

Package ‘npwbs’

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Type Package

Title Nonparametric Multiple Change Point Detection Using Wild Binary Segmentation

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Description Implements nonparametric multiple change-point detection for univariate sequences using Wild Binary Segmentation, as described in Ross (2026) “Nonparametric Detection of Multiple Location-Scale Change Points via Wild Binary Segmentation” <[doi:10.48550/arXiv.2107.01742](https://doi.org/10.48550/arXiv.2107.01742)>. The package provides Mann--Whitney, Mood, Lepage, Cramér--von Mises, modified Baumgartner, and standardised Zhang Z_C rank-based statistics, together with method-specific thresholds for controlling the probability of incorrectly detecting a change point in a homogeneous sequence.

Depends R (>= 4.0.0)

Imports digest, Rcpp

LinkingTo Rcpp

License GPL-3

Encoding UTF-8

NeedsCompilation yes

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detectChanges	<i>Nonparametric detection of multiple change points using Wild Binary Segmentation</i>
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Description

Returns the estimated number and locations of the change points in a sequence of univariate observations. For full details of how this procedure works, please see G. J. Ross (2026) - "Nonparametric Detection of Multiple Location-Scale Change Points via Wild Binary Segmentation" at <https://arxiv.org/abs/2107.01742>

Usage

```
detectChanges(y, alpha=0.05, prune=TRUE, M=10000, d=2,
              displayOutput=FALSE, method="lepage", breakTies=TRUE)
```

Arguments

y	The sequence to test for change points
alpha	Required Type I error rate. Lepage supports 0.05 and 0.01; the other methods support 0.05.
prune	Whether to prune potential excess change points via post-processing. Most likely should be left as TRUE.
M	Number of subsequences to sample during WBS and pruning. The built-in thresholds are calibrated for $M = 10000$, so other values are not supported by the packaged calibration.
d	Endpoint trimming within each sampled interval. The existing methods use $d = 2$; method = "zhang" uses $d = 4$ automatically and accepts only an explicit value of 4.
displayOutput	If TRUE then will print some information while searching for change points
method	Rank statistic: exactly one of "lepage", "mw", "mood", "cvm", "baumgartner", or "zhang".
breakTies	If TRUE, tied inputs receive one random strict ordering before detection; if FALSE, ties are an error.

Details

The built-in thresholds are provided for Lepage, Mann–Whitney, Mood, Cramér–von Mises, and modified Baumgartner statistics using $d = 2$ and $M = 10000$. Lepage at $\alpha = 0.05$ uses the final registered book-chapter calibration, while Lepage at $\alpha = 0.01$ retains the established package calibration. Mann–Whitney, Mood, Cramér–von Mises, and modified Baumgartner support $\alpha = 0.05$ only. The sampled interval minimum length is fixed at 10. Thresholds are provided through segment length $n = 10000$; longer inputs reuse the $n = 10000$ threshold with one warning. Modified-Baumgartner values above $n = 3000$ use the fitted extension accepted for the package rather than direct Monte-Carlo calibration.

The "zhang" method is the exact mean/standard-deviation-standardised Zhang Z_C detector used in the paper. It uses $d = 4$, $M = 10000$, $\alpha = 0.05$, strict threshold exceedance, and registered length-specific thresholds. Exact moments through $n = 1000$ are bundled. Sequence lengths $n = 1001$ through 3000 require one prior call to `download_zhang_moments`; an invalid installed artifact can be replaced with `download_zhang_moments(overwrite = TRUE)`. Lengths above 3000 are unsupported.

If `prune = TRUE`, a post-processing pruning step retests merged neighbouring segments and removes changepoints that are no longer supported.

Value

A vector containing the detected changepoint locations. A returned value k denotes a split between observations k and $k + 1$, i.e. the change occurs after observation k .

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Examples

```
set.seed(100)
y <- c(rnorm(30,0,1), rnorm(30,3,1), rnorm(30,0,1), rnorm(30,0,3))
detectChanges(y)
```

download_zhang_moments

Install the extended exact Zhang moment table

Description

Downloads and verifies the fixed exact-moment artifact required by the standardised Zhang detector for sequence lengths above 1000.

Usage

```
download_zhang_moments(overwrite = FALSE)
```

Arguments

`overwrite` If TRUE, replace an existing installed artifact.

Details

Exact moments through sequence length 1000 are bundled with **npwbs**. The method = "zhang" detector requires this one-time download for lengths 1001 through 3000. The artifact is installed in the package-specific user data directory returned by `tools::R_user_dir("npwbs", "data")`. Use `overwrite = TRUE` to reinstall an invalid or incompatible artifact. Sequence lengths above 3000 are unsupported.

Value

The installed file path, returned invisibly.

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