

# Package ‘xxIRT’

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**Type** Package

**Title** Item Response Theory and Computer-Based Testing in R

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**Author** Xiao Luo [aut, cre]

**Maintainer** Xiao Luo <xluo1986@gmail.com>

**Description** A suite of psychometric analysis tools for research and operation, including:

- (1) computation of probability, information, and likelihood for the 3PL, GPCM, and GRM;
- (2) parameter estimation using joint or marginal likelihood estimation method;
- (3) simulation of computerized adaptive testing using built-in or customized algorithms;
- (4) assembly and simulation of multistage testing.

The full documentation and tutorials are at <<https://github.com/xluo11/xxIRT>>.

**License** GPL (>= 3)

**Depends** R (>= 3.5.0)

**URL** <https://github.com/xluo11/xxIRT>

**BugReports** <https://github.com/xluo11/xxIRT/issues>

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ata	<i>Automated Test Assembly (ATA)</i>
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**Description**

ata initiates an ATA model  
 ata\_obj\_relative adds a relative objective to the model  
 ata\_obj\_absolute adds an absolute objective to the model  
 ata\_constraint adds a constraint to the model  
 ata\_item\_use limits the minimum and maximum usage for items  
 ata\_item\_enemy adds an enemy-item constraint to the model  
 ata\_item\_fixedvalue forces an item to be selected or not selected  
 ata\_solve solves the MIP model

**Usage**

```

ata(pool, num_form = 1, len = NULL, max_use = NULL, ...)

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

## S3 method for class 'ata'
plot(x, ...)

ata_obj_relative(x, coef, mode = c("max", "min"), tol = NULL,
                 negative = FALSE, forms = NULL, collapse = FALSE,
                 internal_index = FALSE, ...)

ata_obj_absolute(x, coef, target, equal_tol = FALSE, tol_up = NULL,
                  tol_down = NULL, forms = NULL, collapse = FALSE,
                  internal_index = FALSE, ...)

ata_constraint(x, coef, min = NA, max = NA, level = NULL,
                  forms = NULL, collapse = FALSE, internal_index = FALSE)

ata_item_use(x, min = NA, max = NA, items = NULL)
  
```

```

ata_item_enemy(x, items)

ata_item_fixedvalue(x, items, min = NA, max = NA, forms)

ata_solve(x, solver = c("lp_solve", "glpk"), as.list = TRUE,
          details = TRUE, time_limit = 10, message = FALSE, ...)

```

## Arguments

pool	item pool, a data.frame
num_form	number of forms to be assembled
len	test length of each form
max_use	maximum use of each item
...	options, e.g. group, common_items, overlap_items
x	an ATA object
coef	coefficients of the objective function
mode	optimization mode: 'max' for maximization and 'min' for minimization
tol	the tolerance paraemter
negative	TRUE when the objective function is expected to be negative
forms	forms where objectives are added. NULL for all forms
collapse	TRUE to collapse into one objective function
internal_index	TRUE to use internal form indices
target	the target values of the objective function
equal_tol	TRUE to force upward and downward tolerance to be equal
tol_up	the range of upward tolerance
tol_down	the range of downward tolerance
min	the lower bound of the constraint
max	the upper bound of the constraint
level	the level of a categorical variable to be constrained
items	a vector of item indices, NULL for all items
solver	use 'lp_solve' for lp_solve 5.5 or 'glpk' for GLPK
as.list	TRUE to return results in a list; otherwise, a data frame
details	TRUE to print detailed information
time_limit	the time limit in seconds passed along to solvers
message	TRUE to print messages from solvers

## Details

The ATA model stores the definition of a MIP model. `ata_solve` converts the model definition to a real MIP object and attempts to solve it.

`ata_obj_relative`: when mode='max', maximize (y-tol), subject to  $y \leq \text{sum}(x) \leq y+\text{tol}$ ; when mode='min', minimize (y+tol), subject to  $y-\text{tol} \leq \text{sum}(x) \leq y$ . When negative is TRUE,  $y < 0$ , tol > 0. coef can be a numeric vector that has the same length with the pool or forms, or a variable name in the pool, or a numeric vector of theta points. When tol is NULL, it is optimized; when FALSE, ignored; when a number, fixed; when a range, constrained with lower and upper bounds.

`ata_obj_absolute` minimizes  $y_0+y_1$  subject to  $t-y_0 \leq \text{sum}(x) \leq t+y_1$ .

When level is NA, it is assumed that the constraint is on a quantitative item property; otherwise, a categorical item property. coef can be a variable name, a constant, or a numeric vector that has the same size as the pool.

`ata_solve` takes control options in .... For lpSolve, see `lpSolveAPI::lp.control.options`. For glpk, see `glpkAPI::glpkConstants`

Once the model is solved, additional data are added to the model. status shows the status of the solution, optimum the optimal value of the objective function found in the solution, obj\_vars the values of two critical variables in the objective function, result the assembly results in a binary matrix, and items the assembled items

## Examples

```
## Not run:
## generate a pool of 100 items
n_items <- 100
pool <- with(model_3pl_gendata(1, n_items), data.frame(id=1:n_items, a=a, b=b, c=c))
pool$content <- sample(1:3, n_items, replace=TRUE)
pool$time <- round(rlnorm(n_items, log(60), .2))
pool$group <- sort(sample(1:round(n_items/3), n_items, replace=TRUE))

## ex. 1: four 10-item forms, maximize b parameter
x <- ata(pool, 4, len=10, max_use=1)
x <- ata_obj_relative(x, "b", "max")
x <- ata_solve(x, timeout=5)
data.frame(form=1:4, b=sapply(x$items, function(x) mean(x$b)))

## ex. 2: four 10-item forms, minimize b parameter
x <- ata(pool, 4, len=10, max_use=1)
x <- ata_obj_relative(x, "b", "min", negative=TRUE)
x <- ata_solve(x, as.list=FALSE, timeout=5)
with(x$items, aggregate(b, by=list(form=form), mean))

## ex. 3: two 10-item forms, mean(b)=0, sd(b)=1
## content = (3, 3, 4), avg. time = 58--62 seconds
constr <- data.frame(name='content', level=1:3, min=c(3,3,4), max=c(3,3,4), stringsAsFactors=F)
constr <- rbind(constr, c('time', NA, 58*10, 62*10))
x <- ata(pool, 2, len=10, max_use=1)
x <- ata_obj_absolute(x, pool$b, 0*10)
x <- ata_obj_absolute(x, (pool$b-0)^2, 1*10)
for(i in 1:nrow(constr))
```

```

x <- with(constr, ata_constraint(x, name[i], min[i], max[i], level=level[i]))
x <- ata_solve(x, timeout=5)
sapply(x$items, function(x) c(mean=mean(x$b), sd=sd(x$b)))

## ex. 4: two 10-item forms, max TIF over (-1, 1), consider item sets
x <- ata(pool, 2, len=10, max_use=1, group="group")
x <- ata_obj_relative(x, seq(-1, 1, .5), 'max')
x <- ata_solve(x, timeout=5)
plot(x)

## End(Not run)

```

## Description

`cat_sim` runs a simulation of CAT. Use `theta` in options to set the starting value of theta estimate.

`cat_estimate_mle` is the maximum likelihood estimation rule. Use `map_len` to apply MAP to the first K items and use `map_prior` to set the prior for MAP.

`cat_estimate_eap` is the expected a posteriori estimation rule, using `eap_mean` and `eap_sd` option parameters as the prior

`cat_estimate_hybrid` is a hybrid estimation rule, which uses MLE for mixed responses and EAP for all 1's or 0's responses

`cat_stop_default` is a three-way stopping rule. When `stop_se` is set in the options, it uses the standard error stopping rule. When `stop_mi` is set in the options, it uses the minimum information stopping rule. When `stop_cut` is set in the options, it uses the confidence interval (set by `ci_width`) stopping rule.

`cat_select_maxinfo` is the maximum information selection rule. Use `group` (a numeric vector) to group items belonging to the same set. Use `info_random` to implement the random-esque item exposure control method.

`cat_select_ccat` is the constrained CAT selection rule. Use `ccat_var` to set the content variable in the pool. Use `ccat_perc` to set the desired content distribution, with the name of each element being the content code and the value of each element being the percentage. Use `ccat_random` to add randomness to initial item selections.

`cat_select_shadow` is the shadow-test selection rule. Use `shadow_id` to group item sets. Use `constraints` to set constraints. Constraints should be in a data.frame with four columns: `var` (variable name), `level` (variable level, NA for quantitative variable), `min` (lower bound), and `max` (upper bound).

`cat_stop_projection` is the projection-based stopping rule. Use `projection_method` to choose the projection method ('info' or 'diff'). Use `stop_cut` to set the cut score. Use `constraints` to set the constraints. Constraints should be a data.frame with columns: `var` (variable name), `level` (variable level, NA for quantitative variable), `min` (lower bound), `max` (upper bound)

**Usage**

```
cat_sim(true, pool, ...)

cat_estimate_mle(len, theta, stats, admin, pool, opts)

cat_estimate_eap(len, theta, stats, admin, pool, opts)

cat_estimate_hybrid(len, theta, stats, admin, pool, opts)

cat_stop_default(len, theta, stats, admin, pool, opts)

cat_select_maxinfo(len, theta, stats, admin, pool, opts)

cat_select_ccat(len, theta, stats, admin, pool, opts)

cat_select_shadow(len, theta, stats, admin, pool, opts)

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

## S3 method for class 'cat'
plot(x, ...)

cat_stop_projection(len, theta, stats, admin, pool, opts)
```

**Arguments**

true	the true theta
pool	the item pool (data.frame)
...	option/control parameters
len	the current test length
theta	the current theta estimate
stats	a matrix of responses, theta estimate, information and std error
admin	a data frame of administered items
opts	a list of option/control parameters
x	a cat object

**Details**

... takes a variety of option/control parameters for the simulations from users. min and max are mandatory for setting limits on the test length. User-defined selection, estimation, and stopping rules are also passed to the simulator via options.

To write a new rule, the function signature must be: `function(len, theta, stats, admin, pool, opts)`. See built-in rules for examples.

**Value**

`cat_sim` returns a `cat` object  
 an estimation rule should return a theta estimate  
 a stopping rule should return a boolean: TRUE to stop the CAT, FALSE to continue  
 a selection rule should return a list of (a) the selected item and (b) the updated pool

**Examples**

```
## Not run:
## generate a 100-item pool
num_items <- 100
pool <- with(model_3pl_gendata(1, num_items), data.frame(a=a, b=b, c=c))
pool$set_id <- sample(1:30, num_items, replace=TRUE)
pool$content <- sample(1:3, num_items, replace=TRUE)
pool$time <- round(rlnorm(num_items, mean=4.1, sd=.2))

## MLE, EAP, and hybrid estimation rule
cat_sim(1.0, pool, min=10, max=20, estimate_rule=cat_estimate_mle)
cat_sim(1.0, pool, min=10, max=20, estimate_rule=cat_estimate_eap)
cat_sim(1.0, pool, min=10, max=20, estimate_rule=cat_estimate_hybrid)

## SE, MI, and CI stopping rule
cat_sim(1.0, pool, min=10, max=20, stop_se=.3)
cat_sim(1.0, pool, min=10, max=20, stop_mi=.6)
cat_sim(1.0, pool, min=10, max=20, stop_cut=0)
cat_sim(1.0, pool, min=10, max=20, stop_cut=0, ci_width=2.58)

## maximum information selection with item sets
cat_sim(1.0, pool, min=10, max=20, group="set_id")$admin

## maximum information with item exposure control
cat_sim(1.0, pool, min=10, max=20, info_random=5)$admin

## Constrained-CAT selection rule with and without initial randomness
cat_sim(1.0, pool, min=10, max=20, select_rule=cat_select_ccat,
        ccat_var="content", ccat_perc=c("1"=.2, "2"=.3, "3"=.5))
cat_sim(1.0, pool, min=10, max=20, select_rule=cat_select_ccat, ccat_random=5,
        ccat_var="content", ccat_perc=c("1"=.2, "2"=.3, "3"=.5))

## Shadow-test selection rule
cons <- data.frame(var='content', level=1:3, min=c(3,3,4), max=c(3,3,4))
cons <- rbind(cons, data.frame(var='time', level=NA, min=55*10, max=65*10))
cat_sim(1.0, pool, min=10, max=10, select_rule=cat_select_shadow, constraints=cons)

## Projection-based stopping rule
cons <- data.frame(var='content', level=1:3, min=5, max=15)
cons <- rbind(cons, data.frame(var='time', level=NA, min=60*20, max=60*40))
cat_sim(1.0, pool, min=20, max=40, select_rule=cat_select_shadow, stop_rule=cat_stop_projection,
        projection_method="diff", stop_cut=0, constraints=cons)

## End(Not run)
```

cronbach_alpha	<i>Cronbach's alpha</i>
----------------	-------------------------

### Description

`cronbach_alpha` computes Cronbach's alpha internal consistency reliability

### Usage

```
cronbach_alpha(responses)
```

### Arguments

responses	the observed responses, 2d matrix
-----------	-----------------------------------

### Examples

```
cronbach_alpha(model_3pl_gendata(1000, 20)$u)
```

expected_raw_score_dist	<i>#' Distribution of Expected Raw Scores</i>
-------------------------	---

### Description

Calculate the distribution of expected raw scores

### Usage

```
expected_raw_score_dist(t, a, b, c)
```

### Arguments

t	the ability parameters, 1d vector
a	the item discrimination parameters, 1d vector
b	the item difficulty parameters, 1d vector
c	the item guessing parameters, 1d vector

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freq	<i>Frequency Counts</i>
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## Description

Frequency counts of a vector

## Usage

```
freq(x, values = NULL, rounding = NULL)
```

## Arguments

x	a numeric or character vector
values	valid values, NULL to include all values
rounding	round percentage to n-th decimal places

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model_3pl	<i>3-parameter-logistic model</i>
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## Description

Routine functions for the 3PL model

## Usage

```
model_3pl_prob(t, a, b, c, D = 1.702)
model_3pl_info(t, a, b, c, D = 1.702)
model_3pl_lh(u, t, a, b, c, D = 1.702, log = FALSE)
model_3pl_rescale(t, a, b, c, param = c("t", "b"), mean = 0, sd = 1)
model_3pl_gendata(n_p, n_i, t = NULL, a = NULL, b = NULL, c = NULL,
D = 1.702, t_dist = c(0, 1), a_dist = c(-0.1, 0.2), b_dist = c(0,
0.7), c_dist = c(5, 46), missing = NULL)
model_3pl_plot(a, b, c, D = 1.702, type = c("prob", "info"),
total = FALSE, xaxis = seq(-4, 4, 0.1))
model_3pl_plot_loglh(u, a, b, c, D = 1.702, xaxis = seq(-4, 4, 0.1),
show_mle = FALSE)
```

### Arguments

<b>t</b>	ability parameters, 1d vector
<b>a</b>	discrimination parameters, 1d vector
<b>b</b>	difficulty parameters, 1d vector
<b>c</b>	guessing parameters, 1d vector
<b>D</b>	the scaling constant, 1.702 by default
<b>u</b>	observed responses, 2d matrix
<b>log</b>	True to return log-likelihood
<b>param</b>	the parameter of the new scale: 't' or 'b'
<b>mean</b>	the mean of the new scale
<b>sd</b>	the standard deviation of the new scale
<b>n_p</b>	the number of people to be generated
<b>n_i</b>	the number of items to be generated
<b>t_dist</b>	parameters of the normal distribution used to generate t-parameters
<b>a_dist</b>	parameters of the lognormal distribution used to generate a-parameters
<b>b_dist</b>	parameters of the normal distribution used to generate b-parameters
<b>c_dist</b>	parameters of the beta distribution used to generate c-parameters
<b>missing</b>	the proportion or number of missing responses
<b>type</b>	the type of plot: 'prob' for item characteristic curve (ICC) and 'info' for item information function curve (IIFC)
<b>total</b>	TRUE to sum values over items
<b>xaxis</b>	the values of x-axis
<b>show_mle</b>	TRUE to print maximum likelihood estimates

### Examples

```
with(model_3pl_gendata(10, 5), model_3pl_prob(t, a, b, c))
with(model_3pl_gendata(10, 5), model_3pl_info(t, a, b, c))
with(model_3pl_gendata(10, 5), model_3pl_lh(u, t, a, b, c))
model_3pl_gendata(10, 5)
model_3pl_gendata(10, 5, a=1, c=0, missing=.1)
with(model_3pl_gendata(10, 5), model_3pl_plot(a, b, c, type="prob"))
with(model_3pl_gendata(10, 5), model_3pl_plot(a, b, c, type="info", total=TRUE))
with(model_3pl_gendata(5, 50), model_3pl_plot_loglh(u, a, b, c, show_mle=TRUE))
```

**Description**

Routine functions for the GPCM

**Usage**

```
model_gpcm_prob(t, a, b, d, D = 1.702, insert_d0 = NULL)

model_gpcm_info(t, a, b, d, D = 1.702, insert_d0 = NULL)

model_gpcm_lh(u, t, a, b, d, D = 1.702, insert_d0 = NULL,
               log = FALSE)

model_gpcm_gendata(n_p, n_i, n_c, t = NULL, a = NULL, b = NULL,
                     d = NULL, D = 1.702, sort_d = FALSE, t_dist = c(0, 1),
                     a_dist = c(-0.1, 0.2), b_dist = c(0, 0.8), missing = NULL)

model_gpcm_rescale(t, a, b, d, param = c("t", "b"), mean = 0, sd = 1)

model_gpcm_plot(a, b, d, D = 1.702, insert_d0 = NULL,
                 type = c("prob", "info"), by_item = FALSE, total = FALSE,
                 xaxis = seq(-6, 6, 0.1))

model_gpcm_plot_loglh(u, a, b, d, D = 1.702, insert_d0 = NULL,
                       xaxis = seq(-6, 6, 0.1), show_mle = FALSE)
```

**Arguments**

t	ability parameters, 1d vector
a	discrimination parameters, 1d vector
b	item location parameters, 1d vector
d	item category parameters, 2d vector
D	the scaling constant, 1.702 by default
insert_d0	insert an initial category value
u	the observed scores (starting from 0), 2d matrix
log	TRUE to return log-likelihood
n_p	the number of people to be generated
n_i	the number of items to be generated
n_c	the number of score categories
sort_d	TRUE to sort d parameters for each item

<b>t_dist</b>	parameters of the normal distribution used to generate t-parameters
<b>a_dist</b>	parameters of the lognormal distribution parameters of a-parameters
<b>b_dist</b>	parameters of the normal distribution used to generate b-parameters
<b>missing</b>	the proportion or number of missing responses
<b>param</b>	the parameter of the new scale: 't' or 'b'
<b>mean</b>	the mean of the new scale
<b>sd</b>	the standard deviation of the new scale
<b>type</b>	the type of plot, prob for ICC and info for IIFC
<b>by_item</b>	TRUE to combine categories
<b>total</b>	TRUE to sum values over items
<b>xaxis</b>	the values of x-axis
<b>show_mle</b>	TRUE to print maximum likelihood values

## Details

Use NA to represent unused category.

## Examples

```

with(model_gpcm_gendata(10, 5, 3), model_gpcm_prob(t, a, b, d))
with(model_gpcm_gendata(10, 5, 3), model_gpcm_info(t, a, b, d))
with(model_gpcm_gendata(10, 5, 3), model_gpcm_lh(u, t, a, b, d))
model_gpcm_gendata(10, 5, 3)
model_gpcm_gendata(10, 5, 3, missing=.1)
# Figure 1 in Muraki, 1992 (APM)
b <- matrix(c(-2,0,2,-.5,0,2,-.5,0,2), nrow=3, byrow=TRUE)
model_gpcm_plot(a=c(1,1,.7), b=rowMeans(b), d=rowMeans(b)-b, D=1.0, insert_d0=0)
# Figure 2 in Muraki, 1992 (APM)
b <- matrix(c(.5,0,NA,0,0,0), nrow=2, byrow=TRUE)
model_gpcm_plot(a=.7, b=rowMeans(b, na.rm=TRUE), d=rowMeans(b, na.rm=TRUE)-b, D=1.0, insert_d0=0)
# Figure 3 in Muraki, 1992 (APM)
b <- matrix(c(1.759,-1.643,3.970,-2.764), nrow=2, byrow=TRUE)
model_gpcm_plot(a=c(.778,.946), b=rowMeans(b), d=rowMeans(b)-b, D=1.0, insert_d0=0)
# Figure 1 in Muraki, 1993 (APM)
b <- matrix(c(0,-2,4,0,-2,2,0,-2,0,0,-2,-2,0,-2,-4), nrow=5, byrow=TRUE)
model_gpcm_plot(a=1, b=rowMeans(b), d=rowMeans(b)-b, D=1.0)
# Figure 2 in Muraki, 1993 (APM)
b <- matrix(c(0,-2,4,0,-2,2,0,-2,0,0,-2,-2,0,-2,-4), nrow=5, byrow=TRUE)
model_gpcm_plot(a=1, b=rowMeans(b), d=rowMeans(b)-b, D=1.0, type='info', by_item=TRUE)
with(model_gpcm_gendata(5, 50, 3), model_gpcm_plot_loglh(u, a, b, d))

```

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<code>model_grm</code>	<i>Graded Response Model</i>
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**Description**

Routine functions for the GRM

**Usage**

```
model_grm_prob(t, a, b, D = 1.702, raw = FALSE)

model_grm_info(t, a, b, D = 1.702)

model_grm_lh(u, t, a, b, D = 1.702, log = FALSE)

model_grm_gendata(n_p, n_i, n_c, t = NULL, a = NULL, b = NULL,
D = 1.702, t_dist = c(0, 1), a_dist = c(-0.1, 0.2), b_dist = c(0,
0.8), missing = NULL)

model_grm_rescale(t, a, b, param = c("t", "b"), mean = 0, sd = 1)

model_grm_plot(a, b, D = 1.702, type = c("prob", "info"),
by_item = FALSE, total = FALSE, xaxis = seq(-6, 6, 0.1),
raw = FALSE)

model_grm_plot_loglh(u, a, b, D = 1.702, xaxis = seq(-6, 6, 0.1),
show_mle = FALSE)
```

**Arguments**

<code>t</code>	ability parameters, 1d vector
<code>a</code>	discrimination parameters, 1d vector
<code>b</code>	item location parameters, 2d matrix
<code>D</code>	the scaling constant, 1.702 by default
<code>raw</code>	TRUE to return P*
<code>u</code>	the observed scores (starting from 0), 2d matrix
<code>log</code>	TRUE to return log-likelihood
<code>n_p</code>	the number of people to be generated
<code>n_i</code>	the number of items to be generated
<code>n_c</code>	the number of score categories
<code>t_dist</code>	parameters of the normal distribution used to generate t-parameters
<code>a_dist</code>	parameters of the lognormal distribution used to generate a-parameters
<code>b_dist</code>	parameters of the normal distribution used to generate b-parameters

<code>missing</code>	the proportion or number of missing responses
<code>param</code>	the parameter of the new scale: 't' or 'b'
<code>mean</code>	the mean of the new scale
<code>sd</code>	the standard deviation of the new scale
<code>type</code>	the type of plot, prob for ICC and info for IIFC
<code>by_item</code>	TRUE to combine categories
<code>total</code>	TRUE to sum values over items
<code>xaxis</code>	the values of x-axis
<code>show_mle</code>	TRUE to print maximum likelihood values

### Examples

```
with(model_grm_gendata(10, 5, 3), model_grm_prob(t, a, b))
with(model_grm_gendata(10, 5, 3), model_grm_info(t, a, b))
with(model_grm_gendata(10, 5, 3), model_grm_lh(u, t, a, b))
model_grm_gendata(10, 5, 3)
model_grm_gendata(10, 5, 3, missing=.1)
with(model_grm_gendata(10, 5, 3), model_grm_plot(a, b, type='prob'))
with(model_grm_gendata(10, 5, 3), model_grm_plot(a, b, type='info', by_item=TRUE))
with(model_grm_gendata(5, 50, 3), model_grm_plot_loglh(u, a, b))
```

## ***mst\_sim***

### *Simulation of Multistage Testing*

### Description

`mst_sim` simulates a MST administration

### Usage

```
mst_sim(x, true, rdp = NULL, ...)

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

## S3 method for class 'mst_sim'
plot(x, ...)
```

### Arguments

<code>x</code>	the assembled MST
<code>true</code>	the true theta parameter (numeric)
<code>rdp</code>	routing decision points (list)
<code>...</code>	additional option/control parameters

## Examples

```

## Not run:
## assemble a MST
nitems <- 200
pool <- with(model_3pl_gendata(1, nitems), data.frame(a=a, b=b, c=c))
pool$content <- sample(1:3, nrow(pool), replace=TRUE)
x <- mst(pool, "1-2-", 2, 'topdown', len=20, max_use=1)
x <- mst_obj(x, theta=-1, indices=1)
x <- mst_obj(x, theta=0, indices=2:3)
x <- mst_obj(x, theta=1, indices=4)
x <- mst_constraint(x, "content", 6, 6, level=1)
x <- mst_constraint(x, "content", 6, 6, level=2)
x <- mst_constraint(x, "content", 8, 8, level=3)
x <- mst_stage_length(x, 1:2, min=5)
x <- mst_assemble(x)

## ex. 1: administer the MST using fixed RDP for routing
x_sim <- mst_sim(x, .5, list(stage1=0, stage2=0))
plot(x_sim)

## ex. 2: administer the MST using the max. info. for routing
x_sim <- mst_sim(x, .5)
plot(x_sim, ylim=c(-5, 5))

## End(Not run)

```

rmse

*Root Mean Squared Error*

## Description

Root mean squared error (RMSE) of two numeric vectors/matrices

## Usage

```
rmse(x, y)
```

## Arguments

- |   |                         |
|---|-------------------------|
| x | a numeric vector/matrix |
| y | a numeric vector/matrix |

---

`spearman_brown`      *Spearman Brown Prophecy*

---

### Description

Use Spearman-brown formula to compute the predicted reliability when the test length is extened to n-fold or reversely the n-fold extension of test length in order to reach the targeted reliability

### Usage

```
spearman_brown(n, rho)  
spearman_brown_reverse(rho, target)
```

### Arguments

n	extend the test length to n-fold
rho	the reliability of current test
target	the targeted reliability

### Examples

```
spearman_brown(2, .70)  
spearman_brown_reverse(.70, .85)
```

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