

Package ‘easyRasch2’

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Title Psychometric Analysis with Rasch Measurement Theory

Version 1.0.0

Description Streamlines reproducible Rasch measurement theory analyses for ordinal item-response data, combining estimation routines from 'eRm', 'psychotools', 'mirt', 'iarm', and 'lavaan' with consistent diagnostic, plotting, and reporting layers. Covers the four basic psychometric criteria summarised by Christensen et al. (2021) [doi:10.1111/sms.13908](https://doi.org/10.1111/sms.13908) -- unidimensionality, local independence, ordered response category thresholds, and invariance across subgroups -- together with item fit, targeting, reliability, category functioning, and descriptive item-response plots. A distinguishing feature is the use of simulation-based critical values to replace rule-of-thumb cutoffs for conditional infit mean-square, Yen's Q3 local-dependence statistic, the largest residual-PCA eigenvalue, ordinal CFA fit indices, and partial-gamma DIF and local-dependence coefficients, optionally augmented with multiplicity-corrected bootstrap p-values. Outputs are knitr::kable() tables and 'ggplot2' figures suitable for direct inclusion in 'Quarto' and 'R Markdown' reports.

License GPL (>= 3)

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URL <https://github.com/pgmj/easyRasch2>,
<https://pgmj.github.io/easyRasch2/>

BugReports <https://github.com/pgmj/easyRasch2/issues>

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Author Magnus Johansson [aut, cre] (ORCID:

<<https://orcid.org/0000-0003-1669-592X>>),

Nicklas Korsell [ctb] (PCM simulation code),

Mirka Henninger [ctb] (ORCID: <<https://orcid.org/0000-0003-4676-2361>>),

MH / partial-gamma effect-size and ETS-classification algorithms in

dif_tree.R, adapted under MIT licence from the raschtreeMH and

effecttree packages),

Jan Radek [ctb] (ORCID: <<https://orcid.org/0009-0003-8842-9206>>),

partial-gamma effect-size and ETS-classification algorithms in

dif_tree.R, adapted under MIT licence from the effecttree package)

Maintainer Magnus Johansson <pgmj@pm.me>

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Contents

phq9	3
RMdifGamma	4
RMdifGammaCutoff	7
RMdifGammaPlot	10
RMdifLR	12
RMdifTree	14
RMdimCFA	18
RMdimCFACutoff	20
RMdimCFAPlot	23
RMdimMartinLof	24
RMdimMartinLofResiduals	27
RMdimResidualPCA	30
RMdimResidualPCACutoff	32
RMitemCatProb	34
RMitemHierarchy	37
RMitemICCPlot	39
RMitemInfit	41
RMitemInfitCutoff	44
RMitemInfitCutoffMI	47
RMitemInfitMI	49
RMitemInfitPlot	51
RMitemParameters	53
RMitemRestscore	55
RMitemRestscoreBoot	57
RMlocdepGamma	60
RMlocdepGammaCutoff	63
RMlocdepGammaPlot	65

RMlocdepQ3	67
RMlocdepQ3Cutoff	70
RMlocdepQ3Plot	73
RMpersonFit	75
RMpersonParameters	78
RMplotBar	81
RMplotStackedbar	83
RMplotTile	85
RMreliability	88
RMscoreSE	90
RMtargeting	92
RMUreliability	95

Index	96
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 phq9

PHQ-9 Depression Screener (NHANES Subsample)

Description

A processed subsample of the Patient Health Questionnaire 9-item (PHQ-9) depression screener from the U.S. National Health and Nutrition Examination Survey (NHANES), September 2024 release. Six hundred respondents were drawn at random from the cycle's PHQ-9 module subject to having complete responses on all nine items, while retaining a realistic share of respondents with a sum-score of zero ($n = 8$) so that floor behaviour can be illustrated in a Rasch analysis.

Usage

phq9

Format

A data frame with 600 rows and 12 variables:

- q1** Little interest or pleasure in doing things. Integer 0–3.
- q2** Feeling down, depressed, or hopeless. Integer 0–3.
- q3** Trouble falling/staying asleep, or sleeping too much. Integer 0–3.
- q4** Feeling tired or having little energy. Integer 0–3.
- q5** Poor appetite or overeating. Integer 0–3.
- q6** Feeling bad about yourself — or that you are a failure or have let yourself or your family down. Integer 0–3.
- q7** Trouble concentrating on things, such as reading the newspaper or watching television. Integer 0–3.
- q8** Moving or speaking so slowly that other people could have noticed — or the opposite, being so fidgety or restless that you have been moving around a lot more than usual. Integer 0–3.
- q9** Thoughts that you would be better off dead, or of hurting yourself in some way. Integer 0–3.

gender Self-reported gender, factor with levels "Female" and "Male" (31 respondents with missing values).

age Age in years (integer, range 15–85).

edu Highest educational attainment, factor with levels "Elementary School", "High school", "University".

Each PHQ-9 item uses a four-point ordinal response scale, scored 0 ("Not at all"), 1 ("Several days"), 2 ("More than half the days") and 3 ("Nearly every day").

Details

The dataset is a *processed subsample* intended for teaching and for the package's worked example; it should not be treated as a canonical NHANES microdata file. Users wishing to validate against NCHS-published figures should download the original public-use microdata directly from the NHANES website (see *Source*).

Source

U.S. Centers for Disease Control and Prevention, National Center for Health Statistics. *National Health and Nutrition Examination Survey*, September 2024 release. <https://www.cdc.gov/nchs/nhanes/search/datapage.aspx?Component=Questionnaire&CycleBeginYear=2024>. NHANES data are released to the public domain by the U.S. federal government (<https://www.cdc.gov/nchs/policy/data-release-policy.html>).

References

Kroenke, K., Spitzer, R. L., & Williams, J. B. W. (2001). The PHQ-9: Validity of a brief depression severity measure. *Journal of General Internal Medicine*, 16(9), 606–613. doi:10.1046/j.1525-1497.2001.016009606.x

Examples

```
data(phq9)
str(phq9)
summary(rowSums(phq9[, 1:9]))
```

Description

Computes partial gamma coefficients for Differential Item Functioning (DIF) using `iar::partgam_DIF()`. Each item is tested for association with a single categorical DIF variable, controlling for the total score.

Usage

```

RMdifGamma(
  data,
  dif_var,
  cutoff = NULL,
  p_value = FALSE,
  correction = c("fwer", "fdr_bh", "fdr_by", "none"),
  alpha = 0.05,
  output = "kable"
)

```

Arguments

data	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed, but at least one complete case must exist after combining data and dif_var.
dif_var	A vector (factor or character) of the same length as nrow(data), representing the grouping variable for DIF analysis.
cutoff	Optional. Default NULL (no cutoff applied). Can be: <ul style="list-style-type: none"> • The return value of RMdifGammaCutoff (a list with \$item_cutoffs): the data.frame is extracted automatically and simulation metadata is included in the kable caption. • The \$item_cutoffs data.frame from RMdifGammaCutoff directly: must have columns Item, gamma_low, gamma_high. When provided, adds columns Gamma_low, Gamma_high, and Flagged (logical; TRUE when the observed partial gamma falls outside the credible range) to the result.
p_value	Logical. When TRUE, adds two-sided bootstrap p-values (p_gamma, padj_gamma) comparing each item's observed partial gamma against its simulated null distribution, and flagged reflects padj_gamma < alpha instead of the credible range. The asymptotic BH-adjusted p-value and star columns from <code>iar::partgam_DIF()</code> are dropped in this mode (two p-value families in one table would invite double-reading); the simulated gamma_low / gamma_high band is kept as the effect-size reference. Requires the full RMdifGammaCutoff object as cutoff (it carries the simulated distributions in \$results). Default FALSE.
correction	Character. Multiplicity correction for the bootstrap p-values: "fwer" (default; Westfall-Young studentised-max step-down), "fdr_bh", "fdr_by", or "none". Ignored when p_value = FALSE.
alpha	Numeric in (0, 1). Significance level used to flag items on the corrected p-value. Default 0.05. Ignored when p_value = FALSE.
output	Character string controlling the return value. Either "kable" (default) for a formatted <code>knitr::kable()</code> table, or "dataframe" for the underlying data.frame.

Details

Partial gamma (Bjorner et al., 1998) measures the association between item response and an exogenous grouping variable, controlling for the total score. Values near 0 indicate no DIF. Recommended interpretive thresholds (Bjorner et al., 1998):

- **No or negligible DIF:** gamma within $[-0.21, 0.21]$, *or* gamma not significantly different from 0.
- **Slight to moderate DIF:** gamma within $[-0.31, 0.31]$ (and outside $[-0.21, 0.21]$), *or* not significantly outside $[-0.21, 0.21]$.
- **Moderate to large DIF:** gamma outside $[-0.31, 0.31]$, **and** significantly outside $[-0.21, 0.21]$.

The `iarm` package must be installed (it is in Suggests, not Imports).

Bootstrap p-values. When `p_value = TRUE`, each item's observed partial gamma is compared against its simulated null distribution (from `cutoff$results`, where the DIF variable is random by construction). The per-item statistic is the residual studentised by the bootstrap mean and SD; the marginal p-value is the two-sided Monte-Carlo p-value $(1 + \#\{|t^*| \geq |t|\}) / (B + 1)$, so it can be no smaller than $1 / (B + 1)$. `correction = "fwer"` uses the Westfall-Young studentised-max step-down, which exploits the bootstrap dependence among items (Ferreira, 2024); it is liberal when the simulation is small, so at least 1000 iterations in `RMdifGammaCutoff()` are recommended (a warning is issued below that). Unlike the asymptotic p-values from `iarm::partgam_DIF()`, these are calibrated against the *simulated Rasch null* rather than the asymptotic SE; they are model-conditional and sample-size-sensitive, and are reported alongside the simulated effect-size band, not in place of it.

Value

- If output = "kable": a `knitr_kable` object with columns "Item", "Partial gamma", "SE", "Lower CI", "Upper CI", "Adj. p-value (BH)", and "p-value sign." (a star-string indicator from `iarm::partgam_DIF()`). When `cutoff` is provided, additional columns "Gamma low", "Gamma high", and "Flagged" are included. With `p_value = TRUE`, the asymptotic p-value columns are replaced by bootstrap "p" and "p (adj)".
- If output = "dataframe": a `data.frame` with columns `Item`, `gamma`, `se`, `lower`, `upper`, `padj_bh`, `Significance`. When `cutoff` is provided, columns `gamma_low`, `gamma_high`, and `flagged` are also included. With `p_value = TRUE`, `padj_bh` and `Significance` are replaced by `p_gamma` and `padj_gamma`.

Multiple comparisons

The marginal p-value controls the error rate of a *single* comparison: for one item (or item pair) decided on in advance it is the relevant value. But scanning all k comparisons and flagging whichever fall below α tests k hypotheses at once, so the chance of at least one false flag inflates to roughly $1 - (1 - \alpha)^k$ (e.g. about 34% for $k = 8$ at $\alpha = 0.05$) – even when every marginal p-value is correctly calibrated. The corrected (adjusted) p-value controls this: `correction = "fwer"` bounds the probability of *any* false flag (strict, lower power), while `"fdr_bh" / "fdr_by"` bound the expected *proportion* of false flags among those raised (a more lenient middle ground). Rule of thumb: use the marginal p-value for a single pre-specified comparison, and a corrected p-value when screening the whole table – the usual workflow.

References

Bjorner, J. B., Kreiner, S., Ware, J. E., Damsgaard, M. T., & Bech, P. (1998). Differential item functioning in the Danish translation of the SF-36. *Journal of Clinical Epidemiology*, *51*(11), 1189–1202. doi:10.1016/S08954356(98)001115

Ferreira, J. A. (2024). Methods of testing a 'small' or 'moderate' number of hypotheses simultaneously. *Journal of Statistical Theory and Practice*, 19(6). doi:10.1007/s42519024004124

Westfall, P. H., & Young, S. S. (1993). *Resampling-Based Multiple Testing*. Wiley.

See Also

[RMdifGammaCutoff](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)
  dif_group <- factor(sample(c("A", "B"), 200, replace = TRUE))

  # Default kable output
  RMdifGamma(sim_data, dif_group)

  # Return as data.frame
  RMdifGamma(sim_data, dif_group, output = "dataframe")

  # Simulation-based cutoffs (100 Monte-Carlo iterations)
  if (requireNamespace("ggdist", quietly = TRUE)) {
    cutoff_res <- RMdifGammaCutoff(sim_data, dif_var = dif_group,
                                   iterations = 100, parallel = FALSE,
                                   seed = 42)
    RMdifGamma(sim_data, dif_group, cutoff = cutoff_res)

    # Bootstrap p-values with family-wise (Westfall-Young) correction
    # (use iterations >= 1000 in real analyses for stable p-values)
    RMdifGamma(sim_data, dif_group, cutoff = cutoff_res, p_value = TRUE,
               output = "dataframe")
  }
}
```

RMdifGammaCutoff

Simulation-Based Partial Gamma DIF Cutoff Determination

Description

Uses parametric bootstrap simulation to determine appropriate cutoff values for partial gamma DIF analysis via [partgam_DIF](#). Under a correctly fitting Rasch model where the DIF variable is unrelated to item responses (i.e., no true DIF), this function generates the expected distribution of absolute partial gamma values per item, providing empirical critical values.

Usage

```

RMdifGammaCutoff(
  data,
  dif_var,
  iterations = 250,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  cutoff_method = "hdci",
  hdci_width = 0.99
)

```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Only complete cases (rows without any NA) are used.
<code>dif_var</code>	A vector (factor, character, or integer) defining group membership for DIF analysis. Must have the same length as <code>nrow(data)</code> . The actual group labels are used to determine the number of groups and their relative sizes; during simulation, respondents are randomly assigned to groups with the same proportions, so there is no true DIF by construction.
<code>iterations</code>	Integer. Number of simulation iterations (default 250).
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> if available (default TRUE).
<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first. If neither is set and <code>parallel = TRUE</code> , a warning is issued and execution falls back to sequential (single core) processing.
<code>verbose</code>	Logical. Show a progress bar (default FALSE).
<code>seed</code>	Integer or NULL. Random seed for reproducibility.
<code>cutoff_method</code>	Character string specifying how cutoff intervals are computed. Either "hdci" (default) for the Highest Density Interval via <code>ggdist::hdci()</code> , or "quantile" for the 2.5th/97.5th percentiles via <code>stats::quantile()</code> .
<code>hdci_width</code>	Numeric. Width of the HDICI when <code>cutoff_method = "hdci"</code> . Default is 0.99 (99\ cutoff_method = "quantile".

Details

For each simulation iteration the function:

1. Resamples person parameters (thetas) with replacement from the WLE person locations.
2. Simulates item response data under a Rasch model (dichotomous via `psychotools::rrm()` or polytomous via an internal partial credit simulator).
3. Creates a random DIF variable by sampling group labels with the same proportions as the observed `dif_var`, so there is **no true DIF** by construction.
4. Computes partial gamma DIF statistics via `iarm::partgam_DIF()`.

The distribution of partial gamma values across iterations provides empirical critical values per item. Values from real data that fall outside these bounds suggest DIF that exceeds what would be expected by chance under a correctly fitting Rasch model. Failed iterations (e.g., due to convergence issues or degenerate data) are silently discarded.

The generating model uses CML item thresholds via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM) and WLE person locations, consistent with the rest of the package; responses are simulated with `psychotools::rrm()` (dichotomous) or an internal partial credit score simulator (polytomous).

Parallel processing is provided by the `mirai` package (optional). Install it with `install.packages("mirai")` to enable parallelisation.

The `iar` package must be installed (it is in Suggests, not Imports).

Value

A list with components:

`results` data.frame with columns `iteration`, `Item`, and `gamma` (one row per item per successful iteration).

`item_cutoffs` data.frame with per-item cutoff summaries: `Item`, `gamma_low`, `gamma_high`. Bounds are computed using the method specified by `cutoff_method`.

`actual_iterations` Number of successful iterations.

`sample_n` Number of complete cases used.

`sample_n_total` Number of respondents in the raw input data, before removing rows with NA in `data` or `dif_var`.

`sample_has_na` Logical. Whether `data` or `dif_var` contained any missing values.

`sample_summary` Summary statistics of estimated person parameters.

`item_names` Character vector of item names from data.

`dif_group_sizes` Named integer vector of group sizes used in the simulation (matches proportions in the observed `dif_var`).

`cutoff_method` The method used to compute cutoffs ("hdci" or "quantile").

`hdci_width` The HDCl width used (only meaningful when `cutoff_method = "hdci"`).

References

Bjorner, J. B., Kreiner, S., Ware, J. E., Damsgaard, M. T., & Bech, P. (1998). Differential item functioning in the Danish translation of the SF-36. *Journal of Clinical Epidemiology*, *51*(11), 1189–1202. doi:[10.1016/S08954356\(98\)001115](https://doi.org/10.1016/S08954356(98)001115)

Henninger, M., Radek, J., Debelak, R., & Strobl, C. (2025). Partial credit trees meet the partial gamma coefficient for quantifying DIF and DSF in polytomous items. *Behaviormetrika*, *52*, 221–257. doi:[10.1007/s41237024002523](https://doi.org/10.1007/s41237024002523)

See Also

[partgam_DIF](#)

Examples

```

if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)
  dif_sex <- sample(c("male", "female"), 200, replace = TRUE)

  # Run 100 iterations sequentially for a quick demo
  cutoff_res <- RMdifGammaCutoff(sim_data, dif_var = dif_sex,
                                iterations = 100, parallel = FALSE,
                                seed = 42)

  cutoff_res$item_cutoffs
}

```

RMdifGammaPlot

Plot Distribution of Simulated Partial Gamma DIF Values

Description

Visualises the distribution of simulation-based partial gamma DIF values from [RMdifGammaCutoff](#), optionally overlaying observed partial gamma values computed from real data via [partgam_DIF](#).

Usage

```
RMdifGammaPlot(simfit, data, dif_var)
```

Arguments

simfit	The return value of RMdifGammaCutoff (a list with components results, item_cutoffs, actual_iterations, sample_n, and item_names).
data	Optional. A data.frame or matrix of item responses for computing and overlaying observed partial gamma values. Items must be scored starting at 0 (non-negative integers). When provided, the plot includes orange diamond markers for the observed partial gamma alongside the simulated distribution, plus segment summaries from the cutoff intervals.
dif_var	Required when data is supplied. A vector (factor, character, or integer) defining group membership for the DIF analysis. Must have the same length as nrow(data).

Details

Uses `ggdist::stat_dotsinterval()` (when data is not supplied) or `ggdist::stat_dots()` (when data is supplied) with `point_interval = "median_hdci"` and `.width = c(0.66, 0.95, 0.99)`.

When data is **not** supplied, the function plots the simulated partial gamma distributions as dot-interval plots using `ggdist::stat_dotsinterval()` with median and Highest Density Continuous Interval (HD CI) summaries.

When data **is** supplied (along with `dif_var`), the function:

1. Computes observed partial gamma values via `iarm::partgam_DIF()`.
2. Overlays observed gamma values as orange diamond markers on the simulated distributions.
3. Shows per-item cutoff intervals (from `simfit$item_cutoffs`) as black line segments, with thicker segments for the 66\ black dots for the median.

The `ggplot2`, `ggdist`, and optionally `iarm` packages must be installed (they are in `Suggests`, not `Imports`).

Value

A `ggplot` object.

See Also

[RMdifGammaCutoff](#), [RMdifGamma](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)
  dif_group <- factor(sample(c("A", "B"), 200, replace = TRUE))

  # Run simulation
  cutoff_res <- RMdifGammaCutoff(sim_data, dif_var = dif_group,
                                iterations = 100, parallel = FALSE,
                                seed = 42)

  # Simulated distribution only
  RMdifGammaPlot(cutoff_res)

  # With observed partial gamma overlaid
  RMdifGammaPlot(cutoff_res, data = sim_data, dif_var = dif_group)
}
```

Description

Splits a Rasch model by an external grouping variable using `eRm::LRtest()` and reports per-group item locations (or per-group threshold locations) together with their standard errors. A single function replaces the four legacy helpers (`RIidifTableLR`, `RIidifThreshTblLR`, `RIidifFigureLR`, `RIidifThreshFigLR`) by exposing the two underlying axes – `level` (item or threshold) and `output` (`data.frame`, `kable`, or `ggplot`) – as arguments. The same data preparation pipeline feeds all six combinations.

Usage

```
RMdifLR(
  data,
  dif_var,
  model = c("auto", "PCM", "RM"),
  level = c("item", "threshold"),
  output = c("kable", "dataframe", "ggplot"),
  cutoff = 0.5,
  conf = 0.95,
  sort = FALSE
)
```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses (non-negative integers, 0-based). One column per item, one row per person. Person IDs and grouping variables must not be included – pass the grouping variable separately via <code>dif_var</code> .
<code>dif_var</code>	Vector of length <code>nrow(data)</code> (factor, character, or numeric) defining the DIF grouping variable. Coerced to factor; unused levels are dropped. Rows where <code>dif_var</code> is NA are dropped with a message. Must result in at least 2 groups after cleaning.
<code>model</code>	One of "auto" (default), "PCM", or "RM". "auto" fits <code>eRm::RM()</code> when the data are dichotomous (max response = 1) and <code>eRm::PCM()</code> otherwise. "RM" errors on polytomous data.
<code>level</code>	One of "item" (default) or "threshold". "item" reports each item's mean threshold location per group; "threshold" reports each individual threshold per group. For dichotomous (RM) data the two views are equivalent (one threshold per item).
<code>output</code>	One of "kable" (default), "dataframe", or "ggplot". The <code>data.frame</code> view always carries a <code>Flagged</code> logical column; the <code>kable</code> view bolds flagged rows; the <code>ggplot</code> view shows confidence intervals.

cutoff	Numeric or NULL. Threshold (in logits) for the Flagged column: a row is flagged when $\text{MaxDiff} > \text{cutoff}$, where MaxDiff is the difference between the largest and smallest per-group location for that item (or threshold). Set to NULL to suppress flagging. Default 0.5.
conf	Numeric in (0, 1). Confidence level used for the ggplot error bars. Default 0.95.
sort	Logical. kable output only: sort rows by MaxDiff (descending). Default FALSE.

Details

The Partial Credit Model (PCM) is fitted by default for polytomous data and the dichotomous Rasch Model (RM) is fitted when all responses are 0/1; this can be overridden via `model`.

For the `data.frame` and `kable` outputs, locations are reported on the centred `eRm` parameterisation returned by `eRm::thresholds()`. Per-group fits come from `eRm::LRtest(..., splitcr = dif_var)`; the unsplit fit (All column) is the model fitted to the full dataset. The Andersen LR statistic, `df`, and `p-value` reported as the `lr_test` attribute / caption come directly from `LRtest()`'s return value.

`cell_spec()`-style HTML cell colouring used in the legacy `easyRasch` package has been dropped in favour of a logical `Flagged` column (and bold rendering in the `kable` output), so the `kable` renders correctly in HTML, LaTeX, and pipe/markdown.

Value

A `data.frame`, a `knitr_kable` object, or a `ggplot` object, depending on output.

The `data.frame` has one row per item (`level = "item"`) or per item x threshold (`level = "threshold"`), with columns `Item` (and `Threshold` at threshold level), one numeric column per group level, an `All` column for the unsplit fit, `MaxDiff`, `Flagged` (when `cutoff` is non-NULL), and matching `SE_*` columns.

The Andersen LR test result is attached as `attr(result, "lr_test")` on the `data.frame`, in the `kable` footnote, and in the `ggplot` caption ($\text{LR } \chi^2$, `df`, `p-value`).

Examples

```
if (requireNamespace("eRm", quietly = TRUE)) {
  set.seed(1)
  data("pcmdat2", package = "eRm")
  grp <- factor(sample(c("A", "B"), nrow(pcmdat2), replace = TRUE))

  # Default: kable of per-group item locations
  RMdifLR(pcmdat2, dif_var = grp)

  # ggplot panel of item locations with 95% CIs
  RMdifLR(pcmdat2, dif_var = grp, output = "ggplot")

  # Threshold-level kable, sorted by MaxDiff
  RMdifLR(pcmdat2, dif_var = grp, level = "threshold", sort = TRUE)

  # Tidy data.frame for downstream use
  df <- RMdifLR(pcmdat2, dif_var = grp, output = "dataframe")
  attr(df, "lr_test")
}
```

```

    df[df$Flagged, ]
  }

```

 RMdifTree

Tree-based DIF analysis with effect-size classification

Description

Detects Differential Item Functioning (DIF) by recursively splitting the sample on one or more covariates using `psychotree::raschtree()` (dichotomous data) or `psychotree::pctree()` (polytomous data), then computes per-split effect-size measures for every item – the Mantel-Haenszel odds-ratio (Holland & Thayer, 1986), on the Delta scale developed at the Educational Testing Service (ETS; Zwick, 2012), for dichotomous data, or the partial gamma coefficient for polytomous data – and classifies them into ETS A/B/C categories (Bjorner et al., 1998). Optionally, an iterative purification step (Henninger et al., 2025) is applied, and tree stability across resamples can be assessed via `stablelearner::stabletree()` (Philipp et al., 2018).

Usage

```

RMdifTree(
  data,
  covariates,
  model = c("auto", "PCM", "RM"),
  effect_size = c("auto", "MH", "pgamma"),
  purification = c("none", "iterative"),
  p_adj = c("none", "fdr", "bonferroni"),
  thresholds = c(0.21, 0.31),
  alpha = 0.05,
  prune_negligible = FALSE,
  stability = FALSE,
  stability_B = 100L,
  stability_sampler = c("subsampling", "bootstrap"),
  min_n_per_level = 20L,
  on_rescale = c("message", "warning", "stop"),
  output = c("kable", "dataframe", "tree", "plot"),
  ...
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses (non-negative integers, 0-based). One column per item. Items only – pass covariates separately via <code>covariates</code> .
<code>covariates</code>	A <code>data.frame</code> with <code>nrow(data)</code> rows giving the DIF covariates. Columns may be numeric (continuous), factor, ordered factor, or logical. At least one column is required.

model	One of "auto" (default), "PCM", or "RM". "auto" picks RM when the data are dichotomous (max response = 1) and PCM otherwise.
effect_size	One of "auto" (default), "MH" (Mantel-Haenszel), or "pgamma" (partial gamma). "auto" uses MH for RM and partial gamma for PCM.
purification	"none" (default) or "iterative". Iterative purification recomputes the effect size while excluding items already classified as DIF from the matching score (Bjorner et al., 1998).
p_adj	Multiple-testing adjustment for the partial-gamma classification: "none" (default), "fdr" (Benjamini & Hochberg), or "bonferroni". Ignored for MH (which uses the ETS test directly).
thresholds	Numeric length-2 vector with the partial-gamma B/C boundaries (default $c(0.21, 0.31)$). Ignored for MH (the ETS Delta-scale boundaries 1.0 / 1.5 are used).
alpha	Significance level for the A/C tests. Default 0.05.
prune_negligible	Logical. If TRUE, splits whose every item is classified as A are pruned from the tree. Default FALSE.
stability	Logical. If TRUE, runs <code>stablelearner::stabetree()</code> on the fitted tree to assess variable-selection and cutpoint stability across resamples. Default FALSE.
stability_B	Integer. Number of resamples for stability assessment. Default 100.
stability_sampler	One of "subsampling" (default) or "bootstrap". Subsampling is recommended for tree stability because bootstrap resamples can drop levels of categorical covariates, breaking the model fit on small subsamples.
min_n_per_level	Integer. Minimum count required for any factor level in covariates. Default 20. Set to 0 to disable.
on_rescale	One of "message" (default), "warning", or "stop". Controls how the function reports the situation in which one or more items have no responses in their lowest category within a terminal node of the tree (psychotree silently rescales those items per node, which leaves the per-node item parameters on a different metric). <i>The MH and partial-gamma effect sizes reported here are computed on the raw responses and are not affected.</i> The diagnostic concerns only the per-node item parameters that are visible via <code>plot(tree)</code> .
output	One of "kable" (default), "dataframe", "tree", or "plot". "kable" renders the per-split per-item effect-size table as a <code>knitr::kable()</code> ; "dataframe" returns the underlying tidy data.frame; "tree" returns the augmented partykit tree object; "plot" returns the partykit tree plot with item names on the terminal-node x-axis (<code>tp_args = list(names = TRUE)</code>). For full control over the plot, use <code>output = "tree"</code> and call <code>plot()</code> on the result with your own <code>tp_args</code> . When <code>stability = TRUE</code> , the stability summary is attached as <code>attr(result, "stability")</code> (a small data.frame) and <code>attr(result, "stability_kable")</code> (pre-rendered kable).
...	Additional arguments forwarded to <code>psychotree::raschtree()</code> or <code>psychotree::pctree()</code> , e.g. <code>minsize</code> , <code>alpha</code> for the parameter-instability test. Note: this <code>alpha</code> (the tree-fitting argument) is independent of the <code>alpha</code> for ETS classification above; pass it via ...

Details

Continuous covariates (e.g., age in years) and interactions among multiple covariates are handled natively by the model-based recursive-partitioning machinery of `partykit` / `psychotree`.

ETS Delta-scale Mantel-Haenszel. The MH common odds ratio $\hat{\alpha}_{MH}$ is mapped to the ETS Delta scale via $\Delta_{MH} = -2.35 \log \hat{\alpha}_{MH}$. The classification rules (Holland & Thayer, 1988; Zwick, 2012) are:

- Class **A**: $|\Delta_{MH}| < 1$ or test of $\Delta_{MH} = 0$ not rejected at alpha.
- Class **C**: $|\Delta_{MH}| \geq 1.5$ and test of $|\Delta_{MH}| \leq 1$ rejected at alpha.
- Class **B**: otherwise.

`easyRasch2` uses the sign convention of `effecttree`: positive Δ indicates that the item is more difficult for the second (reference) group.

Partial gamma. `iarm::partgam_DIF()` provides the gamma estimate and SE per item. ETS-style classification follows Bjorner et al. (1998): A if $|\gamma| < 0.21$ or the test of $\gamma = 0$ is not rejected at alpha; C if $|\gamma| > 0.31$ and the test of $|\gamma| \leq 0.21$ is rejected at alpha; B otherwise.

Rule-of-thumb caveat. The A/B/C boundaries (Delta 1.0 / 1.5; gamma 0.21 / 0.31) are conventions carried over from large-scale educational testing, not values calibrated to the sample and items at hand – in contrast to the simulation-based cutoffs used elsewhere in this package – so the classification is best read as a rough magnitude guide rather than a calibrated test. For a sample-calibrated partial-gamma DIF test, see `RMdifGamma()` with an `RMdifGammaCutoff()` object (optionally with `p_value = TRUE`).

Continuous and interaction effects. The recursive partitioning step automatically handles continuous covariates (the parameter-instability test searches for the optimal cutpoint) and multivariate interactions (later splits are conditional on earlier ones). To assess sensitivity of variable selection and cutpoints to the particular sample, set `stability = TRUE`.

Stability assessment. When `stability = TRUE`, the same tree-fitting call is replayed on `stability_B` resamples of the data. The returned `stabletree` object reports, per covariate, the proportion of resamples in which it was selected at any split, and (for continuous covariates) the empirical distribution of cutpoints. Stability is independent of effect-size classification – a stable split with a negligible effect is still negligible, and a large effect on an unstable split should be interpreted with care. Cost is roughly `stability_B` times the original fitting time.

Acknowledgement. The effect-size machinery – MH and partial gamma per node, iterative purification, ETS A/B/C classification – follows the implementations by Henninger & Radek in the GitHub packages `raschtreeMH` and `effecttree`. The relevant code has been adapted here under the MIT licence (see file header).

Value

Depending on output:

"kable" A `kable` object with one row per (split node x item), grouped by node via `pack_rows`-style section headers. The caption summarises model, effect-size measure, purification, and (if requested) stability.

"dataframe" A `data.frame` with one row per (split node x item): columns `NodeID`, `Split` (human-readable description of the split), `Variable`, `Direction`, `Item`, `EffectSize`, `SE`, `Class (A/B/C)`, `Flagged (TRUE for B or C)`, `n_left`, `n_right`.

"tree" The fitted partykit tree object with class `c("RMdifTree", ...)`, with effect-size results stored at `tree$info$effectsize`.

"plot" A plotted partykit tree.

Stability results (when `stability = TRUE`) are attached to the return value as `attr(result, "stability")` (data.frame) and `attr(result, "stability_kable")` (pre-rendered kable).

References

Bjorner, J. B., Kreiner, S., Ware, J. E., Damsgaard, M. T., & Bech, P. (1998). Differential item functioning in the Danish translation of the SF-36. *Journal of Clinical Epidemiology*, *51*(11), 1189-1202. doi:10.1016/S08954356(98)001115

Henninger, M., Debelak, R., & Strobl, C. (2023). A new stopping criterion for Rasch trees based on the Mantel-Haenszel effect size measure for DIF. *Educational and Psychological Measurement*, *83*, 181-212. doi:10.1177/00131644221077135

Henninger, M., Radek, J., Debelak, R., & Strobl, C. (2025). Partial credit trees meet the partial gamma coefficient for quantifying DIF and DSF in polytomous items. *Behaviormetrika*, *52*, 221-257. doi:10.1007/s41237024002523

Holland, P. W., & Thayer, D. T. (1986). Differential item performance and the Mantel-Haenszel procedure. *ETS Research Report Series*(2). doi:10.1002/j.23308516.1986.tb00186.x

Philipp, M., Rusch, T., Hornik, K., & Strobl, C. (2018). Measuring the stability of results from supervised statistical learning. *Journal of Computational and Graphical Statistics*, *27*, 685-700. doi:10.1080/10618600.2018.1473779

Asamoah, N. A. B., Turner, R. C., Lo, W.-J., Crawford, B. L., & Jozkowski, K. N. (2025). Impacts of DIF Item Balance and Effect Size Incorporation With the Rasch Tree. *Educational and Psychological Measurement*. doi:10.1177/00131644251370605

Zwick, R. (2012). A review of ETS differential item functioning assessment procedures: Flagging rules, minimum sample size requirements, and criterion refinement. *ETS Research Report Series*(1). doi:10.1002/j.23338504.2012.tb02290.x

See Also

[RMdifLR](#), [RMdifGamma](#)

Examples

```
if (requireNamespace("psychotree", quietly = TRUE) &&
    requireNamespace("partykit", quietly = TRUE) &&
    requireNamespace("difR", quietly = TRUE) &&
    requireNamespace("iarm", quietly = TRUE)) {
  data("DIFSimPC", package = "psychotree")

  items <- as.data.frame(as.matrix(DIFSimPC$resp))
  covs <- DIFSimPC[, c("age", "gender", "motivation")]

  # Default: kable of per-split effect sizes
  RMdifTree(items, covariates = covs)
```

```

# Tidy data.frame -- one row per (split node x item)
df <- RMdifTree(items, covariates = covs, output = "dataframe")
df[df$Flagged, ]

# Tree object (for plotting via partykit::plot)
tree <- RMdifTree(items, covariates = covs, output = "tree")
plot(tree)

# Stability assessment refits the tree on B resamples.
# (use more resamples, e.g. 100+, in real analyses)
if (requireNamespace("stablelearner", quietly = TRUE)) {
  kbl <- RMdifTree(items, covariates = covs,
                   purification = "iterative", p_adj = "fdr",
                   stability = TRUE, stability_B = 25)
  kbl # main effect-size kable
  attr(kbl, "stability_kable") # pre-rendered stability kable
  attr(kbl, "stability") # raw stability data.frame
}
}

```

RMdimCFA

Observed one-factor CFA fit and loadings vs a simulated reference

Description

Fits the observed one-factor categorical CFA to data and compares its fit indices and per-item standardized loadings against the simulated null distribution produced by `RMdimCFACutoff`. Returns a list of two tables: model-fit indices and per-item loadings, each with the observed value, the expected reference from the simulation, and a flag.

Usage

```

RMdimCFA(
  data,
  cutoff,
  p_value = FALSE,
  correction = c("fwer", "fdr_bh", "fdr_by", "none"),
  alpha = 0.05,
  output = c("kable", "dataframe")
)

```

Arguments

`data` A data.frame or matrix of item responses (non-negative integers, 0-based), the same items used for the cutoff simulation.

cutoff	The list returned by <code>RMdimCFACutoff</code> . Required: observed CFA fit indices are not interpretable without the simulated reference, so the function errors if it is missing.
p_value	Logical. When TRUE, adds bootstrap p-values from the simulated null distributions: one-sided in the unfavourable direction for the fit indices (CFI low; RMSEA / SRMR high), two-sided for the per-item loadings. The Flagged columns then reflect $\text{p_adj} < \alpha$ instead of the percentile cutoffs. The fit indices and the loadings are corrected as two separate families. Default FALSE.
correction	Character. Multiplicity correction for the p-values: "fwer" (default; Westfall-Young studentised-max step-down), "fdr_bh" (Benjamini-Hochberg), "fdr_by" (Benjamini-Yekutieli), or "none". Ignored when p_value = FALSE.
alpha	Numeric in (0, 1). Significance level used to flag comparisons on the corrected p-value. Default 0.05. Ignored when p_value = FALSE.
output	Character. "kable" (default) returns each table as a <code>knitr::kable()</code> ; "dataframe" returns plain data.frames.

Details

Bootstrap p-values. The per-comparison statistic is the residual studentised by the bootstrap mean and SD. Marginal p-values are Monte-Carlo, $(1 + \text{count}) / (B + 1)$, so they can be no smaller than $1 / (B + 1)$. `correction = "fwer"` uses the Westfall-Young studentised-max step-down, which exploits the bootstrap dependence among the statistics (Ferreira, 2024); it is liberal when the simulation is small, so at least 1000 iterations in `RMdimCFACutoff()` are recommended (a warning is issued below that). These p-values are model-conditional and sample-size-sensitive and are reported alongside the simulated expected ranges, not in place of them.

Value

A named list with two elements, `fit` and `loadings`:

`fit` CFI / RMSEA / SRMR with columns `Index`, `Observed`, `Cutoff`, `Direction`, `Flagged` (one-sided, in the unfavourable direction). With `p_value = TRUE`, columns `p` and `p_adj` are added and `Flagged` reflects $\text{p_adj} < \alpha$.

`loadings` One row per item with columns `Item`, `Observed`, `Expected_low`, `Expected_high`, `Flagged` ("below" / "above" / ""). With `p_value = TRUE`, columns `p_loading` and `p_adj_loading` are added and `Flagged` reflects $\text{p_adj_loading} < \alpha$ (direction from the sign of the deviation from the simulated mean).

Each element is a `knitr_kable` (when `output = "kable"`) or a `data.frame` (when `output = "dataframe"`).

Multiple comparisons

The marginal p-value controls the error rate of a *single* comparison: for one item (or item pair) decided on in advance it is the relevant value. But scanning all k comparisons and flagging whichever fall below α tests k hypotheses at once, so the chance of at least one false flag inflates to roughly $1 - (1 - \alpha)^k$ (e.g. about 34% for $k = 8$ at $\alpha = 0.05$) – even when every marginal p-value is correctly calibrated. The corrected (adjusted) p-value controls this: `correction = "fwer"` bounds the probability of *any* false flag (strict, lower power), while `"fdr_bh"` / `"fdr_by"` bound the expected

proportion of false flags among those raised (a more lenient middle ground). Rule of thumb: use the marginal p-value for a single pre-specified comparison, and a corrected p-value when screening the whole table – the usual workflow.

References

Ferreira, J. A. (2024). Methods of testing a 'small' or 'moderate' number of hypotheses simultaneously. *Journal of Statistical Theory and Practice*, 19(6). doi:10.1007/s42519024004124

Westfall, P. H., & Young, S. S. (1993). *Resampling-Based Multiple Testing*. Wiley.

See Also

[RMdimCFACutoff](#), [RMdimCFAPlot](#)

Examples

```
if (requireNamespace("lavaan", quietly = TRUE) &&
    requireNamespace("eRm", quietly = TRUE)) {
  data("raschdat1", package = "eRm")
  sim <- RMdimCFACutoff(raschdat1[, 1:8], iterations = 50,
                       parallel = FALSE, seed = 1)
  tabs <- RMdimCFA(raschdat1[, 1:8], cutoff = sim)
  tabs$fit
  tabs$loadings

  # Bootstrap p-values with family-wise (Westfall-Young) correction
  # (use iterations >= 1000 in real analyses for stable p-values)
  RMdimCFA(raschdat1[, 1:8], cutoff = sim, p_value = TRUE)
}
```

RMdimCFACutoff

Simulated null distribution for one-factor CFA fit and loadings under PCM unidimensionality

Description

Generates a parametric-bootstrap null distribution against which observed one-factor categorical-CFA results can be compared. The simulation draws `iterations` datasets from the fitted PCM (or RM, for dichotomous data) using the observed item parameters and a resampled person distribution; each simulated dataset is fitted with `lavaan::cfa(..., ordered = TRUE, estimator = "WLSMV")` and both the three fit indices (CFI, RMSEA, SRMR) and the per-item standardized factor loadings are recorded. Because the simulated data satisfy the PCM unidimensional assumption by construction, the resulting distributions are the "expected" reference for what a correctly fitting unidimensional model produces at this sample size and item structure.

Usage

```

RMdimCFACutoff(
  data,
  iterations = 250L,
  percentile = 99,
  output = c("list", "kable"),
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  estimator = "WLSMV"
)

```

Arguments

data	A data.frame or matrix of item responses (non-negative integers, 0-based). One column per item, one row per person.
iterations	Integer. Number of parametric-bootstrap iterations. Default 250.
percentile	Numeric in (50, 100). The strictness of the cutoffs. Default 99. Fit indices use a one-sided cutoff in the unfavourable direction (CFI from below; RMSEA and SRMR from above); standardized loadings use a two-sided central interval covering percentile% of the simulated distribution (an item is flagged when its observed loading falls in the outer 100 - percentile%, split across the two tails).
output	Character. Only "list" (the default) is supported and the function always returns the simulation object. "kable" is retained only to raise an informative error: tables now come from RMdimCFA .
parallel	Logical. If TRUE (default), uses parallel processing via mirai . Falls back to sequential if mirai is not installed or <code>n_cores</code> cannot be resolved.
n_cores	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is consulted; if neither is set, sequential is used.
verbose	Logical. Show a progress bar (default FALSE).
seed	Integer or NULL. Master seed for reproducibility.
estimator	Character. The lavaan estimator passed to <code>lavaan::cfa()</code> . Default "WLSMV". Other limited-information estimators that produce robust/scaled fit indices (e.g., "DWLS", "ULSMV") are also accepted; full-information ML is rejected (incompatible with <code>ordered = TRUE</code>).

Details

This function only generates the simulated reference. To obtain the observed-vs-expected tables, pass its result to [RMdimCFA](#); for the figures, pass it to [RMdimCFAPlot](#).

Generative model. The data-generating process for each simulated dataset is the PCM (or RM) fitted to the observed data, with persons drawn from the empirical theta distribution (resampled with replacement). This means the simulated data perfectly satisfy the PCM unidimensional assumption.

Estimation model. The CFA on each simulated dataset uses a single-factor model with all items as ordinal indicators ($F1 \approx I1 + I2 + \dots$), fitted with WLSMV by default. Reported CFI / RMSEA are the Satorra-Bentler-scaled variants (`cfi.scaled`, `rmsea.scaled`) for consistency across iterations; SRMR is reported unchanged. Standardized loadings are the `est.std` of the `\approx` paths from `lavaan::standardizedSolution()`.

Why a null distribution. A perfectly PCM-unidimensional dataset will typically not yield CFA fit indices at their ideal values (CFI = 1, RMSEA = 0), nor identical loadings across items: PCM uses a logistic threshold structure while WLSMV uses a probit link via the polychoric correlation matrix, and finite samples add sampling variability. The simulated distributions capture both, giving a more honest reference than rule-of-thumb cutoffs derived under continuous-data ML.

Iteration failures. Some simulated datasets cause WLSMV to fail (non-positive-definite polychoric matrix, boundary thresholds, empty categories). Failed iterations are dropped; `actual_iterations` reflects the number that succeeded.

Value

A list (the simulation object), with components:

`simulated` data.frame with one row per successful iteration and columns `iteration`, `cfi`, `rmsea`, `srmr`.

`simulated_loadings` data.frame with one row per successful iteration: an `iteration` column followed by one column per item holding the simulated standardized loading.

`percentile` Numeric: the strictness setting used.

`cutoffs` Named numeric vector (`cfi`, `rmsea`, `srmr`) of one-sided fit-index cutoffs at the chosen percentile.

`loading_cutoffs` data.frame `Item`, `low`, `high` — the two-sided expected loading interval per item.

`actual_iterations` Number of successful MC iterations.

`sample_n` Number of complete cases used.

`sample_n_total` Number of respondents in the raw input data, before the complete-case filter.

`sample_has_na` Logical. Whether the raw input data contained any missing values.

`n_items` Number of items.

`item_names` Character vector of item names.

`is_polytomous` Logical: was a PCM (vs RM) fitted?

`estimator` The lavaan estimator used.

References

Yuan, K.-H., & Bentler, P. M. (2000). Three likelihood-based methods for mean and covariance structure analysis with nonnormal missing data. *Sociological Methodology*, *30*(1), 165-200. doi:10.1111/00811750.00078

Rosseel, Y. (2012). lavaan: An R Package for Structural Equation Modeling. *Journal of Statistical Software*, *48*(2), 1-36. doi:10.18637/jss.v048.i02

See Also

[RMdimCFA](#), [RMdimCFAPlot](#), [RMdimResidualPCA](#), [RMdimMartinLof](#)

Examples

```

if (requireNamespace("lavaan", quietly = TRUE) &&
    requireNamespace("eRm", quietly = TRUE)) {
  data("raschdat1", package = "eRm")

  # Few iterations for a fast example; use 250+ in real analyses
  sim <- RMdimCFACutoff(raschdat1[, 1:8], iterations = 50,
                       parallel = FALSE, seed = 1)

  # Observed-vs-expected tables
  RMdimCFA(raschdat1[, 1:8], cutoff = sim)

  if (requireNamespace("ggplot2", quietly = TRUE)) {
    plots <- RMdimCFAPlot(sim, data = raschdat1[, 1:8])
    plots$loadings
    plots$fit
  }
}

```

RMdimCFAPlot

Plot observed CFA fit and loadings against the simulated null

Description

Returns two figures (in a list) comparing the observed one-factor CFA to the simulated null distribution from [RMdimCFACutoff](#): a per-item standardized-loadings plot (observed marker against each item's simulated distribution and expected range, in the style of [RMitemInfitPlot](#)), and a faceted plot of the CFI / RMSEA / SRMR distributions with the observed value overlaid.

Usage

```
RMdimCFAPlot(simfit, data, percentile = NULL)
```

Arguments

<code>simfit</code>	The list returned by RMdimCFACutoff .
<code>data</code>	The item-response data the CFA was run on (the same items used for the cutoff). Required: the observed values are computed from it.
<code>percentile</code>	Numeric in (50, 100) or NULL. When supplied, the cutoffs and flags are recomputed at this percentile from the stored simulated distributions (no re-simulation). When NULL (default), the percentile from the original <code>RMdimCFACutoff()</code> call is reused.

Value

A named list of two ggplot objects:

`loadings` Per-item standardized loadings: simulated distribution (dots), expected interval, and the observed loading as a diamond (red when flagged).

`fit` Faceted CFI / RMSEA / SRMR simulated distributions with the observed value and cutoff overlaid.

See Also

[RMdimCFACutoff](#), [RMdimCFA](#)

Examples

```
if (requireNamespace("lavaan", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("eRm", quietly = TRUE)) {
  data("raschdat1", package = "eRm")
  sim <- RMdimCFACutoff(raschdat1[, 1:8], iterations = 50,
                       parallel = FALSE, seed = 1)
  plots <- RMdimCFAPlot(sim, data = raschdat1[, 1:8])
  plots$loadings
  plots$fit
}
```

Description

Likelihood-ratio test of unidimensionality against an *a priori* specified multidimensional alternative, generalised to polytomous Rasch / partial credit models (Christensen, Bjorner, Kreiner, & Petersen, 2002). The p-value is obtained by parametric-bootstrap (Monte Carlo) sampling under the unidimensional null, following Christensen & Kreiner (2007), because the asymptotic chi-square approximation is biased toward conservatism for realistic sample sizes – especially with polytomous items, where the degrees of freedom can be very large.

Usage

```
RMdimMartinLof(
  data,
  partition,
  iterations = 1000L,
  stopping = c("none", "sequential"),
  h = 50L,
  alpha = 0.05,
```

```

parallel = TRUE,
n_cores = NULL,
verbose = FALSE,
seed = NULL
)

```

Arguments

data	A data.frame or matrix of item responses (0-based, non-negative integers). Rows with any NA are dropped.
partition	The hypothesised partition of items into subscales. One of: <ul style="list-style-type: none"> • a list of column-name or column-index vectors, e.g. <code>list(c("I1", "I2", "I3"), c("I4", "I5", "I6"))</code>; • a vector of length <code>ncol(data)</code> indicating each item's subscale (factor, character, or integer), e.g. <code>c(1, 1, 1, 2, 2, 2)</code>. Each subscale must contain at least two items. Subscales must not overlap; items not assigned to any subscale are dropped with a warning.
iterations	Integer. Maximum number of Monte Carlo iterations (default 1000).
stopping	Character. "none" (default) runs all iterations. "sequential" uses Besag & Clifford's (1991) sequential rule: stop as soon as h simulated statistics have exceeded the observed value. The sequential strategy substantially reduces compute time when H0 holds but cannot be parallelised.
h	Integer. Sequential-stopping count threshold (default 50). Ignored when stopping = "none".
alpha	Numeric in (0, 1). Nominal significance level used only for the rejected flag in the result; default 0.05.
parallel	Logical. Use parallel processing via mirai (default TRUE). Ignored when stopping = "sequential".
n_cores	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first; if neither is set, falls back to sequential with a warning.
verbose	Logical. Show a progress bar (default FALSE).
seed	Integer or NULL. Random seed for reproducibility.

Details

This is **not** a routine screening tool. The test requires an *a priori* partition of items into subscales; using it post-hoc on, e.g., the partition suggested by `RMdimResidualPCA()`'s PC1 sign would inflate the Type-I error rate. Both source papers state this explicitly.

Test statistic. With items partitioned into D subscales, total score t and subscores (t_1, \dots, t_D) (Christensen et al. 2002, eq. 22):

$$T = 2 \left[\sum_{t_1, \dots, t_D} n_{t_1, \dots, t_D} \log(n_{t_1, \dots, t_D} / N) - \sum_t n_t \log(n_t / N) - \ell_C(\hat{\epsilon}) + \sum_d \ell_C(\hat{\epsilon}^{(d)}) \right]$$

where ℓ_C is the conditional log-likelihood and the $\hat{\epsilon}^{(d)}$ are CML estimates on the d-th subscale alone. CML fits use `psychotools::raschmodel()` (RM) or `psychotools::pcmodel()` (PCM) for speed.

Monte Carlo sampling under H0. Following Christensen & Kreiner (2007): (a) sample N total scores from the empirical score distribution n_t/N ; (b) for each sampled score, sample an item-response vector from the conditional distribution $p(x | t, \hat{\epsilon})$ given by eq. 4 of the paper. For dichotomous data the fast algorithm of Christensen & Kreiner (2007, p. 23) is used (sample without replacement weighted by item easinesses). For polytomous data the recursive γ -function approach is used, with each item's response sampled conditional on the remaining items' joint score distribution (computed via `psychotools::elementary_symmetric_functions()`).

Iterations that fail (e.g., simulated dataset has an empty category for an item) are silently dropped.

Item parameters are estimated once on the observed data and held fixed across MC iterations. Christensen & Kreiner (2007) use the extended likelihood function (Tjur, 1982) with the empirical score distribution as a non-parametric estimate of the latent distribution, so no distributional assumption about θ is needed.

Value

A list with components:

`T_obs` Observed Martin-Löf likelihood-ratio statistic.

`p_value` Monte Carlo p-value with $(n_exceed + 1) / (n + 1)$ correction.

`actual_iterations` Number of successful MC iterations completed.

`rejected` Logical: is `p_value < alpha`?

`partition` Normalised partition (list of integer indices).

`n_subscales` Number of subscales.

`is_polytomous` Whether a PCM was fitted.

`sample_n` Number of complete cases analysed.

`n_items` Number of items.

`stopping` The stopping strategy used.

`h` The sequential-stopping count, or NA for `stopping = "none"`.

`T_rep` Numeric vector of successful MC test statistics.

`wle_scores` data.frame with one row per person and one column per subscale (`subscale_1_wle`, ..., `subscale_D_wle`), giving Warm's Weighted Likelihood Estimate of theta from a CML fit on each subscale alone. Persons whose subscore equals the minimum or maximum on a subscale produce non-finite WLEs ($-\infty$ / ∞) and are excluded from `wle_correlation` pairwise.

`wle_correlation` data.frame of pairwise Pearson correlations between subscale WLEs, with columns `subscale_a`, `subscale_b`, `r`, `ci_lower`, `ci_upper` (95% CI from `stats::cor.test`), `p_value`, and `n` (number of persons with finite WLEs on both subscales). One row per pair; for $D = 2$, a single row. Useful as an effect-size companion to `p_value` – a rejected test with `r` near 1 indicates a small effect; `r` clearly below 1 indicates substantive multidimensionality.

References

Christensen, K. B., Bjorner, J. B., Kreiner, S., & Petersen, J. H. (2002). Testing unidimensionality in polytomous Rasch models. *Psychometrika*, 67(4), 563-574. doi:10.1007/BF02295132

Christensen, K. B., & Kreiner, S. (2007). A Monte Carlo approach to unidimensionality testing in polytomous Rasch models. *Applied Psychological Measurement*, *31*(1), 20-30. doi:10.1177/0146621605286204

Besag, J., & Clifford, P. (1991). Sequential Monte Carlo p-values. *Biometrika*, *78*(2), 301-304. doi:10.1093/biomet/78.2.301

See Also

[RMdimResidualPCA](#), [RMdimResidualPCACutoff](#)

Examples

```
set.seed(1)
# Build 2-dimensional polytomous data: 4 items per subscale, 5 categories
n <- 400
theta1 <- rnorm(n)
theta2 <- 0.6 * theta1 + sqrt(1 - 0.6^2) * rnorm(n)
make_pcm <- function(theta, n_items, taus) {
  sapply(seq_len(n_items), function(j) {
    # ... toy simulation here
    sample(0:4, n, replace = TRUE)
  })
}
dat <- cbind(make_pcm(theta1, 4, NULL), make_pcm(theta2, 4, NULL))
colnames(dat) <- paste0("I", 1:8)

# Few iterations for a fast example; use 1000+ in real analyses
RMdimMartinLof(dat,
  partition = list(c("I1", "I2", "I3", "I4"),
                  c("I5", "I6", "I7", "I8")),
  iterations = 100, parallel = FALSE, seed = 1)

# Sequential stopping: stop as soon as h = 25 simulated statistics exceed
# the observed one (cuts compute time under H0).
RMdimMartinLof(dat,
  partition = c(1,1,1,1,2,2,2,2),
  iterations = 200, stopping = "sequential", h = 25,
  seed = 1)
```

RMdimMartinLofResiduals

Standardised Residuals from the Joint Subscore Distribution

Description

Diagnostic accompanying [RMdimMartinLof](#): per-cell standardised residuals from the joint distribution of subscores under unidimensionality (Christensen, Bjorner, Kreiner, & Petersen, 2002, eq. 13). Useful for identifying *where* a partition deviates from the unidimensional null rather than just whether it does (which [RMdimMartinLof\(\)](#) answers).

Usage

```

RMdimMartinLofResiduals(
  data,
  partition,
  output = c("kable", "dataframe", "ggplot"),
  flag_threshold = 2,
  color_by = c("residual", "n"),
  color_limits = NULL,
  min_expected = NULL
)

```

Arguments

<code>data</code>	A data.frame or matrix of item responses (0-based, non-negative integers). Rows with any NA are dropped.
<code>partition</code>	Same format as in <code>RMdimMartinLof</code> : a list of item-name/index vectors, or a length-ncol(data) vector of group labels. Each subscale must contain at least 2 items.
<code>output</code>	Character. "kable" (default) for a 2-D pipe-format residual table when $D = 2$ (long-format kable when $D > 2$), "dataframe" for the underlying long-format data.frame, or "ggplot" for a diverging-fill heatmap (with <code>facet_wrap</code> over t_3 for $D = 3$, error for $D > 3$).
<code>flag_threshold</code>	Numeric. Cells with $ \text{residual} > \text{flag_threshold}$ are flagged: marked as bold in the kable, shown in the flagged column of the dataframe. Default 2.
<code>color_by</code>	Character. For output = "ggplot", what the tile fill colour encodes. "residual" (default) – diverging red-white-blue scale centred at 0, the most directly diagnostic. "n" – sequential blue scale on the observed cell count, useful for spotting whether large-magnitude residuals are driven by sparse cells. Either way, the numeric residual is printed inside each cell.
<code>color_limits</code>	Numeric length-2 vector or NULL. Caps the colour scale for output = "ggplot". Default <code>c(-5, 5)</code> when <code>color_by = "residual"</code> (sparse-cell residuals from $(o-e)/\sqrt{n \cdot p \cdot (1-p)}$) can be enormous when expected counts are tiny; capping the scale stops outliers from compressing the rest of the plot). The unclipped residual values still appear as cell labels. NULL for <code>color_by = "n"</code> , which uses the natural data range.
<code>min_expected</code>	Numeric or NULL. If set, cells with $\text{expected} < \text{min_expected}$ have their residual set to NA (they appear grey in the heatmap and are not flagged). Default NULL (no filtering). Setting <code>min_expected = 1</code> (or 5) is the analogue of the Cochran rule for sparse-cell chi-square contributions and removes residuals whose asymptotic standard normal approximation is unreliable.

Details

For each cell of the joint subscore table (indexed by (t_1, \dots, t_D)), the conditional probability under H_0 given the total score $t = \sum_d t_d$ is

$$p(t_1, \dots, t_D | t) = \prod_d \gamma_{t_d}^{(d)} / \gamma_t,$$

the expected count is $e = n_t \cdot p$, and the residual is $(o - e) / \sqrt{n_t \cdot p \cdot (1 - p)}$. CML estimates from the unidimensional model are used for the γ -functions.

Reading the table ($D = 2$): under the unidimensional null, residuals should be patternless and roughly $N(0, 1)$. Multidimensionality with positively correlated dimensions typically shows up as **positive** residuals at the corners of each antidiagonal (high t_1 + low t_2 , low t_1 + high t_2) and **negative** residuals near the antidiagonal centre (matched subscores). Negatively correlated dimensions show positive residuals at the table corners (high/low and low/high) and negative residuals at high/high and low/low. See Christensen et al. (2002, section7) for a worked example.

Cells where the total score has no observed cases ($n_t = 0$) are uninformative and are dropped from the output.

Value

- `output = "kable"`: a `knitr_kable` object. For $D = 2$, a wide table with rows = t_1 , columns = t_2 , cells = standardised residual (****bold**** if flagged, em-dash if NA). For $D > 2$, long-format with one row per cell.
- `output = "dataframe"`: a long-format data.frame with columns $t_1, \dots, t_D, \text{total}, \text{observed}, \text{expected}, \text{residual}, \text{flagged}$.
- `output = "ggplot"`: a `geom_tile()` heatmap ($D = 2$ or 3 only).

References

Christensen, K. B., Bjorner, J. B., Kreiner, S., & Petersen, J. H. (2002). Testing unidimensionality in polytomous Rasch models. *Psychometrika*, 67(4), 563-574. doi:10.1007/BF02295132

See Also

[RMdimMartinLof](#)

Examples

```
set.seed(1)
dat <- as.data.frame(matrix(sample(0:1, 400 * 8, replace = TRUE),
                           nrow = 400, ncol = 8))
colnames(dat) <- paste0("I", 1:8)

# Wide kable table for D = 2
RMdimMartinLofResiduals(dat,
  partition = list(c("I1", "I2", "I3", "I4"),
                  c("I5", "I6", "I7", "I8")))

# Heatmap
if (requireNamespace("ggplot2", quietly = TRUE)) {
  RMdimMartinLofResiduals(dat,
    partition = c(1,1,1,1,2,2,2,2),
    output = "ggplot")
}

# Underlying data.frame for custom analysis
df <- RMdimMartinLofResiduals(dat,
```

```

                                partition = c(1,1,1,1,2,2,2,2),
                                output = "dataframe")
df[df$flagged, ]

```

RMdimResidualPCA

PCA of Standardized Rasch Residuals

Description

Fits a Rasch model by CML via `psychotools` (a dichotomous item is a 2-category PCM), extracts the standardized residuals $(x - E)/\sqrt{Var}$ at WLE person locations, and runs an unrotated principal-component analysis on those residuals via `stats::prcomp()`. The function reports the top `n_components` eigenvalues and their proportions of unexplained variance, and optionally compares the first-contrast eigenvalue against a simulation-based bound from [RMdimResidualPCACutoff](#).

Usage

```

RMdimResidualPCA(
  data,
  cutoff = NULL,
  p_value = FALSE,
  n_components = 5L,
  output = "kable"
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Rows with any NA are dropped before PCA, since <code>prcomp()</code> does not accept missing values.
<code>cutoff</code>	Optional. The list returned by RMdimResidualPCACutoff (its <code>suggested_cutoff</code> is used), or a single numeric value to use as the cutoff directly. When provided, the result includes a <code>Flagged</code> column (logical: is the eigenvalue above the simulated bound?) and the kable caption notes the cutoff.
<code>p_value</code>	Logical. When TRUE, adds a one-sided bootstrap p-value for the first-contrast eigenvalue: the proportion of simulated first-contrast eigenvalues at least as large as the observed one, $(1 + \#\{\lambda^* \geq \lambda\}) / (B + 1)$. Requires the full RMdimResidualPCACutoff object as <code>cutoff</code> (it carries the simulated eigenvalues in <code>\$results</code>); a bare numeric cutoff is not sufficient. The simulated null is the distribution of the <i>largest</i> eigenvalue, so the p-value applies to PC1 only (NA for the other components). This is a single test — no multiplicity correction is involved. Default FALSE.
<code>n_components</code>	Integer. Number of eigenvalues to report. Capped at the number of items. Default 5.

output Character. "kable" (default) for a formatted `knitr::kable()` table, "dataframe" for the underlying data.frame, or "ggplot" for a ggplot of PC1 loadings against item locations. "loadings" is accepted as a backward-compatible alias for "ggplot".

Details

Rule-of-thumb thresholds for the first-contrast eigenvalue (e.g., the "> 2" heuristic occasionally cited from *Winsteps* documentation) are not reliable indicators of multidimensionality; the first-contrast eigenvalue under a correctly fitting unidimensional model varies systematically with sample size, test length, and item-parameter spread. Empirical (simulated) bounds tailored to the data structure should be used instead — see `RMdimResidualPCACutoff`, and Chou & Wang (2010) for the underlying simulation argument.

The PCA is performed on the standardized residuals $(x - E)/\sqrt{Var}$ from the shared CML/WLE engine (CML item parameters via `psychotools`, WLE person locations). The reported eigenvalues are unrotated; rotation is appropriate for *interpreting* a multidimensional solution but obscures the dominant first contrast that dimensionality assessment is concerned with.

Item locations on the loadings plot are the per-item mean of the CML Andrich thresholds.

The variance partition follows Linacre's convention: per-item observed variance is compared to per-item *expected* variance under the fitted model, summed across items. Expected scores are computed from the CML item parameters and WLE person locations. WLE is finite at extreme scores, so all persons are retained (the previous MLE partition dropped extreme-score cases).

Bootstrap p-value. When `p_value = TRUE`, the observed first-contrast eigenvalue is compared against the simulated null distribution of largest eigenvalues (from `cutoff$results`), giving the one-sided Monte-Carlo p-value $(1 + \#\{\lambda \geq \lambda\}) / (B + 1)$. Because the maximum eigenvalue is a single family-wise statistic, no multiplicity correction applies. The p-value is model-conditional and sample-size-sensitive; it is reported alongside the simulated cutoff, not in place of it, and can be no smaller than $1 / (B + 1)$.

Value

- If `output = "kable"`: a `knitr_kable` object with columns Component, Eigenvalue, Proportion of variance (and Flagged when cutoff is provided; p when `p_value = TRUE`). The caption gives the variance partition (% of total observed variance explained by measures vs. unexplained), the model fitted, sample size, and cutoff/p-value metadata if applicable.
- If `output = "dataframe"`: a `data.frame` with columns Component, Eigenvalue, Proportion_of_variance (and Flagged when cutoff is provided; p when `p_value = TRUE`, non-NA for PC1 only). The variance partition is attached as the "variance_partition" attribute — a list with elements total, explained, unexplained, pct_explained, pct_unexplained, n_persons. Access via `attr(result, "variance_partition")`.
- If `output = "ggplot"`: a ggplot showing each item's PC1 loading on the x-axis and Rasch item location on the y-axis, with dashed reference lines at zero, and the variance partition in the figure caption. Item names are labelled via `ggrepel::geom_text_repel()` when `ggrepel` is installed; otherwise plain `geom_text()`.

References

Chou, Y.-T., & Wang, W.-C. (2010). Checking dimensionality in item response models with principal component analysis on standardized residuals. *Educational and Psychological Measurement*, 70(5), 717-731. doi:10.1177/0013164410379322

See Also

[RMdimResidualPCACutoff](#)

Examples

```
set.seed(1)
dat <- as.data.frame(
  matrix(sample(0:1, 200 * 12, replace = TRUE), nrow = 200, ncol = 12)
)
colnames(dat) <- paste0("I", 1:12)

# Default kable output
RMdimResidualPCA(dat)

# PC1 loadings vs item location plot
if (requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("ggrepel", quietly = TRUE)) {
  RMdimResidualPCA(dat, output = "ggplot")
}

# Simulation-based cutoff (use 250+ iterations in real analyses)
bound <- RMdimResidualPCACutoff(dat, iterations = 50, parallel = FALSE, seed = 1)
RMdimResidualPCA(dat, cutoff = bound)

# With the one-sided bootstrap p-value for the first contrast
RMdimResidualPCA(dat, cutoff = bound, p_value = TRUE)
```

RMdimResidualPCACutoff

Simulation-based Cutoff for First-Contrast Eigenvalue

Description

Parametric bootstrap producing an empirical upper percentile for the largest eigenvalue from a PCA of standardized residuals under a correctly fitting Rasch model. For each iteration the function re-samples theta values from the data-based estimates, simulates response data, refits the appropriate Rasch model, and extracts the first-contrast eigenvalue. Several upper-tail percentiles of the resulting distribution are returned; the 99th percentile is reported as the suggested cutoff (matching the convention used by [RMlocdepQ3Cutoff](#)).

Usage

```

RMdimResidualPCACutoff(
  data,
  iterations = 250,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses (0-based, non-negative integers).
<code>iterations</code>	Integer. Number of simulation iterations. Default 250.
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> . Default TRUE.
<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first; if neither is set, <code>parallel = TRUE</code> falls back to sequential with a warning.
<code>verbose</code>	Logical. Show a progress bar. Default FALSE.
<code>seed</code>	Integer or NULL. Random seed for reproducibility.

Details

Rule-of-thumb cutoffs for the first-contrast eigenvalue depend strongly on sample size, test length, and item-parameter spread; simulation-based cutoffs tailored to the data are more defensible (Chou & Wang, 2010).

The generating model uses CML item parameters (`psychotools`) and WLE person locations. Per iteration: theta values are sampled with replacement from the WLE estimates; response data are simulated under the model (`psychotools::rrm` for dichotomous, partial-credit simulator for polytomous); CML/WLE standardized residuals are computed (the same engine as the observed analysis); `prcomp()` is run; the first-contrast eigenvalue is recorded.

Iterations that fail (e.g., due to a degenerate simulated dataset where some category isn't represented) are silently dropped. The `iarm` package is **not** required.

Value

A list with components:

`results` `data.frame`: iteration, eigenvalue.

`p95`, `p99`, `p995`, `p999` Empirical percentiles of eigenvalue.

`max` The largest simulated eigenvalue.

`suggested_cutoff` The 99th percentile (p99) — pass this list back into `RMdimResidualPCA` via `cutoff =` , or use `suggested_cutoff` directly.

`suggested_cutoff_percentile` The percentile used for `suggested_cutoff`, currently always 99.

actual_iterations Number of successful iterations.
 sample_n Number of complete cases used.
 item_names Character vector of item names.

References

Chou, Y.-T., & Wang, W.-C. (2010). Checking dimensionality in item response models with principal component analysis on standardized residuals. *Educational and Psychological Measurement*, 70(5), 717-731. doi:10.1177/0013164410379322

See Also

[RMdimResidualPCA](#)

Examples

```
set.seed(1)
dat <- as.data.frame(
  matrix(sample(0:1, 200 * 12, replace = TRUE), nrow = 200, ncol = 12)
)
colnames(dat) <- paste0("I", 1:12)

# Few iterations for a fast example; use 250+ in real analyses
bound <- RMdimResidualPCACutoff(dat, iterations = 50, parallel = FALSE, seed = 1)
bound$suggested_cutoff

RMdimResidualPCA(dat, cutoff = bound)
```

RMitemCatProb

Item Category Probability Curves

Description

Plots model-implied response-category probability curves for each item as a function of the latent trait θ . Item parameters are estimated by conditional maximum likelihood via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM). Each item gets its own facet panel, with one curve per response category coloured from low to high using the viridis palette. Comparable in scope to `eRm::plotICC()` and `mirt`'s trace plots, with a `ggplot2` / `viridis` output and optional descriptive labels for items and categories.

Usage

```
RMitemCatProb(
  data,
  item_labels = NULL,
  category_labels = NULL,
  theta_range = NULL,
```

```

n_points = 200L,
viridis_option = "D",
viridis_end = 0.95,
facet_ncol = NULL,
label_wrap = 25L,
line_width = 0.9,
font = "sans",
output = c("ggplot", "dataframe"),
label_curves = c("legend", "path"),
item = NULL,
text_size = 4
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed — the model fit handles them.
<code>item_labels</code>	Optional character vector of descriptive item labels (facet strip titles). Must be the same length as <code>ncol(data)</code> . If NULL (the default), column names are used.
<code>category_labels</code>	Optional character vector of labels for the response categories (legend). Must be the same length as the number of categories spanning from 0 to the maximum observed value. If NULL (the default), numeric category values are used.
<code>theta_range</code>	Numeric length 2. Range of the latent trait θ (logits) plotted along the x-axis. When NULL (default) the range is <code>c(-4, 4)</code> for <code>label_curves = "legend"</code> and a wider <code>c(-5, 5)</code> for <code>label_curves = "path"</code> — the wider range gives <code>geomtextpath</code> more horizontal room to place per-curve labels at their peaks. Pass an explicit <code>c(lo, hi)</code> to override.
<code>n_points</code>	Integer. Number of evenly-spaced θ values at which the curves are evaluated. Default 200L.
<code>viridis_option</code>	Character. Viridis palette identifier. One of "A" through "H". Default "D" (viridis green).
<code>viridis_end</code>	Numeric in (0, 1]. Upper end of the viridis palette range; lower values keep the palette inside its mid-tones (avoids the very bright yellow at 1.0). Default 0.95.
<code>facet_ncol</code>	Optional integer. Number of columns in the facet layout. Default NULL (<code>ggplot2::facet_wrap()</code> auto-layout).
<code>label_wrap</code>	Integer. Characters per line for facet-strip label wrapping. Default 25L.
<code>line_width</code>	Numeric. Line width for the probability curves. Default 0.9.
<code>font</code>	Character. Font family for all text. Default "sans".
<code>output</code>	Character. Either "ggplot" (default) for a ggplot object, or "dataframe" for the underlying long-format probability table.
<code>label_curves</code>	Character. How response categories are identified. "legend" (default) draws lines and a separate colour legend with one swatch per category — the standard multi-item presentation. "path" uses <code>geomtextpath::geom_textpath()</code>

to write each category's label *along* its own curve (a la classic IRT trace plots) and suppresses the legend; valid for **a single item at a time** because narrow facets do not give path labels enough horizontal room to render legibly. The model is still fit on the full multi-item data (PCM thresholds require multi-item input for CML estimation); the `item` argument then selects which item's curves to plot. Requires the optional `geomtextpath` package.

<code>item</code>	Character or integer. Used only when <code>label_curves = "path"</code> . Either an item name (matching a column in data) or a column index, identifying which item's category curves to plot. Required for path mode.
<code>text_size</code>	Numeric. Used only when <code>label_curves = "path"</code> . Size of the path labels in mm. Default 4.

Details

For each polytomous item i with response categories $0, 1, \dots, K_i$ and threshold parameters $\delta_{i,1}, \dots, \delta_{i,K_i}$ (CML, psychotools), the PCM category probability is

$$P(X_i = k \mid \theta) = \frac{\exp(\sum_{j=1}^k (\theta - \delta_{i,j}))}{\sum_{k'=0}^{K_i} \exp(\sum_{j=1}^{k'} (\theta - \delta_{i,j}))},$$

with the empty sum (when $k = 0$) taken as zero. For dichotomous items the function fits a Rasch model and treats the item difficulty $\delta_i = -\beta_i$ as the single threshold, recovering the standard two-category logistic ICC.

The colour mapping uses `scale_color_viridis_c()` against the integer category value, so the natural ordering of response categories is preserved visually — low categories at one end of the palette, high categories at the other. When `category_labels` is provided, the legend uses those labels (e.g., "Never" / "Sometimes" / "Often") while the colour mapping stays on the integer category value.

Items with fewer response categories than the maximum (e.g., an otherwise four-category scale with one three-category item) contribute only the categories they actually have to their own facet — the y-axis still spans $[0, 1]$.

Value

- If `output = "ggplot"`: a `ggplot2::ggplot` object, one facet per item.
- If `output = "dataframe"`: a long-format `data.frame` with columns `Item` (factor in column order), `Category` (integer), and `Theta, Probability` (numeric), one row per item \times category \times theta gridpoint.

See Also

`RMitemICCPLOT()` for conditional ICCs binned by total score, `RMitemHierarchy()` for item threshold locations on the logit scale.

Examples

```

if (requireNamespace("eRm", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  data(pcmdat2, package = "eRm")

  # Default plot
  RMitemCatProb(pcmdat2)

  # Custom item and category labels
  RMitemCatProb(
    pcmdat2,
    item_labels = c("Mood", "Sleep", "Appetite", "Energy"),
    category_labels = c("Never", "Sometimes", "Often")
  )

  # Underlying probability data
  df <- RMitemCatProb(pcmdat2, output = "dataframe")
  head(df)

  # Single-item plot with labels written along each curve
  # (classic IRT trace-plot style). Model is still fit on all four
  # items; `item` picks which one to plot.
  if (requireNamespace("geomtextpath", quietly = TRUE)) {
    RMitemCatProb(
      pcmdat2,
      category_labels = c("Never", "Sometimes", "Often"),
      label_curves = "path",
      item = "I1"
    )
  }
}

```

RMitemHierarchy

Item-Threshold Hierarchy Plot

Description

Visualises item and threshold locations on the logit scale for a Partial Credit Model. Items are sorted by their (mean-threshold) location; each item shows its location as a black diamond and its individual thresholds as coloured dots with confidence-interval error bars.

Usage

```

RMitemHierarchy(
  data,
  show_numbers = TRUE,
  sem_multiplier = 1.405,

```

```

  item_labels = NULL,
  output = c("ggplot", "dataframe")
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of polytomous item responses (non-negative integers, 0-based, max value > 1). One column per item, one row per person.
<code>show_numbers</code>	Logical. When TRUE (default), prints the numerical item location and threshold values next to the points on the plot. When FALSE, only the threshold labels (T1, T2, ...) are shown.
<code>sem_multiplier</code>	Numeric multiplier for the threshold SE used to draw the error bars. Default 1.405 (84% CI). Common alternatives: 1.96 (95% CI), 2.576 (99% CI).
<code>item_labels</code>	Optional character vector of length <code>ncol(data)</code> providing descriptive labels for items. Default NULL uses the column names of <code>data</code> . Labels are appended to the column names on the y-axis (name - label) and wrapped at 36 characters via base-R <code>strwrap()</code> .
<code>output</code>	One of "ggplot" (default) – a faceted hierarchy figure – or "dataframe" – the long-format underlying data with one row per (item × threshold).

Details

Threshold locations are centred at the grand mean of all thresholds across items, so the dashed reference line at 0 represents the mean threshold location across the scale.

Confidence intervals around thresholds are 84% by default (`sem_multiplier = 1.405`), following Payton, Greenstone, & Schenker (2003) – non-overlap of 84% intervals approximately corresponds to a two-sample significance test at $\alpha = 0.05$. Use `sem_multiplier = 1.96` for 95% intervals.

Polytomous only. Dichotomous items have a single threshold that coincides with the item location; the hierarchy plot is visually degenerate in that case. For dichotomous data use `RMtargeting()` or `RMscoreSE()` instead.

Centring convention. The CML PCM thresholds (estimated via `psychotools::pcmodel()`) are shifted so that their grand mean is zero; each item's location is then the mean of its centred thresholds. The dashed horizontal reference line on the plot marks this zero – i.e., the average threshold across all items.

Value

Either a `ggplot` (default) or a `data.frame` with columns `Item`, `ItemLabel`, `Threshold`, `ThresholdLocation`, `ThresholdSE`, and `ItemLocation` (the per-item mean of the centred thresholds).

References

Payton, M. E., Greenstone, M. H., & Schenker, N. (2003). Overlapping confidence intervals or standard error intervals: What do they mean in terms of statistical significance? *Journal of Insect Science*, 3(34), 1-6. doi:10.1093/jis/3.1.34

See Also

[RMtargeting\(\)](#), [RMscoreSE\(\)](#), [RMitemICCPLOT\(\)](#)

Examples

```
if (requireNamespace("eRm", quietly = TRUE)) {
  data("pcmdat2", package = "eRm")
  RMitemHierarchy(pcmdat2)

  # 95% CI instead of 84%
  RMitemHierarchy(pcmdat2, sem_multiplier = 1.96)

  # Underlying data.frame
  RMitemHierarchy(pcmdat2, output = "dataframe")
}
```

RMitemICCPLOT

Conditional Item Characteristic Curves

Description

Faceted panel of Conditional Item Characteristic Curves (cICCs), one per item. Each panel shows the model-expected conditional item score $E[X_i | R = r]$ against the total score r , together with the average observed item score within class intervals of the total score and their confidence intervals. When a `dif_var` is supplied, observed averages are computed separately per group, turning each panel into a visual DIF check, and the partial-gamma DIF magnitude is reported per item.

Usage

```
RMitemICCPLOT(
  data,
  dif_var = NULL,
  method = c("cut", "score"),
  class_intervals = 4,
  ci = TRUE,
  error_band = FALSE,
  conf_level = 0.95,
  min_n = 8L,
  items = NULL,
  output = c("patchwork", "list")
)
```

Arguments

<code>data</code>	A data.frame or matrix of item responses (non-negative integers, 0-based). One column per item, one row per person.
<code>dif_var</code>	Optional vector of length <code>nrow(data)</code> (factor or coercible to factor) defining a DIF grouping variable. When supplied, observed averages are shown separately per group and the partial-gamma DIF coefficient (<code>item:partgam_DIF()</code> , as in <code>RMdifGamma()</code>) is annotated per panel. Default NULL (no DIF).
<code>method</code>	One of "cut" (default) or "score". "cut" groups respondents into <code>class_intervals</code> total-score bins (equal-count quantile bins, common across groups); "score" uses every observed total score as its own group.
<code>class_intervals</code>	Integer ≥ 2 . Number of class intervals when <code>method = "cut"</code> . Default 4. Ignored when <code>method = "score"</code> .
<code>ci</code>	Logical. Draw confidence intervals (error bars) on the observed class-interval means. Default TRUE.
<code>error_band</code>	Logical. Add a shaded band for the model's interval of the <i>observed mean</i> at each total score, $E \pm z\sqrt{\text{Var}/n_r}$ (n_r = number of respondents at that total score), as in RASCHplot's <code>CICCPLOT</code> . Default FALSE.
<code>conf_level</code>	Numeric in (0, 1). Confidence level for the observed error bars and the model band. Default 0.95.
<code>min_n</code>	Integer. A group-by-interval cell needs at least this many respondents to contribute an observed point + CI; sparser cells are skipped. Default 8 (the package's per-cell stability floor).
<code>items</code>	Optional character or integer vector selecting which items to plot. The model is always fitted on all items; only the rendering is filtered. Default NULL (all items).
<code>output</code>	One of "patchwork" (default) – composite patchwork figure – or "list" – a named list of per-item ggplot objects.

Details

The model curve and its conditional variance come from the shared CML engine (CML item thresholds via `psychotools` and the exact conditional distribution of each item score given the total score, via elementary symmetric functions). The conditional-ICC approach follows Buchardt, Christensen & Jensen (2023) and their RASCHplot package; the implementation here is native to `easyRasch2`'s CML/WLE engine.

Conditioning. The expected curve is the exact conditional expectation of the item score given the total score (it accounts for the item being part of the total), not a marginal ICC.

Class intervals. With `method = "cut"`, total scores are split into `class_intervals` equal-count bins using common boundaries (so groups share the x-axis); each bin contributes one observed point at its mean total score. With `method = "score"`, every observed total score is a point. If the score distribution is too sparse to form `class_intervals` distinct bins, the function falls back to score-level points.

Confidence intervals. Observed error bars use the normal approximation $\bar{x}_i \pm z\sqrt{\text{var}(x_i)/n_i}$ within each (group, interval) cell, clamped to the item's score range; cells with fewer than `min_n`

respondents are dropped. In DIF mode this makes sparse group differences visibly uncertain rather than over-interpreted.

DIF magnitude. The annotated partial gamma (Bjorner et al., 1998) is the association between the item score and the group conditional on the rest score – a non-parametric effect size, complementary to the total-score-conditional visual. It is the same statistic as [RMdifGamma\(\)](#).

Value

Either a patchwork/ggplot composite (default) or a named list of per-item ggplot objects (output = "list"). In DIF mode the per-item partial-gamma table is attached as `attr(, "dif_gamma")`.

References

Buchardt, A.-S., Christensen, K. B., & Jensen, S. N. (2023). Visualizing Rasch item fit using conditional item characteristic curves in R. *Psychological Test and Assessment Modeling*, 65(2), 206-219.

Andersen, E. B. (1995). Polytomous Rasch models and their estimation. In G. H. Fischer & I. W. Molenaar (Eds.), *Rasch Models: Foundations, Recent Developments, and Applications* (pp. 271-291). Springer. (Conditional expectation of item scores given the total score; formula 15.22.)

Bjorner, J. B., Kreiner, S., Ware, J. E., Damsgaard, M. T., & Bech, P. (1998). Differential item functioning in the Danish translation of the SF-36. *Journal of Clinical Epidemiology*, 51(11), 1189-1202.

See Also

[RMdifGamma](#), [RMitemRestscore](#)

RMitemInfit

Conditional Item Infit MSQ

Description

Computes conditional infit mean-square (MSQ) statistics for each item using `iarms::out_infit()`, enriched with item locations relative to the sample mean person location.

Usage

```
RMitemInfit(
  data,
  cutoff = NULL,
  p_value = FALSE,
  correction = c("fwer", "fdr_bh", "fdr_by", "none"),
  alpha = 0.05,
  output = "kable",
  sort
)
```

Arguments

data	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed, but at least one complete case (row with no NA) must be present.
cutoff	Optional. Default NULL (no cutoff applied, behaviour is identical to the current version). Can be: <ul style="list-style-type: none"> • The return value of <code>RMitemInfitCutoff</code> (a list with <code>\$item_cutoffs</code>): the data.frame is extracted automatically and the number of simulation iterations, <code>cutoff_method</code>, and <code>hdcj_width</code> are included in the kable caption. • The <code>\$item_cutoffs</code> data.frame from <code>RMitemInfitCutoff</code> directly: must have columns <code>Item</code>, <code>infit_low</code>, and <code>infit_high</code>. When provided, adds columns <code>Infit_low</code>, <code>Infit_high</code>, and <code>Flagged</code> to the result. Flagged labels the misfit direction: "overfit" (infit below the range – more predictable than the model expects), "underfit" (above the range – noisier than expected), or "" (within range, no misfit).
p_value	Logical. If TRUE, bootstrap p-values are computed from the simulated null distribution and added to the output. This requires cutoff to be the full <code>RMitemInfitCutoff</code> object (which carries the per-item simulated values in its <code>\$results</code> element); the summarised <code>\$item_cutoffs</code> data.frame is not sufficient. Default FALSE, in which case behaviour is unchanged.
correction	Character. Multiple-comparison correction applied across items when <code>p_value = TRUE</code> : "fwer" (default) for the Westfall-Young studentised-max step-down (family-wise error rate), "fdr_bh" / "fdr_by" for Benjamini-Hochberg / Benjamini-Yekutieli false discovery rate control, or "none" for uncorrected per-item p-values.
alpha	Numeric in (0, 1). Significance level for the Flagged column when <code>p_value = TRUE</code> (an item is flagged when its corrected p-value is below alpha). Default 0.05.
output	Character string controlling the return value. Either "kable" (default) for a formatted <code>knitr::kable()</code> table, or "dataframe" for the underlying data.frame.
sort	Optional character string. When <code>sort = "infit"</code> , rows are sorted by <code>Infit_MSQ</code> in descending order before output.

Details

Infit MSQ is a weighted fit statistic that emphasises deviations near the item location. Values close to 1.0 indicate good fit. Values substantially above 1.0 suggest underfit (unexpected responses), while values substantially below 1.0 suggest overfit (overly predictable responses). The definition of "substantially" depends on several factors such as sample size, and needs to be determined by simulation using `RMitemInfitCutoff`. There is no general rule-of-thumb value that is correct.

Conditional infit MSQ statistics are computed via `iarm::out_infit()`, which uses the conditional distribution of the sufficient statistics (Müller, 2020). Only complete cases (rows without any NA) are used in the conditional fit calculation.

Item parameters are estimated by conditional maximum likelihood via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM); the conditional infit/outfit MSQ comes from `iarm::out_infit()`

and is invariant to the estimation engine. Per-item average locations are the means of the CML thresholds, and the person-location reference is the mean of the Warm WLE estimates.

Relative item location is defined as the item's average location minus the sample mean person location, providing a measure of item targeting.

The `iar` package must be installed (it is in `Suggests`, not `Imports`).

Bootstrap p-values. When `p_value = TRUE`, each item's observed infit is compared against its simulated null distribution (from `cutoff$results`). The per-item statistic is the residual studentised by the bootstrap mean and SD – deliberately the empirical SD rather than the Wilson-Hilferty / ZSTD transform, which is uninformative for conditional MSQ (Müller, 2020). The marginal p-value is the two-sided Monte-Carlo p-value $(1 + \#\{|t^*| \geq |t|\}) / (B + 1)$. For `correction = "fwer"` the family-wise adjustment uses the Westfall-Young studentised-max step-down, which exploits the bootstrap dependence among items and is more powerful than Bonferroni/Holm (Ferreira, 2024); its validity rests on subset pivotality. `"fdr_bh"/"fdr_by"` apply Benjamini-Hochberg / Benjamini- Yekutieli instead. These are model-conditional, sample-size-sensitive p-values and are reported alongside the simulated effect-size band, not in place of it. p-values can be no smaller than $1 / (B + 1)$, and the studentised-max (FWER) correction is *liberal* when the simulation is small (the bootstrap mean/SD used for studentisation are then too noisy). At least 1000 iterations in `RMitemInfitCutoff()` are recommended – in simulations the family-wise error rate is then controlled at the nominal level – and a warning is issued when the simulation is smaller. The marginal p-values are well calibrated even at a few hundred iterations.

Value

- If `output = "kable"`: a `knitr_kable` object (plain text table via `format = "pipe"`) with columns "Item", "Infit MSQ", and "Relative location", and a caption showing the number of complete cases. When `cutoff` is provided, columns "Infit low", "Infit high", and "Flagged" are also included, and the caption notes the simulation-based cutoffs.
- If `output = "dataframe"`: a `data.frame` with columns `Item`, `Infit_MSQ`, and `Relative_location`. When `cutoff` is provided, columns `Infit_low`, `Infit_high`, and `Flagged` are also included (inserted after `Infit_MSQ`, before `Relative_location`). `Flagged` is a character column with values "overfit", "underfit", or "" (not the previous logical). When `p_value = TRUE`, columns `p_infit` (marginal two-sided p-value) and `padj_infit` (corrected p-value) are added and `Flagged` reflects items with `padj_infit < alpha` (direction from `Infit_MSQ` relative to 1).

Multiple comparisons

The marginal p-value controls the error rate of a *single* comparison: for one item (or item pair) decided on in advance it is the relevant value. But scanning all k comparisons and flagging whichever fall below α tests k hypotheses at once, so the chance of at least one false flag inflates to roughly $1 - (1 - \alpha)^k$ (e.g. about 34% for $k = 8$ at $\alpha = 0.05$) – even when every marginal p-value is correctly calibrated. The corrected (adjusted) p-value controls this: `correction = "fwer"` bounds the probability of *any* false flag (strict, lower power), while `"fdr_bh" / "fdr_by"` bound the expected *proportion* of false flags among those raised (a more lenient middle ground). Rule of thumb: use the marginal p-value for a single pre-specified comparison, and a corrected p-value when screening the whole table – the usual workflow.

References

- Müller, M. (2020). Item fit statistics for Rasch analysis: Can we trust them? *Journal of Statistical Distributions and Applications*, 7(5). doi:10.1186/s40488020001087
- Ferreira, J. A. (2024). Methods of testing a 'small' or 'moderate' number of hypotheses simultaneously. *Journal of Statistical Theory and Practice*, 19(6). doi:10.1007/s42519024004124
- Westfall, P. H., & Young, S. S. (1993). *Resampling-Based Multiple Testing*. Wiley.

See Also

[RMitemInfitCutoff](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE)) {
  # Simulate binary item response data (5 items, 40 persons)
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 40 * 5, replace = TRUE), nrow = 40, ncol = 5)
  )
  colnames(sim_data) <- paste0("Item", 1:5)

  # Default kable output
  RMitemInfit(sim_data)

  # Sorted by infit MSQ descending
  RMitemInfit(sim_data, sort = "infit")

  # Return as data.frame for further processing
  df <- RMitemInfit(sim_data, output = "dataframe")

  # Simulation-based cutoffs (100 Monte-Carlo iterations)
  if (requireNamespace("ggdist", quietly = TRUE)) {
    cutoff_res <- RMitemInfitCutoff(sim_data, iterations = 100,
                                   parallel = FALSE, seed = 42)
    RMitemInfit(sim_data, cutoff = cutoff_res)
    RMitemInfit(sim_data, cutoff = cutoff_res, output = "dataframe")

    # Bootstrap p-values with family-wise (Westfall-Young) correction
    # (use iterations >= 1000 in real analyses for stable p-values)
    RMitemInfit(sim_data, cutoff = cutoff_res, p_value = TRUE,
                output = "dataframe")
  }
}
```

Description

Uses parametric bootstrap simulation to determine appropriate cutoff values for `RMitemInfit`. This function simulates data from a correctly fitting Rasch model that mimics your data and returns per-item empirical cutoffs.

Usage

```
RMitemInfitCutoff(
  data,
  iterations = 250,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  cutoff_method = "hdci",
  hdci_width = 0.999,
  dgp = c("resample", "conditional")
)
```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Only complete cases (rows without any NA) are used.
<code>iterations</code>	Integer. Number of simulation iterations (default 250).
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> if available (default TRUE).
<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first. If neither is set and <code>parallel = TRUE</code> , a warning is issued and execution falls back to sequential (single core) processing.
<code>verbose</code>	Logical. Show a progress bar (default FALSE).
<code>seed</code>	Integer or NULL. Random seed for reproducibility.
<code>cutoff_method</code>	Character string specifying how cutoff intervals are computed. Either "hdci" (default) for the Highest Density Interval via <code>ggdist::hdci()</code> , or "quantile" for the 2.5th/97.5th percentiles via <code>stats::quantile()</code> .
<code>hdci_width</code>	Numeric. Width of the HD CI when <code>cutoff_method = "hdci"</code> . Default is 0.999 (99.9% HD CI). Ignored when <code>cutoff_method = "quantile"</code> .
<code>dgp</code>	Character. Data-generating process for the parametric bootstrap. "resample" (default) resamples WLE person locations with replacement and simulates responses under the model (a <i>marginal</i> null). "conditional" simulates each respondent's pattern from the exact Rasch conditional distribution given their observed total score, item parameters fixed (a <i>conditional</i> null). Because the conditional infit/outfit statistic is itself conditional on the total score, "conditional" is its naturally matched null. Experimental.

Details

The generating model is CML item parameters (via `psychotools`) with WLE person locations. For each iteration a dataset is simulated under the chosen `dgp`, the model is refitted by CML

(`psychotools::pcmodel()`, which handles dichotomous and polytomous data and is accepted by `iarm`), and conditional infit and outfit MSQ are computed via `iarm::out_infit()`. The distribution of these statistics across iterations provides empirical critical values per item. Failed iterations (e.g., degenerate simulated data) are silently discarded.

Parallel processing is provided by the `mirai` package (optional). Install it with `install.packages("mirai")` to enable parallelisation.

The `iarm` package must be installed (it is in Suggests, not Imports).

Value

A list with components:

`results` data.frame with columns `iteration`, `Item`, `InfitMSQ`, `OutfitMSQ` (one row per item per successful iteration).

`item_cutoffs` data.frame with per-item cutoff summaries: `Item`, `infit_low`, `infit_high`, `outfit_low`, `outfit_high`. Bounds are computed using the method specified by `cutoff_method`.

`actual_iterations` Number of successful iterations.

`sample_n` Number of complete cases used.

`sample_n_total` Number of respondents in the raw input data, before the complete-case filter.

`sample_has_na` Logical. Whether the raw input data contained any missing values.

`sample_summary` Summary statistics of estimated person parameters.

`item_names` Character vector of item names from data.

`cutoff_method` The method used to compute cutoffs ("hdci" or "quantile").

`hdci_width` The HDCl width used (only meaningful when `cutoff_method = "hdci"`).

`dgp` The data-generating process used ("resample" or "conditional").

See Also

[RMitemInfit](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)

  # Run 100 iterations sequentially for a quick demo
  cutoff_res <- RMitemInfitCutoff(sim_data, iterations = 100,
                                parallel = FALSE, seed = 42)

  cutoff_res$item_cutoffs

  # Use the cutoffs in RMitemInfit()
  RMitemInfit(sim_data)
}
```

RMitemInfitCutoffMI *Simulation-Based Infit MSQ Cutoff Determination for Multiply Imputed Data*

Description

Extends [RMitemInfitCutoff](#) to work with multiply imputed datasets produced by the `mice` package. Runs the parametric bootstrap simulation on each imputed dataset and stacks the resulting distributions, so that the final cutoff intervals reflect both sampling variability and imputation uncertainty.

Usage

```
RMitemInfitCutoffMI(
  mids_object,
  iterations = 500,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  cutoff_method = "hdci",
  hdci_width = 0.999
)
```

Arguments

<code>mids_object</code>	A <code>mids</code> object (multiply imputed dataset) as returned by <code>mice::mice()</code> . Each completed dataset must contain only the item response columns to be analysed (i.e., no ID or grouping variables). Items must be scored starting at 0 (non-negative integers).
<code>iterations</code>	Integer. Total number of simulation iterations to run across all imputations. These are distributed approximately evenly across the <code>m</code> imputed datasets (default 500).
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> within each imputed dataset (default TRUE). Passed to RMitemInfitCutoff .
<code>n_cores</code>	Integer or NULL. Number of parallel workers. Passed to RMitemInfitCutoff .
<code>verbose</code>	Logical. Show progress messages (default FALSE).
<code>seed</code>	Integer or NULL. Master random seed for reproducibility. A unique per-imputation seed is derived from this value.
<code>cutoff_method</code>	Character string specifying how cutoff intervals are computed from the stacked distribution. Either "hdci" (default) for the Highest Density Interval via <code>ggdist::hdci()</code> , or "quantile" for the 2.5th/97.5th percentiles via <code>stats::quantile()</code> .
<code>hdci_width</code>	Numeric. Width of the HD CI when <code>cutoff_method = "hdci"</code> . Default is 0.999 (99.9% HD CI). Ignored when <code>cutoff_method = "quantile"</code> .

Details

The function completes each of the m imputed datasets via `mice::complete()`, then calls `RMitemInfitCutoff` on each one. The total number of iterations is split approximately evenly across imputations (i.e., each imputed dataset receives `ceiling(iterations / m)` or `floor(iterations / m)` iterations). The per-imputation simulation results are stacked into a single distribution from which cutoff intervals are computed, naturally incorporating imputation uncertainty.

Imputed datasets that cause model convergence failures are dropped with a warning. If all imputations fail, the function stops with an error.

The `mice` package must be installed (it is in `Suggests`, not `Imports`).

Value

A list with the same structure as `RMitemInfitCutoff`, so that the result can be passed directly to `RMitemInfit`, `RMitemInfitMI`, and `RMitemInfitPlot`:

`results` `data.frame` with columns `iteration`, `imputation`, `Item`, `InfitMSQ`, `OutfitMSQ` — the stacked simulation results from all imputed datasets.

`item_cutoffs` `data.frame` with per-item cutoff summaries: `Item`, `infit_low`, `infit_high`, `outfit_low`, `outfit_high`. Computed from the stacked distribution.

`actual_iterations` Total number of successful iterations across all imputations.

`sample_n` Number of rows (respondents) per imputed dataset.

`sample_summary` Summary statistics of estimated person parameters from the first imputed dataset.

`item_names` Character vector of item names.

`cutoff_method` The method used to compute cutoffs.

`hdc_i_width` The HDCI width used.

`n_imputations` Number of imputed datasets used.

`iterations_per_imputation` Integer vector of requested iterations per imputed dataset.

`actual_iterations_per_imputation` Integer vector of successful iterations per imputed dataset.

See Also

[RMitemInfitCutoff](#), [RMitemInfitMI](#), [RMitemInfitPlot](#)

Examples

```
if (requireNamespace("mice", quietly = TRUE) &&
    requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE)) {
  # Create example data with ~10% MCAR missingness
  set.seed(42)
  mat <- matrix(sample(0:1, 200 * 8, replace = TRUE), nrow = 200, ncol = 8)
  mat[sample(length(mat), round(0.10 * length(mat)))] <- NA
  sim_data <- as.data.frame(mat)
  colnames(sim_data) <- paste0("Item", 1:8)

  # mice's ordinal method (`polr`) requires the items to be ordered
```

```

# factors, so code them as such before imputing. RMitemInfitCutoffMI()
# converts the completed factors back to numeric internally.
sim_data[] <- lapply(sim_data, function(x) factor(x, ordered = TRUE))

# Impute (use more imputations, e.g. m = 5+, in real analyses)
imp <- mice::mice(sim_data, m = 2, method = "polr", seed = 123,
  printFlag = FALSE)

# Compute simulation-based cutoffs across imputations
# (use more iterations, e.g. 250+, in real analyses)
cutoff_mi <- RMitemInfitCutoffMI(imp, iterations = 50, parallel = FALSE,
  seed = 42)

cutoff_mi$item_cutoffs

# Use with RMitemInfitMI()
RMitemInfitMI(imp, cutoff = cutoff_mi)
}

```

RMitemInfitMI

Conditional Item Infit MSQ for Multiply Imputed Data

Description

Extends [RMitemInfit](#) to work with multiply imputed datasets produced by the `mice` package. Computes conditional infit MSQ on each imputed dataset and pools the results using Rubin's rules.

Usage

```
RMitemInfitMI(mids_object, cutoff = NULL, output = "kable", sort)
```

Arguments

<code>mids_object</code>	A <code>mids</code> object (multiply imputed dataset) as returned by <code>mice::mice()</code> . Each completed dataset must contain only the item response columns to be analysed (i.e., no ID or grouping variables). Items must be scored starting at 0 (non-negative integers).
<code>cutoff</code>	Optional. Default NULL (no cutoff applied). Can be: <ul style="list-style-type: none"> The return value of RMitemInfitCutoff or RMitemInfitCutoffMI (a list with <code>\$item_cutoffs</code>): the data.frame is extracted automatically and meta-data is included in the kable caption. The <code>\$item_cutoffs</code> data.frame directly: must have columns <code>Item</code>, <code>infit_low</code>, and <code>infit_high</code>. When provided, adds columns <code>Infit_low</code>, <code>Infit_high</code>, and <code>Flagged</code> to the result. <code>Flagged</code> is a character column labelling the misfit direction: "overfit" (pooled infit below the range), "underfit" (above), or "" (within range).
<code>output</code>	Character string controlling the return value. Either "kable" (default) for a formatted <code>knitr::kable()</code> table, or "dataframe" for the underlying data.frame.

sort Optional character string. When `sort = "infit"`, rows are sorted by `Infit_MSQ` in descending order before output.

Details

For each of the m imputed datasets, the function:

1. Fits a Rasch model by CML via `psychotools::pcmodel()` (a dichotomous item is a 2-category partial credit model), consistent with `RMitemInfit` and the rest of the package.
2. Computes conditional infit MSQ and its standard error via `iarm::out_infit()`.
3. Computes item locations (mean of the grand-mean-centred CML Andrich thresholds) and the mean WLE person location.

The per-imputation estimates are then pooled using Rubin's rules:

Pooled MSQ The mean of the m infit MSQ point estimates.

Within-imputation variance The mean of the m squared standard errors.

Between-imputation variance The sample variance of the m point estimates.

Total variance Within + $(1 + 1/m) * \text{Between}$.

Pooled SE The square root of the total variance.

Relative item location is the mean of per-imputation relative locations (item location minus sample mean person location).

Caveat on the pooled SE. The within-imputation variance is the squared conditional infit SE from `iarm::out_infit()`. Müller (2020) showed that this asymptotic SE is an unreliable measure of uncertainty for the conditional infit statistic; Rubin's pooled SE inherits that limitation, so the `Infit_SE/Infit SE` column should be read as an approximate indication of imputation-related variability rather than a trustworthy inferential standard error. For item misfit decisions, prefer the simulation-based cutoffs from `RMitemInfitCutoffMI`.

Imputed datasets that cause model convergence failures are dropped with a warning. If all imputations fail, the function stops with an error. At least two successful imputations are required to estimate between-imputation variance.

The `mice` and `iarm` packages must be installed (they are in Suggests, not Imports).

Value

- If `output = "kable"`: a `knitr_kable` object (plain text table via `format = "pipe"`) with columns "Item", "Infit MSQ", "Infit SE", "Relative location", and a caption noting the number of imputations and complete cases. When `cutoff` is provided, columns "Infit low", "Infit high", and "Flagged" are also included.
- If `output = "dataframe"`: a `data.frame` with columns `Item`, `Infit_MSQ`, `Infit_SE`, and `Relative_location`. When `cutoff` is provided, columns `Infit_low`, `Infit_high`, and `Flagged` are also included (inserted after `Infit_SE`, before `Relative_location`). `Flagged` is a character column ("overfit" / "underfit" / ""), not the previous logical.

References

Müller, M. (2020). Item fit statistics for Rasch analysis: Can we trust them? *Journal of Statistical Distributions and Applications*, 7(5). doi:10.1186/s40488020001087

See Also

[RMitemInfit](#), [RMitemInfitCutoffMI](#)

Examples

```

if (requireNamespace("mice", quietly = TRUE) &&
    requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE)) {
  # Create example data with ~10% MCAR missingness
  set.seed(42)
  mat <- matrix(sample(0:1, 200 * 8, replace = TRUE), nrow = 200, ncol = 8)
  mat[sample(length(mat), round(0.10 * length(mat)))] <- NA
  sim_data <- as.data.frame(mat)
  colnames(sim_data) <- paste0("Item", 1:8)

  # mice's ordinal method (`polr`) requires the items to be ordered
  # factors, so code them as such before imputing. RMitemInfitMI()
  # converts the completed factors back to numeric internally.
  sim_data[] <- lapply(sim_data, function(x) factor(x, ordered = TRUE))

  # Impute (use more imputations, e.g. m = 5+, in real analyses)
  imp <- mice::mice(sim_data, m = 2, method = "polr", seed = 123,
                   printFlag = FALSE)

  # Pooled infit table (no cutoffs)
  RMitemInfitMI(imp)

  # With simulation-based cutoffs
  # (use more iterations, e.g. 250+, in real analyses)
  cutoff_mi <- RMitemInfitCutoffMI(imp, iterations = 50, parallel = FALSE,
                                  seed = 42)
  RMitemInfitMI(imp, cutoff = cutoff_mi)

  # As data.frame
  df <- RMitemInfitMI(imp, cutoff = cutoff_mi, output = "dataframe")
}

```

RMitemInfitPlot

Plot Distribution of Simulated Infit and Outfit MSQ Values

Description

Visualises the distribution of simulation-based conditional item fit values from [RMitemInfitCutoff](#), optionally overlaying observed item fit from the original data.

Usage

```
RMitemInfitPlot(simfit, data, statistic = "infit")
```

```
RMitemInfitCutoffPlot(...)
```

Arguments

<code>simfit</code>	The return value of <code>RMitemInfitCutoff</code> (a list with components <code>results</code> , <code>item_cutoffs</code> , <code>actual_iterations</code> , <code>sample_n</code> , and <code>item_names</code>).
<code>data</code>	Optional. A <code>data.frame</code> or matrix of item responses for computing and overlaying observed conditional item fit values. Items must be scored starting at 0 (non-negative integers). When provided, the plot includes orange diamond markers for the observed infit/outfit MSQ alongside the simulated distribution, plus segment summaries from the cutoff intervals.
<code>statistic</code>	Character string. Either <code>"infit"</code> (default) to show only the infit panel, <code>"outfit"</code> to show only the outfit panel, or <code>"both"</code> to show infit and outfit side by side (requires the <code>patchwork</code> package when data is supplied).
<code>...</code>	Arguments passed on to <code>RMitemInfitPlot()</code> .

Details

Uses `ggdist::stat_dotsinterval()` (when data is not supplied) or `ggdist::stat_dots()` (when data is supplied) with `point_interval = "median_hdci"` and `.width = c(0.66, 0.999)`.

When data is **not** supplied, the function plots the simulated MSQ distributions as dot-interval plots using `ggdist::stat_dotsinterval()` with median and Highest Density Continuous Interval (HD CI) summaries, faceted by `statistic` (InfitMSQ / OutfitMSQ).

When data **is** supplied, the function:

1. Fits a Rasch / Partial Credit model by CML via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM) and computes observed conditional infit and outfit MSQ via `iarm::out_infit()`.
2. Overlays observed fit values as orange diamond markers on the simulated distributions.
3. Shows per-item cutoff intervals (from `simfit$item_cutoffs`) as black line segments, with thicker segments for the 66% HD CI range and black dots for the median.

The `ggplot2`, `ggdist`, and optionally `patchwork` packages must be installed (they are in `Suggests`, not `Imports`).

`RMitemInfitCutoffPlot()` is a deprecated alias for `RMitemInfitPlot()`, retained for backward compatibility with code written against `easyRasch2` 0.8.0. It warns and forwards to `RMitemInfitPlot()`.

Value

A `ggplot` object (or a `patchwork` object when `statistic = "both"` and data is supplied).

See Also

[RMitemInfitCutoff](#), [RMitemInfit](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  set.seed(42)
```

```

sim_data <- as.data.frame(
  matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
)
colnames(sim_data) <- paste0("Item", 1:10)

# Run simulation
cutoff_res <- RMitemInfitCutoff(sim_data, iterations = 100,
                               parallel = FALSE, seed = 42)

# Simulated distribution only (infit + outfit faceted)
RMitemInfitPlot(cutoff_res)

# With observed fit overlaid (infit only, the default)
RMitemInfitPlot(cutoff_res, data = sim_data)

# Both infit and outfit panels side by side
if (requireNamespace("patchwork", quietly = TRUE)) {
  RMitemInfitPlot(cutoff_res, data = sim_data, statistic = "both")
}
}

```

RMitemParameters

Item Parameters for a Rasch / Partial Credit Model

Description

Estimates item difficulty (dichotomous) or item-category threshold (polytomous) parameters and returns them in long or wide format, with optional standard errors and Wald confidence intervals. Item parameters are estimated by conditional maximum likelihood (CML, via **psychotools**) by default, with marginal maximum likelihood (MML, via **mirt**) available for sparse data where CML can be unstable.

Usage

```

RMitemParameters(
  data,
  estimator = c("CML", "MML"),
  format = c("long", "wide"),
  se = TRUE,
  ci_level = 0.95,
  center = TRUE,
  output = c("kable", "dataframe", "file"),
  filename = NULL
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed; both estimators handle them.
<code>estimator</code>	Character. "CML" (default) estimates item parameters with <code>psychotools::pcmodel()</code> (a dichotomous item is a 2-category PCM); "MML" uses <code>mirt::mirt()</code> with <code>itemtype = "Rasch"</code> . CML is preferred for Rasch measurement; MML can be more robust when data are sparse. When <code>estimator = "CML"</code> and sparse response categories are detected, a warning suggests switching to MML.
<code>format</code>	Character. "long" (default) returns one row per item (dichotomous) or per item-threshold (polytomous); "wide" returns one row per item with threshold columns <code>t1</code> , <code>t2</code> , ... plus a mean location column.
<code>se</code>	Logical. If TRUE (default), standard-error and confidence-interval columns are added.
<code>ci_level</code>	Numeric in (0, 1). Confidence level for the Wald interval (estimate +/- z * SE). Default 0.95.
<code>center</code>	Logical. If TRUE (default), all thresholds are shifted so their grand mean is zero, the usual Rasch identification. CML estimates are already centred; the shift mainly affects the MML path, keeping the two estimators on a common scale.
<code>output</code>	Character. "kable" (default) for a formatted <code>knitr::kable()</code> table, "dataframe" for the underlying <code>data.frame</code> , or "file" to write that <code>data.frame</code> to a CSV at <code>filename</code> (the <code>data.frame</code> is also returned invisibly).
<code>filename</code>	Character. Path to the CSV file to write when <code>output = "file"</code> . Required in that case; ignored otherwise.

Details

Items are detected as dichotomous (maximum score 1) or polytomous (maximum score > 1), and the Rasch or Partial Credit model is chosen accordingly. Thresholds are reported as Andrich thresholds (the person locations at which adjacent response categories are equally probable) on the logit difficulty scale, matching `RMtargeting()`.

Standard errors. For the CML path, threshold SEs are the square roots of the diagonal of the threshold-parameter covariance from `psychotools::threshpar(vcov = TRUE)`. For the MML path, SEs come from the `mirt` parameter covariance, propagated by the delta method through the linear threshold map. Confidence intervals are Wald intervals and are symmetric on the logit scale.

Value

For `output = "dataframe"`, a `data.frame`. In **long** format the columns are `item`, `threshold` (integer; 1 for dichotomous items), `location`, and – when `se = TRUE` – `se`, `ci_lower`, `ci_upper`. In **wide** format the columns are `item`, the threshold locations (`t1`, `t2`, ... or `location` for dichotomous items), and a mean location; when `se = TRUE`, matching `se_t1`, `se_t2`, ... columns are appended. For `output = "kable"`, the same content as a `knitr_kable` object.

References

- Andrich, D. (1978). A rating formulation for ordered response categories. *Psychometrika*, 43(4), 561-573. doi:10.1007/BF02293814
- Mair, P., & Hatzinger, R. (2007). Extended Rasch modeling: The eRm package for the application of IRT models in R. *Journal of Statistical Software*, 20(9), 1-20. doi:10.18637/jss.v020.i09

See Also

[RMpersonParameters\(\)](#), [RMscoreSE\(\)](#), [RMtargeting\(\)](#)

Examples

```
set.seed(1)
poly <- as.data.frame(
  matrix(sample(0:2, 250 * 5, replace = TRUE), nrow = 250, ncol = 5)
)
colnames(poly) <- paste0("Item", 1:5)

# Default: long-format kable with SE and 95% CI
RMitemParameters(poly)

# Wide format, point estimates only
RMitemParameters(poly, format = "wide", se = FALSE, output = "dataframe")

# Dichotomous data
dich <- as.data.frame(
  matrix(sample(0:1, 250 * 6, replace = TRUE), nrow = 250, ncol = 6)
)
colnames(dich) <- paste0("Item", 1:6)
RMitemParameters(dich, output = "dataframe")

# Write the parameter table to a CSV (also returned invisibly)
RMitemParameters(poly, output = "file",
  filename = tempfile(fileext = ".csv"))
```

RMitemRestscore

Item Restscore Analysis

Description

Computes observed and model-expected item-restscore correlations using `iarms::item_restscore()`, and enriches the output with the absolute difference between observed and expected values, item average locations, and item locations relative to the sample mean person location.

Usage

```
RMitemRestscore(data, output = "kable", sort, p_adj = "BH")
```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed, but at least one complete case (row with no NA) must be present.
<code>output</code>	Character string controlling the return value. Either "kable" (default) for a formatted <code>knitr::kable()</code> table, or "dataframe" for the underlying <code>data.frame</code> .
<code>sort</code>	Optional character string. When <code>sort = "diff"</code> , rows are sorted by the absolute magnitude of Difference in descending order, so that both over- and underfitting items appear near the top.
<code>p_adj</code>	Character string specifying the p-value adjustment method passed to <code>iarms::item_restscore()</code> . Default "BH" (Benjamini-Hochberg); use "none" for unadjusted p-values. Run <code>?stats::p.adjust</code> for the list of available methods.

Details

Item-restscore correlations using Goodman-Kruskal's gamma (Kreiner, 2011) measure the association between a person's score on a single item and their total score on the remaining items (the "restscore"). Under a correctly fitting Rasch model, observed and model-expected correlations should agree closely.

Item parameters are estimated by conditional maximum likelihood via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM); the item-restscore statistic itself comes from `iarms::item_restscore()` and is conditional on the total score, so it is invariant to the estimation engine. Per-item average locations are the means of the CML thresholds, and the person-location reference is the mean of the Warm WLE estimates.

Relative item location is defined as the item's average location minus the sample mean person location, providing a measure of item targeting.

The `iarms` package must be installed (it is in Suggests, not Imports).

Value

- If `output = "kable"`: a `knitr_kable` object (plain text table via `format = "pipe"`) with columns for item name, observed and expected restscore correlations, the signed difference (observed minus expected), adjusted p-value, the Flagged misfit label, and item location relative to the sample mean person location.
- If `output = "dataframe"`: a `data.frame` with columns `Item`, `Observed`, `Expected`, `Difference`, `p_adjusted`, `Flagged`, and `Relative_location`. `Flagged` is "overfit" (observed above expected, $\text{adj. } p < .05$), "underfit" (below, $\text{adj. } p < .05$), or "" (not flagged).

The `Difference` column is signed (observed minus expected): *positive* values indicate that the item correlates more strongly with the rest-score than the Rasch model predicts (over-discrimination / *overfit*, often associated with local dependence), and *negative* values indicate weaker-than-expected association (under-discrimination / *underfit*, often associated with multidimensionality or noise).

References

Kreiner, S. (2011). A Note on Item–Restscore Association in Rasch Models. *Applied Psychological Measurement*, 35(7), 557–561. doi:10.1177/0146621611410227

Examples

```

if (requireNamespace("iarm", quietly = TRUE)) {
  # Simulate binary item response data (8 items, 200 persons)
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 8, replace = TRUE), nrow = 200, ncol = 8)
  )
  colnames(sim_data) <- paste0("Item", 1:8)

  # Default kable output
  RMitemRestscore(sim_data)

  # Sorted by absolute difference
  RMitemRestscore(sim_data, sort = "diff")

  # Return as data.frame for further processing
  df <- RMitemRestscore(sim_data, output = "dataframe")
}

```

RMitemRestscoreBoot *Bootstrap Item-Restscore Misfit Detection*

Description

Non-parametric bootstrap of item-restscore fit using `iarm::item_restscores()`. For each iteration, a sample of size `samplesize` is drawn from data with replacement, the appropriate Rasch model is refitted, and item-restscore results are classified as "overfit", "underfit", or "no misfit" based on the BH-adjusted p-value ($< .05$) and the sign of expected - observed. The function returns the percentage of iterations in which each item is flagged.

Usage

```

RMitemRestscoreBoot(
  data,
  iterations = 200,
  samplesize = 600,
  parallel = TRUE,
  n_cores = NULL,
  cutoff = 5,
  verbose = FALSE,
  seed = NULL,
  output = "kable"
)

```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers).
<code>iterations</code>	Integer. Number of bootstrap samples (default 200).
<code>samplesize</code>	Integer. Size of each bootstrap sample (default 600). Must not exceed <code>nrow(data)</code> .
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> if available (default TRUE).
<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first. If neither is set and <code>parallel = TRUE</code> , a warning is issued and execution falls back to sequential processing.
<code>cutoff</code>	Numeric. Items flagged in fewer than this percentage of iterations are excluded from the kable output (default 5). Has no effect when <code>output = "dataframe"</code> or <code>output = "raw"</code> .
<code>verbose</code>	Logical. Show a progress bar (default FALSE).
<code>seed</code>	Integer or NULL. Random seed for reproducibility.
<code>output</code>	Either "kable" (default) for a formatted <code>knitr::kable()</code> table, "dataframe" for the per-item summary data.frame, or "raw" for the per-iteration long data.frame (useful for custom plotting).

Details

Useful with large samples, where the asymptotic test underlying `RMitemRestscore` can flag items that are not practically misfitting; bootstrapping gives a more nuanced view of the probability of an item actually being misfit.

The full-sample model is fitted by CML via `psychotools::pcmodel()` (a dichotomous item is a 2-category partial credit model), and item locations (mean of the grand-mean-centred CML Andrich thresholds) and the mean WLE person location are computed from it — consistent with `RMitemRestscore` and the rest of the package. Each bootstrap iteration draws a sample of size `samplesize` with replacement and refits via `psychotools::pcmodel(..., hessian = FALSE)` for speed; `iarm::item_restscore()` accepts the fitted model.

Conditional infit MSQ (computed once on the full sample via `iarm::out_infit()`) and relative item locations are reported alongside the bootstrap percentages for context. The item-restscore classification and the infit statistic are conditional and engine-invariant; only the relative-item location shifts slightly relative to the previous eRm implementation, because it now uses the WLE person mean (finite at extreme scores) rather than the eRm MLE mean.

Iterations that fail (e.g., due to convergence issues on a degenerate bootstrap sample) are silently discarded; the `caption / actual_iterations` reflects only successful runs.

Parallel processing is provided by the `mirai` package (optional). Install it with `install.packages("mirai")` to enable parallelisation.

The `iarm` package must be installed (it is in Suggests, not Imports).

Value

- If `output = "kable"`: a `knitr_kable` object listing items flagged in more than `cutoff%` of iterations, with columns Item, Item-restscore result, % of iterations, Conditional MSQ infit,

and Relative item location, and a caption noting iteration count, bootstrap size, and number of complete cases.

- If output = "dataframe": a data.frame with one row per item × classification combination (Item, item_restscore, n, percent, Infit_MSQ, Relative_location), including "no misfit" rows.
- If output = "raw": a long data.frame with one row per item × successful iteration (iteration, Item, item_restscore, diff, diff_abs), where diff = expected - observed.

References

Kreiner, S. (2011). A Note on Item-Restscore Association in Rasch Models. *Applied Psychological Measurement*, 35(7), 557-561. doi:10.1177/0146621611410227

See Also

[RMitemRestscore](#), [RMitemInfit](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 400 * 8, replace = TRUE), nrow = 400, ncol = 8)
  )
  colnames(sim_data) <- paste0("Item", 1:8)

  # Few iterations for a fast example; use 100+ in real analyses
  # Default kable output (only items flagged > cutoff%)
  RMitemRestscoreBoot(sim_data, iterations = 50, samplesize = 300,
    parallel = FALSE, seed = 1)

  # Per-item summary data.frame (all classifications, including "no misfit")
  summary_df <- RMitemRestscoreBoot(sim_data, iterations = 50, samplesize = 300,
    parallel = FALSE, seed = 1,
    output = "dataframe")

  # Per-iteration long data for custom plotting
  raw_df <- RMitemRestscoreBoot(sim_data, iterations = 50, samplesize = 300,
    parallel = FALSE, seed = 1, output = "raw")

  # Distribution of (expected - observed) across iterations, per item
  if (requireNamespace("ggplot2", quietly = TRUE)) {
    library(ggplot2)
    ggplot(raw_df, aes(x = Item, y = diff)) +
      geom_hline(yintercept = 0, linetype = "dashed", colour = "grey50") +
      geom_violin(fill = "grey90", colour = NA) +
      geom_jitter(aes(colour = item_restscore),
        width = 0.15, alpha = 0.5, size = 0.8) +
      scale_colour_manual(values = c("overfit" = "#377eb8",
        "underfit" = "#e41a1c",
        "no misfit" = "grey60")) +
```

```

labs(y = "Expected - observed restscore correlation",
      colour = NULL) +
theme_minimal() +
theme(axis.text.x = element_text(angle = 45, hjust = 1))
}
}

```

RMlocdepGamma

Partial Gamma Local Dependence Analysis

Description

Computes partial gamma coefficients for Local Dependence (LD) assessment using `iar::partgam_LD()`. Each pair of items is tested for residual association, controlling for the rest score (total score minus one of the items in the pair).

Usage

```

RMlocdepGamma(
  data,
  cutoff = NULL,
  p_value = FALSE,
  correction = c("fwer", "fdr_bh", "fdr_by", "none"),
  alpha = 0.05,
  output = "kable",
  n_pairs = NULL
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed, but at least one complete case must exist.
<code>cutoff</code>	Optional. Default NULL (no cutoff applied). Can be: <ul style="list-style-type: none"> The return value of <code>RMlocdepGammaCutoff</code> (a list with <code>\$pair_cutoffs</code>): the <code>data.frame</code> is extracted automatically and simulation metadata is included in the kable caption. The <code>\$pair_cutoffs</code> <code>data.frame</code> from <code>RMlocdepGammaCutoff</code> directly: must have columns <code>Item1</code>, <code>Item2</code>, <code>gamma_low</code>, <code>gamma_high</code>. When provided, adds columns <code>Gamma_low</code>, <code>Gamma_high</code>, and <code>Flagged</code> (logical; TRUE when the observed partial gamma falls outside the credible range) to the result.
<code>p_value</code>	Logical. When TRUE, adds one-sided bootstrap p-values for <i>excess positive</i> local dependence (<code>p_gamma</code> , <code>padj_gamma</code>), matching the <code>p_value</code> semantics of <code>RMlocdepQ3</code> , and <code>flagged</code> reflects <code>padj_gamma < alpha</code> (positive deviations

only) instead of the credible range. One test per item pair: the p-value is computed in the canonical direction (direction 1, rest score = total - Item2, the direction that was simulated) and repeated in the direction-2 table for the same pair. The asymptotic BH-adjusted p-value and star columns from `iar::partgam_LD()` are **dropped** in this mode; the simulated `gamma_low / gamma_high` band is kept as the effect-size reference. Requires the **full** `RMlocdepGammaCutoff` object as `cutoff` (it carries the simulated distributions in `$results`). Default `FALSE`.

correction	Character. Multiplicity correction for the bootstrap p-values, applied over the family of all item pairs (before any <code>n_pairs</code> display filter): "fwer" (default; Westfall-Young studentised-max step-down), "fdr_bh", "fdr_by", or "none". Ignored when <code>p_value = FALSE</code> .
alpha	Numeric in (0, 1). Significance level used to flag pairs on the corrected p-value. Default <code>0.05</code> . Ignored when <code>p_value = FALSE</code> .
output	Character string controlling the return value. Either "kable" (default) for a formatted <code>knitr::kable()</code> table, or "dataframe" for the underlying <code>data.frame</code> .
n_pairs	Optional positive integer. When supplied, only the <code>n_pairs</code> item pairs with the largest absolute partial-gamma values (i.e., strongest residual dependence in either direction) are retained per rest-score direction, sorted by <code> gamma </code> descending. When <code>NULL</code> (default), all pairs are returned in <code>iar</code> 's native ordering. Values larger than the total number of pairs are silently capped at that total.

Details

Partial gamma (Christensen, Kreiner & Mesbah, 2013) measures the residual association between pairs of items after controlling for the rest score (total score minus one item). Because it matters which item is subtracted, calculations are done for each pair in both directions, yielding two `data.frames`.

Values near 0 indicate no local dependence. Large positive values suggest positive LD (items share variance beyond the latent trait), while large negative values suggest negative LD.

The `iar` package must be installed (it is in `Suggests`, not `Imports`).

Bootstrap p-values. When `p_value = TRUE`, each pair's observed partial gamma (canonical direction) is compared against its simulated null distribution (from `cutoff$results`, simulated under local independence). The per-pair statistic is the residual studentised by the bootstrap mean and SD; the marginal p-value is the one-sided Monte-Carlo p-value $(1 + \#\{t^* \geq t\}) / (B + 1)$ for excess *positive* LD (redundancy, the diagnostic target — matching `RMlocdepQ3`), so it can be no smaller than $1 / (B + 1)$. The band still shows both bounds for reference. `correction = "fwer"` uses the Westfall-Young studentised-max step-down over the family of all pairs, which exploits the bootstrap dependence among them (Ferreira, 2024); it is liberal when the simulation is small, so at least 1000 iterations in `RMlocdepGammaCutoff()` are recommended (a warning is issued below that). Unlike the asymptotic p-values from `iar::partgam_LD()`, these are calibrated against the *simulated Rasch null* rather than the asymptotic SE; they are model-conditional and sample-size-sensitive, and are reported alongside the simulated effect-size band, not in place of it.

Value

- If `output = "kable"`: an object of class "RMlocdepGamma". Internally a list with two `knitr_kable` elements, `$direction1` and `$direction2`. In both, the rest score is the total score minus

Item 2 (the second column); the two elements list each item pair in the two possible orders, so together they cover both rest-score directions for every pair. Each has columns "Item 1", "Item 2", "Partial gamma", "Adj. p-value (BH)", and "p-value sign." (a star-string indicator from `iarm::partgam_LD()`). When `cutoff` is provided, additional columns "Gamma low", "Gamma high", and "Flagged" are included.

The object has custom `print()` and `knitr::knit_print()` methods: in the R console it prints the two tables stacked vertically; in a Quarto / R Markdown chunk it renders as two distinct pipe tables. Access the individual tables explicitly as `result$direction1` and `result$direction2` if needed.

- If `output = "dataframe"`: a named list of two data.frames (`$direction1`, `$direction2`) with columns `Item1`, `Item2`, `gamma`, `padj_bh`, `Significance`. When `cutoff` is provided, columns `gamma_low`, `gamma_high`, and `flagged` are also included. With `p_value = TRUE`, `padj_bh` and `Significance` are replaced by `p_gamma` and `padj_gamma` (identical for a pair in both directions).

Multiple comparisons

The marginal p-value controls the error rate of a *single* comparison: for one item (or item pair) decided on in advance it is the relevant value. But scanning all k comparisons and flagging whichever fall below α tests k hypotheses at once, so the chance of at least one false flag inflates to roughly $1 - (1 - \alpha)^k$ (e.g. about 34% for $k = 8$ at $\alpha = 0.05$) – even when every marginal p-value is correctly calibrated. The corrected (adjusted) p-value controls this: `correction = "fwer"` bounds the probability of *any* false flag (strict, lower power), while `"fdr_bh" / "fdr_by"` bound the expected *proportion* of false flags among those raised (a more lenient middle ground). Rule of thumb: use the marginal p-value for a single pre-specified comparison, and a corrected p-value when screening the whole table – the usual workflow.

References

- Christensen, K. B., Kreiner, S. & Mesbah, M. (Eds.) (2013). *Rasch Models in Health*, pp. 133–135. ISTE & Wiley. doi:10.1002/9781118574454
- Ferreira, J. A. (2024). Methods of testing a 'small' or 'moderate' number of hypotheses simultaneously. *Journal of Statistical Theory and Practice*, 19(6). doi:10.1007/s42519024004124
- Westfall, P. H., & Young, S. S. (1993). *Resampling-Based Multiple Testing*. Wiley.

See Also

[RMlocdepGammaCutoff](#), [RMlocdepGammaPlot](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)

  # Default kable output
```

```

RMlocdepGamma(sim_data)

# Return as data.frame list
RMlocdepGamma(sim_data, output = "dataframe")

# Simulation-based cutoffs (slow): 100+ Monte-Carlo iterations
if (requireNamespace("ggdist", quietly = TRUE)) {
  cutoff_res <- RMlocdepGammaCutoff(sim_data, iterations = 100,
                                   parallel = FALSE, seed = 42)
  RMlocdepGamma(sim_data, cutoff = cutoff_res)

  # Bootstrap p-values with family-wise (Westfall-Young) correction
  # (use iterations >= 1000 in real analyses for stable p-values)
  RMlocdepGamma(sim_data, cutoff = cutoff_res, p_value = TRUE,
                output = "dataframe")
}
}

```

RMlocdepGammaCutoff *Simulation-Based Partial Gamma LD Cutoff Determination*

Description

Uses parametric bootstrap simulation to determine appropriate cutoff values for partial gamma Local Dependence analysis via `partgam_LD`. Under a correctly fitting Rasch model where items are locally independent, this function generates the expected distribution of partial gamma values per item pair, providing empirical critical values.

Usage

```

RMlocdepGammaCutoff(
  data,
  iterations = 250,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  cutoff_method = "hdci",
  hdci_width = 0.99
)

```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Only complete cases (rows without any NA) are used.
<code>iterations</code>	Integer. Number of simulation iterations (default 250).
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> if available (default TRUE).

<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first. If neither is set and <code>parallel = TRUE</code> , a warning is issued and execution falls back to sequential (single core) processing.
<code>verbose</code>	Logical. Show a progress bar (default FALSE).
<code>seed</code>	Integer or NULL. Random seed for reproducibility.
<code>cutoff_method</code>	Character string specifying how cutoff intervals are computed. Either "hdci" (default) for the Highest Density Interval via <code>ggdist::hdci()</code> , or "quantile" for the 2.5th/97.5th percentiles via <code>stats::quantile()</code> .
<code>hdci_width</code>	Numeric. Width of the HD CI when <code>cutoff_method = "hdci"</code> . Default is 0.99 (99\ cutoff_method = "quantile").

Details

For each simulation iteration the function:

1. Resamples person parameters (thetas) with replacement from the WLE person locations.
2. Simulates item response data under a Rasch model (dichotomous via `psychotools::rrm()` or polytomous via an internal partial credit simulator).
3. Computes partial gamma LD statistics via `iarm::partgam_LD()`.

Because the data are simulated under the Rasch model, items are locally independent by construction. The distribution of partial gamma values across iterations provides empirical critical values per item pair. Values from real data that fall outside these bounds suggest local dependence that exceeds what would be expected by chance. Failed iterations (e.g., due to convergence issues or degenerate data) are silently discarded.

The generating model uses CML item thresholds via `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM) and WLE person locations, consistent with the rest of the package; responses are simulated with `psychotools::rrm()` (dichotomous) or an internal partial credit score simulator (polytomous).

Parallel processing is provided by the `mirai` package (optional). Install it with `install.packages("mirai")` to enable parallelisation.

The `iarm` package must be installed (it is in Suggests, not Imports).

Value

A list with components:

`results` data.frame with columns `iteration`, `Item1`, `Item2`, and `gamma` (one row per item pair per successful iteration). Contains results from direction 1 only (rest score = total - `Item2`), which is the conventional direction.

`pair_cutoffs` data.frame with per-pair cutoff summaries: `Item1`, `Item2`, `gamma_low`, `gamma_high`. Bounds are computed using the method specified by `cutoff_method`.

`actual_iterations` Number of successful iterations.

`sample_n` Number of complete cases used.

`sample_n_total` Number of respondents in the raw input data, before the complete-case filter.

`sample_has_na` Logical. Whether the raw input data contained any missing values.

sample_summary Summary statistics of estimated person parameters.
 item_names Character vector of item names from data.
 cutoff_method The method used to compute cutoffs ("hdci" or "quantile").
 hdci_width The HDCl width used (only meaningful when cutoff_method = "hdci").

References

Christensen, K. B., Kreiner, S. & Mesbah, M. (Eds.) (2013). *Rasch Models in Health*, pp. 133–135. ISTE & Wiley. doi:10.1002/9781118574454

See Also

[partgam_LD](#), [RMlocdepGamma](#), [RMlocdepGammaPlot](#)

Examples

```
if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)

  # Run 100 iterations sequentially for a quick demo
  cutoff_res <- RMlocdepGammaCutoff(sim_data, iterations = 100,
                                   parallel = FALSE, seed = 42)

  cutoff_res$pair_cutoffs
}
```

RMlocdepGammaPlot *Plot Distribution of Simulated Partial Gamma LD Values*

Description

Visualises the distribution of simulation-based partial gamma LD values from [RMlocdepGammaCutoff](#), optionally overlaying observed partial gamma values computed from real data via [partgam_LD](#).

Usage

```
RMlocdepGammaPlot(simfit, data, items = NULL, n_pairs = NULL)
```

Arguments

<code>simfit</code>	The return value of <code>RMlocdepGammaCutoff</code> (a list with components <code>results</code> , <code>pair_cutoffs</code> , <code>actual_iterations</code> , <code>sample_n</code> , and <code>item_names</code>).
<code>data</code>	Optional. A <code>data.frame</code> or matrix of item responses for computing and overlaying observed partial gamma values. Items must be scored starting at 0 (non-negative integers). When provided, the plot includes orange diamond markers for the observed partial gamma alongside the simulated distribution, plus segment summaries from the cutoff intervals.
<code>items</code>	Optional character vector of item names to include in the plot. Only item pairs where both items are in this vector will be shown. When <code>NULL</code> (default), all item pairs are plotted.
<code>n_pairs</code>	Optional positive integer. When supplied, only the <code>n_pairs</code> item pairs with the largest absolute partial gamma values are plotted, sorted by <code> gamma </code> descending. When <code>data</code> is supplied, the ranking uses the <i>observed</i> partial gammas (the diamonds you actually want to interpret); otherwise it falls back to the per-pair median of the simulated distributions. Applied <i>after</i> the <code>items</code> filter when both are supplied. Values larger than the number of available pairs are silently capped.

Details

Uses `ggdist::stat_dotsinterval()` (when `data` is not supplied) or `ggdist::stat_dots()` (when `data` is supplied) with `point_interval = "median_hdci"` and `.width = c(0.66, 0.95, 0.99)`.

The plot shows one row per item pair (labelled as "Item1 - Item2"). Only direction 1 (rest score = total - Item2) is plotted, matching the convention used in the simulation.

When `data` is **not** supplied, the function plots the simulated partial gamma distributions as dot-interval plots using `ggdist::stat_dotsinterval()` with median and Highest Density Continuous Interval (HD CI) summaries.

When `data` **is** supplied, the function:

1. Computes observed partial gamma values via `iarm::partgam_LD()`.
2. Overlays observed gamma values as orange diamond markers on the simulated distributions.
3. Shows per-pair cutoff intervals (from `simfit$pair_cutoffs`) as black line segments, with thicker segments for the 66\ black dots for the median.

The `ggplot2`, `ggdist`, and optionally `iarm` packages must be installed (they are in `Suggests`, not `Imports`).

Value

A `ggplot` object.

See Also

[RMlocdepGammaCutoff](#), [RMlocdepGamma](#)

Examples

```

if (requireNamespace("iarm", quietly = TRUE) &&
    requireNamespace("ggdist", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)

  # Run simulation
  cutoff_res <- RMlocdepGammaCutoff(sim_data, iterations = 100,
                                   parallel = FALSE, seed = 42)

  # Simulated distribution only
  RMlocdepGammaPlot(cutoff_res)

  # With observed partial gamma overlaid
  RMlocdepGammaPlot(cutoff_res, data = sim_data)

  # Plot only a subset of items
  RMlocdepGammaPlot(cutoff_res, data = sim_data,
                    items = c("Item1", "Item2", "Item3"))
}

```

 RMlocdepQ3

Q₃ Residual Correlations for Local Dependence Assessment

Description

Computes Yen's Q_3 residual correlations between item pairs. By default the Rasch model is fitted by conditional maximum likelihood with WLE person locations (`estimator = "CML"`); marginal ML via mirt is available with `estimator = "MML"`. High correlations (above the dynamic cut-off) indicate potential local dependence between items. See [RMlocdepQ3Cutoff](#) for how to determine the appropriate dynamic cut-off for your data.

Usage

```

RMlocdepQ3(
  data,
  cutoff = NULL,
  output = "kable",
  n_pairs = NULL,
  p_value = FALSE,
  correction = c("fwer", "fdr_bh", "fdr_by", "none"),
  alpha = 0.05,
  estimator = c("CML", "MML")
)

```

Arguments

data	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed.
cutoff	Optional. NULL (default) returns the raw Q_3 matrix. A single numeric value returns the Q_3 matrix with a global dynamic cut-off (the value added to the mean off-diagonal Q_3). The full list returned by <code>RMlocdepQ3Cutoff</code> returns a <i>list of two tables</i> (see Value): the cut-off matrix plus a per-pair table.
output	Character string controlling the return value. Either "kable" (default) for formatted <code>knitr::kable()</code> table(s), or "dataframe" for the underlying data.frame(s).
n_pairs	Integer or NULL (default). When the full cutoff object is supplied, limits the per-pair table to the n_pairs pairs with the largest departure from their expected range. NULL shows all pairs.
p_value	Logical. If TRUE (requires the full <code>RMlocdepQ3Cutoff</code> object), the per-pair table also reports one-sided bootstrap p-values (<code>p_q3</code> , <code>padj_q3</code>) and flags above pairs (only) on <code>padj_q3 < alpha</code> instead of the expected range. Default FALSE.
correction	Character. Multiple-comparison correction across item pairs when <code>p_value = TRUE</code> : "fwer" (default) for the Westfall-Young studentised-max step-down, "fdr_bh" / "fdr_by" for Benjamini-Hochberg / Benjamini-Yekutieli, or "none".
alpha	Numeric in (0, 1). Significance level for Flagged when <code>p_value = TRUE</code> . Default 0.05.
estimator	Character. Estimation engine for the Q_3 residual correlations. "CML" (default) fits item parameters by conditional maximum likelihood (psychotools) and person locations by Warm's weighted likelihood (WLE) – true to the Rasch tradition and finite at extreme scores. "MML" uses the marginal-ML / EAP engine (mirt), retained for backward compatibility. The estimator must match the one used by <code>RMlocdepQ3Cutoff</code> ; when the full cutoff object is supplied, its stored estimator takes precedence (a mismatching estimator argument is overridden with a warning).

Details

The Q_3 statistic (Yen, 1984) is the correlation between residuals of pairs of items after accounting for the latent trait. Under local independence, Q_3 values are expected to be around $-1/(k - 1)$ where k is the number of items. When `cutoff` is supplied, the dynamic cut-off is the mean of all off-diagonal Q_3 values plus `cutoff`, following the approach of Christensen et al. (2017). Use `RMlocdepQ3Cutoff` to obtain a simulation-based cutoff recommendation.

Q_3 is the column-wise correlation matrix of the model standardized residuals $(x - E)/\sqrt{Var}$. By default (`estimator = "CML"`) item parameters are estimated by conditional maximum likelihood (psychotools) and person locations by Warm's weighted likelihood; `estimator = "MML"` instead uses mirt's marginal-ML model and its built-in Q_3 residuals. The two estimators give very similar Q_3 values (off-diagonal correlation typically > 0.95); what matters for inference is that the observed Q_3 and the simulated cut-off in `RMlocdepQ3Cutoff` use the *same* estimator, which the functions enforce.

Two views of local dependence. Given the full `RMlocdepQ3Cutoff` object, two complementary tables are returned. The `$matrix` applies a single *global* cut-off (the Christensen et al. approach:

the 99th percentile of the simulated max-minus-mean Q_3) – a family-wise "is there any local dependence" overview. The \$pairs table is the per-comparison view: each observed Q_3 against its own simulated expected range (the Low/High bounds), so individual dependent pairs can be read off and ranked.

Bootstrap p-values. When p_value = TRUE, the \$pairs table also tests each observed Q_3 against its simulated null (from cutoff\$pair_results) with a one-sided (upper-tail) test for excess local dependence. The pair statistic is studentised by the bootstrap mean and SD; the marginal p-value is $(1 + \#\{Q_3 \geq Q_3\}) / (B + 1)$, and correction applies the family-wise (Westfall-Young step-down) or FDR adjustment across the $k(k-1)/2$ pairs. As for item fit, the family-wise correction is liberal when the simulation is small, so ≥ 1000 iterations in `RMlocdepQ3Cutoff()` are recommended (a warning is issued otherwise).

Value

With cutoff = NULL or a bare numeric cut-off, a single object (kable or data.frame) holding the lower triangle of the Q_3 matrix; a numeric cut-off adds a Flagged row flag and a caption describing the dynamic cut-off.

With the **full** `RMlocdepQ3Cutoff()` **object**, a named list of two:

\$matrix the Q_3 lower-triangle matrix with the *global* dynamic cut-off (mean off-diagonal Q_3 + suggested cut-off), as above.

\$pairs one row per item pair: Item1, Item2, Observed (Q_3), Low/High (the per-pair expected range, i.e. the simulated bounds), and Flagged – "above" (Q_3 above the upper bound, indicating local dependence), "below" (below the lower bound), or "". Sorted by absolute departure from the per-pair simulated median and truncated to n_pairs. With p_value = TRUE, columns p_q3 and padj_q3 are added and Flagged reflects padj_q3 < alpha and **only flags** "above".

The Q_3 tile heatmap that earlier versions returned as \$plot is now produced by `RMlocdepQ3Plot` (as its \$matrix element), so the table and plot outputs share the same \$matrix/\$pairs structure.

Multiple comparisons

The marginal p-value controls the error rate of a *single* comparison: for one item (or item pair) decided on in advance it is the relevant value. But scanning all k comparisons and flagging whichever fall below alpha tests k hypotheses at once, so the chance of at least one false flag inflates to roughly $1 - (1 - \alpha)^k$ (e.g. about 34% for $k = 8$ at $\alpha = 0.05$) – even when every marginal p-value is correctly calibrated. The corrected (adjusted) p-value controls this: correction = "fwer" bounds the probability of *any* false flag (strict, lower power), while "fdr_bh" / "fdr_by" bound the expected *proportion* of false flags among those raised (a more lenient middle ground). Rule of thumb: use the marginal p-value for a single pre-specified comparison, and a corrected p-value when screening the whole table – the usual workflow.

References

Yen, W. M. (1984). Effects of local item dependence on the fit and equating performance of the three-parameter logistic model. *Applied Psychological Measurement*, 8(2), 125–145. doi:10.1177/014662168400800201

Christensen, K. B., Makransky, G., & Horton, M. (2017). Critical values for Yen's Q_3 : Identification of local dependence in the Rasch model. *Applied Psychological Measurement*, 41(3), 178–194. doi:10.1177/0146621616677520

Ferreira, J. A. (2024). Methods of testing a 'small' or 'moderate' number of hypotheses simultaneously. *Journal of Statistical Theory and Practice*, 19(6). doi:10.1007/s42519024004124

Examples

```
# Simulate binary item response data (10 items, 200 persons)
set.seed(42)
sim_data <- as.data.frame(
  matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
)
colnames(sim_data) <- paste0("Item", 1:10)

# Raw Q3 matrix (no cutoff)
RMlocdepQ3(sim_data)

# Get the underlying data.frame
q3_df <- RMlocdepQ3(sim_data, output = "dataframe")

# Simulation-based cutoff (use 500+ iterations in real analyses)
if (requireNamespace("ggdist", quietly = TRUE)) {
  cutoff_res <- RMlocdepQ3Cutoff(sim_data, iterations = 50, parallel = FALSE)

  # Bare numeric cutoff -> just the matrix
  RMlocdepQ3(sim_data, cutoff = cutoff_res$suggested_cutoff)

  # Full object -> list of two tables: $matrix and $pairs
  res <- RMlocdepQ3(sim_data, cutoff = cutoff_res, output = "dataframe")
  res$pairs

  # Top 5 pairs, with bootstrap p-values (use iterations >= 1000 in practice)
  RMlocdepQ3(sim_data, cutoff = cutoff_res, n_pairs = 5, p_value = TRUE,
    output = "dataframe")$pairs
}
```

RMlocdepQ3Cutoff

Simulation-Based Q_3 Cutoff Determination

Description

Uses parametric bootstrap simulation to determine an appropriate cutoff value for `RMlocdepQ3`. Under a correctly fitting Rasch model, Q_3 residuals have an unknown distribution; this function simulates that distribution and returns empirical percentiles.

Usage

```

RMlocdepQ3Cutoff(
  data,
  iterations = 500,
  parallel = TRUE,
  n_cores = NULL,
  verbose = FALSE,
  seed = NULL,
  cutoff_method = "hdci",
  hdci_width = 0.99,
  estimator = c("CML", "MML"),
  dgp = c("resample", "conditional")
)

```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers).
<code>iterations</code>	Integer. Number of simulation iterations (default 500).
<code>parallel</code>	Logical. Use parallel processing via <code>mirai</code> if available (default TRUE).
<code>n_cores</code>	Integer or NULL. Number of parallel workers. When NULL, <code>getOption("mc.cores")</code> is checked first. If neither is set and <code>parallel = TRUE</code> , a warning is issued and execution falls back to sequential (single core) processing.
<code>verbose</code>	Logical. Show a progress bar (default FALSE).
<code>seed</code>	Integer or NULL. Random seed for reproducibility.
<code>cutoff_method</code>	Character. Method used to compute per-pair Q_3 credible intervals in <code>pair_cutoffs</code> . One of "hdci" (the default, Highest Density Continuous Interval via <code>ggdist::hdci()</code>) or "quantile" (symmetric 2.5th / 97.5th percentiles). Only affects <code>pair_cutoffs</code> ; the global <code>\$suggested_cutoff</code> (99th percentile of $\max(Q_3) - \text{mean}(Q_3)$) is unaffected.
<code>hdci_width</code>	Numeric in (0, 1). Width of the HDCl when <code>cutoff_method = "hdci"</code> . Default 0.99. Ignored when <code>cutoff_method = "quantile"</code> .
<code>estimator</code>	Character. Estimation engine for the simulated Q_3 values, passed through to the per-iteration computation. "CML" (default) uses CML item parameters and WLE person locations; "MML" uses <code>mirt</code> . This must match the estimator later given to <code>RMlocdepQ3</code> ; the value is stored in the returned object's <code>\$estimator</code> and reused automatically.
<code>dgp</code>	Character. Data-generating process for the parametric bootstrap. "resample" (default) draws person locations by resampling the WLE estimates with replacement and simulates responses under the model – a <i>marginal</i> null. "conditional" instead simulates each respondent's pattern from the exact Rasch conditional distribution given their observed total score (and answered items), with item parameters fixed – a <i>conditional</i> null that fixes the score margin and needs no latent distribution, avoiding the over-dispersion of resampled point estimates. The two give different cut-offs; see the package's comparison study. Experimental.

Details

The generating model is fitted once: CML item parameters (via `psychotools`) and WLE person locations. For each simulation iteration, those WLE thetas are resampled with replacement, response data are simulated under the Rasch / Partial Credit model, the model is refitted, and Q_3 residuals are computed under `estimator`. The distribution of $\max(Q_3) - \text{mean}(Q_3)$ across iterations provides empirical critical values. Failed iterations (e.g., due to convergence issues) are silently discarded.

Supports both **dichotomous** data (simulated via `psychotools::rrm()`) and **polytomous** data (via an internal partial credit score simulator).

Parallel processing is provided by the `mirai` package (optional). Install it with `install.packages("mirai")` to enable parallelisation.

Value

A list with components:

`results` data.frame with columns `mean`, `max`, `diff` (one row per successful iteration).

`pair_results` Long data.frame with columns `Item1`, `Item2`, `Q3`, `iteration` — one row per item pair per successful iteration. Used by [RMlocdepQ3Plot](#).

`pair_cutoffs` data.frame with per-pair cutoff summaries: `Item1`, `Item2`, `Q3_low`, `Q3_high`. Boundaries are computed via the method specified by `cutoff_method`.

`actual_iterations` Number of successful iterations.

`sample_n` Number of persons in the original data.

`sample_n_total` Equal to `sample_n`: no respondents are dropped (incomplete responses are retained). Stored for consistency with the other `*Cutoff()` objects.

`sample_has_na` Logical. Whether the data contained any missing values.

`sample_summary` Summary statistics of estimated person parameters.

`item_names` Character vector of item names from data.

`max_diff`, `sd_diff` Max and SD of the `diff` distribution.

`p95`, `p99`, `p995`, `p999` Empirical percentiles of `diff`.

`suggested_cutoff` The 99th percentile (`p99`) — recommended scalar cutoff for [RMlocdepQ3](#).

`cutoff_method` The method used for `pair_cutoffs` ("`hdci`" or "`quantile`").

`hdci_width` The HDCl width used (only meaningful when `cutoff_method = "hdci"`).

`estimator` The estimator used for the simulated Q_3 ("`CML`" or "`MML`"); reused by [RMlocdepQ3](#) and [RMlocdepQ3Plot](#).

`dgp` The data-generating process used ("`resample`" or "`conditional`").

See Also

[RMlocdepQ3](#)

Examples

```

if (requireNamespace("ggdist", quietly = TRUE)) {
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_data) <- paste0("Item", 1:10)

  # Few iterations for a fast example; use 500+ in real analyses
  cutoff_res <- RMlocdepQ3Cutoff(sim_data, iterations = 50, parallel = FALSE,
                                seed = 42)
  cutoff_res$suggested_cutoff # 99th percentile

  # Use the cutoff in RMlocdepQ3()
  RMlocdepQ3(sim_data, cutoff = cutoff_res$suggested_cutoff)
}

```

RMlocdepQ3Plot

Plot Distribution of Simulated Q_3 Residual Correlations

Description

Visualises the distribution of simulation-based Yen's Q_3 residual correlations per item pair from [RMlocdepQ3Cutoff](#), optionally overlaying observed Q_3 values computed from real data via `mirt::residuals(..., type = "Q3")`.

Usage

```
RMlocdepQ3Plot(simfit, data, items = NULL, n_pairs = NULL)
```

Arguments

<code>simfit</code>	The return value of RMlocdepQ3Cutoff (a list with components <code>pair_results</code> , <code>pair_cutoffs</code> , <code>actual_iterations</code> , <code>sample_n</code> , and <code>item_names</code>).
<code>data</code>	Optional. A <code>data.frame</code> or matrix of item responses for computing and overlaying observed Q_3 values. Items must be scored starting at 0 (non-negative integers). When provided, the plot includes orange diamond markers for the observed Q_3 alongside the simulated distribution, plus segment summaries from the cutoff intervals.
<code>items</code>	Optional character vector of item names to include in the plot. Only item pairs where both items are in this vector will be shown. When <code>NULL</code> (default), all item pairs are plotted.
<code>n_pairs</code>	Optional positive integer. When supplied, only the <code>n_pairs</code> item pairs with the largest deviation from the simulated null are plotted, sorted by <code> observed Q3 - median(simulated Q3 per pair) </code> descending when <code>data</code> is supplied, or by <code> median(simulated Q3 per pair) </code> otherwise. Applied <i>after</i> the <code>items</code> filter when both are supplied. Values larger than the number of available pairs are silently capped.


```

# Simulated distribution only
RMlocdepQ3Plot(cutoff_res)

# With observed Q3 overlaid
RMlocdepQ3Plot(cutoff_res, data = sim_data)

# Top 10 pairs by departure from null
RMlocdepQ3Plot(cutoff_res, data = sim_data, n_pairs = 10)
}

```

RMpersonFit

Person-Fit Statistics for a Rasch / Partial Credit Model

Description

Computes per-respondent person-fit statistics and resampling-based p-values. Three statistics are reported: conditional **infit** and **outfit** mean-squares (MSQ) – the magnitude (effect-size) measures familiar from Rasch analysis – and the standardized log-likelihood statistic **lz**. The conditional MSQ statistics use response probabilities conditional on the total score, which require no person estimate and are therefore unbiased (Kreiner & Christensen, 2011); they are computed on each person’s observed response pattern, so partial missingness is handled directly.

Usage

```

RMpersonFit(
  data,
  statistics = c("infit", "outfit", "lz"),
  estimator = c("CML", "MML"),
  theta_method = c("WLE", "EAP"),
  iterations = 500L,
  flag_alpha = 0.05,
  flag = c("both", "underfit"),
  zstd = FALSE,
  parallel = FALSE,
  n_cores = NULL,
  seed = NULL,
  output = c("kable", "dataframe", "ggplot")
)

```

Arguments

data	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed.
statistics	Character vector. Which statistics to report; any of "infit", "outfit", "lz". Defaults to all three.
estimator	Character. How item parameters are estimated: "CML" (default) or "MML" (via mirt).

theta_method	Character. Person-location estimator used for the lz statistic: "WLE" (default) or "EAP". Ignored if "lz" is not requested.
iterations	Integer. Number of Monte-Carlo replications per person. 0 skips resampling and returns statistics only. Default 500.
flag_alpha	Numeric in (0, 1). Significance level for the flagged column and the plot highlighting. Default 0.05.
flag	Character. Which misfit direction drives flagging for the MSQ statistics: "both" (default) flags either direction with a two-sided p-value; "underfit" flags only underfit (MSQ > 1, noisy responding) with a one-sided upper p-value, which is more powerful for detecting it and ignores (benign) overfit. The reported p_infit / p_outfit follow this choice. lz is one-sided regardless. Overfit can occasionally be suspicious (e.g. fabricated or copied response patterns), so "both" is the default.
zstd	Logical. If TRUE, also report the Wilson-Hilferty standardized (ZSTD) versions of the MSQ statistics. These are provided only as a familiar cross-person comparability metric and are not used for inference (see Müller, 2020). Default FALSE.
parallel, n_cores	Logical / integer. Parallelise the resampling across persons via mirai when available. Default sequential.
seed	Optional integer for reproducible resampling.
output	Character. "kable" (default), "dataframe", or "ggplot". For "ggplot", a named list of person-fit maps is returned – one per requested statistic (e.g. \$infit, \$outfit, \$lz) – each plotting the statistic against person location, with respondents flagged by <i>that</i> statistic highlighted and a caption reporting the assessed sample size and the proportion flagged. For the MSQ maps the flagged count is split into underfit (MSQ > 1, noisy/erratic responding) and overfit (MSQ < 1, overly deterministic responding).

Details

Statistical significance is assessed by Monte-Carlo resampling under the fitted model rather than by an assumed asymptotic distribution. The asymptotic null distributions of MSQ and lz are known to be unreliable – the Wilson-Hilferty (ZSTD) transformation of MSQ in particular adds nothing once conditional estimation is used (Müller, 2020) – so resampling provides the valid reference (Sinharay, 2016).

Conditional MSQ. For person v with answered items A_v and total score r_v , the conditional residual is $z_{vi} = (x_{vi} - E(X_{vi} | R_v = r_v)) / \sqrt{\text{Var}(X_{vi} | R_v = r_v)}$, with conditional moments obtained from elementary symmetric functions of the answered items' parameters. Outfit is the unweighted mean of z_{vi}^2 ; infit is the information-weighted mean. Because the conditional moments use only item parameters, no (biased) person estimate enters the residual.

Interpreting MSQ direction. Values near 1 indicate fit. MSQ > 1 (*underfit*) means the responses are noisier / more erratic than the model expects – the validity-relevant direction, indicating careless or aberrant responding. MSQ < 1 (*overfit*) means responses are overly deterministic (Guttman-like); usually benign for score validity, though a suspiciously perfect pattern can occasionally signal copied or fabricated data. Use flag = "underfit" to flag only the former. lz is one-sided: low (negative) values flag the aberrant (underfit-like) direction.

lz. The standardized log-likelihood of the response pattern evaluated at the estimated person location (Drasgow, Levine & Williams, 1985); small (negative) values indicate misfit. Because the location is estimated rather than known, the variance of lz is below 1 and its asymptotic standard-normal null is invalid, which makes a naive test conservative (Snijders, 2001; Sinharay, 2016). Instead of applying the analytic lz^* standardization – derived by Snijders (2001) for dichotomous items and extended to polytomous / mixed-format items by Sinharay (2016, 2026) – easyRasch2 obtains the reference distribution by resampling with the person location **re-estimated for every simulated pattern** (see **Resampling**). This reproduces the ability-estimation effect and is the resampling analogue of lz^* , so the resampled p-value is well calibrated.

Resampling. Each statistic is referenced against the null that matches it, removing the need to choose a scheme. The conditional MSQ statistics use patterns sampled **conditional on the person's total score** – the exact Rasch-native null, requiring no person estimate and fully consistent with the (conditional) statistic. lz, which is defined at the estimated location, uses patterns **simulated at that location and then scored with the location re-estimated from each simulated pattern**, so the null carries the same ability-estimation effect as the observed lz (for a Rasch / PCM model the location is a function of the total score, so this re-estimation is a cheap score-based lookup). Both schemes are computed per person over the items actually answered, so partial missingness is handled by either. The p-value is the proportion of the iterations replicates at least as extreme as the observed value. This follows the resampling-based person-fit approach (Sinharay, 2016) and the bootstrap recommendation of Müller (2020).

Value

For output = "dataframe", a data.frame with one row per respondent (input order): id, n_answered, sum_score, the requested statistics (infit_msq, outfit_msq, lz), their resampled p-values (p_infit, p_outfit, p_lz) when iterations > 0, flagged, and – if zstd = TRUE – infit_zstd, outfit_zstd. The flagged column is TRUE when the marginal (uncorrected) p-value of **any** requested statistic is below flag_alpha for that respondent; it is therefore a per-person screening flag, not corrected for the number of respondents tested (so under fit expect about flag_alpha of respondents to be flagged by chance). Each output = "ggplot" map instead colours and counts respondents flagged by its **own** statistic alone. Extreme scorers (minimum or maximum possible given the items they answered) receive NA statistics and are not assessed. For output = "kable" the same content as a knitr_kable; for output = "ggplot" the named list of maps described under that argument.

References

- de la Torre, J., & Deng, W. (2008). Improving person-fit assessment by correcting the ability estimate and its reference distribution. *Journal of Educational Measurement*, 45(2), 159-177. doi:10.1111/j.17453984.2008.00058.x
- Drasgow, F., Levine, M. V., & Williams, E. A. (1985). Appropriateness measurement with polytomous item response models and standardized indices. *British Journal of Mathematical and Statistical Psychology*, 38(1), 67-86. doi:10.1111/j.20448317.1985.tb00817.x
- Kreiner, S., & Christensen, K. B. (2011). Exact evaluation of bias in Rasch model residuals. *Advances in Mathematics Research*, 12, 19-40.
- Müller, M. (2020). Item fit statistics for Rasch analysis: can we trust them? *Journal of Statistical Distributions and Applications*, 7(5). doi:10.1186/s40488020001087
- Sinharay, S. (2016). Assessment of person fit using resampling-based approaches. *Journal of Educational Measurement*, 53(1), 63-85. doi:10.1111/jedm.12101

Sinharay, S. (2016). Asymptotically correct standardization of person-fit statistics beyond dichotomous items. *Psychometrika*, 81(4), 992-1013. doi:10.1007/s113360159465x

Sinharay, S. (2026). Refining the asymptotically correct standardization of person-fit statistics for mixed-format tests. *British Journal of Mathematical and Statistical Psychology*. doi:10.1111/bmsp.70049

Snijders, T. A. B. (2001). Asymptotic null distribution of person fit statistics with estimated person parameter. *Psychometrika*, 66(3), 331-342. doi:10.1007/BF02294440

See Also

[RMpersonParameters\(\)](#), [RMitemInfit\(\)](#), [RMitemParameters\(\)](#)

Examples

```
set.seed(1)
dat <- as.data.frame(
  matrix(sample(0:2, 200 * 8, replace = TRUE), nrow = 200, ncol = 8)
)
colnames(dat) <- paste0("Item", 1:8)

# Conditional infit/outfit MSQ + lz with resampled p-values
RMpersonFit(dat, iterations = 200, output = "dataframe") |> head()

# Person-fit maps: a named list with one plot per statistic
if (requireNamespace("ggplot2", quietly = TRUE)) {
  plots <- RMpersonFit(dat, iterations = 200, output = "ggplot")
  plots$infit # infit map (each plot's caption reports the % flagged)
}

# Flag only underfit (noisy responding), the validity-relevant direction
RMpersonFit(dat, iterations = 200, flag = "underfit",
  output = "dataframe") |> head()
```

RMpersonParameters

Person Locations for a Rasch / Partial Credit Model

Description

Estimates a person location (θ) and its standard error of measurement (SEM) for every respondent. Estimation is performed directly on each person's observed response pattern, so partial missingness is handled correctly: two respondents with the same sum score on different subsets of items receive different estimates. This avoids the sum-score lookup used by [RMscoreSE\(\)](#), which assumes complete data.

Usage

```

RMpersonParameters(
  data,
  method = c("WLE", "EAP"),
  item_params = NULL,
  estimator = c("CML", "MML"),
  theta_range = c(-10, 10),
  prior_mean = 0,
  prior_sd = NULL,
  output = c("kable", "dataframe", "ggplot", "file"),
  filename = NULL
)

```

Arguments

data	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed.
method	Character. "WLE" (default) for Warm's Weighted Likelihood Estimate (lower bias than MLE; Warm, 1989), or "EAP" for the Expected A Posteriori estimate under a normal prior.
item_params	Optional pre-specified item parameters, e.g. for anchoring or equating. Either a named list of Andrich-threshold vectors (one per item) or the long-format data.frame returned by <code>RMitemParameters()</code> . When NULL (default) item parameters are estimated from data.
estimator	Character. How item parameters are estimated when <code>item_params</code> is NULL: "CML" (default, via <code>psychotools</code>) or "MML" (via <code>mirt</code>). Ignored when <code>item_params</code> is supplied.
theta_range	Numeric length 2. Search range for the WLE root and bounds for the EAP quadrature grid. Default <code>c(-10, 10)</code> . Only if the WLE root falls outside this range is the boundary returned.
prior_mean	Numeric. Mean of the normal prior used by <code>method = "EAP"</code> . Default 0, the natural choice when item parameters are centred at mean difficulty zero. Ignored for WLE.
prior_sd	Numeric or NULL. Standard deviation of the normal prior used by <code>method = "EAP"</code> . When NULL (default) it is estimated from the data by marginal maximum likelihood, holding the item parameters fixed. Supply a number (e.g. 1 for a standard $N(0, 1)$ prior, or a value carried over from a reference sample for equating) to fix it. Ignored for WLE.
output	Character. "kable" (default) for a formatted <code>knitr::kable()</code> table, "dataframe" for the underlying data.frame, "ggplot" for a histogram of the estimated person locations, or "file" to write the data.frame to a CSV at filename (the data.frame is also returned invisibly).
filename	Character. Path to the CSV file to write when <code>output = "file"</code> . Required in that case; ignored otherwise.

Details

Item parameters are obtained once (by CML or MML, or taken from `item_params`) and treated as fixed. Each person's θ is then estimated from the items they answered.

WLE solves Warm's weighted-likelihood score equation $l'(\theta) + J(\theta) / (2 I(\theta)) = 0$ by bracketed root finding, where the bias-correction term $J / (2 I)$ keeps the equation solvable at the boundaries. The SEM is $1 / \sqrt{I(\theta)}$. Unlike the MLE, Warm's estimator therefore yields *finite* locations for the minimum and maximum possible scores (a sensible step beyond the next-most extreme score rather than $\pm\infty$; cf. Warm, 1989), matching established implementations such as **catR** and **TAM**. Such scores are still marked in the extreme column because they are extrapolated and carry large standard errors. Only if the root lies outside `theta_range` is the boundary returned with NA SEM.

EAP integrates the pattern likelihood against a normal prior over a quadrature grid; the estimate is the posterior mean and the SEM is the posterior standard deviation. Unlike WLE, EAP is finite at extreme scores because the prior shrinks them inward, at the cost of depending on the assumed prior. The prior actually used – including the marginal-ML estimate of `prior_sd` when it is left NULL – is reported in the kable caption and attached to the result as `attr(result, "prior")`.

Value

For output = "dataframe", a data.frame with one row per respondent (in input order; respondents with no responses are dropped with a message) and columns `theta` (the person location), `sem` (standard error of measurement), `sum_score`, `n_answered` (number of non-missing responses), and `extreme` (logical: a minimum or maximum possible score given the items answered). For output = "kable", the same content as a knitr_kable object. For output = "ggplot", a histogram of `theta`.

References

- Warm, T. A. (1989). Weighted likelihood estimation of ability in item response theory. *Psychometrika*, 54(3), 427-450. doi:10.1007/BF02294627
- Bock, R. D., & Mislevy, R. J. (1982). Adaptive EAP estimation of ability in a microcomputer environment. *Applied Psychological Measurement*, 6(4), 431-444. doi:10.1177/014662168200600405
- Magis, D. (2015). A note on weighted likelihood and Jeffreys modal estimation of proficiency levels in polytomous item response models. *Psychometrika*, 80(1), 200-204. doi:10.1007/s11336-01393785

See Also

[RMitemParameters\(\)](#), [RMscoreSE\(\)](#), [RMreliability\(\)](#)

Examples

```
set.seed(1)
dat <- as.data.frame(
  matrix(sample(0:2, 200 * 6, replace = TRUE), nrow = 200, ncol = 6)
)
colnames(dat) <- paste0("Item", 1:6)
# Introduce some missingness
```

```
dat[cbind(sample(200, 30), sample(6, 30, replace = TRUE))] <- NA

# Default: WLE person locations
RMpersonParameters(dat, output = "dataframe") |> head()

# EAP with a data-estimated prior SD
eap <- RMpersonParameters(dat, method = "EAP", output = "dataframe")
attr(eap, "prior")

# EAP with a fixed N(0, 1) prior
RMpersonParameters(dat, method = "EAP", prior_sd = 1, output = "dataframe") |>
  head()

# Write the person-location table to a CSV (also returned invisibly)
RMpersonParameters(dat, output = "file",
  filename = tempfile(fileext = ".csv"))
```

RMplotBar

Item Response Distribution Bar Chart

Description

Creates a faceted bar chart showing the response distribution for each item, with counts and percentages displayed on each bar. Each item gets its own panel, with response categories on the x-axis and percentage of responses on the y-axis. This is a descriptive data visualization tool intended for use before model fitting.

Usage

```
RMplotBar(
  data,
  item_labels = NULL,
  category_labels = NULL,
  ncol = 1L,
  label_wrap = 25L,
  text_y = 6,
  viridis_option = "A",
  viridis_end = 0.9,
  font = "sans"
)
```

Arguments

data A data.frame in wide format containing only the item response columns. Each column is one item, each row is one person. All columns must be numeric (integer-valued). Response categories may be coded starting from 0 or 1. Do not include person IDs, grouping variables, or other non-item columns.

<code>item_labels</code>	An optional character vector of descriptive labels for the items (facet strips). Must be the same length as <code>ncol(data)</code> . If NULL (the default), column names are used. Labels are displayed as "column_name - label".
<code>category_labels</code>	An optional character vector of labels for the response categories (x-axis). Must be the same length as the number of response categories spanning from the minimum to the maximum observed value. If NULL (the default), numeric category values are used.
<code>ncol</code>	Integer. Number of columns in the faceted layout. Default is 1L.
<code>label_wrap</code>	Integer. Number of characters per line in facet strip labels before wrapping. Default is 25L.
<code>text_y</code>	Numeric. Vertical position (in percent units) for the count labels on each bar. Adjust upward if bars are tall. Default is 6.
<code>viridis_option</code>	Character. Viridis palette option for the count-text colour. One of "A" through "H". Default is "A".
<code>viridis_end</code>	Numeric in [0, 1]. End point of the viridis colour scale for count text. Adjust if text is hard to read against the bar colours. Default is 0.9.
<code>font</code>	Character. Font family for all text. Default is "sans".

Details

Each item is displayed as a separate facet panel with the item label in the strip on the left side. Bars are coloured by response category using the viridis palette. Each bar shows the count ($n = X$) as text.

The plot caption reports the sample in the standard $n = X$ respondents (policy) form; item-level NAs are retained – each bar counts the non-missing responses for that item.

Input requirements:

- All columns must be numeric (integer-valued).
- The data frame must contain at least 2 columns (items) and at least 1 row (person).

Value

A `ggplot2::ggplot` object.

See Also

[RMplotStackedbar\(\)](#), [RMplotTile\(\)](#)

Examples

```
if (requireNamespace("eRm", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  data(pcmdat2, package = "eRm")

  # Basic response distribution plot
  RMplotBar(pcmdat2)
```

```

# With custom item labels
RMplotBar(
  pcmdat2,
  item_labels = c("Mood", "Sleep", "Appetite", "Energy")
)

# Two-column layout with wrapped labels
RMplotBar(
  pcmdat2,
  item_labels = c(
    "General mood and emotional wellbeing",
    "Quality of sleep at night",
    "Appetite and eating habits",
    "Overall energy level during the day"
  ),
  ncol = 2, label_wrap = 20
)

# With custom category labels
RMplotBar(
  pcmdat2,
  category_labels = c("Never", "Sometimes", "Often")
)
}

```

RMplotStackedbar

Stacked Bar Chart of Item Response Distributions

Description

Creates a horizontal stacked bar chart showing the response distribution for all items. Each bar represents one item, with segments coloured by response category. Counts are displayed as text labels within each segment. This is a descriptive data visualization tool intended for use before model fitting.

Usage

```

RMplotStackedbar(
  data,
  item_labels = NULL,
  category_labels = NULL,
  show_n = TRUE,
  show_percent = FALSE,
  text_color = "sienna1",
  text_size = 3,
  min_label_n = 0L,
  viridis_option = "D",
  viridis_end = 0.99,

```

```

    title = "Item responses"
  )

```

Arguments

<code>data</code>	A <code>data.frame</code> in wide format containing only the item response columns. Each column is one item, each row is one person. All columns must be numeric (integer-valued). Response categories may be coded starting from 0 or 1. Do not include person IDs, grouping variables, or other non-item columns.
<code>item_labels</code>	An optional character vector of descriptive labels for the items (y-axis). Must be the same length as <code>ncol(data)</code> . If <code>NULL</code> (the default), column names are used.
<code>category_labels</code>	An optional character vector of labels for the response categories (legend). Must be the same length as the number of response categories spanning from the minimum to the maximum observed value, ordered from lowest to highest category. If <code>NULL</code> (the default), numeric category values are used.
<code>show_n</code>	Logical. If <code>TRUE</code> (the default), the count of responses is displayed as a text label inside each bar segment.
<code>show_percent</code>	Logical. If <code>TRUE</code> , the percentage of responses is displayed instead of (or in addition to) counts. Default is <code>FALSE</code> .
<code>text_color</code>	Character. Colour for the count/percentage labels. Default is <code>"sienna1"</code> .
<code>text_size</code>	Numeric. Size of the count/percentage labels. Default is 3.
<code>min_label_n</code>	Integer. Minimum count required for a label to be displayed within a bar segment. Segments with fewer responses are left unlabelled to avoid clutter. Default is 0 (all segments labelled).
<code>viridis_option</code>	Character. Viridis palette option. One of "A" through "H". Default is "D".
<code>viridis_end</code>	Numeric in $[0, 1]$. End point of the viridis colour scale. Default is 0.99.
<code>title</code>	Character. Plot title. Default is <code>"Item responses"</code> .

Details

Items are displayed on the y-axis in the same order as the columns in `data` (first column at the top). Each bar is divided into segments representing response categories, with the lowest category on the left and the highest on the right. The total bar length equals the number of non-missing responses for that item.

Categories with zero responses still appear in the legend but produce no visible bar segment, which helps identify gaps in the response distribution.

The plot caption reports the sample in the standard $n = X$ respondents (policy) form; item-level NAs are retained – each bar counts the non-missing responses for that item.

Input requirements:

- All columns must be numeric (integer-valued).
- The data frame must contain at least 2 columns (items) and at least 1 row (person).

Value

A `ggplot2::ggplot` object.

See Also

`RMplotBar()`, `RMplotTile()`

Examples

```
if (requireNamespace("eRm", quietly = TRUE) &&
    requireNamespace("ggplot2", quietly = TRUE)) {
  data(pcmdat2, package = "eRm")

  # Basic stacked bar chart
  RMplotStackedbar(pcmdat2)

  # With custom item and category labels
  RMplotStackedbar(
    pcmdat2,
    item_labels = c("Mood", "Sleep", "Appetite", "Energy"),
    category_labels = c("Never", "Sometimes", "Often")
  )

  # Show percentages, suppress small segments
  RMplotStackedbar(
    pcmdat2,
    show_percent = TRUE,
    show_n = FALSE,
    min_label_n = 5
  )
}
```

RMplotTile

Tile Plot of Item Response Distributions

Description

Creates a tile (heat map) plot showing the distribution of responses across all items and response categories. Each cell displays the count (or percentage) of responses, with optional conditional highlighting for cells with low counts. Optional faceting by a grouping variable is provided for inspecting subgroup response distributions before DIF analyses – particularly useful for spotting empty categories or under-represented subgroups before fitting Rasch models per group.

Usage

```
RMplotTile(
  data,
  group = NULL,
```

```

  cutoff = 10,
  highlight = TRUE,
  percent = FALSE,
  text_color = "orange",
  item_labels = NULL,
  category_labels = NULL,
  group_labels = NULL,
  facet_ncol = NULL,
  output = c("ggplot", "dataframe")
)

```

Arguments

<code>data</code>	A <code>data.frame</code> in wide format containing only the item response columns. Each column is one item, each row is one person. All columns must be numeric (integer-valued). Response categories may be coded starting from 0 or 1. Do not include person IDs, grouping variables, or other non-item columns – supply the grouping variable separately via <code>group</code> .
<code>group</code>	Optional vector of length <code>nrow(data)</code> (factor, character, or numeric) defining a grouping variable. When provided, the plot is faceted by <code>group</code> and counts / percentages are computed within each group. Default <code>NULL</code> (no faceting). Persons with <code>NA</code> <code>group</code> are excluded, with a <code>message()</code> reporting how many rows were dropped.
<code>cutoff</code>	Integer. Cells with counts below this value are highlighted (when <code>highlight = TRUE</code>). Default 10.
<code>highlight</code>	Logical. If <code>TRUE</code> (default), cell labels with counts below <code>cutoff</code> are displayed in red. This includes empty cells ($n = 0$), useful for identifying gaps in the response distribution.
<code>percent</code>	Logical. If <code>TRUE</code> , cell labels show percentages instead of raw counts. Percentages are computed within item (and within group, when <code>group</code> is supplied). Default <code>FALSE</code> .
<code>text_color</code>	Character. Colour for non-highlighted cell labels. Default "orange".
<code>item_labels</code>	Optional character vector of descriptive labels for the items (y-axis), same length as <code>ncol(data)</code> . Default <code>NULL</code> uses the column names.
<code>category_labels</code>	Optional character vector of labels for the response categories (x-axis), same length as the number of categories spanning <code>min</code> to <code>max</code> observed value. Default <code>NULL</code> uses the numeric category values.
<code>group_labels</code>	Optional character vector of length <code>nlevels(as.factor(group))</code> to override the displayed facet labels. Order corresponds to <code>levels(as.factor(group))</code> .
<code>facet_ncol</code>	Integer or <code>NULL</code> . Number of columns in the facet grid when <code>group</code> is supplied. Default <code>NULL</code> (<code>ggplot2</code> chooses).
<code>output</code>	Character. "ggplot" (default) returns the plot; "dataframe" returns the underlying per-cell counts (one row per item x category, plus <code>group</code> when supplied).

Details

Adapted from `easyRaschBayes::plot_tile()` and extended with the `group` parameter for faceted display.

Items are placed on the y-axis (in the same order as the columns of data, top to bottom) and response categories on the x-axis. Cell shading represents the count of responses (darker = more responses). Categories with zero responses are explicitly shown ($n = 0$), which helps identify gaps in the response distribution – one of the primary purposes of the plot, especially before DIF analyses where under-represented categories within a subgroup can break model fitting on that subgroup.

When `group` is supplied, percentages and the highlight cutoff are applied within each group, so a cell labelled "5" in the group-A facet contains the count for group A only.

The plot caption reports the sample in the standard $n = X$ of Y respondents (policy) form: rows with NA group are dropped (and counted in Y only), while item-level NAs are retained – each cell simply counts the non-missing responses for that item.

Value

Either a `ggplot` object or a `data.frame`, depending on output.

Examples

```
if (requireNamespace("eRm", quietly = TRUE)) {
  data("pcmdat2", package = "eRm")

  # Basic tile plot
  RMplotTile(pcmdat2)

  # With percentages
  RMplotTile(pcmdat2, percent = TRUE)

  # Faceted by an external grouping variable
  set.seed(1)
  grp <- sample(c("A", "B"), nrow(pcmdat2), replace = TRUE)
  RMplotTile(pcmdat2, group = grp)

  # With custom labels and tighter cutoff
  RMplotTile(pcmdat2,
             group = grp,
             group_labels = c("Female", "Male"),
             cutoff = 5,
             facet_ncol = 2)

  # Underlying counts as a data.frame
  RMplotTile(pcmdat2, group = grp, output = "dataframe")
}
```

RMreliability

*Reliability metrics for a Rasch model***Description**

Computes three reliability indices for a Rasch / partial credit model: the Person Separation Index (PSI) – WLE-based separation reliability – the marginal reliability (native, CML test information integrated over the estimated normal latent density), and Relative Measurement Uncertainty (RMU) via [RMUreliability\(\)](#) applied to plausible values from `mirt::fcores()`.

Usage

```
RMreliability(
  data,
  conf_int = 0.95,
  draws = 1000,
  rmu_iter = 50,
  estim = "WLE",
  boot = FALSE,
  boot_iter = 200,
  parallel = TRUE,
  n_cores = NULL,
  seed = NULL,
  verbose = FALSE,
  theta_range = c(-10, 10),
  output = "kable"
)
```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers).
<code>conf_int</code>	Numeric in (0, 1). HDCI width for both bootstrap CIs and RMU. Default 0.95.
<code>draws</code>	Integer. Number of plausible-value draws drawn from the mirt model for the RMU calculation. Default 1000. More gives a more stable RMU; computational cost is mostly linear.
<code>rmu_iter</code>	Integer. Number of times RMUreliability() is repeated on the same set of plausible-value draws (each repetition uses a fresh random column split). Estimates are averaged across repetitions to stabilise against split-induced variability. Default 50.
<code>estim</code>	Character. Theta estimator used by <code>mirt::fcores()</code> for the RMU plausible-value seed. One of "WLE" (default), "EAP", "MAP", "ML". Plausible draws themselves are produced by Metropolis-Hastings. (PSI and marginal reliability are computed natively and do not use this.)
<code>boot</code>	Logical. If TRUE, run a non-parametric bootstrap to obtain CIs for PSI and Marginal reliability. Default FALSE.

boot_iter	Integer. Number of bootstrap iterations when boot = TRUE. Default 200.
parallel	Logical. Use parallel processing via mirai for the bootstrap if available. Default TRUE.
n_cores	Integer or NULL. Number of parallel workers. When NULL, getOption("mc.cores") is checked first; if neither is set, bootstrapping falls back to sequential.
seed	Integer or NULL. Master random seed for reproducibility.
verbose	Logical. Print progress messages and a progress bar for the bootstrap. Default FALSE.
theta_range	Numeric length-2 vector. Theta limits passed to mirt::fscores(). Default c(-10, 10).
output	Character. "kable" (default) for a formatted knitr::kable() table, or "dataframe" for the underlying data.frame.

Details

Confidence intervals for **PSI** and **Marginal** reliability are obtained by non-parametric bootstrap (resampling respondents; all three indices are recomputed natively per resample, no model is refitted by mirt). The RMU interval is the HDCI of correlations across plausible-value draws, averaged over rmu_iter random splits of the draws.

Marginal reliability is the native Green (1984) coefficient, $1 - \overline{1/I(\theta)}/\sigma^2$, where the test information $I(\theta)$ is summed from the CML item parameters and the average error variance is taken over the estimated normal latent density $N(0, \sigma^2)$ (σ from marginal ML). Unlike mirt::marginal_rxx(), which assumes $N(0, 1)$, this integrates over the estimated latent variance, so it is correct on the Rasch logit scale (where σ is typically well above 1, and the $N(0, 1)$ assumption underestimates reliability). It is the model-based complement to the sample-based PSI; a large gap between the two flags an off-target or non-normal sample.

PSI is the WLE-based separation reliability, $1 - \overline{SEM^2}/\text{Var}(\hat{\theta})$, computed from CML item thresholds (psychotools) and Warm's WLE person locations / analytic SEMs. Respondents with extreme (min/max) raw scores are excluded – their boundary estimates would inflate the person variance and overstate reliability. (Earlier versions used eRm::SepRel() with MLE; the values can differ, most noticeably for scales with many extreme scorers, e.g. dichotomous items.)

RMU is from Bignardi, Kievit, & Bürkner (2025), modified here to use mirt plausible values rather than fully Bayesian posterior draws (see Mislevy, 1991, for the plausible-values framework).

Bootstrap iterations that fail to converge are silently dropped.

Value

- If output = "kable": a knitr_kable object with one row per metric.
- If output = "dataframe": a data.frame with columns metric, estimate, lower, upper, notes.

References

Bignardi, G., Kievit, R., & Bürkner, P. C. (2025). A general method for estimating reliability using Bayesian Measurement Uncertainty. *PsyArXiv*. doi:10.31234/osf.io/h54k8_v1

Green, B. F., Bock, R. D., Humphreys, L. G., Linn, R. L., & Reckase, M. D. (1984). Technical Guidelines for Assessing Computerized Adaptive Tests. *Journal of Educational Measurement*, 21(4), 347–360. doi:10.1111/j.17453984.1984.tb01039.x

Mislevy, R. J. (1991). Randomization-Based Inference about Latent Variables from Complex Samples. *Psychometrika*, 56(2), 177-196. doi:10.1007/BF02294457

Adams, R. J. (2005). Reliability as a measurement design effect. *Studies in Educational Evaluation*, 31(2), 162-172. doi:10.1016/j.stueduc.2005.05.008

See Also

[RMUreliability\(\)](#)

Examples

```
if (requireNamespace("ggdist", quietly = TRUE) &&
    requireNamespace("eRm", quietly = TRUE)) {
  set.seed(1)
  RMreliability(eRm::raschdat1[, 1:20], draws = 1000)

  # Bootstrap CI for PSI and Marginal
  # (use more bootstrap iterations, e.g. 200+, in real analyses)
  RMreliability(eRm::raschdat1[, 1:20], draws = 1000,
               boot = TRUE, boot_iter = 25, parallel = FALSE, seed = 42)
}
```

RMscoreSE

Raw-Score to Logit Score Transformation Table

Description

For a given set of items, returns the score-to-theta lookup that maps each possible raw sum score to a person-location estimate (in logits) and its standard error. Useful when reporting a scale's measurement properties or converting raw totals to interval-scaled scores for downstream analysis.

Usage

```
RMscoreSE(
  data,
  method = "WLE",
  output = "kable",
  ci_multiplier = 1.96,
  point_size = 3,
  error_width = 0.5,
  theta_range = c(-10, 10)
)
```

Arguments

<code>data</code>	A <code>data.frame</code> or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed; the underlying model fit handles them.
<code>method</code>	Character string. Either "WLE" (default) for Warm's Weighted Likelihood Estimator computed from a CML-fitted Rasch / Partial Credit Model via <code>psychotools</code> , or "EAP" for Expected A Posteriori sum-score estimates from an MML-fitted model via <code>mirt</code> .
<code>output</code>	Character string controlling the return value: "kable" (default) for a formatted <code>knitr::kable()</code> table, "dataframe" for the underlying <code>data.frame</code> , or "ggplot" for a <code>ggplot2</code> figure showing each raw score's logit estimate with <code>ci_multiplier</code> -scaled error bars.
<code>ci_multiplier</code>	Numeric. Multiplier applied to the standard error to draw error bars on the figure. Default 1.96 ($\approx 95\%$ CI under a Gaussian approximation). Ignored when <code>output != "ggplot"</code> .
<code>point_size</code>	Numeric. Point size for the figure. Default 3.
<code>error_width</code>	Numeric. Cap width for error bars on the figure. Default 0.5.
<code>theta_range</code>	Numeric length 2. Theta search range used for boundary raw scores under WLE estimation. Default <code>c(-10, 10)</code> . Ignored when <code>method = "EAP"</code> .

Details

The function automatically detects whether the data is dichotomous (max score 1) or polytomous (max score > 1) and selects the appropriate Rasch / Partial Credit model.

`method = "WLE"` fits the model by CML with `psychotools::pcmodel()`, centres the item thresholds to grand-mean-zero, and solves Warm's weighted-likelihood equation for each raw score with the same engine used by `RMpersonParameters()`; the two functions therefore report identical locations and standard errors. Warm's bias correction yields finite locations even at the minimum and maximum scores (only a root outside `theta_range` is clamped to the boundary with NA SE). The reported `logit_se` is the information-based standard error $1 / \sqrt{I(\theta)}$, matching `catR`, TAM and most Rasch software.

`method = "EAP"` fits the model with `mirt::mirt(..., itemtype = "Rasch")` (MML) and obtains sum-score-based EAP estimates and posterior SDs via `mirt::fscores(method = "EAPsum", full.scores = FALSE, full.scores.SE = TRUE)`. EAP estimates are finite at all score boundaries (the prior shrinks them inward), but they depend on the assumed normal prior on theta. Item parameters from MML differ slightly from the CML values used by the WLE path; for well-behaved data the difference is small.

Value

- If `output = "kable"`: a `knitr_kable` object with columns "Ordinal sum score", "Logit score", and "Logit std.error", and a caption noting the estimation method.
- If `output = "dataframe"`: a `data.frame` with columns `raw_score`, `logit_score`, and `logit_se` (one row per possible raw sum score from 0 to the theoretical maximum).
- If `output = "ggplot"`: a `ggplot` object — points at each (`logit_score`, `raw_score`) with horizontal error bars at $\pm ci_multiplier \times logit_se$.

References

- Warm, T. A. (1989). Weighted likelihood estimation of ability in item response theory. *Psychometrika*, 54(3), 427-450. doi:10.1007/BF02294627
- Bock, R. D., & Mislevy, R. J. (1982). Adaptive EAP estimation of ability in a microcomputer environment. *Applied Psychological Measurement*, 6(4), 431-444. doi:10.1177/014662168200600405

Examples

```
set.seed(42)
sim_data <- as.data.frame(
  matrix(sample(0:3, 200 * 6, replace = TRUE), nrow = 200, ncol = 6)
)
colnames(sim_data) <- paste0("Item", 1:6)

# Default kable output, WLE
RMscoreSE(sim_data)

# Underlying data.frame
RMscoreSE(sim_data, output = "dataframe")

# ggplot figure
if (requireNamespace("ggplot2", quietly = TRUE)) {
  RMscoreSE(sim_data, output = "ggplot")
}

# EAP via mirt
RMscoreSE(sim_data, method = "EAP")
```

RMtargeting

Person-Item Targeting Plot (Wright Map)

Description

Produces a three-panel targeting plot with a shared logit scale x-axis:

1. **Top:** Histogram of person location estimates, with a reference line for the mean (or median) and shading for ± 1 SD (or ± 1 MAD).
2. **Middle:** Inverted histogram of item threshold locations, with the same summary annotations.
3. **Bottom:** Dot-and-whisker plot of individual item thresholds with confidence intervals based on threshold standard errors.

Usage

```
RMtargeting(
  data,
  robust = FALSE,
  sort_items = c("data", "location"),
```

```

    bins,
    xlim = c(-4, 4),
    ci_level = 0.95,
    person_fill = "#0072B2",
    threshold_fill = "#D55E00",
    height_ratios = c(3, 2, 5),
    output = "patchwork"
  )

```

Arguments

<code>data</code>	A data.frame or matrix of item responses. Items must be scored starting at 0 (non-negative integers). Missing values (NA) are allowed.
<code>robust</code>	Logical. If FALSE (the default), histogram annotations use mean \pm SD. If TRUE, median \pm MAD is used instead.
<code>sort_items</code>	Character string controlling item ordering on the y-axis of the bottom panel. "data" (the default) preserves the column order in data (first item at top). "location" sorts items by their average threshold location (easiest at top, hardest at bottom).
<code>bins</code>	Integer. Number of bins for both histograms. Default is number of unique scores plus one, but no less than 15.
<code>xlim</code>	Numeric vector of length 2. Initial lower and upper limits for the shared x-axis. Automatically expanded if any person or item threshold values fall outside these limits.
<code>ci_level</code>	Numeric. Confidence level for the item threshold error bars. Default is 0.95 (95% CI). Set to NULL to hide error bars.
<code>person_fill</code>	Fill colour for the person histogram. Default "#0072B2" (blue).
<code>threshold_fill</code>	Fill colour for the item threshold histogram. Default "#D55E00" (vermillion).
<code>height_ratios</code>	Numeric vector of length 3 specifying the relative heights of the top (person), middle (threshold), and bottom (dot-whisker) panels. Default c(3, 2, 5).
<code>output</code>	Character string. "patchwork" (the default) returns the combined patchwork plot. "list" returns a named list of the three ggplot objects (p1, p2, p3) for further customisation.

Details

Together, the top and middle panels form a back-to-back histogram that makes it easy to assess whether the test is well-targeted to the sample.

Estimation method selection. The function checks whether any item response category has fewer than 3 observations. If all categories have at least 3 responses, item threshold locations and their standard errors are estimated via Conditional Maximum Likelihood (CML) using `psychotools::pcmodel()` (a dichotomous item is a 2-category PCM). If any category has fewer than 3 responses, the function falls back to Marginal Maximum Likelihood (MML) estimation via `mirt::mirt()` with `itemtype = "Rasch"` and `SE = TRUE`, which is more numerically stable under sparse-category conditions. A message is emitted when the MML fallback is used.

In both cases, item threshold locations are centered (shifted so the grand mean of all thresholds equals zero).

Person estimates are obtained by Warm's weighted likelihood (WLE) from the fitted item thresholds, consistent with the rest of the package. WLE is finite at extreme scores, so all-zero and perfect responders are located rather than dropped.

Confidence intervals for item thresholds are based on Wald-type intervals: threshold estimate $\pm z \times \text{SE}$, where z is the standard normal quantile corresponding to `ci_level`.

The `ggplot2` and `patchwork` packages must be installed (they are in Suggests, not Imports).

Value

- If `output = "patchwork"`: a patchwork object (combined `ggplot`).
- If `output = "list"`: a named list with elements `p1` (person histogram), `p2` (threshold histogram), and `p3` (item threshold dot-whisker plot).

References

Wright, B. D. & Stone, M. H. (1979). *Best Test Design*. MESA Press.

See Also

`psychotools::pcmodel()`, `mirt::mirt()`

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("patchwork", quietly = TRUE)) {
  # Polytomous example
  set.seed(42)
  sim_data <- as.data.frame(
    matrix(sample(0:3, 200 * 8, replace = TRUE), nrow = 200, ncol = 8)
  )
  colnames(sim_data) <- paste0("Item", 1:8)

  # Default: mean/SD, data order, 95% CI
  RMtargeting(sim_data)

  # Robust (median/MAD), sorted by location, 84% CI
  RMtargeting(sim_data, robust = TRUE, sort_items = "location",
              ci_level = 0.84)

  # Get list of sub-plots for customisation
  plots <- RMtargeting(sim_data, output = "list")
  plots$p1 + ggplot2::ggtitle("My custom title")

  # Dichotomous example
  sim_bin <- as.data.frame(
    matrix(sample(0:1, 200 * 10, replace = TRUE), nrow = 200, ncol = 10)
  )
  colnames(sim_bin) <- paste0("Item", 1:10)
```

```

  RMtargeting(sim_bin)
}

```

RMUreliability	<i>Relative Measurement Uncertainty (RMU)</i>
----------------	---

Description

Bayesian-style reliability estimate (Bignardi, Kievit & Bürkner, 2025) computed from a matrix of posterior or plausible-value draws. The columns of `input_draws` are split at random into two halves; reliability is the Pearson correlation across persons of paired columns from the two halves, summarised across pairs as a posterior mean with HDCI.

Usage

```
RMUreliability(input_draws, level = 0.95, verbose = FALSE)
```

Arguments

<code>input_draws</code>	Numeric matrix or <code>data.frame</code> of draws. Rows are subjects; columns are draws. Must have at least two columns; ideally many.
<code>level</code>	Numeric in (0, 1). Width of the HDCI returned. Default 0.95.
<code>verbose</code>	Logical. Print summary information about the input. Default FALSE.

Details

Adapted (with permission, GPL-2/3) from <https://github.com/giac01/gbtoolbox/blob/main/R/reliability.R>.

The function silently returns 0 for any column pair where either side has zero variance (the correlation is undefined there).

Requires the `ggdist` package (Suggests).

Value

A 1-row `data.frame` with columns `rmu_estimate`, `hdc_lowerbound`, `hdc_upperbound`, plus the `.width/.point/.interval` metadata columns added by `ggdist::mean_hdc()`.

References

Bignardi, G., Kievit, R., & Bürkner, P. C. (2025). A general method for estimating reliability using Bayesian Measurement Uncertainty. *PsyArXiv*. doi:10.31234/osf.io/h54k8_v1

See Also

[RMreliability\(\)](#)

Index

* **datasets**
 phq9, 3

ggplot2::ggplot, 36, 82, 85

knitr::kable(), 54, 79

mirt::mirt(), 54, 94

partgam_DIF, 7, 9, 10
partgam_LD, 63, 65
phq9, 3
psychotools::pcmodel(), 54, 94

RMdifGamma, 4, 11, 17, 41
RMdifGamma(), 16, 40, 41
RMdifGammaCutoff, 5, 7, 7, 10, 11
RMdifGammaCutoff(), 6, 16
RMdifGammaPlot, 10
RMdifLR, 12, 17
RMdifTree, 14
RMdimCFA, 18, 21, 22, 24
RMdimCFACutoff, 18–20, 20, 23, 24
RMdimCFACutoff(), 19
RMdimCFAPlot, 20–22, 23
RMdimMartinLof, 22, 24, 27–29
RMdimMartinLofResiduals, 27
RMdimResidualPCA, 22, 27, 30, 33, 34
RMdimResidualPCACutoff, 27, 30–32, 32
RMitemCatProb, 34
RMitemHierarchy, 37
RMitemHierarchy(), 36
RMitemICCPlot, 39
RMitemICCPlot(), 36, 39
RMitemInfit, 41, 45, 46, 48–52, 59
RMitemInfit(), 78
RMitemInfitCutoff, 42, 44, 44, 47–49, 51, 52
RMitemInfitCutoff(), 43
RMitemInfitCutoffMI, 47, 49–51
RMitemInfitCutoffPlot
 (RMitemInfitPlot), 51
RMitemInfitMI, 48, 49
RMitemInfitPlot, 23, 48, 51
RMitemParameters, 53
RMitemParameters(), 78–80
RMitemRestscore, 41, 55, 58, 59
RMitemRestscoreBoot, 57
RMlocdepGamma, 60, 65, 66
RMlocdepGammaCutoff, 60–62, 63, 65, 66
RMlocdepGammaCutoff(), 61
RMlocdepGammaPlot, 62, 65, 65, 74
RMlocdepQ3, 60, 61, 67, 70–72, 74
RMlocdepQ3Cutoff, 32, 67, 68, 70, 73, 74
RMlocdepQ3Cutoff(), 69
RMlocdepQ3Plot, 69, 72, 73
RMpersonFit, 75
RMpersonParameters, 78
RMpersonParameters(), 55, 78, 91
RMplotBar, 81
RMplotBar(), 85
RMplotStackedbar, 83
RMplotStackedbar(), 82
RMplotTile, 85
RMplotTile(), 82, 85
RMreliability, 88
RMreliability(), 80, 95
RMscoreSE, 90
RMscoreSE(), 38, 39, 55, 78, 80
RMtargeting, 92
RMtargeting(), 38, 39, 54, 55
RMUreliability, 95
RMUreliability(), 88, 90