolation-interpolation method described by Woods (2007). NOTE: to improve stability in the presence of extreme response styles (i.e., all highest or lowest in each item) the technical option \texttt{zeroExtreme = TRUE} may be required to down-weight the contribution of these problematic patterns.
- 'Davidian-#' estimates semi-parametric Davidian curves described by Woods and Lin (2009), where the # placeholder represents the number of Davidian parameters to estimate (e.g., 'Davidian-6' will estimate 6 smoothing parameters). By default, the number of quadpts is increased to 121, and this method is only applicable for unidimensional models estimated with the EM algorithm.

pars: a data.frame with the structure of how the starting values, parameter numbers, estimation logical values, etc, are defined. The user may observe how the model defines the values by using \texttt{pars = 'values'}, and this object can in turn be modified and input back into the estimation with \texttt{pars = mymodifiedpars}.

constrain: a list of user declared equality constraints. To see how to define the parameters correctly use \texttt{pars = 'values'} initially to see how the parameters are labeled. To constrain parameters to be equal create a list with separate concatenated vectors signifying which parameters to constrain. For example, to set parameters 1 and 5 equal, and also set parameters 2, 6, and 10 equal use \texttt{constrain = list(c(1,5),c(2,6,10))}. Constraints can also be specified using the \texttt{mirt.model} syntax (recommended).

parprior: a list of user declared prior item probabilities. To see how to define the parameters correctly use \texttt{pars = 'values'} initially to see how the parameters are labeled. Can define either normal (e.g., intercepts, lower/guessing and upper bounds), log-normal (e.g., for univariate slopes), or beta prior probabilities. To specify a prior the form is \texttt{c('priortype',...)}, where normal priors are \texttt{parprior = list(c(parnumbers,'norm',mean,sd))}, \texttt{parprior = list(c(parnumbers,'lnorm',log_mean,log_sd))} for log-normal, and \texttt{parprior = list(c(parnumbers,'beta',alpha,beta))} for beta, and \texttt{parprior = list(c(parnumbers,'expbeta',alpha,beta))} for the beta distribution after applying the function \texttt{plogis} to the input value (note, this is specifically for applying a beta prior to the lower/upper-bound parameters in 3/4PL models). Priors can also be specified using \texttt{mirt.model} syntax (recommended).
calcNull logical; calculate the Null model for additional fit statistics (e.g., TLI)? Only applicable if the data contains no NA’s and the data is not overly sparse

draws the number of Monte Carlo draws to estimate the log-likelihood for the MH-RM algorithm. Default is 5000

survey.weights a optional numeric vector of survey weights to apply for each case in the data (EM estimation only). If not specified, all cases are weighted equally (the standard IRT approach). The sum of the survey.weights must equal the total sample size for proper weighting to be applied

quadpts number of quadrature points per dimension (must be larger than 2). By default the number of quadrature uses the following scheme: switch(as.character(nfact),'1'=61,'2'=31,'3'=15,'4'=9,'5'=7,3). However, if the method input is set to 'QMCEM' and this argument is left blank then the default number of quasi-Monte Carlo integration nodes will be set to 5000 in total

TOL convergence threshold for EM or MH-RM; defaults are .0001 and .001. If SE.type = 'SEM' and this value is not specified, the default is set to 1e-5. If dentype = 'empiricalhist' (i.e., 'EH') or 'empiricalhist_Woods' (i.e., 'EHW') and TOL is not specified then the default 3e-5 will be used. To evaluate the model using only the starting values pass TOL = NaN, and to evaluate the starting values without the log-likelihood pass TOL = NA

gpcm_mats a list of matrices specifying how the scoring coefficients in the (generalized) partial credit model should be constructed. If omitted, the standard gpcm format will be used (i.e., seq(0,k,by = 1) for each trait). This input should be used if traits should be scored different for each category (e.g., matrix(c(0:3,1,0,0,0),4,2) for a two-dimensional model where the first trait is scored like a gpcm, but the second trait is only positively indicated when the first category is selected). Can be used when itemtypes are 'gpcm' or 'Rasch', but only when the respective element in gpcm_mats is not NULL

grsm.block an optional numeric vector indicating where the blocking should occur when using the grsm, NA represents items that do not belong to the grsm block (other items that may be estimated in the test data). For example, to specify two blocks of 3 with a 2PL item for the last item: grsm.block = c(rep(1,3),rep(2,3),NA). If NULL the all items are assumed to be within the same group and therefore have the same number of item categories

rsm.block same as grsm.block, but for 'rsm' blocks

monopoly.k a vector of values (or a single value to repeated for each item) which indicate the degree of the monotone polynomial fitted, where the monotone polynomial corresponds to monopoly.k * 2 + 1 (e.g., monopoly.k = 2 fits a 5th degree polynomial). Default is monopoly.k = 1, which fits a 3rd degree polynomial

key a numeric vector of the response scoring key. Required when using nested logit item types, and must be the same length as the number of items used. Items that are not nested logit will ignore this vector, so use NA in item locations that are not applicable

large a logical indicating whether unique response patterns should be obtained prior to performing the estimation so as to avoid repeating computations on identical patterns. The default TRUE provides the correct degrees of freedom for the model since all unique patterns are tallied (typically only affects goodness of fit
statistics such as G2, but also will influence nested model comparison methods such as `anova(mod1, mod2)`, while `FALSE` will use the number of rows in data as a placeholder for the total degrees of freedom. As such, model objects should only be compared if all flags were set to `TRUE` or all were set to `FALSE` Alternatively, if the collapse table of frequencies is desired for the purpose of saving computations (i.e., only computing the collapsed frequencies for the data oste-time) then a character vector can be passed with the argument `large = 'return'` to return a list of all the desired table information used by `mirt`. This list object can then be reused by passing it back into the `large` argument to avoid re-tallying the data again (again, useful when the dataset are very large and computing the tabulated data is computationally burdensome). This strategy is shown below:

**Compute organized data**  
`e.g., internaldat <- mirt(Science, 1, large = 'return')`

**Pass the organized data to all estimation functions**  
`e.g., mod <- mirt(Science, 1, large = internaldat)`

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>GenRandomPars</code></td>
<td>logical; generate random starting values prior to optimization instead of using the fixed internal starting values?</td>
</tr>
<tr>
<td><code>accelerate</code></td>
<td>a character vector indicating the type of acceleration to use. Default is 'Ramsay', but may also be 'squarem' for the SQUAREM procedure (specifically, the gSqS3 approach) described in Varadhan and Roldand (2008). To disable the acceleration, pass 'none'</td>
</tr>
<tr>
<td><code>verbose</code></td>
<td>logical; print observed- (EM) or complete-data (MHRM) log-likelihood after each iteration cycle? Default is TRUE</td>
</tr>
<tr>
<td><code>solnp_args</code></td>
<td>a list of arguments to be passed to the <code>solnp::solnp()</code> function for equality constraints, inequality constraints, etc</td>
</tr>
<tr>
<td><code>nloptr_args</code></td>
<td>a list of arguments to be passed to the <code>nloptr::nloptr()</code> function for equality constraints, inequality constraints, etc</td>
</tr>
<tr>
<td><code>spline_args</code></td>
<td>a named list of lists containing information to be passed to the <code>bs</code> (default) and <code>ns</code> for each spline itemtype. Each element must refer to the name of the itemtype with the spline, while the internal list names refer to the arguments which are passed. For example, if item 2 were called 'read2', and item 5 were called 'read5', both of which were of itemtype 'spline' but item 5 should use the <code>ns</code> form, then a modified list for each input might be of the form: <code>spline_args = list(read2 = list(degree = 4),read5 = list(fun = 'ns',knots = c(-2,2)))</code> This code input changes the <code>bs()</code> splines function to have a <code>degree = 4</code> input, while the second element changes to the <code>ns()</code> function with knots set a <code>c(-2,2)</code></td>
</tr>
<tr>
<td><code>control</code></td>
<td>a list passed to the respective optimizers (i.e., <code>optim()</code>, <code>nlminb()</code>, etc). Additional arguments have been included for the 'NR' optimizer: 'tol' for the convergence tolerance in the M-step (default is <code>TOL/1000</code>), while the default number of iterations for the Newton-Raphson optimizer is 50 (modified with the 'maxit' control input)</td>
</tr>
<tr>
<td><code>technical</code></td>
<td>a list containing lower level technical parameters for estimation. May be:</td>
</tr>
<tr>
<td></td>
<td><strong>NCYCLES</strong> maximum number of EM or MH-RM cycles; defaults are 500 and 2000</td>
</tr>
</tbody>
</table>
MAXQUAD  maximum number of quadratures, which you can increase if you have more than 4GB or RAM on your PC; default 20000
theta_lim  range of integration grid for each dimension; default is c(-6, 6)
set.seed  seed number used during estimation. Default is 12345
SEtol  standard error tolerance criteria for the S-EM and MHRM computation of the information matrix. Default is 1e-3
symmetric  logical; force S-EM/Oakes information matrix estimates to be symmetric? Default is TRUE so that computation of standard errors are more stable. Setting this to FALSE can help to detect solutions that have not reached the ML estimate
SEM_window  ratio of values used to define the S-EM window based on the observed likelihood differences across EM iterations. The default is c(0, 1 -SEtol), which provides nearly the very full S-EM window (i.e., nearly all EM cycles used). To use a smaller SEM window change the window to to something like c(.9, .999) to start at a point farther into the EM history
warn  logical; include warning messages during estimation? Default is TRUE
message  logical; include general messages during estimation? Default is TRUE
customK  a numeric vector used to explicitly declare the number of response categories for each item. This should only be used when constructing mirt model for reasons other than parameter estimation (such as to obtain factor scores), and requires that the input data all have 0 as the lowest category. The format is the same as the extract.mirt(mod, 'K') slot in all converged models
customPriorFun  a custom function used to determine the normalized density for integration in the EM algorithm. Must be of the form function(Theta, Etable){...}, and return a numeric vector with the same length as number of rows in Theta. The Etable input contains the aggregated table generated from the current E-step computations. For proper integration, the returned vector should sum to 1 (i.e., normalized). Note that if using the Etable it will be NULL on the first call, therefore the prior will have to deal with this issue accordingly
zeroExtreme  logical; assign extreme response patterns a survey.weight of 0 (formally equivalent to removing these data vectors during estimation)? When dentype = 'EHW', where Woods’ extrapolation is utilized, this option may be required if the extrapolation causes expected densities to tend towards positive or negative infinity. The default is FALSE
customTheta  a custom Theta grid, in matrix form, used for integration. If not defined, the grid is determined internally based on the number of quadpts
delta  the deviation term used in numerical estimates when computing the ACOV matrix with the 'forward' or 'central' numerical approaches, as well as Oakes’ method with the Richardson extrapolation. Default is 1e-5
parallel  logical; use the parallel cluster defined by mirtCluster? Default is TRUE
removeEmptyRows  logical; remove response vectors that only contain NA’s? Default is FALSE
internal_constraints  logical; include the internal constraints when using certain IRT models (e.g., 'grsm' itemtype). Disable this if you want to use
special optimizers such as the solnp. Default is `TRUE`.

**gain** a vector of two values specifying the numerator and exponent values for the RM gain function \((v_{al1}/cycle)^{va2}\). Default is \(c(0.10,0.75)\)

**BURNIN** number of burn in cycles (stage 1) in MH-RM; default is 150

**SEMCYCLES** number of SEM cycles (stage 2) in MH-RM; default is 100

**MHDRAWS** number of Metropolis-Hasting draws to use in the MH-RM at each iteration; default is 5

**MHcand** a vector of values used to tune the MH sampler. Larger values will cause the acceptance ratio to decrease. One value is required for each group in unconditional item factor analysis (mixedmirt() requires additional values for random effect). If null, these values are determined internally, attempting to tune the acceptance of the draws to be between .1 and .4.

**MHRM_SE_draws** number of fixed draws to use when `SE=TRUE` and `SE.type = 'FMHRM'` and the maximum number of draws when `SE.type = 'MHRM'`. Default is 2000

**MCEM_draws** a function used to determine the number of quadrature points to draw for the `FMHRM` method. Must include one argument which indicates the iteration number of the EM cycle. Default is `function(cycles) 500 + (cycles -1)*2`, which starts the number of draws at 500 and increases by 2 after each full EM iteration

**info_if_converged** logical; compute the information matrix when using the MH-RM algorithm only if the model converged within a suitable number of iterations? Default is `TRUE`

**logLik_if_converged** logical; compute the observed log-likelihood when using the MH-RM algorithm only if the model converged within a suitable number of iterations? Default is `TRUE`

**keep_vcov_PD** logical; attempt to keep the variance-covariance matrix of the latent traits positive definite during estimation in the EM algorithm? This generally improves the convergence properties when the traits are highly correlated. Default is `TRUE`

... additional arguments to be passed

**Value**

function returns an object of class `SingleGroupClass` (`SingleGroupClass-class`)

**Confirmatory and Exploratory IRT**

Specification of the confirmatory item factor analysis model follows many of the rules in the structural equation modeling framework for confirmatory factor analysis. The variances of the latent factors are automatically fixed to 1 to help facilitate model identification. All parameters may be fixed to constant values or set equal to other parameters using the appropriate declarations. Confirmatory models may also contain ‘explanatory’ person or item level predictors, though including predictors is currently limited to the `mixedmirt` function.

When specifying a single number greater than 1 as the model input to mirt an exploratory IRT model will be estimated. Rotation and target matrix options are available if they are passed to
generic functions such as `summary-method` and `fscores`. Factor means and variances are fixed to ensure proper identification.

If the model is an exploratory item factor analysis estimation will begin by computing a matrix of quasi-polychoric correlations. A factor analysis with `nfact` is then extracted and item parameters are estimated by \( a_{ij} = f_{ij}/u_j \), where \( f_{ij} \) is the factor loading for the \( j \)th item on the \( i \)th factor, and \( u_j \) is the square root of the factor uniqueness, \( \sqrt{1 - h^2_j} \). The initial intercept parameters are determined by calculating the inverse normal of the item facility (i.e., item easiness), \( q_j \), to obtain \( d_j = q_j/u_j \). A similar implementation is also used for obtaining initial values for polytomous items.

A note on upper and lower bound parameters

Internally the \( g \) and \( u \) parameters are transformed using a logit transformation \( \log(x/(1-x)) \), and can be reversed by using \( 1/(1 + \exp(-x)) \) following convergence. This also applies when computing confidence intervals for these parameters, and is done so automatically if `coef(mod, rawug = FALSE)`.

As such, when applying prior distributions to these parameters it is recommended to use a prior that ranges from negative infinity to positive infinity, such as the normally distributed prior via the 'norm' input (see `mirt.model`).

Convergence for quadrature methods

Unrestricted full-information factor analysis is known to have problems with convergence, and some items may need to be constrained or removed entirely to allow for an acceptable solution. As a general rule dichotomous items with means greater than .95, or items that are only .05 greater than the guessing parameter, should be considered for removal from the analysis or treated with prior parameter distributions. The same type of reasoning is applicable when including upper bound parameters as well. For polytomous items, if categories are rarely endorsed then this will cause similar issues. Also, increasing the number of quadrature points per dimension, or using the quasi-Monte Carlo integration method, may help to stabilize the estimation process in higher dimensions. Finally, solutions that are not well defined also will have difficulty converging, and can indicate that the model has been misspecified (e.g., extracting too many dimensions).

Convergence for MH-RM method

For the MH-RM algorithm, when the number of iterations grows very high (e.g., greater than 1500) or when `Max Change = .2500` values are repeatedly printed to the console too often (indicating that the parameters were being constrained since they are naturally moving in steps greater than 0.25) then the model may either be ill defined or have a very flat likelihood surface, and genuine maximum-likelihood parameter estimates may be difficult to find. Standard errors are computed following the model convergence by passing `SE = TRUE`, to perform an addition MH-RM stage but treating the maximum-likelihood estimates as fixed points.

Additional helper functions

Additional functions are available in the package which can be useful pre- and post-estimation. These are:
mirt.model Define the IRT model specification use special syntax. Useful for defining between and within group parameter constraints, prior parameter distributions, and specifying the slope coefficients for each factor.

coeff-method Extract raw coefficients from the model, along with their standard errors and confidence intervals.

summary-method Extract standardized loadings from model. Accepts a rotate argument for exploratory item response model.

anova-method Compare nested models using likelihood ratio statistics as well as information criteria such as the AIC and BIC.

residuals-method Compute pairwise residuals between each item using methods such as the LD statistic (Chen & Thissen, 1997), as well as response pattern residuals.

plot-method Plot various types of test level plots including the test score and information functions and more.

itemplot Plot various types of item level plots, including the score, standard error, and information functions, and more.

createItem Create a customized itemtype that does not currently exist in the package.

imputeMissing Impute missing data given some computed Theta matrix.

fscores Find predicted scores for the latent traits using estimation methods such as EAP, MAP, ML, WLE, and EAPsum.

wald Compute Wald statistics follow the convergence of a model with a suitable information matrix.

M2 Limited information goodness of fit test statistic based to determine how well the model fits the data.

itemfit and personfit Goodness of fit statistics at the item and person levels, such as the S-X2, infit, outfit, and more.

boot.mirt Compute estimated parameter confidence intervals via the bootstrap methods.

mirtCluster Define a cluster for the package functions to use for capitalizing on multi-core architecture to utilize available CPUs when possible. Will help to decrease estimation times for tasks that can be run in parallel.

IRT Models

The parameter labels use the follow convention, here using two factors and $K$ as the total number of categories (using $k$ for specific category instances).

Rasch Only one intercept estimated, and the latent variance of $\theta$ is freely estimated. If the data have more than two categories then a partial credit model is used instead (see `gpcm` below).

$$P(x = 1|\theta, d) = \frac{1}{1 + \exp(-(\theta + d))}$$

2-4PL Depending on the model $u$ may be equal to 1 and $g$ may be equal to 0.

$$P(x = 1|\theta, \psi) = g + \frac{(u - g)}{1 + \exp(-(a_1 * \theta_1 + a_2 * \theta_2 + d))}$$
The graded model consists of sequential 2PL models,
\[ P(x = k|\theta, \psi) = P(x \geq k|\theta, \phi) - P(x \geq k + 1|\theta, \phi) \]
Note that \( P(x \geq 1|\theta, \phi) = 1 \) while \( P(x \geq K + 1|\theta, \phi) = 0 \)

**grsm and grsmIRT** A more constrained version of the graded model where graded spacing is equal across item blocks and only adjusted by a single 'difficulty' parameter \( c \) while the latent variance of \( \theta \) is freely estimated. Again,
\[ P(x = k|\theta, \psi) = P(x \geq k|\theta, \phi) - P(x \geq k + 1|\theta, \phi) \]
but now
\[ P = \frac{1}{1 + \exp(-(a_1 \theta_1 + a_2 \theta_2 + d_k + c))} \]
The grsmIRT model is similar to the grsm item type, but uses the IRT parameterization instead (see Muraki, 1990 for this exact form). This is restricted to unidimensional models only, whereas grsm may be used for unidimensional or multidimensional models and is more consistent with the form of other IRT models in `mirt`

**gpcm/nominal** For the gpcm the \( d \) values are treated as fixed and ordered values from 0 : \((K - 1)\) (in the nominal model \( d_0 \) is also set to 0). Additionally, for identification in the nominal model \( a_{k_0} = 0, a_{k(K-1)} = (K - 1) \).
\[ P(x = k|\theta, \psi) = \frac{\exp(a_{k-1} \theta_1 + a_2 \theta_2 + d_k)}{\sum_{k=1}^{K} \exp(a_{k-1} \theta_1 + a_2 \theta_2 + d_{k-1})} \]
For the partial credit model (when `itemtype` = 'Rasch'; unidimensional only) the above model is further constrained so that \( ak = (0, 1, \ldots, K - 1) \), \( a_1 = 1 \), and the latent variance of \( \theta_1 \) is freely estimated. Alternatively, the partial credit model can be obtained by containing all the slope parameters in the gpcms to be equal. More specific scoring function may be included by passing a suitable list or matrices to the `gpcm_mats` input argument.

In the nominal model this parametrization helps to identify the empirical ordering of the categories by inspecting the \( ak \) values. Larger values indicate that the item category is more positively related to the latent trait(s) being measured. For instance, if an item was truly ordinal (such as a Likert scale), and had 4 response categories, we would expect to see \( a_{k_0} < a_{k_1} < a_{k_2} < a_{k_3} \) following estimation. If on the other hand \( a_{k_0} > a_{k_1} \) then it would appear that the second category is less related to the trait than the first, and therefore the second category should be understood as the 'lowest score'.

NOTE: The nominal model can become numerical unstable if poor choices for the high and low values are chosen, resulting in \( ak \) values greater than \( \text{abs}(\theta) \) or more. It is recommended to choose high and low anchors that cause the estimated parameters to fall between 0 and \( K - 1 \) either by theoretical means or by re-estimating the model with better values following convergence.

**gpcmIRT and rsm** The gpcmIRT model is the classical generalized partial credit model for unidimensional response data. It will obtain the same fit as the gpcm presented above, however the parameterization allows for the Rasch/generalized rating scale model as a special case.
E.g., for a \( K = 4 \) category response model,
\[ P(x = 0|\theta, \psi) = \exp(1)/G \]
\[ P(x = 1|\theta, \psi) = \exp(1 + a(\theta - b_1) + c)/G \]
\[ P(x = 2|\theta, \psi) = \exp(1 + a(2\theta - b_1 - b_2) + 2c)/G \]
\[ P(x = 3|\theta, \psi) = \exp(1 + a(3\theta - b_1 - b_2 - b_3) + 3c)/G \]

where

\[ G = \exp(1)+\exp(1+a(\theta-b_1)+c)+\exp(1+a(2\theta-b_1-b_2)+2c)+\exp(1+a(3\theta-b_1-b_2-b_3)+3c) \]

Here \( a \) is the slope parameter, the \( b \) parameters are the threshold values for each adjacent category, and \( c \) is the so-called difficulty parameter when a rating scale model is fitted (otherwise, \( c = 0 \) and it drops out of the computations).

The gpcmIRT can be constrained to the partial credit IRT model by either constraining all the slopes to be equal, or setting the slopes to 1 and freeing the latent variance parameter.

Finally, the rsr is a more constrained version of the (generalized) partial credit model where the spacing is equal across item blocks and only adjusted by a single ‘difficulty’ parameter \( c \). Note that this is analogous to the relationship between the graded model and the grsm (with an additional constraint regarding the fixed discrimination parameters).

**sequential/Tutz** The multidimensional sequential response model has the form

\[ P(x = k|\theta, \psi) = \prod (1 - F(a_1 \theta_1 + a_2 \theta_2 + d_{sk})) F(a_1 \theta_1 + a_2 \theta_2 + d_{jk}) \]

where \( F(\cdot) \) is the cumulative logistic function. The Tutz variant of this model (Tutz, 1990) (via \texttt{ihtype} = ‘Tutz’) assumes that the slope terms are all equal to 1 and the latent variance terms are estimated (i.e., is a Rasch variant).

**ideal** The ideal point model has the form, with the upper bound constraint on \( d \) set to 0:

\[ P(x = 1|\theta, \psi) = \exp(-0.5 \times (a_1 + \theta_1 + a_2 + \theta_2 + d)^2) \]

**partcomp** Partially compensatory models consist of the product of 2PL probability curves.

\[ P(x = 1|\theta, \psi) = g + (1 - g) \left( \frac{1}{1 + \exp(-a_1 \theta_1 + d_1)} \right) \times \frac{1}{1 + \exp(-(a_2 + \theta_2 + d_2))} \]

Note that constraining the slopes to be equal across items will reduce the model to Embretson’s (a.k.a. Whitely’s) multicomponent model (1980).

**2-4PLNRM** Nested logistic curves for modeling distractor items. Requires a scoring key. The model is broken into two components for the probability of endorsement. For successful endorsement the probability trace is the 1-4PL model, while for unsuccessful endorsement:

\[ P(x = 0|\theta, \psi) = (1 - P_{1-4PL}(x = 1|\theta, \psi)) \times P_{nominal}(x = k|\theta, \psi) \]

which is the product of the complement of the dichotomous trace line with the nominal response model. In the nominal model, the slope parameters defined above are constrained to be 1’s, while the last value of the \( ak \) is freely estimated.

**ggum** The (multidimensional) generalized graded unfolding model is a class of ideal point models useful for ordinal response data. The form is

\[ P(z = k|\theta, \psi) = \frac{\exp{\left( z \sqrt{\sum_{d=1}^{D} a_{id}^2 (\theta_{jd} - b_{id})^2} + \sum_{k=0}^{z} \psi_{ik} \right)}}{\sum_{w=0}^{C} \exp{\left( w \sqrt{\sum_{d=1}^{D} a_{id}^2 (\theta_{jd} - b_{id})^2} + \sum_{k=0}^{z} \psi_{ik} \right)}} + \exp{\left( (M - z) \sqrt{\sum_{d=1}^{D} a_{id}^2 (\theta_{jd} - b_{id})^2} \right)} + \exp{\left( (M - w) \sqrt{\sum_{d=1}^{D} a_{id}^2 (\theta_{jd} - b_{id})^2} \right)} \]
where \( \theta_{jd} \) is the location of the \( j \)th individual on the \( d \)th dimension, \( b_{id} \) is the difficulty location of the \( i \)th item on the \( d \)th dimension, \( a_{jd} \) is the discrimination of the \( j \)th individual on the \( d \)th dimension (where the discrimination values are constrained to be positive), \( \psi_{ik} \) is the \( k \)th subjective response category threshold for the \( i \)th item, assumed to be symmetric about the item and constant across dimensions, where \( \psi_{ik} = \sum_{d=1}^{D} a_{jd} t_{ik} z = 1, 2, \ldots, C \) (where \( C \) is the number of categories minus 1), and \( M = 2C + 1 \).

**spline**  Spline response models attempt to model the response curves uses non-linear and potentially non-monotonic patterns. The form is

\[
P(x = 1|\theta, \eta) = \frac{1}{1 + \exp(- (\eta_1 \ast X_1 + \eta_2 \ast X_2 + \cdots + \eta_n \ast X_n))}
\]

where the \( X_n \) are from the spline design matrix \( X \) organized from the grid of \( \theta \) values. B-splines with a natural or polynomial basis are supported, and the intercept input is set to TRUE by default.

**monopoly**  Monotone polynomial model for polytomous response data of the form

\[
P(x = k|\theta, \psi) = \frac{\exp(\sum_{i=1}^{k} (m^*(\psi) + \xi_{c-1}))}{\sum_{i=1}^{C} \exp(\sum_{i=1}^{K} (m^*(\psi) + \xi_{c-1}))}
\]

where \( m^*(\psi) \) is the monotone polynomial function without the intercept.

**HTML help files, exercises, and examples**

To access examples, vignettes, and exercise files that have been generated with knitr please visit [https://github.com/philchalmers/mirt/wiki](https://github.com/philchalmers/mirt/wiki).

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**References**


See Also

`bfactor`, `multipleGroup`, `mixedmirt`, `expand.table`, `key2binary`, `mod2values`, `extract.item`, `iteminfo`, `testinfo`, `protrace`, `simdata`, `averageMI`, `fixef`, `extract.mirt`

Examples

```r
# load LSAT section 7 data and compute 1 and 2 factor models
data <- expand.table(LSAT7)

(mod1 <- mirt(data, 1))
coef(mod1)
summary(mod1)
plot(mod1)
plot(mod1, type = 'trace')

## Not run:
(mod2 <- mirt(data, 1, SE = TRUE)) # standard errors via the Oakes method
(mod2 <- mirt(data, 1, SE = TRUE, SE.type = 'SEM')) # standard errors with SEM method

# estimated 3PL model for item 5 only
(mod1.3PL <- mirt(data, 1, itemtype = c('2PL', '2PL', '2PL', '2PL', '3PL')))
coef(mod1.3PL)

# internally g and u pars are stored as logits, so usually a good idea to include normal prior
# to help stabilize the parameters. For a value around .182 use a mean
# of -1.5 (since 1 / (1 + exp(-(-1.5))) == .182)
model <- 'F = 1-5
PRIOR = (5, g, norm, -1.5, 3)
mod1.3PL.norm <- mirt(data, model, itemtype = c('2PL', '2PL', '2PL', '2PL', '3PL'))
coef(mod1.3PL.norm)

# unidimensional ideal point model
idealpt <- mirt(data, 1, itemtype = 'ideal')
plot(idealpt, type = 'trace', facet_items = TRUE)
plot(idealpt, type = 'trace', facet_items = FALSE)
```

# two factors (exploratory)
mod2 <- mirt(data, 2)
coef(mod2)
summary(mod2, rotate = 'oblimin') #oblimin rotation
residuals(mod2)
plot(mod2)
plot(mod2, rotate = 'oblimin')

anova(mod1, mod2) #compare the two models
scoresfull <- fscores(mod2) #factor scores for each response pattern
head(scoresfull)
scorestable <- fscores(mod2, full.scores = FALSE) #save factor score table
head(scorestable)

#confirmatory (as an example, model is not identified since you need 3 items per factor)
# Two ways to define a confirmatory model: with mirt.model, or with a string

# these model definitions are equivalent

(cmodel <- mirt.model('F1 = 1,4,5
F2 = 2,3'))
cmodel2 <- 'F1 = 1,4,5
F2 = 2,3'

(cmod <- mirt(data, cmodel))

anova(cmod, mod2)

(cmod <- mirt(data, cmodel, SE = TRUE))

########
#data from the 'ltm' package in numeric format

pmod1 <- mirt(Science, 1)
plot(pmod1)
plot(pmod1, type = 'trace')
plot(pmod1, type = 'itemscore')
summary(pmod1)

#Constrain all slopes to be equal with the constrain = list() input or mirt.model() syntax
#first obtain parameter index
values <- mirt(Science, 1, pars = 'values')
values #note that slopes are numbered 1,5,9,13, or index with values$parnum[values$name == 'a1']
(pmod1_equalslopes <- mirt(Science, 1, constrain = list(c(1,5,9,13))))
coef(pmod1_equalslopes)

# using mirt.model syntax, constrain all item slopes to be equal
model <- 'F = 1-4
CONSTRRAIN = (1-4, a1)'
(pmod1_equalslopes <- mirt(Science, model))
coef(pmod1_equalslopes)

anova(pmod1_equalslopes, pmod1) #significantly worse fit with almost all criteria
mirt

```r
pmod2 <- mirt(Science, 2)
summary(pmod2)
plot(pmod2, rotate = 'oblimin')
itemplot(pmod2, 1, rotate = 'oblimin')
anova(pmod1, pmod2)

# unidimensional fit with a generalized partial credit and nominal model
(gpcmod <- mirt(Science, 1, 'gpcm'))
coef(gpcmod)

# for the nominal model the lowest and highest categories are assumed to be the
# theoretically lowest and highest categories that related to the latent trait(s)
(nomod <- mirt(Science, 1, 'nominal'))
coef(nomod) # ordering of ak values suggest that the items are indeed ordinal
anova(gpcmod, nomod)
itemplot(nomod, 3)

# generalized graded unfolding model
(ggum <- mirt(Science, 1, 'ggum'))
coef(ggum, simplify=TRUE)
plot(ggum)
plot(ggum, type = 'trace')
plot(ggum, type = 'itemscore')

# monotonic polynomial models
(monopoly <- mirt(Science, 1, 'monopoly'))
coef(monopoly, simplify=TRUE)
plot(monopoly)
plot(monopoly, type = 'true')
plot(monopoly, type = 'itemscore')

## example applying survey weights.
# weight the first half of the cases to be more representative of population
survey.weights <- c(rep(2, nrow(Science)/2), rep(1, nrow(Science)/2))
survey.weights <- survey.weights/sum(survey.weights) * nrow(Science)
unweighted <- mirt(Science, 1)
weighted <- mirt(Science, 1, survey.weights=survey.weights)

###########
# empirical dimensionality testing that includes 'guessing'

data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,4,5))

mod1 <- mirt(data, 1)
extract.mirt(mod1, 'time') # time elapsed for each estimation component

# optionally use Newton-Raphson for (generally) faster convergence in the M-step's
mod1 <- mirt(data, 1, optimizer = 'NR')
extract.mirt(mod1, 'time')
```
mod2 <- mirt(data, 2, optimizer = 'NR')
#difficulty converging with reduced quadpts, reduce TOL
mod3 <- mirt(data, 3, TOL = .001, optimizer = 'NR')
anova(mod1, mod2)
anova(mod2, mod3)  # negative AIC, 2 factors probably best

# same as above, but using the QMCEM method for generally better accuracy in mod3
mod3 <- mirt(data, 3, method = 'QMCEM', TOL = .001, optimizer = 'NR')
anova(mod2, mod3)

# with fixed guessing parameters
mod1g <- mirt(data, 1, guess = .1)
coef(mod1g)

# graded rating scale example

# make some data
set.seed(1234)
a <- matrix(rep(1, 10))
d <- matrix(c(1, 0.5, -0.5, -1), 10, 4, byrow = TRUE)
c <- seq(-1, 1, length.out = 10)
data <- simdata(a, d + c, 2000, itemtype = rep('graded', 10))

mod1 <- mirt(data, 1)
mod2 <- mirt(data, 1, itemtype = 'grsm')
coef(mod2)
anova(mod2, mod1)  # not sig, mod2 should be preferred
itemplot(mod2, 1)
itemplot(mod2, 5)
itemplot(mod2, 10)

# 2PL nominal response model example (Suh and Bolt, 2010)
data(SAT12)
SAT12[SAT12 == 8] <- NA  # set 8 as a missing value
head(SAT12)

# correct answer key
key <- c(1, 4, 5, 2, 3, 1, 2, 4, 2, 1, 5, 3, 4, 1, 4, 3, 3, 4, 1, 3, 5, 1, 3, 1, 5, 4, 5)
scoredSAT12 <- key2binary(SAT12, key)
mod0 <- mirt(scoredSAT12, 1)

# for first 5 items use 2PLNRM and nominal
scoredSAT12[, 1:5] <- as.matrix(SAT12[, 1:5])
mod1 <- mirt(scoredSAT12, 1, c(rep('nominal', 5), rep('2PL', 27)))
mod2 <- mirt(scoredSAT12, 1, c(rep('2PLNRM', 5), rep('2PL', 27)), key = key)
coef(mod0)$Item.1
coef(mod1)$Item.1
coef(mod2)$Item.1
itemplot(mod0, 1)
itemplot(mod1, 1)
itemplot(mod2, 1)
# compare added information from distractors
Theta <- matrix(seq(-4, 4, .01))
par(mfrow = c(2, 3))
for(i in 1:5){
  info <- iteminfo(extract.item(mod0, i), Theta)
  info2 <- iteminfo(extract.item(mod2, i), Theta)
  plot(Theta, info2, type = 'l', main = paste('Information for item', i), ylab = 'Information')
  lines(Theta, info, col = 'red')
}
par(mfrow = c(1, 1))

# test information
plot(Theta, testinfo(mod2, Theta), type = 'l', main = 'Test information', ylab = 'Information')
lines(Theta, testinfo(mod0, Theta), col = 'red')

###########
# using the MH-RM algorithm
data(LSAT7)
fulldata <- expand.table(LSAT7)
(mod1 <- mirt(fulldata, 1, method = 'MHRM'))

# Confirmatory models

# simulate data
a <- matrix(c(1.5, NA,
  0.5, NA,
  1.0, NA,
  1.0, 0.5,
  NA, 1.5,
  NA, 0.5,
  NA, 1.0,
  NA, 1.0), ncol=2, byrow=TRUE)
d <- matrix(c(-1.0, NA, NA,
  -1.5, NA, NA,
  1.5, NA, NA,
  0.0, NA, NA,
  3.0, 2.0, -0.5,
  2.5, 1.0, -1,
  2.0, 0.0, NA,
  1.0, NA, NA), ncol=3, byrow=TRUE)
sigma <- diag(2)
sigma[1, 2] <- sigma[2, 1] <- .4
items <- c(rep('2PL', 4), rep('graded', 3), '2PL')
dataset <- simdata(a, d, 2000, items, sigma)

# analyses
# CIFA for 2 factor crossed structure
model.1 <- 'F1 = 1-4
F2 = 4-8
COV = F1*F2'

#compute model, and use parallel computation of the log-likelihood
mirtCluster()
mod1 <- mirt(dataset, model.1, method = 'MHRM')
coef(mod1)
summary(mod1)
residuals(mod1)

#####
#bifactor
model.3 <- 'G = 1-8
F1 = 1-4
F2 = 5-8'

mod3 <- mirt(dataset, model.3, method = 'MHRM')
coef(mod3)
summary(mod3)
residuals(mod3)
anova(mod1, mod3)

#####
#polynomial/combinations
data(SAT12)
data <- key2binary(SAT12,
                   key = c(1,4,5,2,3,1,2,1,3,1,2,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

model.quad <- '
F1 = 1-32
(F1*F1) = 1-32'

model.combo <- '
F1 = 1-16
F2 = 17-32
(F1*F2) = 1-8'

(mod.quad <- mirt(data, model.quad))
summary(mod.quad)
(mod.combo <- mirt(data, model.combo))
anova(mod.quad, mod.combo)

#non-linear item and test plots
plot(mod.quad)
plot(mod.combo, type = 'SE')
itemplot(mod.quad, 1, type = 'score')
itemplot(mod.combo, 2, type = 'score')
itemplot(mod.combo, 2, type = 'infocontour')
## empirical histogram examples (normal, skew and bimodality)

# make some data

```r
go set.seed(1234)
a <- matrix(rlnorm(50, .2, .2))
d <- matrix(rnorm(50))
ThetaNormal <- matrix(rnorm(2000))
ThetaBimodal <- scale(matrix(c(rnorm(1000, -2), rnorm(1000, 2)))) # bimodal
ThetaSkew <- scale(matrix(rchisq(2000, 3))) # positive skew

datNormal <- simdata(a, d, 2000, itemtype = '2PL', Theta=ThetaNormal)
datBimodal <- simdata(a, d, 2000, itemtype = '2PL', Theta=ThetaBimodal)
datSkew <- simdata(a, d, 2000, itemtype = '2PL', Theta=ThetaSkew)
```

normal <- mirt(datNormal, 1, dentype = "empiricalhist")
plot(normal, type = 'empiricalhist')
histogram(ThetaNormal, breaks=30)

bimodal <- mirt(datBimodal, 1, dentype = "empiricalhist")
plot(bimodal, type = 'empiricalhist')
histogram(ThetaBimodal, breaks=30)

skew <- mirt(datSkew, 1, dentype = "empiricalhist")
plot(skew, type = 'empiricalhist')
histogram(ThetaSkew, breaks=30)

#####
# non-linear parameter constraints with Rsolnp package (nloptr supported as well):
# Find Rasch model subject to the constraint that the intercepts sum to 0

dat <- expand.table(LSAT6)

# free latent mean and variance terms
model <- 'Theta = 1-5
MEAN = Theta
COV = Theta*Theta'

# view how vector of parameters is organized internally
sv <- mirt(dat, model, itemtype = 'Rasch', pars = 'values')
sv[sVest, ]

# constraint: create function for solnp to compute constraint, and declare value in eqB
eqfun <- function(p, optim_args) sum(p[1:5]) # could use browser() here, if it helps
LB <- c(rep(-15, 6), 1e-4) # more reasonable lower bound for variance term

mod <- mirt(dat, model, sv=sv, itemtype = 'Rasch', optimizer = 'solnp',
solnp_args=list(eqfun=eqfun, eqB=0, LB=LB))
print(mod)
coef(mod)
(ds <- sapply(coef(mod)[1:5], function(x) x[, 'd']))
sum(ds)

# same likelihood location as: mirt(dat, 1, itemtype = 'Rasch')
# latent regression Rasch model

## simulate data

```r
set.seed(1234)
N <- 1000

# covariates
X1 <- rnorm(N); X2 <- rnorm(N)
covdata <- data.frame(X1, X2)
Theta <- matrix(0.5 * X1 + -1 * X2 + rnorm(N, sd = 0.5))

# items and response data
a <- matrix(1, 20); d <- matrix(rnorm(20))
dat <- simdata(a, d, 1000, itemtype = '2PL', Theta=Theta)

# unconditional Rasch model
mod0 <- mirt(dat, 1, 'Rasch')

# conditional model using X1 and X2 as predictors of Theta
mod1 <- mirt(dat, 1, 'Rasch', covdata=covdata, formula = ~ X1 + X2)
coef(mod1, simplify=TRUE)
anova(mod0, mod1)

# bootstrapped confidence intervals
boot.mirt(mod1, R=5)

# draw plausible values for secondary analyses
pv <- fscores(mod1, plausible.draws = 10)
pvmods <- lapply(pv, function(x, covdata) lm(x ~ covdata$X1 + covdata$X2),
    covdata=covdata)

# population characteristics recovered well, and can be averaged over
so <- lapply(pvmods, summary)
so

# compute Rubin's multiple imputation average
par <- lapply(so, function(x) x$coefficients[, 'Estimate'])
SEpar <- lapply(so, function(x) x$coefficients[, 'Std. Error'])
averageMI(par, SEpar)
```

## Example using Gauss-Hermite quadrature with custom input functions

```r
library(fastGHQuad)
data(SAT12)
data <- key2binary(SAT12, key = c(1,4,5,2,3,1,2,13,1,2,4,1,5,3,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
GH <- gaussHermiteData(50)
Theta <- matrix(GH$x)

# This prior works for uni- and multi-dimensional models
prior <- function(Theta, Etable){
    P <- grid <- GH$w / sqrt(pi)
    # ...
mirt.model

Specify model loadings

Description

The mirt.model function scans/reads user input to specify the confirmatory model. Item locations must be used in the specifications if no itemnames argument is supplied. This is called implicitly by estimation functions when a string is passed to the model argument.

Usage

mirt.model(
  input = NULL,
  itemnames = NULL,
  file = ""
)
```r
mirt.model

COV = NULL,
quiet = TRUE,
...
)

Arguments

input       input for writing out the model syntax. Can either be a string declaration of class
color character or the so-called Q-matrix or class matrix that specifies the model ei-
ter with integer or logical values. If the Q-matrix method is chosen covariances
terms can be specified with the COV input

itemnames   a character vector or factor indicating the item names. If a data.frame or matrix
object is supplied the names will be extracted using colnames(itemnames). Supplying this input allows the syntax to be specified with the raw item names
rather than item locations

file        a input specifying an external file that declares the input.

COV         a symmetric, logical matrix used to declare which covariance terms are esti-
mated

quiet       logical argument passed to scan() to suppress console read message

...         additional arguments for scan()

Details

Factors are first named and then specify which numerical items they affect (i.e., where the slope is
not equal to 0), separated either by commas or by - to indicate a range of items. Products between
factors may be specified by enclosing the left hand term within brackets. To finish the declaration
of a model simply enter a blank line with only a carriage return (i.e., the 'enter' or 'return' key), or
instead read in an input version of the model syntax. The associated slopes throughout the package
label these coefficients as a1,a2,...,ak, where the associated number is assigned according to the
respective order of the defined factors.

For example, if the syntax were

"G = 1-10 F = 1-5 A = 6-10"

then the G factor would be assigned the slopes a1 for each item, F assigned the slopes a2, and A
assigned the slopes a3. The same principle applies to the bfactor function whereby the slopes are
automatically included for the specific factors after the general factor structure has been assigned.

There is an optional keyword for specifying the correlation between relationships between factors
called COV, and non-linear factor products can be included by enclosing the product combination on
the left hand side of the declaration (e.g., (F1*F1) would create a quadratic factor for F1).

The keywords CONSTRAIN, CONSTRAINTB, PRIOR, FIXED, FREE, START, UBOUND, LBOUND can be ap-
plied to specific sub-groups in multiple-group models by included square brackets before the = sign,
where groups are separated by commas. For example, to apply within-group equality constraints to
a group called "male", then specifying:

CONSTRAIN [male] = (1-5,a1)

is appropriate, while specifying the same constraints to the sub-groups "male" and "female" would appear as
```
CONstrain [male,female] = (1-5,a1)

For all other groups in the multi-group model, these within-group equality constraints would not appear. Therefore, these bracketed group specifications are useful when modifying priors, starting values, between/within group equality constraints, and so on when the specifications for each subgroup may differ.

Finally, the keyword GROUP can be used to specify the group-level hyper-parameter terms, such as the means and variance of the default Gaussian distribution. For example, to set the starting value of the variance parameter (COV.11) to 1.5:

START = (GROUP,COV.11,1.5)

COV Specify the relationship between the latent factors. Estimating a correlation between factors is declared by joining the two factors with an asterisk (e.g., F1*F2), or with an asterisk between three or more factors to estimate all the possible correlations (e.g., F1*F2*F3)

MEAN A comma separated list specifying which latent factor means to freely estimate. E.g., MEAN = F1,F2 will free the latent means for factors F1 and F2

CONstrain A bracketed, comma separated list specifying equality constrains between items.

The input format is CONstrain = (items,...,parameterName(s)),(items,...,parameterName).

For example, in a single group 10-item dichotomous tests, using the default 2PL model, the first and last 5 item slopes (a1) can be constrained to be equal by using CONstrain = (1-5,a1),(6-10,a1), or some combination such as CONstrain = (1-3,4,5,a1),(6,7,8-10,a1).

When constraining parameters to be equal across items with different parameter names, a balanced bracketed vector must be supplied. E.g., setting the first slope for item 1 equal to the second slope in item 3 would be CONstrain = (1,3,a1,a2)

CONstrainB A bracketed, comma separate list specifying equality constrains between groups.

The input format is CONstrainB = (items,...,parameterName),(items,...,parameterName).

For example, in a two group 10-item dichotomous tests, using the default 2PL model, the first 5 item slopes (a1) can be constrained to be equal across both groups by using CONstrainB = (1-5,a1)

PRIOR A bracketed, comma separate list specifying prior parameter distributions. The input format is PRIOR = (items,...,parameterName,priorType,val1,val2),(items,...,parameterName,priorType,val1,val2).

For example, in a single group 10-item dichotomous tests, using the default 2PL model, defining a normal prior of N(0,2) for the first 5 item intercepts (d) can be defined by PRIOR = (1-5,d,norm,0,2)

Currently supported priors are of the form: (items,norm,mean,sd) for the normal/Gaussian, (items,lnorm,log_mean,log_sd) for log-normal, (items,beta,alpha,beta) for beta, and (items,expbeta,alpha,beta) for the beta distribution after applying the function plogis to the input value (note, this is specifically for applying a beta prior to the lower-bound parameters in 3/4PL models)

LBOUND A bracketed, comma separate list specifying lower bounds for estimated parameters (used in optimizers such as L-BFGS-B and nlminb). The input format is LBOUND = (items,...,parameterName,value).

For example, in a single group 10-item dichotomous tests, using the 3PL model and setting lower bounds for the ‘g’ parameters for the first 5 items to 0.2 is accomplished with LBOUND = (1-5,g,0.2)

UBOUND same as LBOUND, but specifying upper bounds in estimated parameters
**START** A bracketed, comma separate list specifying the starting values for individual parameters. The input is of the form (items,...,parameterName,value). For instance, setting the 10th and 12th to 15th item slope parameters (a1) to 1.0 is specified with START = (10,12-15,a1,1.0)

For more hands on control of the starting values pass the argument pars = 'values' through whatever estimation function is being used

**FIXED** A bracketed, comma separate list specifying which parameters should be fixed at their starting values (i.e., not freely estimated). The input is of the form (items,...,parameterName).

For instance, fixing the 10th and 12th to 15th item slope parameters (a1) is accomplished with FIXED = (10,12-15,a1)

For more hands on control of the estimated values pass the argument pars = 'values' through whatever estimation function is being used

**FREE** Equivalent to the FIXED input, except that parameters are freely estimated instead of fixed at their starting value

**NEXPLORE** Number of exploratory factors to extract. Usually this is not required because passing a numeric value to the model argument in the estimation function will generate an exploratory factor analysis model, however if different start values, priors, lower and upper bounds, etc, are desired then this input can be used

**Value**

Returns a model specification object to be used in mirt, bfactor, multipleGroup, or mixedmirt

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com> and Alexander Robitzsch

**References**


**Examples**

```r
## Not run:

# interactively through the console (not run)
#model <- mirt.model()
# F1 = 1,2,3,4-10
# F2 = 10-20
# (F1xF2) = 1,2,3,4-10
# COV = F1xF2

#Or alternatively with a string input
s <- 'F1 = 1,2,3,4-10
F2 = 10-20
(F1xF2) = 1,2,3,4-10
```
COV = F1*F2'
model <- mirt.model(s)

# strings can also be passed to the estimation functions directly,
# which silently calls mirt.model(). E.g., using the string above:
# mod <- mirt(data, s)

# Q-matrix specification
Q <- matrix(c(1,1,1,0,0,0,0,0,0,1,1,1), ncol=2, dimnames = list(NULL, c('Factor1', 'Factor2')))
COV <- matrix(c(FALSE, TRUE, TRUE, FALSE), 2)
model <- mirt.model(Q, COV=COV)

## constrain various items slopes and all intercepts in single group model to be equal,
# and use a log-normal prior for all the slopes
s <-'F = 1-10
   CONSTRAIN = (1-3, 5, 6, a1), (1-10, d)
   PRIOR = (1-10, a1, lnorm, .2, .2)'
model <- mirt.model(s)

## constrain various items slopes and intercepts across groups for use in multipleGroup(),
# and constrain first two slopes within 'group1' to be equal
s <-'F = 1-10
   CONSTRAINT = (1-2, a1)
   CONSTRAINTB = (1-3, 5, 6, a1), (1-10, d)'
model <- mirt.model(s)

## specify model using raw item names
data(data.read, package = 'sirt')
dat <- data.read

# syntax with variable names
mirtsyn2 <- "
   F1 = A1,B2,B3,C4
   F2 = A1-A4,C2,C4
   MEAN = F1
   COV = F1*F1, F1*F2
   CONSTRAINT=(A2-A4,a2),(A3,C2,d)
   PRIOR = (C3,A2-A4,a2,lnorm, .2, .2),(B3,d,norm,0,.00001)"
# create a mirt model
mirtmodel <- mirt.model(mirtsyn2, itemnames=dat)
# or equivalently:
# mirtmodel <- mirt.model(mirtsyn2, itemnames=colnames(dat))

# mod <- mirt(dat , mirtmodel)

## End(Not run)
mirtCluster

Define a parallel cluster object to be used in internal functions

Description

This function defines an object that is placed in a relevant internal environment defined in mirt. Internal functions such as calcLogLik, fscores, etc, will utilize this object automatically to capitalize on parallel processing architecture. The object defined is a call from parallel::makeCluster(). Note that if you are defining other parallel objects (for simulation designs, for example) it is not recommended to define a mirtCluster.

Usage

mirtCluster(spec, omp_threads, remove = FALSE, ...)

Arguments

spec input that is passed to parallel::makeCluster(). If no input is given the maximum number of available local cores will be used

omp_threads number of OpenMP threads to use (currently applies to E-step computations only). Not used when argument input is missing

remove logical; remove previously defined mirtCluster()? 

... additional arguments to pass to parallel::makeCluster

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

## Not run:

#make 4 cores available for parallel computing
mirtCluster(4)

#stop and remove cores
mirtCluster(remove = TRUE)

# create 3 core architecture in R, and 4 thread architecture with OpenMP
mirtCluster(spec = 3, omp_threads = 4)

## End(Not run)
MixedClass-class

Class "MixedClass"

Description

Defines the object returned from mixedmirt.

Slots

Call: function call
Data: list of data, sometimes in different forms
Options: list of estimation options
Fit: a list of fit information
Model: a list of model-based information
ParObjects: a list of the S4 objects used during estimation
OptimInfo: a list of arguments from the optimization process
Internals: a list of internal arguments for secondary computations (inspecting this object is generally not required)
v cov: a matrix represented the asymptotic covariance matrix of the parameter estimates
time: a data.frame indicating the breakdown of computation times in seconds

Methods

coef signature(object = "MixedClass")
print signature(x = "MixedClass")
residuals signature(object = "MixedClass")
show signature(object = "MixedClass")
summary signature(object = "MixedClass")
logLik signature(object = "MixedClass")
anova signature(object = "MixedClass")

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

mixedmirt

Mixed effects modeling for MIRT models

Description

mixedmirt fits MIRT models using FIML estimation to dichotomous and polytomous IRT models conditional on fixed and random effect of person and item level covariates. This can also be understood as 'explanatory IRT' if only fixed effects are modeled, or multilevel/mixed IRT if random and fixed effects are included. The method uses the MH-RM algorithm exclusively. Additionally, computation of the log-likelihood can be sped up by using parallel estimation via mirtCluster.

Usage

mixedmirt(
  data,
  covdata = NULL,
  model,
  fixed = ~1,
  random = NULL,
  itemtype = "Rasch",
  lr.fixed = ~1,
  lr.random = NULL,
  itemdesign = NULL,
  constrain = NULL,
  pars = NULL,
  return.design = FALSE,
  SE = TRUE,
  internal_constraints = TRUE,
  technical = list(SEtol = 1e-04),
  ...
)

Arguments

data a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
covdata a data.frame that consists of the nrow(data) by K 'person level' fixed and random predictors. If missing data are present in this object then the observations from covdata and data will be removed row-wise via the rowSums(is.na(covdata)) > 0
model an object returned from, or a string to be passed to, mirt.model() to declare how the IRT model is to be estimated. See mirt.model for more details
fixed a right sided R formula for specifying the fixed effect (aka 'explanatory') predictors from covdata and itemdesign. To estimate the intercepts for each item the keyword items is reserved and automatically added to the itemdesign input. If any polytomous items are being model the items argument is not
valid since all intercept parameters are freely estimated and identified with the parameterizations found in mirt, and the first column in the fixed design matrix (commonly the intercept or a reference group) is omitted.

random a right sided formula or list of formulas containing crossed random effects of the form \(v_1 + ... v_n | G\), where \(G\) is the grouping variable and \(v_n\) are random numeric predictors within each group. If no intercept value is specified then by default the correlations between the \(v\)'s and \(G\) are estimated, but can be suppressed by including the \(~ -1 + ... or 0\) constant. \(G\) may contain interaction terms, such as \(group:items\) to include cross or person-level interactions effects.

itemtype same as itemtype in mirt, except when the fixed or random inputs are used does not support the following item types: c("PC2PL", "PC3PL", "2PLNRM", "3PLNRM", "3PLuNRM", "4PLNRM")

lr.fixed an R formula (or list of formulas) to specify regression effects in the latent variables from the variables in covdata. This is used to construct models such as the so-called 'latent regression model' to explain person-level ability/trait differences. If a named list of formulas is supplied (where the names correspond to the latent trait names in model) then specific regression effects can be estimated for each factor. Supplying a single formula will estimate the regression parameters for all latent traits by default.

lr.random a list of random effect terms for modeling variability in the latent trait scores, where the syntax uses the same style as in the random argument. Useful for building so-called 'multilevel IRT' models which are non-Rasch (multilevel Rasch models do not technically require these because they can be built using the fixed and random inputs alone)

itemdesign a data.frame object used to create a design matrix for the items, where each \(nrow(itemdesign) == nitems\) and the number of columns is equal to the number of fixed effect predictors (i.e., item intercepts). By default an items variable is reserved for modeling the item intercept parameters

constrain a list indicating parameter equality constraints. See mirt for more detail

pars used for parameter starting values. See mirt for more detail

return.design logical; return the design matrices before they have (potentially) been reassembled?

SE logical; compute the standard errors by approximating the information matrix using the MHRM algorithm? Default is TRUE

internal_constraints logical; use the internally defined constraints for constraining effects across persons and items? Default is TRUE. Setting this to FALSE runs the risk of under-identification

technical the technical list passed to the MH-RM estimation engine, with the SEtol default increased to .0001. Additionally, the argument RANDSTART is available to indicate at which iteration (during the burn-in stage) the additional random effect variables should begin to be approximated (i.e., elements in lr.random and random). The default for RANDSTART is to start at iteration 100, and when random effects are included the default number of burn-in iterations is increased from 150 to 200. See mirt for further details

... additional arguments to be passed to the MH-RM estimation engine. See mirt for more details and examples
For dichotomous response models, `mixedmirt` follows the general form

\[
P(x = 1|\theta, \psi) = g + \frac{(u - g)}{1 + \exp(-1 * (\theta a + X \beta + Z \delta))}
\]

where \(X\) is a design matrix with associated \(\beta\) fixed effect intercept coefficients, and \(Z\) is a design matrix with associated \(\delta\) random effects for the intercepts. For simplicity and easier interpretation, the unique item intercept values typically found in \(X \beta\) are extracted and reassigned within mirt’s 'intercept' parameters (e.g., 'd'). To observe how the design matrices are structured prior to reassignment and estimation pass the argument `return.design = TRUE`.

Polytomous IRT models follow a similar format except the item intercepts are automatically estimated internally, rendering the `items` argument in the fixed formula redundant and therefore must be omitted from the specification. If there are a mixture of dichotomous and polytomous items the intercepts for the dichotomous models are also estimated for consistency.

The decomposition of the \(\theta\) parameters is also possible to form latent regression and multilevel IRT models by using the `lr.fixed` and `lr.random` inputs. These effects decompose \(\theta\) such that

\[
\theta = VT + W\zeta + \epsilon
\]

where \(V\) and \(W\) are fixed and random effects design matrices for the associated coefficients.

To simulate maximum a posteriori estimates for the random effect terms use the `randef` function.

Value

function returns an object of class `MixedClass` (MixedClass-class).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

mirt, randef, fixef, boot.mirt
Examples

```r
## Not run:

# make some data
set.seed(1234)
N <- 750
a <- matrix(rlnorm(10,.3,1),10,1)
d <- matrix(rnorm(10), 10)
Theta <- matrix(sort(rnorm(N)))
pseudoIQ <- Theta * 5 + 100 + rnorm(N, 0, 5)
pseudoIQ <- (pseudoIQ - mean(pseudoIQ))/10 # rescale variable for numerical stability
group <- factor(rep(c("VarG1", "VarG2", "VarG3"), each = N/3))
data <- simdata(a,d,N, itemtype = rep("2PL", 10), Theta=Theta)
covdata <- data.frame(group, pseudoIQ)

# use parallel computing
mirtCluster()

# specify IRT model
model <- 'Theta = 1-10'

# model with no person predictors
mod0 <- mirt(data, model, itemtype = 'Rasch')

# group as a fixed effect predictor (aka, uniform dif)
mod1 <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items)
anova(mod0, mod1)
summary(mod1)
coef(mod1)

# same model as above in lme4
wide <- data.frame(id=1:nrow(data),data,covdata)
long <- reshape2::melt(wide, id.vars = c('id', 'group', 'pseudoIQ'))
library(lme4)
lmod0 <- glmer(value ~ 0 + variable + (1|id), long, family = binomial)
lmod1 <- glmer(value ~ 0 + group + variable + (1|id), long, family = binomial)
anova(lmod0, lmod1)

# model using 2PL items instead of Rasch
mod1b <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items, itemtype = '2PL')
anova(mod1, mod1b) # better with 2PL models using all criteria (as expected, given simdata pars)

# continuous predictor with group
mod2 <- mixedmirt(data, covdata, model, fixed = ~ 0 + group + items + pseudoIQ)
summary(mod2)
anova(mod1b, mod2)

# view fixed design matrix with and without unique item level intercepts
withinint <- mixedmirt(data, covdata, model, fixed = ~ 0 + items + group, return.design = TRUE)
withoutint <- mixedmirt(data, covdata, model, fixed = ~ 0 + group, return.design = TRUE)

# notice that in result above, the intercepts 'items1' to items 10' were reassigned to 'd'
```
### random effects

# make the number of groups much larger
covdata$group <- factor(rep(paste0('G',1:50), each = N/50))

# random groups
rmod1 <- mixedmirt(data, covdata, 1, fixed = ~ 0 + items, random = ~ 1|group)
summary(rmod1)
coef(rmod1)

# random groups and random items
rmod2 <- mixedmirt(data, covdata, 1, random = list(~ 1|group, ~ 1|items))
summary(rmod2)
eff <- randef(rmod2) # estimate random effects

# random slopes with fixed intercepts (suppressed correlation)
rmod3 <- mixedmirt(data, covdata, 1, fixed = ~ 0 + items, random = ~ -1 + pseudoIQ|group)
summary(rmod3)
eff <- randef(rmod3)
str(eff)

### LLTM, and 2PL version of LLTM

data(SAT12)
data <- key2binary(SAT12,
  key = c(1,4,5,2,3,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))

model <- 'Theta = 1-32'

# Suppose that the first 16 items were suspected to be easier than the last 16 items, # and we wish to test this item structure hypothesis (more intercept designs are possible # by including more columns).
itemdesign <- data.frame(itemorder = factor(c(rep('easier', 16), rep('harder', 16))))

# notice that the 'fixed = ~ ... + items' argument is omitted
LLTM <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemdesign = itemdesign,
  SE = TRUE) # SE argument ensures that the information matrix is computed accurately
summary(LLTM)
coef(LLTM)
wald(LLTM)
L <- matrix(c(-1, 1, 0), 1)
wald(LLTM, L) # first half different from second

# compare to items with estimated slopes (2PL)
twoPL <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemtype = '2PL',
  itemdesign = itemdesign)

# twoPL not mixing too well (AR should be between .2 and .5), decrease MHcand
twoPL <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, itemtype = '2PL',
  itemdesign = itemdesign, technical = list(MHcand = 0.8))
anova(twoPL, LLTM) #much better fit
summary(twoPL)
coef(twoPL)

wald(twoPL)
L <- matrix(0, 1, 34)
L[1, 1] <- 1
L[1, 2] <- -1
wald(twoPL, L) #n.s., which is the correct conclusion. Rasch approach gave wrong inference

#LLTM with item error term
LLTMwithError <- mixedmirt(data, model = model, fixed = ~ 0 + itemorder, random = ~ 1|items,
itemdesign = itemdesign)
summary(LLTMwithError)
#large item level variance after itemorder is regressed; not a great predictor of item difficulty
coef(LLTMwithError)

###################################################
### Polytomous example
###################################################

#make an arbitrary group difference
covdat <- data.frame(group = rep(c("m", "f"), nrow(Science)/2))

#partial credit model
mod <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group)
coef(mod)

#gpcm to estimate slopes
mod2 <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group,
itemtype = 'gpcm')
summary(mod2)
anova(mod, mod2)

#graded model
mod3 <- mixedmirt(Science, covdat, model=1, fixed = ~ 0 + group,
itemtype = 'graded')
coef(mod3)

###################################################
# latent regression with Rasch and 2PL models

set.seed(1)
n <- 300
a <- matrix(1, 10)
d <- matrix(rnorm(10))
Theta <- matrix(c(rnorm(n, 0), rnorm(n, 1), rnorm(n, 2)))
covdata <- data.frame(group=rep(c('g1', 'g2', 'g3'), each=n))
dat <- simdata(a, d, N=n*3, Theta=Theta, itemtype = '2PL')

#had we known the latent abilities, we could have computed the regression coefs
summary(lm(Theta ~ covdata$group))
# but all we have is observed test data. Latent regression helps to recover these coefs
# Rasch model approach (and mirt equivalent)
rmod0 <- mirt(dat, 1, 'Rasch') # unconditional

# these two models are equivalent
rmod1a <- mirt(dat, 1, 'Rasch', covdata = covdata, formula = ~ group)
rmod1b <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items + group)
aova(rmod0, rmod1b)
coef(rmod1a, simplify=TRUE)
summary(rmod1b)

# 2PL, requires different input to allow Theta variance to remain fixed
mod0 <- mirt(dat, 1) # unconditional
mod1a <- mirt(dat, 1, covdata = covdata, formula = ~ group, itemtype = '2PL')
mod1b <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items, lr.fixed = ~group, itemtype = '2PL')
aova(mod0, mod1b)
coef(mod1a)$lr.betas
summary(mod1b)

# specifying specific regression effects is accomplished by passing a list of formula
model <- c(F1 = 1-5, F2 = 6-10)
covdata$contvar <- rnorm(nrow(covdata))
mod2 <- mirt(dat, model, itemtype = 'Rasch', covdata=covdata, formula = list(F1 = ~ group + contvar, F2 = ~ group))
coef(mod2)[11:12]
mod2b <- mixedmirt(dat, covdata, model, fixed = ~ 0 + items, lr.fixed = list(F1 = ~ group + contvar, F2 = ~ group))
summary(mod2b)

####################################################
## Simulated Multilevel Rasch Model
set.seed(1)
N <- 2000
a <- matrix(rep(1,10),10,1)
d <- matrix(rnorm(10))
covdata$group_pred <- rep(random_intercept, each = N/cluster)
cluster = 100
random_intercept = rnorm(cluster,0,1)
Theta = numeric()
for (i in 1:cluster)
  Theta <- c(Theta, rnorm(N/cluster,0,1) + random_intercept[i])
group = factor(rep(paste0('G',1:cluster), each = N/cluster))
covdata <- data.frame(group)
dat <- simdata(a,d,N, itemtype = rep('2PL',10), Theta=matrix(Theta))

# null model
mod1 <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items, random = ~ 1|group)
summary(mod1)

# include level 2 predictor for 'group' variance
covdata$group_pred <- rep(random_intercept, each = N/cluster)
mod2 <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items + group_pred, random = ~ 1|group)

# including group means predicts nearly all variability in 'group'
summary(mod2)
anova(mod1, mod2)

# can also be fit for Rasch/non-Rasch models with the lr.random input
mod1b <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items, lr.random = ~ 1|group)
summary(mod1b)

mod2b <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items + group_pred, lr.random = ~ 1|group)
summary(mod2b)
anova(mod1b, mod2b)

mod3 <- mixedmirt(dat, covdata, 1, fixed = ~ 0 + items, lr.random = ~ 1|group, itemtype = '2PL')
summary(mod3)
anova(mod1b, mod3)

head(cbind(randef(mod3)$group, random_intercept))

## End(Not run)
mod2values

Methods

  coef signature(object = "MixtureClass")
  print signature(x = "MixtureClass")
  show signature(object = "MixtureClass")
  anova signature(object = "MixtureClass")

Author(s)

  Phil Chalmers <rphilip.chalmers@gmail.com>

References


mod2values

*Convert an estimated mirt model to a data.frame*

Description

  Given an estimated model from any of mirt's model fitting functions this function will convert the model parameters into the design data frame of starting values and other parameter characteristics (similar to using the pars = 'values' for obtaining starting values).

Usage

  mod2values(x)

Arguments

  x  
an estimated model x from the mirt package

Author(s)

  Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

  *extract.mirt*
Examples

```r
## Not run:
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)
values <- mod2values(mod)
values

#use the converted values as starting values in a new model, and reduce TOL
mod2 <- mirt(dat, 1, pars = values, TOL=1e-5)

## End(Not run)
```

multipleGroup

Multiple Group Estimation

Description

multipleGroup performs a full-information maximum-likelihood multiple group analysis for any combination of dichotomous and polytomous data under the item response theory paradigm using either Cai's (2010) Metropolis-Hastings Robbins-Monro (MHRM) algorithm or with an EM algorithm approach. This function may be used for detecting differential item functioning (DIF), thought the DIF function may provide a more convenient approach. If the grouping variable is not specified then the dentype input can be modified to fit mixture models to estimate any latent group components.

Usage

```r
multipleGroup(
  data,
  model,
  group,
  invariance = "",
  method = "EM",
  dentype = "Gaussian",
  ...
)
```

Arguments

data a matrix or data.frame that consists of numerically ordered data, with missing data coded as NA
model string to be passed to, or a model object returned from, mirt.model declaring how the global model is to be estimated (useful to apply constraints here)
group a character or factor vector indicating group membership. If a character vector is supplied this will be automatically transformed into a factor variable. As well, the first level of the (factorized) grouping variable will be treated as the "reference" group
invariance a character vector containing the following possible options:
  'free_mean' or 'free_means' freely estimate all latent means in all focal groups
  (reference group constrained to a vector of 0’s)
  'free_var', 'free_vars', 'free_variance', or 'free_variances' freely estimate all latent variances in focal groups (reference group variances all constrained to 1)
  'slopes' to constrain all the slopes to be equal across all groups
  'intercepts' to constrain all the intercepts to be equal across all groups, note for nominal models this also includes the category specific slope parameters
  Additionally, specifying specific item name bundles (from colnames(data)) will constrain all freely estimated parameters in each item to be equal across groups. This is useful for selecting 'anchor' items for vertical and horizontal scaling, and for detecting differential item functioning (DIF) across groups

method a character object that is either 'EM', 'QMEM', or 'MHRM' (default is 'EM'). See mirt for details

dentype type of density form to use for the latent trait parameters. Current options include all of the methods described in mirt, as well as
  • 'mixture-#' estimates mixtures of Gaussian distributions, where the # placeholder represents the number of potential grouping variables (e.g., 'mixture-3' will estimate 3 underlying classes). Each class is assigned the group name MIXTURE_#, where # is the class number. Note that internally the mixture coefficients are stored as log values where the first mixture group coefficient is fixed at 0

... additional arguments to be passed to the estimation engine. See mirt for details and examples

Details

By default the estimation in multipleGroup assumes that the models are maximally independent, and therefore could initially be performed by sub-setting the data and running identical models with mirt and aggregating the results (e.g., log-likelihood). However, constrains may be automatically imposed across groups by invoking various invariance keywords. Users may also supply a list of parameter equality constraints to by constrain argument, of define equality constraints using the mirt.model syntax (recommended).

Value

function returns an object of class MultipleGroupClass (MultipleGroupClass-class).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

See Also

mirt, DIF, extract.group, DRF

Examples

## Not run:

# single factor
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('2PL', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
models <- 'F1 = 1-15'
mod_configural <- multipleGroup(dat, models, group = group) # completely separate analyses
# limited information fit statistics
M2(mod_configural)

mod_metric <- multipleGroup(dat, models, group = group, invariance=c('slopes')) # equal slopes
# equal intercepts, free variance and means
mod_scalar2 <- multipleGroup(dat, models, group = group,
invariance=c('slopes', 'intercepts', 'free_var', 'free_means'))
mod_scalar1 <- multipleGroup(dat, models, group = group, # fixed means
invariance=c('slopes', 'intercepts', 'free_var'))
mod_fullconstrain <- multipleGroup(dat, models, group = group,
invariance=c('slopes', 'intercepts'))
extract.mirt(mod_fullconstrain, 'time') # time of estimation components

# optionally use Newton-Raphson for (generally) faster convergence in the M-step's
mod_fullconstrain <- multipleGroup(dat, models, group = group, optimizer = 'NR',
invariance=c('slopes', 'intercepts'))
extract.mirt(mod_fullconstrain, 'time') # time of estimation components

summary(mod_scalar2)
coef(mod_scalar2, simplify=TRUE)
residuals(mod_scalar2)
plot(mod_configural)
plot(mod_configural, type = 'info')
plot(mod_configural, type = 'trace')
plot(mod_configural, type = 'trace', which.items = 1:4)
itemplot(mod_configural, 2)
itemplot(mod_configural, 2, type = 'RE')

anova(mod_metric, mod_configural) # equal slopes only
anova(mod_scalar2, mod_metric) # equal intercepts, free variance and mean
anova(mod_scalar1, mod_scalar2) # fix mean
anova(mod_fullconstrain, mod_scalar1) # fix variance
#test whether first 6 slopes should be equal across groups
values <- multipleGroup(dat, models, group = group, pars = 'values')
values
constrain <- list(c(1, 63), c(5,67), c(9,71), c(13,75), c(17,79), c(21,83))
equalslopes <- multipleGroup(dat, models, group = group, constrain = constrain)
anova(equalslopes, mod_configural)

#same as above, but using mirt.model syntax
newmodel <- '
  F = 1-15
  CONSTRAINTB = (1-6, a1)'
equalslopes <- multipleGroup(dat, newmodel, group = group)
coef(equalslopes, simplify=TRUE)

########################
# vertical scaling (i.e., equating when groups answer items others do not)
dat2 <- dat
head(dat2)
tail(dat2)

# items with missing responses need to be constrained across groups for identification
nms <- colnames(dat2)
mod <- multipleGroup(dat2, 1, group, invariance = nms[c(1:2, 14:15)])

# this will throw an error without proper constraints (SEs cannot be computed either)
# mod <- multipleGroup(dat2, 1, group)

# model still does not have anchors, therefore need to add a few (here use items 3-5)
mod_anchor <- multipleGroup(dat2, 1, group,
  invariance = c(nms[c(1:5, 14:15)], 'free_means', 'free_var'))
coef(mod_anchor, simplify=TRUE)

# check if identified by computing information matrix
mod_anchor <- multipleGroup(dat2, 1, group, pars = mod2values(mod_anchor), TOL=NaN, SE=TRUE,
  invariance = c(nms[c(1:5, 14:15)], 'free_means', 'free_var'))
mod_anchor
coef(mod_anchor)
coef(mod_anchor, printSE=TRUE)

########################
#DIF test for each item (using all other items as anchors)
itemnames <- colnames(dat)
refmodel <- multipleGroup(dat, models, group = group, SE=TRUE,
  invariance=c('free_means', 'free_var', itemnames))

#loop over items (in practice, run in parallel to increase speed). May be better to use ?DIF
estmodels <- vector('list', ncol(dat))
for(i in 1:ncol(dat))
estmodels[[i]] <- multipleGroup(dat, models, group = group, verbose = FALSE, calcNull=FALSE,
multipleGroup

invariance=c('free_means', 'free_var', itemnames[-i]))

(anozas <- lapply(estmodels, anova, object2=refmodel, verbose=FALSE))

#family-wise error control
p <- do.call(rbind, lapply(anozas, function(x) x[2, 'p']))
p.adjust(p, method = 'BH')

#same as above, except only test if slopes vary (1 df)
#constrain all intercepts
estmodels <- vector('list', ncol(dat))
for(i in 1:ncol(dat))
estmodels[[i]] <- multipleGroup(dat, models, group = group, verbose = FALSE, calcNull=FALSE,
invariance=c('free_means', 'free_var', intercepts, itemnames[-i]))

(anozas <- lapply(estmodels, anova, object2=refmodel, verbose=FALSE))

#quickly test with Wald test using DIF()
mod_configural2 <- multipleGroup(dat, models, group = group, SE=TRUE)
DIF(mod_configural2, which.par = c('a1', 'd'), Wald=TRUE, p.adjust = 'fdr')

#multiple factors

a <- matrix(c(abs(rnorm(5,1,.3)), rep(0,15), abs(rnorm(5,1,.3)),
             rep(0,15), abs(rnorm(5,1,.3))), 15, 3)
d <- matrix(rnorm(15,0,.7), ncol=1)
mu <- c(-.4, -.7, .1)
sigma <- matrix(c(1.21, .297, 1.232, .297, .81, .252, 1.232, .252, 1.96),3,3)
itemtype <- rep('2PL', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = mu, sigma = sigma)
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))

#group models
model <- '
F1 = 1-5
F2 = 6-10
F3 = 11-15'

#define mirt cluster to use parallel architecture
mirtCluster()

#EM approach (not as accurate with 3 factors, but generally good for quick model comparisons)
mod_configural <- multipleGroup(dat, model, group = group) #completely separate analyses
mod_metric <- multipleGroup(dat, model, group = group, invariance=c('slopes')) #equal slopes
mod_fullconstrain <- multipleGroup(dat, model, group = group, #equal means, slopes, intercepts
        invariance=c('slopes', 'intercepts'))

anova(mod_metric, mod_configural)
anova(mod_fullconstrain, mod_metric)

#same as above, but with MHRM (generally more accurate with 3+ factors, but slower)
mod_configural <- multipleGroup(dat, model, group = group, method = 'MHRM')
mod_metric <- multipleGroup(dat, model, group = group, invariance=c('slopes'), method = 'MHRM')
mod_fullconstrain <- multipleGroup(dat, model, group = group, method = 'MHRM',
    invariance=c('slopes', 'intercepts'))

anova(mod_metric, mod_configural)
anova(mod_fullconstrain, mod_metric)

#################################################################
#polytomous item example
set.seed(12345)
a <- matrix(abs(rnorm(15,1,.3)), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
d <- cbind(d, d-1, d-2)
itemtype <- rep('graded', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, mu = .1, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
model <- 'F1 = 1-15'

mod_configural <- multipleGroup(dat, model, group = group)
plot(mod_configural)
plot(mod_configural, type = 'SE')
itemplot(mod_configural, 1)
itemplot(mod_configural, 1, type = 'info')
plot(mod_configural, type = 'trace') # messy, score function typically better
plot(mod_configural, type = 'itemscore')

fs <- fscores(mod_configural, full.scores = FALSE)
head(fs["D1"[:]])
fscores(mod_configural, method = 'EAPsum', full.scores = FALSE)

# constrain slopes within each group to be equal (but not across groups)
model2 <- 'F1 = 1-15
    CONSTRAINT = (1-15, a1)'
mod_configural2 <- multipleGroup(dat, model2, group = group)
plot(mod_configural2)
plot(mod_configural2, type = 'SE')
itemplot(mod_configural2, 10)

####################
## empirical histogram example (normal and bimodal groups)
set.seed(1234)
a <- matrix(rlnorm(50, .2, .2))
d <- matrix(rnorm(50))
ThetaNormal <- matrix(rnorm(2000))
ThetaBimodal <- scale(matrix(c(rnorm(1000, -2), rnorm(1000, 2)))) #bimodal
Theta <- rbind(ThetaNormal, ThetaBimodal)
dat <- simdata(a, d, 4000, itemtype = '2PL', Theta=Theta)
group <- rep(c('G1', 'G2'), each=2000)

EH <- multipleGroup(dat, 1, group=group, dentity="empiricalhist", invariance = colnames(dat))
coef(EH, simplify=TRUE)
plot(EH, type = 'empiricalhist', npts = 60)

# DIF test for item 1
EH1 <- multipleGroup(dat, 1, group=group, dentity="empiricalhist", invariance = colnames(dat)[-1])
anova(EH, EH1)

#--------------------------------
# Mixture model (no prior group variable specified)
set.seed(12345)
nitems <- 20
a1 <- matrix(.75, ncol=1, nrow=nitems)
a2 <- matrix(1.25, ncol=1, nrow=nitems)
d1 <- matrix(rnorm(nitems,0,1),ncol=1)
d2 <- matrix(rnorm(nitems,0,1),ncol=1)
itemtype <- rep('2PL', nrow(a1))
N1 <- 500
N2 <- N1*2 # second class twice as large
dataset1 <- simdata(a1, d1, N1, itemtype)
dataset2 <- simdata(a2, d2, N2, itemtype)
dat <- rbind(dataset1, dataset2)
# group <- c(rep('D1', N1), rep('D2', N2))

# Mixture Rasch model (Rost, 1990)
models <- 'F1 = 1-20
                     CONSTRAIN = (1-20, a1)'
mod_mix <- multipleGroup(dat, models, dentity = 'mixture-2', GenRandomPars = TRUE)
coef(mod_mix, simplify=TRUE)
summary(mod_mix)
plot(mod_mix)
plot(mod_mix, type = 'trace')
itemplot(mod_mix, 1, type = 'info')

head(fscores(mod_mix)) # theta estimates
head(fscores(mod_mix, method = 'classify')) # classification probability
itemfit(mod_mix)

# Mixture 2PL model
mod_mix2 <- multipleGroup(dat, 1, dentity = 'mixture-2', GenRandomPars = TRUE)
anova(mod_mix2, mod_mix)
coef(mod_mix2, simplify=TRUE)
itemfit(mod_mix2)

# Zero-inflated 2PL IRT model
model <- "F = 1-20
START [MIXTURE_1] = (GROUP, MEAN_1, -100), (GROUP, COV_11, .00001),
(1-20, a1, 1.0), (1-20, d, 0.0)"
**MultipleGroupClass-class**

**Fixed**

```r
FIXED \langle \text{MIXTURE}_1 \rangle = (\text{GROUP}, \text{MEAN}_1), (\text{GROUP}, \text{COV}_{11}),
(1-20, a_1), (1-20, d)"
```

```r
zip <- multipleGroup(dat, model, dentity = 'mixture-2')
coef(zip, simplify=TRUE)
```

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

---

**MultipleGroupClass-class**

**Class** "MultipleGroupClass"

---

**Description**

Defines the object returned from `multipleGroup`.

**Slots**

- **Call**: function call
- **Data**: list of data, sometimes in different forms
- **Options**: list of estimation options
- **Fit**: a list of fit information
- **Model**: a list of model-based information
- **ParObjects**: a list of the S4 objects used during estimation
- **OptimInfo**: a list of arguments from the optimization process
- **Internals**: a list of internal arguments for secondary computations (inspecting this object is generally not required)
- **vcov**: a matrix represented the asymptotic covariance matrix of the parameter estimates
- **time**: a data.frame indicating the breakdown of computation times in seconds

**Methods**

- **coef** signature(object = "MultipleGroupClass")
- **print** signature(x = "MultipleGroupClass")
- **show** signature(object = "MultipleGroupClass")
- **anova** signature(object = "MultipleGroupClass")

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**

compute numerical derivatives using forward/backward difference, central difference, or Richardson extrapolation.

Usage

numerical_deriv(
    f,
    par,
    ...,
    delta = 1e-05,
    gradient = TRUE,
    type = "Richardson"
)

Arguments

f                  the objective function being evaluated
par                a vector of parameters
                    additional arguments to be passed to f
delta              the term used to perturb the f function. Default is 1e-5
gradient           logical; compute the gradient terms? If FALSE then the Hessian is computed instead
                    type of difference to compute. Can be either 'forward' for the forward difference, 'central' for the central difference, or 'Richardson' for the Richardson extrapolation (default). Backward difference is achieved by supplying a negative delta value with 'forward'. When type = 'Richardson', the default value of delta is increased to delta * 1000 for the Hessian and delta * 10 for the gradient to provide a reasonable perturbation starting location (each delta is halved at each iteration).

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

Examples

## Not run:
f <- function(x) 3*x[1]^3 - 4*x[2]^2
par <- c(3,8)
personfit

# grad = 9 * x^2 , -8 * y
(actual <- c(9 * par[1]^2, -8 * par[2]))
numerical_deriv(f, par, type = 'forward')
numerical_deriv(f, par, type = 'central')
numerical_deriv(f, par, type = 'Richardson') # default

# Hessian = h11 -> 18 * x, h22 -> -8, h12 -> h21 -> 0
(actual <- matrix(c(18 * par[1], 0, 0, -8), 2, 2))
numericalderiv(f, par, type = 'forward', gradient = FALSE)
numerical_deriv(f, par, type = 'central', gradient = FALSE)
numerical_deriv(f, par, type = 'Richardson', gradient = FALSE) # default

## End(Not run)

---

personfit **Person fit statistics**

**Description**

personfit calculates the Zh values from Drasgow, Levine and Williams (1985) for unidimensional and multidimensional models, as well as the infit and outfit statistics. The returned object is a data.frame consisting either of the tabulated data or full data with the statistics appended to the rightmost columns.

**Usage**

personfit(x, method = "EAP", Theta = NULL, stats.only = TRUE, ...)

**Arguments**

- **x**
  - a computed model object of class SingleGroupClass or MultipleGroupClass
- **method**
  - type of factor score estimation method. See fscores for more detail
- **Theta**
  - a matrix of factor scores used for statistics that require empirical estimates. If supplied, arguments typically passed to fscores() will be ignored and these values will be used instead
- **stats.only**
  - logical; return only the person fit statistics without their associated response pattern?
- **...**
  - additional arguments to be passed to fscores()

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>
References


See Also

* itemfit

Examples

```r
## Not run:

#make some data
set.seed(1)
a <- matrix(rlnorm(20),ncol=1)
d <- matrix(rnorm(20),ncol=1)
items <- rep('2PL', 20)
data <- simdata(a,d, 2000, items)

x <- mirt(data, 1)
fit <- personfit(x)
head(fit)

#using precomputed Theta
Theta <- fscores(x, method = 'MAP', full.scores = TRUE)
head(personfit(x, Theta=Theta))

#multiple group Rasch model example
set.seed(12345)
a <- matrix(rep(1, 15), ncol=1)
d <- matrix(rnorm(15,0,.7),ncol=1)
itemtype <- rep('dich', nrow(a))
N <- 1000
dataset1 <- simdata(a, d, N, itemtype)
dataset2 <- simdata(a, d, N, itemtype, sigma = matrix(1.5))
dat <- rbind(dataset1, dataset2)
group <- c(rep('D1', N), rep('D2', N))
models <- 'F1 = 1-15'
mod_Rasch <- multipleGroup(dat, models, itemtype = 'Rasch', group = group)
coef(mod_Rasch, simplify=TRUE)
pf <- personfit(mod_Rasch, method='MAP')
head(pf)
```
PLCI.mirt

Compute profiled-likelihood (or posterior) confidence intervals

Description

Computes profiled-likelihood based confidence intervals. Supports the inclusion of equality constraints. Object returns the confidence intervals and whether the respective interval could be found.

Usage

PLCI.mirt(
  mod,
  parnum = NULL,
  alpha = 0.05,
  search_bound = TRUE,
  step = 0.5,
  lower = TRUE,
  upper = TRUE,
  inf2val = 30,
  NealeMiller = FALSE,
  ...
)

Arguments

mod a converged mirt model
parnum a numeric vector indicating which parameters to estimate. Use mod2values to determine parameter numbers. If NULL, all possible parameters are used
alpha two-tailed alpha critical level
search_bound logical; use a fixed grid of values around the ML estimate to determine more suitable optimization bounds? Using this has much better behaviour than setting fixed upper/lower bound values and searching from more extreme ends
step magnitude of steps used when search_bound is TRUE. Smaller values create more points to search a suitable bound for (up to the lower bound value visible with mod2values). When upper/lower bounds are detected this value will be adjusted accordingly
lower logical; search for the lower CI?
upper logical; search for the upper CI?
inf2val a numeric used to change parameter bounds which are infinity to a finite number. Decreasing this too much may not allow a suitable bound to be located. Default is 30
NealeMiller logical; use the Neale and Miller 1997 approximation? Default is FALSE
... additional arguments to pass to the estimation functions
Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


See Also

`boot.mirt`

Examples

```r
## Not run:
mirtCluster() #use all available cores to estimate CI's in parallel
dat <- expand.table(LSAT7)
mod <- mirt(dat, 1)

result <- PLCI.mirt(mod)
result

# model with constraints
mod <- mirt(dat, 'F = 1-5
    CONSTRAIN = (1-5, a1)')

result <- PLCI.mirt(mod)
result

mod2 <- mirt(Science, 1)
result2 <- PLCI.mirt(mod2)
result2

#only estimate CI's slopes
sv <- mod2values(mod2)
parnum <- sv$parnum[sv$name == 'a1']
result3 <- PLCI.mirt(mod2, parnum)
result3

## End(Not run)
```
Description

Plot various test implied response functions from models estimated in the mirt package.

Usage

```r
## S4 method for signature 'SingleGroupClass,missing'
plot(
  x,
  y,
  type = "score",
  npts = 200,
  degrees = 45,
  theta_lim = c(-6, 6),
  which.items = 1:extract.mirt(x, "nitems"),
  MI = 0,
  CI = 0.95,
  rot = list(xaxis = -70, yaxis = 30, zaxis = 10),
  facet_items = TRUE,
  main = NULL,
  drape = TRUE,
  colorkey = TRUE,
  ehist.cut = 1e-10,
  add.ylab2 = TRUE,
  par.strip.text = list(cex = 0.7),
  par.settings = list(strip.background = list(col = "#9ECAE1"), strip.border = list(col = "black")),
  auto.key = list(space = "right", points = FALSE, lines = TRUE),
  profile = FALSE,
  ...
)
```

Arguments

- `x`: an object of class SingleGroupClass, MultipleGroupClass, or DiscreteClass
- `y`: an arbitrary missing argument required for R CMD check
- `type`: type of plot to view. Can be
  - 'info' for test information function
  - 'rxx' for the reliability function
  - 'infocontour' for the test information contours
  - 'SE' for the test standard error function
  - 'infotrace' for item information traceline plots
'infoSE' a combined test information and standard error plot
'trace' item probability traceline plots
'itemscore' item scoring traceline plots
'score' expected total score surface
'scorecontour' expected total score contour plot

Note that if dentype = 'empiricalhist' was used in estimation then the type 'empiricalhist' also will be available to generate the empirical histogram plot, and if dentype = 'Davidian-' was used then the type 'Davidian' will also be available to generate the curve estimates at the quadrature nodes used during estimation

npts number of quadrature points to be used for plotting features. Larger values make plots look smoother

degrees numeric value ranging from 0 to 90 used in plot to compute angle for information-based plots with respect to the first dimension. If a vector is used then a bubble plot is created with the summed information across the angles specified (e.g., degrees = seq(0,90,by=10))

theta_lim lower and upper limits of the latent trait (theta) to be evaluated, and is used in conjunction with npts

which.items numeric vector indicating which items to be used when plotting. Default is to use all available items

MI a single number indicating how many imputations to draw to form bootstrapped confidence intervals for the selected test statistic. If greater than 0 a plot will be drawn with a shaded region for the interval

CI a number from 0 to 1 indicating the confidence interval to select when MI input is used. Default uses the 95% confidence (CI = .95)

rot allows rotation of the 3D graphics

facet.items logical; apply grid of plots across items? If FALSE, items will be placed in one plot for each group

main argument passed to lattice. Default generated automatically

drape logical argument passed to lattice. Default generated automatically

colorkey logical argument passed to lattice. Default generated automatically

ehist.cut a probability value indicating a threshold for excluding cases in empirical histogram plots. Values larger than the default will include more points in the tails of the plot, potentially squishing the 'meat' of the plot to take up less area than visually desired

add.ylab2 logical argument passed to lattice. Default generated automatically

par.strip.text plotting argument passed to lattice

par.settings plotting argument passed to lattice

auto.key plotting argument passed to lattice

profile logical: provide a profile plot of response probabilities (objects returned from mdirt only)

... additional arguments to be passed to lattice
Examples

```r
## Not run:
x <- mirt(Science, 1, SE=TRUE)
plot(x)
plot(x, type = 'info')
plot(x, type = 'infotrace')
plot(x, type = 'infotrace', facet_items = FALSE)
plot(x, type = 'infoSE')
plot(x, type = 'rxx')

# confidence interval plots when information matrix computed
plot(x)
plot(x, MI=100)
plot(x, type='info', MI=100)
plot(x, type='SE', MI=100)
plot(x, type='rxx', MI=100)

# use the directlabels package to put labels on tracelines
library(directlabels)
plt <- plot(x, type = 'trace')
direct.label(plt, 'top.points')

set.seed(1234)
group <- sample(c('g1', 'g2'), nrow(Science), TRUE)
x2 <- multipleGroup(Science, 1, group)
plot(x2)
plot(x2, type = 'trace')
plot(x2, type = 'trace', which.items = 1:2)
plot(x2, type = 'itemscore', which.items = 1:2)
plot(x2, type = 'trace', which.items = 1, facet_items = FALSE) # facet by group
plot(x2, type = 'info')

x3 <- mirt(Science, 2)
plot(x3, type = 'info')
plot(x3, type = 'SE', theta_lim = c(-3,3))

## End(Not run)
```
**Description**

Transforms a matrix of items into a new matrix where the select polytomous items have been converted into comparable dichotomous items with the same information.

**Usage**

```r
poly2dich(data, which.items = 1:ncol(data))
```

**Arguments**

- `data`: an object of class `data.frame` or `matrix`

- `which.items`: a vector indicating which items should be transformed into the dichotomous form. Default uses all input items

**Value**

Returns an integer matrix

**Author(s)**

Phil Chalmers <rphilip.chalmers@gmail.com>

**References**


**Examples**

```r
## Not run:
data(Science)

head(Science)
newScience <- poly2dich(Science)
head(newScience)

newScience2 <- poly2dich(Science, which.items = 2)
head(newScience2)

## End(Not run)
```
print-method

Print the model objects

Description

Print model object summaries to the console.

Usage

## S4 method for signature 'SingleGroupClass'
print(x)

Arguments

x an object of class SingleGroupClass, MultipleGroupClass, or MixedClass

References


Examples

## Not run:
x <- mirt(Science, 1)
print(x)
## End(Not run)

print.mirt_df

Print generic for customized data.frame console output

Description

Provides a nicer output for most printed data.frame objects defined by functions in mirt.

Usage

## S3 method for class 'mirt_df'
print(x, digits = 3, ...)

Arguments

x object of class 'mirt_df'
digits number of digits to round
... additional arguments passed to print(...)
### Description

Provides a nicer output for most printed list objects defined by functions in `mirt`.

### Usage

```r
## S3 method for class 'mirt_list'
print(x, digits = 3, ...)
```

### Arguments

- `x`: object of class 'mirt_list'
- `digits`: number of digits to round
- `...`: additional arguments passed to `print(...)`

### Description

Provides a nicer output for most printed matrix objects defined by functions in `mirt`.

### Usage

```r
## S3 method for class 'mirt_matrix'
print(x, digits = 3, ...)
```

### Arguments

- `x`: object of class 'mirt_matrix'
- `digits`: number of digits to round
- `...`: additional arguments passed to `print(...)`
Function to calculate probability trace lines

Description
Given an internal mirt object extracted from an estimated model, or the single-group estimated model itself, compute the probability trace lines for all categories.

Usage
probtrace(x, Theta)

Arguments
- x: either an extracted internal mirt object containing item information (see `extract.item`) or a model of class SingleGroupClass typically returned by the function `mirt` or `bfactor`
- Theta: a vector (unidimensional) or matrix (unidimensional/multidimensional) of latent trait values

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

References

See Also
`extract.item`, `extract.group`

Examples

```r
mod <- mirt(Science, 1)

# single item probability tracelines for Item 2
eextr.2 <- extract.item(mod, 2)
Theta <- matrix(seq(-4, 4, by = .1))
traceline <- probtrace(extr.2, Theta)
head(data.frame(traceline, Theta=Theta))

# probability tracelines for all items in test
tracelines <- probtrace(mod, Theta)
head(tracelines)
```
randef

Compute posterior estimates of random effect

Description
Stochastically compute random effects for MixedClass objects with Metropolis-Hastings samplers and averaging over the draws. Returns a list of the estimated effects.

Usage
randef(x, ndraws = 1000, thin = 10, return.draws = FALSE)

Arguments
- x: an estimated model object from the mixedmirt function
- ndraws: total number of draws to perform. Default is 1000
- thin: amount of thinning to apply. Default is to use every 10th draw
- return.draws: logical; return a list containing the thinned draws of the posterior?

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

References

Examples
## Not run:
#make an arbitrary groups
covdat <- data.frame(group = rep(paste0('group', 1:49), each=nrow(Science)/49))

#partial credit model
mod <- mixedmirt(Science, covdat, model=1, random = ~ 1|group)
summary(mod)

effects <- randef(mod, ndraws = 2000, thin = 20)
head(effects$Theta)
head(effects$group)

## End(Not run)
Description

Return model implied residuals for linear dependencies between items or at the person level. If the latent trait density was approximated (e.g., Davidian curves, Empirical histograms, etc) then passing use_dentype_estimate = TRUE will use the internally saved quadrature and density components (where applicable).

Usage

```r
## S4 method for signature 'SingleGroupClass'
residuals(
  object,
  type = "LD",
  df.p = FALSE,
  full.scores = FALSE,
  QMC = FALSE,
  printvalue = NULL,
  tables = FALSE,
  verbose = TRUE,
  Theta = NULL,
  suppress = 1,
  theta_lim = c(-6, 6),
  quadpts = NULL,
  fold = TRUE,
  technical = list(),
  ...
)
```

Arguments

- `object`: an object of class SingleGroupClass or MultipleGroupClass. Bifactor models are automatically detected and utilized for better accuracy.
- `type`: type of residuals to be displayed. Can be either 'LD' or 'LDG2' for a local dependence matrix based on the X2 or G2 statistics (Chen & Thissen, 1997), 'Q3' for the statistic proposed by Yen (1984), 'JSI' for the jack-knife statistic proposed Edwards et al. (2018), 'exp' for the expected values for the frequencies of every response pattern, and 'expfull' for the expected values for every theoretically observable response pattern. For the 'LD' and 'LDG2' types, the upper diagonal elements represent the standardized residuals in the form of signed Cramers V coefficients.
- `df.p`: logical; print the degrees of freedom and p-values?
- `full.scores`: logical; compute relevant statistics for each subject in the original data?
QMC logical; use quasi-Monte Carlo integration? If quadpts is omitted the default number of nodes is 5000
printvalue a numeric value to be specified when using the res='exp' option. Only prints patterns that have standardized residuals greater than abs(printvalue). The default (NULL) prints all response patterns
tables logical; for LD type, return the observed, expected, and standardized residual tables for each item combination?
verbose logical; allow information to be printed to the console?
Theta a matrix of factor scores used for statistics that require empirical estimates (i.e., Q3). If supplied, arguments typically passed to fscores() will be ignored and these values will be used instead
suppress a numeric value indicating which parameter local dependency combinations to flag as being too high. Absolute values for the standardized estimates greater than this value will be returned, while all values less than this value will be set to NA
theta_lim range for the integration grid
quadpts number of quadrature nodes to use. The default is extracted from model (if available) or generated automatically if not available
fold logical; apply the sum 'folding' described by Edwards et al. (2018) for the JSI statistic?
technical list of technical arguments when models are re-estimated (see mirt for details)
... additional arguments to be passed to fscores()

References


Examples

```r
## Not run:
x <- mirt(Science, 1)
residuals(x)
residuals(x, tables = TRUE)
residuals(x, type = 'exp')
residuals(x, suppress = .15)
residuals(x, df.p = TRUE)
```
# Pearson's X2 estimate for goodness-of-fit
full_table <- residuals(x, type = 'expfull')
head(full_table)
X2 <- with(full_table, sum((freq - exp)^2 / exp))
df <- nrow(full_table) - extract.mirt(x, 'nest') - 1
p <- pchisq(X2, df = df, lower.tail=FALSE)
data.frame(X2, df, p, row.names='Pearson-X2')

# above FOG test as a function
PearsonX2 <- function(x){
    full_table <- residuals(x, type = 'expfull')
    X2 <- with(full_table, sum((freq - exp)^2 / exp))
    df <- nrow(full_table) - extract.mirt(x, 'nest') - 1
    p <- pchisq(X2, df = df, lower.tail=FALSE)
    data.frame(X2, df, p, row.names='Pearson-X2')
}
PearsonX2(x)

# extract results manually
out <- residuals(x, df.p = TRUE, verbose=FALSE)
str(out)
out$df.p[1,2]

# with and without supplied factor scores
Theta <- fscores(x)
residuals(x, type = 'Q3', Theta=Theta)
residuals(x, type = 'Q3', method = 'ML')

# Edwards et al. (2018) JSI statistic
N <- 250
a <- rnorm(10, 1.7, 0.3)
d <- rnorm(10)
dat <- simdata(a, d, N=250, itemtype = '2PL')
mod <- mirt(dat, 1)
residuals(mod, type = 'JSI')
residuals(mod, type = 'JSI', fold=FALSE) # unfolded

# LD between items 1-2
aLD <- numeric(10)
aLD[1:2] <- rnorm(2, 2.55, 0.15)
a2 <- cbind(a, aLD)
dat <- simdata(a2, d, N=250, itemtype = '2PL')
mod <- mirt(dat, 1)

# JSI executed in parallel over multiple cores
mirtCluster()
residuals(mod, type = 'JSI')

## End(Not run)
Description

Data obtained from the TESTFACT (Woods et al., 2003) manual, with 32 response pattern scored items for a grade 12 science assessment test (SAT) measuring topics of chemistry, biology, and physics. The scoring key for these data is [1, 4, 5, 2, 3, 1, 2, 1, 3, 1, 2, 4, 2, 1, 5, 3, 4, 4, 1, 4, 3, 3, 4, 1, 3, 5, 1, 3, 1, 5, 4, 5], respectively. However, careful analysis using the nominal response model suggests that the scoring key for item 32 may be incorrect, and should be changed from 5 to 3.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
#score the data (missing scored as 0)
head(SAT12)
data <- key2binary(SAT12,
   key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
head(data)

#score the data, missing (value of 8) treated as NA
SAT12missing <- SAT12
SAT12missing[SAT12missing == 8] <- NA
data <- key2binary(SAT12missing,
   key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,5))
head(data)

#potentially better scoring for item 32 (based on nominal model finding)
data <- key2binary(SAT12,
   key = c(1,4,5,2,3,1,2,1,3,1,2,4,2,1,5,3,4,4,1,4,3,3,4,1,3,5,1,3,1,5,4,3))
## End(Not run)
```
Description

A 4-item data set borrowed from ltm package in R, first example of the grm() function. See more complete documentation therein.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
mod <- mirt(Science, 1)
plot(mod, type = 'trace')

## End(Not run)
```

show-method

Show model object

Description

Print model object summaries to the console.

Usage

```r
## S4 method for signature 'SingleGroupClass'
show(object)
```

Arguments

- **object**
  - an object of class `SingleGroupClass`, `MultipleGroupClass`, or `MixedClass`

References

Examples

```r
## Not run:
x <- mirt(Science, 1)
show(x)

## End(Not run)
```

---

SIBTEST

**Simultaneous Item Bias Test (SIBTEST)**

Description

Classical test theory approach to detecting unidirectional and bidirectional (with one crossing location) DIF. This family of statistics is intended for unidimensional tests, and applies a regression-corrected matched-total score approach to quantify the response bias between two groups. Can be used for DIF, DBF, and DTF testing.

Usage

```r
SIBTEST(
  dat,
  group,
  suspect_set,
  match_set,
  focal_name = unique(group)[2],
  guess_correction = 0,
  Jmin = 5,
  na.rm = FALSE,
  LiStout1996 = FALSE,
  permute = 1000,
  pk_focal = FALSE,
  correction = TRUE,
  details = FALSE,
  plot = "none",
  ...
)
```

Arguments

- **dat**: integer-based dataset to be tested, containing dichotomous or polytomous responses
- **group**: a vector indicating group membership with the same length as the number of rows in `dat`
suspect_set an integer vector indicating which items to inspect with SIBTEST. Including only one value will perform a DIF test, while including more than one will perform a simultaneous bundle test (DBF); including all non-matched items will perform DTF. If missing, a simultaneous test using all the items not listed in match_set will be used (i.e., DTF)

match_set an integer vector indicating which items to use as the items which are matched (i.e., contain no DIF). These are analogous to 'anchor' items in the likelihood method to locate DIF. If missing, all items other than the items found in the suspect_set will be used

focal_name name of the focal group; e.g., 'focal'. If not specified then one will be selected automatically using unique(group)[2]

guess_correction a vector of numbers from 0 to 1 indicating how much to correct the items for guessing. It’s length should be the same as ncol(dat)

Jmin the minimum number of observations required when splitting the data into focal and reference groups conditioned on the matched set

na.rm logical; remove rows in dat with any missing values? If TRUE, rows with missing data will be removed, as well as the corresponding elements in the group input

LiStout1996 logical; perform the crossing test for non-compensatory bias using Li and Stout’s (1996) permutation approach? Default is FALSE, which uses the Chalmers (2018) mixed degrees of freedom method

permute number of permutations to perform when LiStout1996 = TRUE. Default is 1000

pk_focal logical; using the group weights from the focal group instead of the total sample? Default is FALSE as per Shealy and Stout’s recommendation

correction logical; apply the composite correction for the difference between focal composite scores using the true-score regression technique? Default is TRUE, reflecting Shealy and Stout’s linear extrapolation method

details logical; return a data.frame containing the details required to compute SIBTEST?

plot a character input indicating the type of plot to construct. Options are 'none' (default), 'observed' for the scaled focal subtest scores against the matched subtest scores, 'weights' for the proportion weights used (i.e., the proportion of observations at each matched score), 'difference' for the difference between the scaled focal subtest scores against the matched subtest scores, and 'wdifference' for the conditional differences multiplied by each respective weight. Note that the last plot reflects the components used in SIBTEST, and therefore the sum of these plotted observations will equal the beta coefficient for SIBTEST

... additional plotting arguments to be passed

Details

SIBTEST is similar to the Mantel-Haenszel approach for detecting DIF but uses a regression correction based on the KR-20/coefficient alpha reliability index to correct the observed differences when the latent trait distributions are not equal. Function supports the standard SIBTEST for
dichotomous and polytomous data (compensatory) and supports crossing DIF testing (i.e., non-compensatory/non-uniform) using the asymptotic sampling distribution version of the Crossing-SIBTEST (CSIBTEST) statistic described by Chalmers (2018) and the permutation method described by Li and Stout (1996). For convenience, the beta coefficient for CSIBTEST is always reported as an absolute value.

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
set.seed(1234)
n <- 30
N <- 500
a <- matrix(1, n)
d <- matrix(rnorm(n), n)
group <- c(rep('reference', N), rep('focal', N*2))

## ---------------
# groups completely equal
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a, d, N*2, itemtype = 'dich')
dat <- rbind(dat1, dat2)

# DIF (all other items as anchors)
SIBTEST(dat, group, suspect_set = 6)

# Some plots depicting the above tests
SIBTEST(dat, group, suspect_set = 6, plot = 'observed')
SIBTEST(dat, group, suspect_set = 6, plot = 'weights')
SIBTEST(dat, group, suspect_set = 6, plot = 'wdifference')
```
SIBTEST

# Include CSIBTEST with randomization method
SIBTEST(dat, group, suspect_set = 6, LiStout1996 = TRUE)

# DIF (specific anchors)
SIBTEST(dat, group, match_set = 1:5, suspect_set = 6)
SIBTEST(dat, group, match_set = 1:5, suspect_set = 6, LiStout1996=TRUE)

# DBF (all and specific anchors, respectively)
SIBTEST(dat, group, suspect_set = 11:30)
SIBTEST(dat, group, match_set = 1:5, suspect_set = 11:30)

# DTF
SIBTEST(dat, group, suspect_set = 11:30)
SIBTEST(dat, group, match_set = 1:10) #equivalent

# different hyper pars
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a, d, N*2, itemtype = 'dich', mu = .5, sigma = matrix(1.5))
dat <- rbind(dat1, dat2)
SIBTEST(dat, group, 6:30)
SIBTEST(dat, group, 11:30)

# DIF testing with anchors 1 through 5
SIBTEST(dat, group, 6, match_set = 1:5)
SIBTEST(dat, group, 7, match_set = 1:5)
SIBTEST(dat, group, 8, match_set = 1:5)

# DIF testing with all other items as anchors
SIBTEST(dat, group, 6)
SIBTEST(dat, group, 7)
SIBTEST(dat, group, 8)

## ----------------
## systematic differing slopes and intercepts (clear DTF)
dat1 <- simdata(a, d, N, itemtype = 'dich')
dat2 <- simdata(a + c(numeric(15), rnorm(n-15, 1, .25)), d + c(numeric(15), rnorm(n-15, 1, 1)),
N*2, itemtype = 'dich')
dat <- rbind(dat1, dat2)
SIBTEST(dat, group, 6:30)
SIBTEST(dat, group, 11:30)

# Some plots depicting the above tests
SIBTEST(dat, group, suspect_set = 11:30, plot = 'observed')
SIBTEST(dat, group, suspect_set = 11:30, plot = 'weights')
SIBTEST(dat, group, suspect_set = 11:30, plot = 'wdifference')

# DIF testing using valid anchors
SIBTEST(dat, group, suspect_set = 6, match_set = 1:5)
SIBTEST(dat, group, suspect_set = 7, match_set = 1:5)
SIBTEST(dat, group, suspect_set = 30, match_set = 1:5)

# randomization method is fairly poor when smaller matched-set used
SIBTEST(dat, group, suspect_set = 30, match_set = 1:5, LiStout1996=TRUE)
simdata

Description
Simulates response patterns for compensatory and noncompensatory MIRT models from multivariate normally distributed factor ($\theta$) scores, or from a user input matrix of $\theta$'s.

Usage
```r
simdata(
  a,
  d,
  N,
  itemtype,
  sigma = NULL,
  mu = NULL,
  guess = 0,
  upper = 1,
  nominal = NULL,
  t = NULL,
  Theta = NULL,
  gpcm_mats = list(),
  returnList = FALSE,
  model = NULL,
  equal.K = TRUE,
  which.items = NULL,
  mins = 0,
  lca_cats = NULL,
  prob.list = NULL
)
```

Arguments
- `a`: a matrix/vector of slope parameters. If slopes are to be constrained to zero then use NA or simply set them equal to 0
- `d`: a matrix/vector of intercepts. The matrix should have as many columns as the item with the largest number of categories, and filled empty locations with NA. When a vector is used the test is assumed to consist only of dichotomous items (because only one intercept per item is provided). When `itemtype = 'lca'` intercepts will not be used
- `N`: sample size
Simdata

itemtype

a character vector of length nrow(a) (or 1, if all the item types are the same) specifying the type of items to simulate. Inputs can either be the same as the inputs found in the itemtype argument in mirt or the internal classes defined by the package. Typical itemtype inputs that are passed to mirt are used then these will be converted into the respective internal classes automatically.

If the internal class of the object is specified instead, the inputs can be 'dich', 'graded', 'gpcm', 'sequential', 'nominal', nested logit, partially compensatory, generalized graded unfolding model, and latent class analysis model. Note that for the gpcm, nominal, and nested logit models there should be as many parameters as desired categories, however to parametrize them for meaningful interpretation the first category intercept should equal 0 for these models (second column for 'nestlogit', since first column is for the correct item trace line). For nested logit models the 'correct' category is always the lowest category (i.e., == 1). It may be helpful to use mod2values on data-sets that have already been estimated to understand the itemtypes more intimately.

sigma

da covariance matrix of the underlying distribution. Default is the identity matrix. Used when Theta is not supplied.

mu

da mean vector of the underlying distribution. Default is a vector of zeros. Used when Theta is not supplied.

guess

da vector of guessing parameters for each item; only applicable for dichotomous items. Must be either a scalar value that will affect all of the dichotomous items, or a vector with as many values as to be simulated items.

upper

same as guess, but for upper bound parameters.

nominal

da matrix of specific item category slopes for nominal models. Should be the dimensions as the intercept specification with one less column, with NA in locations where not applicable. Note that during estimation the first slope will be constrained to 0 and the last will be constrained to the number of categories minus 1, so it is best to set these as the values for the first and last categories as well.

t

matrix of t-values for the 'ggun' itemtype, where each row corresponds to a given item. Also determines the number of categories, where NA can be used for non-applicable categories.

Theta

a user specified matrix of the underlying ability parameters, where nrow(Theta) == N and ncol(Theta) == ncol(a). When this is supplied the N input is not required.

gpcm_mats

da list of matrices specifying the scoring scheme for generalized partial credit models (see mirt for details).

returnList

logical; return a list containing the data, item objects defined by mirt containing the population parameters and item structure, and the latent trait matrix Theta? Default is FALSE.

model

a single group object, typically returned by functions such as mirt or bfactor. Supplying this will render all other parameter elements (excluding the Theta, N, mu, and sigma inputs) redundant (unless explicitly provided).
equal.K logical; when a model input is supplied, should the generated data contain the same number of categories as the original data indicated by extract.mirt(model, 'K')? Default is TRUE, which will redraw data until this condition is satisfied.

which.items an integer vector used to indicate which items to simulate when a model input is included. Default simulates all items.

mins an integer vector (or single value to be used for each item) indicating what the lowest category should be. If model is supplied then this will be extracted from slot(mod, 'Data')$mins, otherwise the default is 0.

lca_cats a vector indicating how many categories each lca item should have. If not supplied then it is assumed that 2 categories should be generated for each item.

prob.list an optional list containing matrix/data.frames of probabilities values for each category to be simulated. This is useful when creating customized probability functions to be sampled from.

Details
Returns a data matrix simulated from the parameters, or a list containing the data, item objects, and Theta matrix.

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

References


Examples
### Parameters from Reckase (2009), p. 153

```r
set.seed(1234)

a <- matrix(c(
  .7471, .0250, .1428,
  .4595, .0097, .0692,
  .8613, .0067, .4040,
  1.0141, .0080, .0470,
  .5521, .0204, .1482,
  1.3547, .0064, .5362,
  1.3761, .0861, .4676,
  .8525, .0383, .2574,
  1.0113, .0055, .2024,
  .9212, .0119, .3044,
  .0026, .0119, .8036,
  .0008, .1905, 1.1945,
  1.0000, .0000, .0000), nrow = 10, byrow = TRUE)
```

```r
```
.0575, .0853, .7077,
.0182, .3307, 2.1414,
.0256, .0478, .8551,
.0246, .1496, .9348,
.0262, .2872, 1.3561,
.0038, .2229, .8993,
.0039, .4720, .7318,
.0068, .0949, .6416,
.3073, .9704, .0031,
.1819, .4980, .0020,
.4115, 1.1136, .2008,
.1536, 1.7251, .0345,
.1530, .6688, .0020,
.2890, 1.2419, .0220,
.1341, 1.4882, .0050,
.0524, .4754, .0012,
.2139, .4612, .0063,
.1761, 1.1200, .0870),
byrow=TRUE)*1.702

d <- matrix(c(.1826,-.1924,-.4656,-.4336,-.4428,-.5845,-1.0403,
.6431,.0122,.0912,.8082,-.1867,.4533,-1.8398,.4139,
-.3004,-.1824,.5125,1.1342,.0230,.6172,-.1955,-.3668,
-1.7590,-.2434,.4925,-.3410,.3410,.006,.0329),ncol=1)*1.702

mu <- c(-.4, -.7, .1)
sigma <- matrix(c(1.21,.297,1.232,.297,.81,.252,1.232,.252,1.96),3,3)

dataset1 <- simdata(a, d, 2000, itemtype = '2PL')
dataset2 <- simdata(a, d, 2000, itemtype = '2PL', mu = mu, sigma = sigma)

#mod <- mirt(dataset1, 3, method = 'MHRM')
#coef(mod)

## Not run:
### Unidimensional graded response model with 5 categories each

a <- matrix(rlnorm(20,.2,.3))

# for the graded model, ensure that there is enough space between the intercepts,
# otherwise closer categories will not be selected often (minimum distance of 0.3 here)
diffs <- t(apply(matrix(runif(20*4, .3, 1), 20), 1, cumsum))
diffs <- -(diffs - rowMeans(diffs))
d <- diffs + rnorm(20)
dat <- simdata(a, d, 500, itemtype = 'graded')
# mod <- mirt(dat, 1)

### An example of a mixed item, bifactor loadings pattern with correlated specific factors

a <- matrix(c(
.8,.4,NA,
.4,.4,NA,
```r
# simdata

```

```r
.7,.4,NA,
.8,NA,.4,
.4,NA,.4,
.7,NA,.4),ncol=3,byrow=TRUE)

d <- matrix(c(
-1.0,NA,NA,
 1.5,NA,NA,
 0.0,NA,NA,
 0.0,-1.0,1.5, #the first 0 here is the recommended constraint for nominal
 0.0,1.0,-1, #the first 0 here is the recommended constraint for gpcm
 2.0,0.0,NA),ncol=3,byrow=TRUE)

nominal <- matrix(NA, nrow(d), ncol(d))
#the first 0 and last (ncat - 1) = 2 values are the recommended constraints
nominal[4, ] <- c(0,1.2,2)

sigma <- diag(3)
sigma[2,3] <- sigma[3,2] <- .25

items <- c('2PL','2PL','2PL','nominal','gpcm','graded')

dataset <- simdata(a,d,2000,items,sigma=sigma,nominal=nominal)

mod <- bfactor(dataset, c(1,1,1,2,2,2), itemtype=c(rep('2PL', 3), 'nominal', 'gpcm', 'graded'))
#coef(mod)

```
simdata

a <- matrix(c(0.8, 0.4, 
0.4, 0.4, 
0.7, 0.4, 
0.8, NA, 
0.4, NA, 
0.7, NA), ncol=2, byrow=TRUE)
d <- matrix(rnorm(6))
itemtype <- rep('2PL', 6)
nonlindata <- simdata(a=a, d=d, itemtype=itemtype, Theta=Theta)

#model <-
#F1 = 1-6
#(F1 * F1) = 1-3
#mod <- mirt(nonlindata, model)
#coef(mod)

### 2PLNRM model for item 4 (with 4 categories), 2PL otherwise

a <- matrix(rlnorm(4, 0, 0.2))
#first column of item 4 is the intercept for the correct category of 2PL model,
# otherwise nominal model configuration
d <- matrix(c(-1.0, NA, NA, NA, 
1.5, NA, NA, NA, 
0.0, NA, NA, NA, 
1, 0, 0, -0.5, 0.5), ncol=4, byrow=TRUE)
nominal <- matrix(NA, nrow(d), ncol(d))
nominal[4, ] <- c(NA, 0, 0.5, 0.6)
items <- c(rep('2PL', 3), 'nestlogit')
dataset <- simdata(a, d, 2000, items, nominal=nominal)
mod <- mirt(dataset, 1, itemtype = c('2PL', 3), 
2PLNRM), key=c(NA, NA, NA, 1))
#coef(mod)
#itemplot(mod, 4)

#return list of simulation parameters
listobj <- simdata(a, d, 2000, items, nominal=nominal, returnList=TRUE)
str(listobj)

# generate dataset from converged model
mod <- mirt(Science, 1, itemtype = c(rep('gpcm', 3), 'nominal'))
sim <- simdata(model=mod, N=1000)
head(sim)

Theta <- matrix(rnorm(100))
sim <- simdata(model=mod, Theta=Theta)
head(sim)
# alternatively, define a suitable object with functions from the mirtCAT package
# help(generate.mirt_object)
library(mirtCAT)

nitems <- 50
a1 <- rlnorm(nitems, .2,.2)
d <- rnorm(nitems)
g <- rbeta(nitems, 20, 80)
pars <- data.frame(a1=a1, d=d, g=g)
head(pars)

obj <- generate.mirt_object(pars, '3PL')
dat <- simdata(N=200, model=obj)

### 10 item GGUMs test with 4 categories each
a <- rlnorm(10, .2, .2)
b <- rnorm(10) # passed to d= input, but used as the b parameters
diffs <- t(apply(matrix(runif(10*3, .3, 1), 10), 1, cumsum))
t <- +(diffs - rowMeans(diffs))
dat <- simdata(a, b, 1000, 'ggum', t)
apply(dat, 2, table)

# mod <- mirt(dat, 1, 'ggum')
# coef(mod)

#####
# prob.list example

# custom probability function that returns a matrix
fun <- function(a, b, theta){
P <- 1 / (1 + exp(-a * (theta-b)))
cbind(1-P, P)
}

set.seed(1)
theta <- matrix(rnorm(100))
prob.list <- list()
nitems <- 5
a <- rlnorm(nitems, .2, .2); b <- rnorm(nitems, 0, 1/2)
for(i in 1:nitems) prob.list[[i]] <- fun(a[i], b[i], theta)
str(prob.list)

dat <- simdata(prob.list=prob.list)
head(dat)

# prob.list input is useful when defining custom items as well
name <- 'old2PL'
par <- c(a = .5, b = -2)
est <- c(TRUE, TRUE)
P.old2PL <- function(par,Theta, ncat){
a <- par[1]
b <- par[2]
}
```r
P1 <- 1 / (1 + exp(-a*(Theta - b)))
cbind(1-P1, P1)
}
x <- createItem(name, par=par, est=est, P=P.old2PL)
prob.list[[1]] <- x@P(x@par, theta)

## End(Not run)
```

---

**SingleGroupClass-class**

*Class "SingleGroupClass"

**Description**

Defines the object returned from `mirt` when model is exploratory.

**Slots**

- **Call**: function call
- **Data**: list of data, sometimes in different forms
- **Options**: list of estimation options
- **Fit**: a list of fit information
- **Model**: a list of model-based information
- **ParObjects**: a list of the S4 objects used during estimation
- **OptimInfo**: a list of arguments from the optimization process
- **Internals**: a list of internal arguments for secondary computations (inspecting this object is generally not required)
- **vcov**: a matrix represented the asymptotic covariance matrix of the parameter estimates
- **time**: a data.frame indicating the breakdown of computation times in seconds

**Methods**

- `anova` signature(object = "SingleGroupClass")
- `coef` signature(object = "SingleGroupClass")
- `plot` signature(x = "SingleGroupClass", y = "missing")
- `print` signature(x = "SingleGroupClass")
- `residuals` signature(object = "SingleGroupClass")
- `show` signature(object = "SingleGroupClass")
- `summary` signature(object = "SingleGroupClass")
summary-method

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


summary-method

Summary of model object

Description

Transforms coefficients into a standardized factor loading’s metric. For MixedClass objects, the fixed and random coefficients are printed. Note that while the output to the console is rounded to three digits, the returned list of objects is not. For simulations, use output <- summary(mod, verbose = FALSE) to suppress the console messages.

Usage

## S4 method for signature 'SingleGroupClass'
summary(
  object,
  rotate = "oblimin",
  Target = NULL,
  suppress = 0,
  verbose = TRUE,
  ...
)

Arguments

object an object of class SingleGroupClass, MultipleGroupClass, or MixedClass
rotate a string indicating which rotation to use for exploratory models, primarily from the GPArotation package (see documentation therein).
 Rotations currently supported are: 'promax', 'oblimin', 'varimax', 'quartimin', 'targetT', 'targetQ', 'pstT', 'pstQ', 'oblimax', 'entropy', 'quartimax', 'simplimax', 'bentlerT', 'bentlerQ', 'tandemI', 'tandemII', 'geominT', 'geominQ', 'cfT', 'cfQ', 'infomaxT', 'infomaxQ', 'mccammon', 'bifactorT', 'bifactorQ'.
 For models that are not exploratory this input will automatically be set to 'none'
Target a dummy variable matrix indicting a target rotation pattern. This is required for rotations such as 'targetT', 'targetQ', 'pstT', and 'pstQ'
suppress a numeric value indicating which (possibly rotated) factor loadings should be suppressed. Typical values are around .3 in most statistical software. Default is 0 for no suppression
verbose logical; allow information to be printed to the console?

... additional arguments to be passed

References


See Also

coeff-method

Examples

```r
## Not run:
x <- mirt(Science, 2)
summary(x)
summary(x, rotate = 'varimax')

## End(Not run)
```

Function to calculate test information

testinfo

Description

Given an estimated model compute the test information.

Usage

testinfo(
  x, 
  Theta, 
  degrees = NULL, 
  group = NULL, 
  individual = FALSE, 
  which.items = 1:extract.mirt(x, "nitems")
)

Arguments

- **x** an object of class 'SingleGroupClass', or an object of class 'MultipleGroupClass' if a suitable group input were supplied
- **Theta** a matrix of latent trait values
- **degrees** a vector of angles in degrees that are between 0 and 90. Only applicable when the input object is multidimensional
thetaComb

Create all possible combinations of vector input

Description

This function constructs all possible k-way combinations of an input vector. It is primarily useful when used in conjunction with the mirt function, though users may have other uses for it as well. See expand.grid for more flexible combination formats.
usage

thetaComb(theta, nfact, intercept = FALSE)

Arguments

theta  the vector from which all possible combinations should be obtained
nfact  the number of observations (and therefore the number of columns to return in
       the matrix of combinations)
intercept  logical; should a vector of 1’s be appended to the first column of the result to
           include an intercept design component? Default is FALSE

Value

a matrix with all possible combinations

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References

ronment. Journal of Statistical Software, 48(6), 1-29. doi: 10.18637/jss.v048.i06

Examples

# all possible joint combinations for the vector -4 to 4
thetaComb(-4:4, 2)

# all possible binary combinations for four observations
thetaComb(c(0,1), 4)

# all possible binary combinations for four observations (with intercept)
thetaComb(c(0,1), 4, intercept=TRUE)

Description

This is a helper function for users who have previously available traditional/classical IRT parame-
ters and want to know the equivalent slope-intercept translation used in mirt. Note that this func-
tion assumes that the supplied models are unidimensional by definition (i.e., will have only one
slope/discrimination). If there is no supported slope-intercept transformation available then the
original vector of parameters will be returned by default.
Usage

\texttt{traditional2mirt(x, cls, ncat)}

Arguments

\begin{itemize}
  \item \texttt{x} a vector of parameters to transform
  \item \texttt{cls} the class or itemtype of the supplied model
  \item \texttt{ncat} the number of categories implied by the IRT model
\end{itemize}

Details

Supported class transformations for the \texttt{cls} input are:

- \textbf{Rasch, 2PL, 3PL, 3PLu, 4PL}. Form must be: (discrimination, difficulty, lower-bound, upper-bound)
- \textbf{graded}. Form must be: (discrimination, difficulty 1, difficulty 2, ..., difficulty \textit{k}-1)
- \textbf{gpcm}. Form must be: (discrimination, difficulty 1, difficulty 2, ..., difficulty \textit{k}-1)
- \textbf{nominal}. Form must be: (discrimination 1, discrimination 2, ..., discrimination \textit{k}, difficulty 1, difficulty 2, ..., difficulty \textit{k})

Value

a named vector of slope-intercept parameters (if supported)

Examples

\begin{verbatim}
# classical 3PL model
vec <- c(a=1.5, b=-1, g=.1, u=1)
slopeint <- traditional2mirt(vec, '3PL', ncat=2)
slopeint

# classical graded model (four category)
vec <- c(a=1.5, b1=-1, b2=0, b3=1.5)
slopeint <- traditional2mirt(vec, 'graded', ncat=4)
slopeint

# classical generalize partial credit model (four category)
vec <- c(a=1.5, b1=-1, b2=0, b3=1.5)
slopeint <- traditional2mirt(vec, 'gpcm', ncat=4)
slopeint

# classical nominal model (4 category)
vec <- c(a1=.5, a2 = -1, a3=1, a4=-.5, d1=1, d2=-1, d3=-.5, d4=.5)
slopeint <- traditional2mirt(vec, 'nominal', ncat=4)
slopeint
\end{verbatim}
vcov-method

Extract parameter variance covariance matrix

Description
Extract parameter variance covariance matrix

Usage

```r
## S4 method for signature 'SingleGroupClass'
vcov(object)
```

Arguments

- `object`: an object of class `SingleGroupClass`, `MultipleGroupClass`, or `MixedClass`

References


Examples

```r
## Not run:
x <- mirt(Science, 1, SE=TRUE)
vcov(x)
```

## End(Not run)

wald

Wald statistics for mirt models

Description
Compute a Wald test given an \( L \) vector or matrix of numeric contrasts. Requires that the model information matrix be computed (including \( \mathbf{SE} = \text{TRUE} \) when using the EM method). Use `wald(model)` to observe how the information matrix columns are named, especially if the estimated model contains constrained parameters (e.g., 1PL).

Usage

```r
wald(object, L, C = 0)
```
Arguments

- **object**: estimated object from `mirt`, `bfactor`, `multipleGroup`, `mixedmirt`, or `mdirt`
- **L**: a coefficient matrix with dimensions nconstants x npars. Omitting this value will return the column names of the information matrix used to identify the (potentially constrained) parameters
- **C**: a constant vector of population parameters to be compared along side L, where length(C) == ncol(L). By default a vector of 0’s is constructed

Author(s)

Phil Chalmers <rphilip.chalmers@gmail.com>

References


Examples

```r
## Not run:
#View parnumber index
data(LSAT7)
data <- expand.table(LSAT7)
mod <- mirt(data, 1, SE = TRUE)
coef(mod)

# see how the information matrix relates to estimated parameters, and how it lines up
# with the parameter index
(infonames <- wald(mod))
index <- mod2values(mod)
index[index$est, ]

# second item slope equal to 0?
L <- matrix(0, 1, 10)
L[1,3] <- 1
wald(mod, L)

# simultaneously test equal factor slopes for item 1 and 2, and 4 and 5
L <- matrix(0, 2, 10)
L[1,1] <- L[2, 7] <- 1
L[1,3] <- L[2, 9] <- -1
L
wald(mod, L)

# logLikelihood tests (requires estimating a new model)
cmodel <- 'theta = 1-5
    CONSTRAINT = (1,2, a1), (4,5, a1)'
mod2 <- mirt(data, cmodel)
# or, equivalently
#mod2 <- mirt(data, 1, constrain = list(c(1,5), c(13,17)))
anova(mod2, mod)
```
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