

Package ‘exactGMH’

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Type Package

Title Exact and Permutation-Based Mantel Tests for Differential Item Functioning in Dichotomous and Polytomous Items

Version 0.1.0

Description Screens dichotomous and polytomous test items for Differential Item Functioning (DIF) using an extension of the Mantel (1963) <[doi:10.1080/01621459.1963.10500879](https://doi.org/10.1080/01621459.1963.10500879)> and generalized Mantel-Haenszel statistic, with statistical significance computed via permutation rather than the conventional asymptotic chi-square approximation. Following Hemerik and Goeman (2018) <[doi:10.1007/s11749-017-0571-1](https://doi.org/10.1007/s11749-017-0571-1)>, the permutation p-value is exact at the nominal level rather than an approximation, even for a finite number of permutations. This makes the test valid for small samples (fewer than 200 examinees per group), a condition common in classroom-, program-, and institution-level assessment where existing exact-inference options in other software are restricted to dichotomous items only. An optional Benjamini-Hochberg or Bonferroni correction addresses multiple comparisons when screening many items at once.

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Encoding UTF-8

RoxygenNote 7.3.1

Depends R (>= 4.0)

Imports stats

Suggests testthat (>= 3.0.0), shiny

Config/testthat/edition 3

URL <https://github.com/exactGMH-project/exactGMH>

BugReports <https://github.com/exactGMH-project/exactGMH/issues>

NeedsCompilation no

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exact_mantel_dif	<i>Exact/permutation Mantel test for a single item</i>
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Description

Computes the Mantel (1963) / Mantel-Haenszel DIF statistic for a single dichotomous or polytomous item, with statistical significance obtained via permutation of group membership within score-matched strata. Following Hemerik and Goeman (2018), the observed statistic is included among the reference draws (the "+1" correction), which guarantees the resulting p-value is exact at the nominal level rather than merely an asymptotic approximation, even for a finite number of permutations.

Usage

```
exact_mantel_dif(item_score, group, total_score, n_perm = 5000, seed = 123)
```

Arguments

item_score	Numeric vector of item scores: 0/1 for dichotomous items, or 0..C-1 for polytomous items (e.g., a 5-point rubric coded 0-4).
group	Vector of group membership (exactly 2 levels, e.g., "Reference" / "Focal").
total_score	Numeric vector used as the matching/stratification variable, typically the total test score computed after removing the item under study.
n_perm	Integer; number of permutations (default 5000). Larger values give a more precise p-value at the cost of computation time.
seed	Integer; random seed for reproducibility (default 123).

Value

A one-row data frame with columns:

item_type "Dichotomous" or "Polytomous" (auto-detected).

z_statistic Standardized Mantel statistic.

effect_size Delta-MH (dichotomous) or standardized difference (polytomous).

effect_label Label describing the effect size column.

chi_asymp Asymptotic chi-square statistic (for comparison).

p_asymptotic p-value from the conventional asymptotic chi-square approximation.

p_exact_perm Exact permutation-based p-value (recommended).

classification ETS-style DIF classification: "A (negligible)", "B (moderate)", or "C (large)".

n_permutations Number of permutations used.

References

Mantel, N. (1963). Chi-square tests with one degree of freedom: Extensions of the Mantel-Haenszel procedure. *Journal of the American Statistical Association*, 58(303), 690-700. doi:10.1080/01621459.1963.10500879

Hemerik, J., & Goeman, J. (2018). Exact testing with random permutations. *TEST*, 27(4), 811-825. doi:10.1007/s1174901705711

Examples

```
set.seed(1)
n <- 60
group <- rep(c("Reference", "Focal"), each = n / 2)
item <- rbinom(n, 1, 0.5)
total <- rowSums(replicate(5, rbinom(n, 1, 0.5)))
exact_mantel_dif(item, group, total, n_perm = 500)
```

run_dif_screening	<i>Screen all items in a test for Differential Item Functioning</i>
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Description

Runs the exact/permutation Mantel test (see [exact_mantel_dif](#)) on every column of a response matrix. Dichotomous (0/1) and polytomous (0..C-1) items may be freely mixed within the same matrix; item type is auto-detected per column.

Usage

```
run_dif_screening(
  response_matrix,
  group,
  n_perm = 5000,
  seed = 123,
  p_adjust_method = "none"
)
```

Arguments

<code>response_matrix</code>	A numeric matrix or data frame of item responses: rows are examinees, columns are items.
<code>group</code>	Vector of group membership (2 levels), of the same length as <code>nrow(response_matrix)</code> .
<code>n_perm</code>	Integer; number of permutations per item (default 5000).
<code>seed</code>	Integer; base random seed (default 123). Each item uses <code>seed + column_index</code> internally for reproducible but non-identical permutation draws across items.
<code>p_adjust_method</code>	Character; multiple-testing correction method passed to <code>p.adjust</code> (e.g., "BH" for Benjamini-Hochberg, "bonferroni"). Default "none" returns unadjusted per-item p-values.

Value

A data frame with one row per item; see `exact_mantel_dif` for column descriptions. An additional item column identifies each item (from `colnames(response_matrix)` if available), and, when `p_adjust_method != "none"`, a `p_exact_adjusted` column is added and used to update the classification column.

Examples

```
set.seed(42)
n <- 80
group <- rep(c("Reference", "Focal"), each = n / 2)
# 3 dichotomous items, 2 polytomous items (0-3)
resp <- data.frame(
  Item1 = rbinom(n, 1, 0.5),
  Item2 = rbinom(n, 1, 0.5),
  Item3 = rbinom(n, 1, 0.5),
  Item4 = sample(0:3, n, replace = TRUE),
  Item5 = sample(0:3, n, replace = TRUE)
)
run_dif_screening(resp, group, n_perm = 500, p_adjust_method = "BH")
```

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