

Package ‘CptNonPar’

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Type Package

Title Nonparametric Change Point Detection for Multivariate Time Series

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Depends R (>= 4.1.0)

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Description Implements the nonparametric moving sum procedure for detecting changes in the joint characteristic function (NP-MOJO) for multiple change point detection in multivariate time series. See McGonigle, E. T., Cho, H. (2025) <[doi:10.1093/biomet/asaf024](https://doi.org/10.1093/biomet/asaf024)> for description of the NP-MOJO methodology.

Encoding UTF-8

LinkingTo Rcpp

Imports Rcpp, doParallel, parallel, parallelly, foreach, Rfast, iterators, stats

URL <https://github.com/EuanMcGonigle/CptNonPar>

BugReports <https://github.com/EuanMcGonigle/CptNonPar/issues>

RoxygenNote 7.3.2

Suggests covr, testthat (>= 3.0.0)

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multilag.cpts.merge *Merge Change Point Estimators from Multiple Lags*

Description

Merges change point estimators from different lagged values into a final set of overall change point estimators.

Usage

```
multilag.cpts.merge(
  x.c,
  eta.merge = 1,
  merge.type = c("sequential", "bottom-up")[1]
)
```

Arguments

<code>x.c</code>	A list object, where each element of the list is the output of the np.mojo function computed at a different lag.
<code>eta.merge</code>	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth, used to merge change point estimators across different lags.
<code>merge.type</code>	String indicating the method used to merge change point estimators from different lags. Possible choices are <ul style="list-style-type: none"> • "sequential": starting from the left-most change point estimator and proceeding forward in time, estimators are grouped into clusters based on mutual distance. The estimator yielding the largest corresponding importance score is chosen as the change point estimator for that cluster. See McGonigle and Cho (2025) for details. • "bottom-up": starting with the largest importance score, the change points are merged using bottom-up merging (Messer et al. (2014)).

Details

See McGonigle and Cho (2025) for further details.

Value

A list object which contains the following fields

cpts	A matrix with rows corresponding to final change point estimators, with estimated change point location and associated lag and importance score given in columns.
cpt.clusters	A list object of length given by the number of detected change points. Each field contains a matrix of all change point estimators that are declared to be associated to the corresponding change point in the cpts field.

References

McGonigle, E.T., Cho, H. (2025). Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Messer M., Kirchner M., Schiemann J., Roeper J., Neininger R., Schneider G. (2014). A Multiple Filter Test for the Detection of Rate Changes in Renewal Processes with Varying Variance. *The Annals of Applied Statistics*, 8(4), 2027-2067.

See Also

[np.mojo](#), [np.mojo.multilag](#)

Examples

```
set.seed(1)
n <- 500
noise <- c(rep(1, 300), rep(0.4, 200)) * stats::arima.sim(model = list(ar = 0.3), n = n)
signal <- c(rep(0, 100), rep(2, 400))
x <- signal + noise
x.c0 <- np.mojo(x, G = 83, lag = 0)
x.c1 <- np.mojo(x, G = 83, lag = 1)
x.c <- multilag.cpts.merge(list(x.c0, x.c1))
x.c
```

Description

For a given set of bandwidths and lagged values of the time series, performs multiscale nonparametric change point detection of a possibly multivariate time series.

Usage

```
multiscale.np.mojo(
  x,
  G,
  lags = c(0, 1),
  kernel.f = c("quad.exp", "gauss", "euclidean", "laplace", "sine")[1],
  kern.par = 1,
  data.driven.kern.par = TRUE,
  threshold = c("bootstrap", "manual")[1],
  threshold.val = NULL,
  alpha = 0.1,
  reps = 200,
  boot.dep = 1.5 * (nrow(as.matrix(x))^(1/3)),
  parallel = FALSE,
  boot.method = c("mean.subtract", "no.mean.subtract")[1],
  criterion = c("eta", "epsilon", "eta.and.epsilon")[3],
  eta = 0.4,
  epsilon = 0.02,
  use.mean = FALSE,
  scale.data = TRUE,
  eta.merge = 1,
  merge.type = c("sequential", "bottom-up")[1],
  eta.bottom.up = 0.8
)
```

Arguments

<code>x</code>	Input data (a <code>numeric</code> vector or an object of classes <code>ts</code> and <code>timeSeries</code> , or a <code>numeric</code> matrix with rows representing observations and columns representing variables).
<code>G</code>	A numeric vector containing the moving sum bandwidths; all values in the vector <code>G</code> should be less than half the length of the time series.
<code>lags</code>	A numeric vector giving the range of lagged values of the time series that will be used to detect changes. See np.mojo.multilag for further details.
<code>kernel.f</code>	String indicating which kernel function to use when calculating the NP-MOJO detector statistics; with <code>kern.par = a</code> , possible values are <ul style="list-style-type: none"> • "quad.exp": kernel h_2 in McGonigle and Cho (2025), kernel 5 in Fan et al. (2017):

$$h(x, y) = \prod_{i=1}^{2p} \frac{(2a - (x_i - y_i)^2) \exp(-\frac{1}{4a}(x_i - y_i)^2)}{2a}.$$

- "gauss": kernel h_1 in McGonigle and Cho (2025), the standard Gaussian kernel:

$$h(x, y) = \exp\left(-\frac{a^2}{2}\|x - y\|^2\right).$$

- "euclidean": kernel h_3 in McGonigle and Cho (2025), the Euclidean distance-based kernel:

$$h(x, y) = \|x - y\|^a.$$

- "laplace": kernel 2 in Fan et al. (2017), based on a Laplace weight function:

$$h(x, y) = \prod_{i=1}^{2p} (1 + a^2(x_i - y_i)^2)^{-1}.$$

- "sine": kernel 4 in Fan et al. (2017), based on a sinusoidal weight function:

$$h(x, y) = \prod_{i=1}^{2p} \frac{-2|x_i - y_i| + |x_i - y_i - 2a| + |x_i - y_i + 2a|}{4a}.$$

kern.par The tuning parameter that appears in the expression for the kernel function, which acts as a scaling parameter.

data.driven.kern.par A logical variable, if set to TRUE, then the kernel tuning parameter is calculated using the median heuristic, if FALSE it is given by **kern.par**.

threshold String indicating how the threshold is computed. Possible values are

- "bootstrap": the threshold is calculated using the bootstrap method with significance level **alpha**.
- "manual": the threshold is set by the user and must be specified using the **threshold.val** parameter.

threshold.val The value of the threshold used to declare change points, only to be used if **threshold** = "manual". Can be either a single numeric value, in which case the same threshold is used for *all* bandwidths and lags, or a list of vectors, with the length of the list equal to the number of bandwidths, that corresponds to the **G** argument, where the elements of each vector in the list corresponds to the threshold value for the corresponding element of the **lags** argument.

alpha a numeric value for the significance level with $0 \leq \alpha \leq 1$; use iff **threshold** = "bootstrap".

reps An integer value for the number of bootstrap replications performed, if **threshold** = "bootstrap".

boot.dep A positive value for the strength of dependence in the multiplier bootstrap sequence, if **threshold** = "bootstrap".

parallel A logical variable, if set to TRUE, then parallel computing is used in the bootstrapping procedure if bootstrapping is performed.

boot.method A string indicating the method for creating bootstrap replications. It is not recommended to change this. Possible choices are

- "mean.subtract": the default choice, as described in McGonigle and Cho (2025). Empirical mean subtraction is performed to the bootstrapped replicates, improving power.
- "no.mean.subtract": empirical mean subtraction is not performed, improving size control.

criterion	String indicating how to determine whether each point k at which NP-MOJO statistic exceeds the threshold is a change point; possible values are <ul style="list-style-type: none"> • "epsilon": k is the maximum of its local exceeding environment, which has at least size $\text{epsilon} \times G$. • "eta": there is no larger exceeding in an $\text{eta} \times G$ environment of k. • "eta.and.epsilon": the recommended default option; k satisfies both the eta and epsilon criterion. Recommended to use with the standard value of eta that would be used if <code>criterion = "eta"</code> (e.g. 0.4), but much smaller value of epsilon than would be used if <code>criterion = "epsilon"</code>, e.g. 0.02.
eta	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth (if <code>criterion = "eta"</code> or <code>criterion = "eta.and.epsilon"</code>).
epsilon	a numeric value in (0,1] for the minimal size of exceeding environments, relative to moving sum bandwidth (if <code>criterion = "epsilon"</code> or <code>criterion = "eta.and.epsilon"</code>).
use.mean	Logical variable, only to be used if <code>data.drive.kern.par=TRUE</code> . If set to TRUE, the mean of pairwise distances is used to set the kernel function tuning parameter, instead of the median. May be useful for binary data, not recommended to be used otherwise.
scale.data	Logical variable, whether to scale the data in each dimension before performing change point detection. Performance is generally improved by scaling the data.
eta.merge	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth, used to merge change point estimators across different lags.
merge.type	String indicating the method used to merge change point estimators from different lags. Possible choices are <ul style="list-style-type: none"> • "sequential": Starting from the left-most change point estimator and proceeding forward in time, estimators are grouped into clusters based on mutual distance. The estimator yielding the largest corresponding importance score is chosen as the change point estimator for that cluster. See McGonigle and Cho (2025) for details. • "bottom-up": starting with the largest importance score, the change points are merged using bottom-up merging (Messer et al. (2014)).
eta.bottom.up	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth, for use in bottom-up merging of change point estimators across multiple bandwidths.

Details

The multi-lag NP-MOJO algorithm for nonparametric change point detection is described in McGonigle, E. T. and Cho, H. (2025) Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear). The multiscale version uses bottom-up merging to combine the results of the multi-lag NP-MOJO algorithm performed over a given set of bandwidths.

Value

A list object that contains the following fields:

G	Set of moving window bandwidths
lags	Lags used to detect changes
kernel.f, data.driven.kern.par, use.mean	Input parameters
threshold, alpha, reps, boot.dep, boot.method, parallel	Input parameters
criterion, eta, epsilon	Input parameters
cpts	A matrix with rows corresponding to final change point estimators, with estimated change point location and associated detection bandwidth, lag and importance score given in columns.

References

McGonigle, E.T., Cho, H. (2025). Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Fan, Y., de Micheaux, P.L., Penev, S. and Salopek, D. (2017). Multivariate nonparametric test of independence. *Journal of Multivariate Analysis*, 153, pp.189-210.

Messer M., Kirchner M., Schiemann J., Roeper J., Neininger R., Schneider G. (2014). A Multiple Filter Test for the Detection of Rate Changes in Renewal Processes with Varying Variance. *The Annals of Applied Statistics*, 8(4), 2027-2067.

See Also

[np.mojo.multilag](#)

Examples

```
set.seed(1)
n <- 500
noise <- c(rep(1, 300), rep(0.4, 200)) * stats::arima.sim(model = list(ar = 0.3), n = n)
signal <- c(rep(0, 100), rep(2, 400))
x <- signal + noise
x.c <- multiscale.np.mojo(x, G = c(50, 80), lags = c(0, 1))
x.c$cpts
```

np.mojo

Nonparametric Single Lag Change Point Detection

Description

For a given lagged value of the time series, performs nonparametric change point detection of a possibly multivariate time series. If lag $\ell = 0$, then only marginal changes are detected. If lag $\ell \neq 0$, then changes in the pairwise distribution of $(X_t, X_{t+\ell})$ are detected.

Usage

```
np.mojo(
  x,
  G,
  lag = 0,
  kernel.f = c("quad.exp", "gauss", "euclidean", "laplace", "sine")[1],
  kern.par = 1,
  data.driven.kern.par = TRUE,
  alpha = 0.1,
  threshold = c("bootstrap", "manual")[1],
  threshold.val = NULL,
  reps = 200,
  boot.dep = 1.5 * (nrow(as.matrix(x))^(1/3)),
  parallel = FALSE,
  boot.method = c("mean.subtract", "no.mean.subtract")[1],
  criterion = c("eta", "epsilon", "eta.and.epsilon")[3],
  eta = 0.4,
  epsilon = 0.02,
  use.mean = FALSE,
  scale.data = TRUE
)
```

Arguments

x	Input data (a numeric vector or an object of classes <code>ts</code> and <code>timeSeries</code> , or a numeric matrix with rows representing observations and columns representing variables).
G	An integer value for the moving sum bandwidth; G should be less than half the length of the time series.
lag	The lagged values of the time series used to detect changes. If lag $\ell = 0$, then only marginal changes are detected. If lag $\ell \neq 0$, then changes in the pairwise distribution of $(X_t, X_{t+\ell})$ are detected.
kernel.f	String indicating which kernel function to use when calculating the NP-MOJO detectors statistics; with <code>kern.par = a</code> , possible values are

- "quad.exp": kernel h_2 in McGonigle and Cho (2025), kernel 5 in Fan et al. (2017):

$$h(x, y) = \prod_{i=1}^{2p} \frac{(2a - (x_i - y_i)^2) \exp(-\frac{1}{4a}(x_i - y_i)^2)}{2a}.$$

- "gauss": kernel h_1 in McGonigle and Cho (2025), the standard Gaussian kernel:

$$h(x, y) = \exp\left(-\frac{a^2}{2}\|x - y\|^2\right).$$

- "euclidean": kernel h_3 in McGonigle and Cho (2025), the Euclidean distance-based kernel:

$$h(x, y) = \|x - y\|^a.$$

- "laplace": kernel 2 in Fan et al. (2017), based on a Laplace weight function:

$$h(x, y) = \prod_{i=1}^{2p} (1 + a^2(x_i - y_i)^2)^{-1}.$$

- "sine": kernel 4 in Fan et al. (2017), based on a sinusoidal weight function:

$$h(x, y) = \prod_{i=1}^{2p} \frac{-2|x_i - y_i| + |x_i - y_i - 2a| + |x_i - y_i + 2a|}{4a}.$$

kern.par	The tuning parameter that appears in the expression for the kernel function, which acts as a scaling parameter, only to be used if data.driven.kern.par = FALSE. If kernel.f = "euclidean", then kern.par $\in (0, 2)$, otherwise kern.par > 0 .
data.driven.kern.par	A logical variable, if set to TRUE, then the kernel tuning parameter is calculated using the median heuristic, if FALSE it is given by kern.par.
alpha	A numeric value for the significance level with $0 \leq \alpha \leq 1$; use iff threshold = "bootstrap".
threshold	String indicating how the threshold is computed. Possible values are <ul style="list-style-type: none"> • "bootstrap": the threshold is calculated using the bootstrap method with significance level alpha. • "manual": the threshold is set by the user and must be specified using the threshold.val parameter.
threshold.val	The value of the threshold used to declare change points, only to be used if threshold = "manual".
reps	An integer value for the number of bootstrap replications performed, if threshold = "bootstrap".
boot.dep	A positive value for the strength of dependence in the multiplier bootstrap sequence, if threshold = "bootstrap".
parallel	A logical variable, if set to TRUE, then parallel computing is used in the bootstrapping procedure if bootstrapping is performed.

boot.method	A string indicating the method for creating bootstrap replications. It is not recommended to change this. Possible choices are <ul style="list-style-type: none"> • "mean.subtract": the default choice, as described in McGonigle and Cho (2025). Empirical mean subtraction is performed to the bootstrapped replicates, improving power. • "no.mean.subtract": empirical mean subtraction is not performed, improving size control.
criterion	String indicating how to determine whether each point k at which NP-MOJO statistic exceeds the threshold is a change point; possible values are <ul style="list-style-type: none"> • "epsilon": k is the maximum of its local exceeding environment, which has at least size $\text{epsilon} \times G$. • "eta": there is no larger exceeding in an $\eta \times G$ environment of k. • "eta.and.epsilon": the recommended default option; k satisfies both the eta and epsilon criterion. Recommended to use with the standard value of eta that would be used if <code>criterion = "eta"</code> (e.g. 0.4), but much smaller value of epsilon than would be used if <code>criterion = "epsilon"</code>, e.g. 0.02.
eta	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth (if <code>criterion = "eta"</code> or <code>criterion = "eta.and.epsilon"</code>).
epsilon	a numeric value in (0,1] for the minimal size of exceeding environments, relative to moving sum bandwidth (if <code>criterion = "epsilon"</code> or <code>criterion = "eta.and.epsilon"</code>).
use.mean	Logical variable, only to be used if <code>data.drive.kern.par=TRUE</code> . If set to TRUE, the mean of pairwise distances is used to set the kernel function tuning parameter, instead of the median. May be useful for binary data, not recommended to be used otherwise.
scale.data	Logical variable, whether to scale the data in each dimension before performing change point detection. Performance is generally improved by scaling the data.

Details

The single-lag NP-MOJO algorithm for nonparametric change point detection is described in McGonigle, E. T. and Cho, H. (2025) Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Value

A list object that contains the following fields:

x	Input data
G	Moving window bandwidth
lag	Lag used to detect changes
kernel.f, data.driven.kern.par, use.mean	Input parameters
kern.par	The value of the kernel tuning parameter

threshold, alpha, reps, boot.dep, boot.method, parallel	
	Input parameters
threshold.val	Threshold value for declaring change points
criterion, eta, epsilon	
	Input parameters
test.stat	A vector containing the NP-MOJO detector statistics computed from the input data
cpts	A vector containing the estimated change point locations
scores	The corresponding importance scores of the estimated change points. The larger the score is, the more likely that there exists a change point close to the estimated location. If the bootstrap method is used, this a value between 0 and 1 corresponding to the proportion of times the observed detector statistic was larger than the bootstrapped detector statistics. Otherwise, the importance score is simply the value of the detector statistic at the estimated change point location (which is not necessarily less than 1).

References

McGonigle, E.T., Cho, H. (2025). Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Fan, Y., de Micheaux, P.L., Penev, S. and Salopek, D. (2017). Multivariate nonparametric test of independence. *Journal of Multivariate Analysis*, 153, pp.189-210.

See Also

[np.mojo.multilag](#)

Examples

```
set.seed(1)
n <- 500
noise <- c(rep(1, 300), rep(0.4, 200)) * stats::arima.sim(model = list(ar = 0.3), n = n)
signal <- c(rep(0, 100), rep(2, 400))
x <- signal + noise
x.c <- np.mojo(x, G = 83, lag = 0)
x.c$cpts
x.c$scores
```

Description

For a given set of lagged values of the time series, performs nonparametric change point detection of a possibly multivariate time series.

Usage

```
np.mojo.multilag(
  x,
  G,
  lags = c(0, 1),
  kernel.f = c("quad.exp", "gauss", "euclidean", "laplace", "sine")[1],
  kern.par = 1,
  data.driven.kern.par = TRUE,
  threshold = c("bootstrap", "manual")[1],
  threshold.val = NULL,
  alpha = 0.1,
  reps = 200,
  boot.dep = 1.5 * (nrow(as.matrix(x))^(1/3)),
  parallel = FALSE,
  boot.method = c("mean.subtract", "no.mean.subtract")[1],
  criterion = c("eta", "epsilon", "eta.and.epsilon")[3],
  eta = 0.4,
  epsilon = 0.02,
  use.mean = FALSE,
  scale.data = TRUE,
  eta.merge = 1,
  merge.type = c("sequential", "bottom-up")[1]
)
```

Arguments

x Input data (a numeric vector or an object of classes `ts` and `timeSeries`, or a numeric matrix with rows representing observations and columns representing variables).

G An integer value for the moving sum bandwidth; `G` should be less than half the length of the time series.

lags A numeric vector giving the range of lagged values of the time series that will be used to detect changes. See [np.mojo](#) for further details.

kernel.f String indicating which kernel function to use when calculating the NP-MOJO detector statistics; with `kern.par = a`, possible values are

- "quad.exp": kernel h_2 in McGonigle and Cho (2025), kernel 5 in Fan et al. (2017):

$$h(x, y) = \prod_{i=1}^{2p} \frac{(2a - (x_i - y_i)^2) \exp(-\frac{1}{4a}(x_i - y_i)^2)}{2a}.$$

- "gauss": kernel h_1 in McGonigle and Cho (2025), the standard Gaussian kernel:

$$h(x, y) = \exp\left(-\frac{a^2}{2} \|x - y\|^2\right).$$

- "euclidean": kernel h_3 in McGonigle and Cho (2025), the Euclidean distance-based kernel:

$$h(x, y) = \|x - y\|^a.$$

- "laplace": kernel 2 in Fan et al. (2017), based on a Laplace weight function:

$$h(x, y) = \prod_{i=1}^{2p} (1 + a^2(x_i - y_i)^2)^{-1}.$$

- "sine": kernel 4 in Fan et al. (2017), based on a sinusoidal weight function:

$$h(x, y) = \prod_{i=1}^{2p} \frac{-2|x_i - y_i| + |x_i - y_i - 2a| + |x_i - y_i + 2a|}{4a}.$$

kern.par	The tuning parameter that appears in the expression for the kernel function, which acts as a scaling parameter.
data.driven.kern.par	A logical variable, if set to TRUE, then the kernel tuning parameter is calculated using the median heuristic, if FALSE it is given by kern.par.
threshold	String indicating how the threshold is computed. Possible values are <ul style="list-style-type: none"> • "bootstrap": the threshold is calculated using the bootstrap method with significance level alpha. • "manual": the threshold is set by the user and must be specified using the threshold.val parameter.
threshold.val	The value of the threshold used to declare change points, only to be used if threshold = "manual". Can be either a single numeric value, in which case the same threshold is used for all lags, or a vector with length equal to the number of lags, where each elements in the vector gives the threshold value of the corresponding lag from the lags argument.
alpha	a numeric value for the significance level with $0 \leq \alpha \leq 1$; use iff threshold = "bootstrap".
reps	An integer value for the number of bootstrap replications performed, if threshold = "bootstrap".
boot.dep	A positive value for the strength of dependence in the multiplier bootstrap sequence, if threshold = "bootstrap".
parallel	A logical variable, if set to TRUE, then parallel computing is used in the bootstrapping procedure if bootstrapping is performed.
boot.method	A string indicating the method for creating bootstrap replications. It is not recommended to change this. Possible choices are <ul style="list-style-type: none"> • "mean.subtract": the default choice, as described in McGonigle and Cho (2025). Empirical mean subtraction is performed to the bootstrapped replicates, improving power. • "no.mean.subtract": empirical mean subtraction is not performed, improving size control.
criterion	String indicating how to determine whether each point k at which NP-MOJO statistic exceeds the threshold is a change point; possible values are <ul style="list-style-type: none"> • "epsilon": k is the maximum of its local exceeding environment, which has at least size $\epsilon \times G$. • "eta": there is no larger exceeding in an $\eta \times G$ environment of k.

	<ul style="list-style-type: none"> • "eta.and.epsilon": the recommended default option; k satisfies both the eta and epsilon criterion. Recommended to use with the standard value of eta that would be used if <code>criterion = "eta"</code> (e.g. 0.4), but much smaller value of epsilon than would be used if <code>criterion = "epsilon"</code>, e.g. 0.02.
<code>eta</code>	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth (if <code>criterion = "eta"</code> or <code>criterion = "eta.and.epsilon"</code>).
<code>epsilon</code>	a numeric value in (0,1] for the minimal size of exceeding environments, relative to moving sum bandwidth (if <code>criterion = "epsilon"</code> or <code>criterion = "eta.and.epsilon"</code>).
<code>use.mean</code>	Logical variable, only to be used if <code>data.drive.kern.par=TRUE</code> . If set to TRUE, the mean of pairwise distances is used to set the kernel function tuning parameter, instead of the median. May be useful for binary data, not recommended to be used otherwise.
<code>scale.data</code>	Logical variable, whether to scale the data in each dimension before performing change point detection. Performance is generally improved by scaling the data.
<code>eta.merge</code>	A positive numeric value for the minimal mutual distance of changes, relative to bandwidth, used to merge change point estimators across different lags.
<code>merge.type</code>	String indicating the method used to merge change point estimators from different lags. Possible choices are <ul style="list-style-type: none"> • "sequential": Starting from the left-most change point estimator and proceeding forward in time, estimators are grouped into clusters based on mutual distance. The estimator yielding the largest corresponding importance score is chosen as the change point estimator for that cluster. See McGonigle and Cho (2025) for details. • "bottom-up": starting with the largest importance score, the change points are merged using bottom-up merging (Messer et al. (2014)).

Details

The multi-lag NP-MOJO algorithm for nonparametric change point detection is described in McGonigle, E. T. and Cho, H. (2025) Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Value

A list object that contains the following fields:

<code>G</code>	Moving window bandwidth
<code>lags</code>	Lags used to detect changes
<code>kernel.f</code> , <code>data.driven.kern.par</code> , <code>use.mean</code>	Input parameters
<code>threshold</code> , <code>alpha</code> , <code>reps</code> , <code>boot.dep</code> , <code>boot.method</code> , <code>parallel</code>	Input parameters
<code>criterion</code> , <code>eta</code> , <code>epsilon</code>	Input parameters

cpts	A matrix with rows corresponding to final change point estimators, with estimated change point location and associated lag and importance score given in columns.
cpt.clusters	A list object of length given by the number of detected change points. Each field contains a matrix of all change point estimators that are declared to be associated to the corresponding change point in the cpts field.

References

McGonigle, E.T., Cho, H. (2025). Nonparametric data segmentation in multivariate time series via joint characteristic functions. *Biometrika* (to appear).

Fan, Y., de Micheaux, P.L., Penev, S. and Salopek, D. (2017). Multivariate nonparametric test of independence. *Journal of Multivariate Analysis*, 153, pp.189-210.

Messer M., Kirchner M., Schiemann J., Roeper J., Neininger R., Schneider G. (2014). A Multiple Filter Test for the Detection of Rate Changes in Renewal Processes with Varying Variance. *The Annals of Applied Statistics*, 8(4), 2027-2067.

See Also

[np.mojo](#), [multilag.cpts.merge](#)

Examples

```
set.seed(1)
n <- 500
noise <- c(rep(1, 300), rep(0.4, 200)) * stats::arima.sim(model = list(ar = 0.3), n = n)
signal <- c(rep(0, 100), rep(2, 400))
x <- signal + noise
x.c <- np.mojo.multilag(x, G = 83, lags = c(0, 1))
x.c$cpts
x.c$cpt.clusters
```

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