Package ‘tsmp’

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**analyze**

Runs an appropriate workflow based on the parameters passed in.

---

**Description**

The goal of this function is to compute all fundamental algorithms on the provided time series data. See details for more information.

**Usage**

```r
analyze(
  ts,
  windows = NULL,
  query = NULL,
  sample_pct = 1,
  threshold = 0.98,
  n_jobs = 1L
)
```

**Arguments**

- `ts` a matrix or a vector. The time series to analyze.
- `windows` an int or a vector. The window(s) to compute the Matrix Profile. Note that it may be an int for a single matrix profile computation or a vector of int for computing the Pan-Matrix Profile.
- `query` a matrix or a vector. Optional The query to analyze. Note that when computing the Pan-Matrix Profile the query is ignored!
sample_pct  a numeric. A number between 0 and 1 representing how many samples to compute for the Matrix Profile or Pan-Matrix Profile. When it is 1, the exact algorithm is used. (default is 1.0).

threshold  a numeric. Correlation threshold. See details. (Default is 0.98).

n_jobs  an int. The number of cpu cores to use when computing the MatrixProfile. (default is 1).

Details

For now the following is computed:

1. Matrix Profile - exact or approximate based on sample_pct given that a single windows is provided. By default is the exact algorithm;
2. Top 3 Motifs;
3. Top 3 Discords;
4. Plot Matrix Profile, Motifs and Discords.

When windows is not provided or more than a single window is provided, the Pan-Matrix Profile is computed:

1. Compute the upper bound when a threshold is provided (it is, by default);
2. Compute Pan-Matrix Profile for all windows provided, below the upper bound, or a default range when no windows is provided;
3. Top Motifs;
4. Top Discords;
5. Plot Pan-Matrix Profile, motifs and discords.

Value

The appropriate Matrix Profile or Pan-Matrix Profile profile object and also plots the graphics.

References

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Main API: compute(), discords(), motifs(), visualize()

Examples

# Matrix Profile
result <- analyze(mp_toy$data[, 1], 80)

# Pan Matrix Profile
result <- analyze(mp_toy$data[, 1])
as.matrixprofile  

Convert a TSMP object into another if possible

Description

The base Classes are MatrixProfile and MultiMatrixProfile, but as other functions are used, classes are pushed behind, since the last output normally is the most significant. If you want, for example, to plot the Matrix Profile from a Fluss object, you may use as.matrixprofile() to cast it back.

Usage

as.matrixprofile(.mp)

as.multimatrixprofile(.mp)

as.pmp(.mp)

as.valmod(.mp)

as.fluss(.mp)

as.chain(.mp)

as.discord(.mp)

as.motif(.mp)

as.multimotif(.mp)

as.arccount(.mp)

as.salient(.mp)

Arguments

.mp  a TSMP object.

Value

Returns the object with the new class, if possible.

Functions

• as.matrixprofile: Cast an object changed by another function back to MatrixProfile.

• as.multimatrixprofile: Cast an object changed by another function back to MultiMatrixProfile.

• as.pmp: Cast an object changed by another function back to PMP.
• as.valmod: Cast an object changed by another function back to MultiMatrixProfile.
• as.fluss: Cast an object changed by another function back to Fluss.
• as.chain: Cast an object changed by another function back to Chain.
• as.discord: Cast an object changed by another function back to Discord.
• as.motif: Cast an object changed by another function back to Motif.
• as.multimotif: Cast an object changed by another function back to MultiMotif.
• as.arccount: Cast an object changed by another function back to ArcCount.
• as.salient: Cast an object changed by another function back to Salient.

Examples

```r
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1 / 4, verbose = 0)
mp <- find_motif(mp)
class(mp) # first class will be "Motif"

plot(mp) # plots a motif plot

plot(as.matrixprofile(mp)) # plots a matrix profile plot
```

---

**av_apply**

**Corrects the matrix profile using an annotation vector**

**Description**

This function overwrites the current Matrix Profile using the Annotation Vector. Use with caution.

**Usage**

`av_apply(.mp)`

**Arguments**

- `.mp` A Matrix Profile with an Annotation Vector.

**Value**

Returns the input `.mp` object corrected by the embedded annotation vector.

**References**

av_complexity

See Also

Other Annotation vectors: `av_complexity()`, `av_hardlimit_artifact()`, `av_motion_artifact()`, `av_stop_word()`, `av_zerocrossing()`

Examples

data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tsmp(data, window_size = w, verbose = 0)
mp <- av_complexity(mp)
av <- av_apply(mp)

---

av_complexity Computes the annotation vector that favors complexity

Description

Computes the annotation vector that favors complexity

Usage

`av_complexity(.mp, data, dilution_factor = 0, apply = FALSE)`

Arguments

- `.mp` a Matrix Profile object.
- `data` a vector or a column matrix of numeric.
- `dilution_factor` a numeric. (Default is 0). Larger numbers means more dilution.
- `apply` logical. (Default is FALSE). Applies the Annotation Vector over the Matrix Profile. Use with caution.

Value

Returns the input .mp object with an embedded annotation vector.

References


See Also

Other Annotation vectors: `av_apply()`, `av_hardlimit_artifact()`, `av_motion_artifact()`, `av_stop_word()`, `av_zerocrossing()`
Examples

```r
data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tsmp(data, window_size = w, verbose = 0)
av <- av_complexity(mp, apply = TRUE)
```

---

**av_hardlimit_artifact**  
*Computes the annotation vector that suppresses hard-limited artifacts*

---

**Description**
Computes the annotation vector that suppresses hard-limited artifacts

**Usage**

```r
av_hardlimit_artifact(.mp, data, apply = FALSE)
```

**Arguments**
- `.mp`  
a Matrix Profile object.
- `data`  
a vector or a column matrix of numeric.
- `apply`  
logical. (Default is FALSE). Applies the Annotation Vector over the Matrix Profile. Use with caution.

**Value**
Returns the input `.mp` object with an embedded annotation vector.

**References**

**See Also**
Other Annotation vectors: `av_apply()`, `av_complexity()`, `av_motion_artifact()`, `av_stop_word()`, `av_zerocrossing()`

**Examples**

```r
data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tsmp(data, window_size = w, verbose = 0)
av <- av_hardlimit_artifact(mp, apply = TRUE)
```
av_motion_artifact

Description

Computes the annotation vector that suppresses motion artifacts

Usage

av_motion_artifact(.mp, data, apply = FALSE)

Arguments

- `.mp` a Matrix Profile object.
- `data` a vector or a column matrix of numeric.
- `apply` logical. (Default is FALSE). Applies the Annotation Vector over the Matrix Profile. Use with caution.

Value

Returns the input `.mp` object with an embedded annotation vector.

References


See Also

Other Annotation vectors: av_apply(), av_complexity(), av_hardlimit_artifact(), av_stop_word(), av_zerocrossing()

Examples

data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tsmp(data, window_size = w, verbose = 0)
av <- av_motion_artifact(mp, apply = TRUE)
av_stop_word  Computes the annotation vector that suppresses stop-word motifs

Description

Computes the annotation vector that suppresses stop-word motifs

Usage

av_stop_word(
  .mp,
  data,
  stop_word_loc,
  exclusion_zone = NULL,
  threshold = 0.1,
  apply = FALSE
)

Arguments

- \texttt{.mp} | a Matrix Profile object.
- \texttt{data} | a vector or a column matrix of numeric.
- \texttt{stop_word_loc} | an int. The index of stop word location.
- \texttt{exclusion_zone} | a numeric. Size of the exclusion zone, based on \texttt{window_size} (default is NULL). See details.
- \texttt{threshold} | a numeric. (default is 0.1).
- \texttt{apply} | logical. (Default is FALSE). Applies the Annotation Vector over the Matrix Profile. Use with caution.

Details

The function is intended to be generic. However, its parameters (\texttt{stop_word_loc}, \texttt{exclusion_zone} and \texttt{threshold}) are highly dataset dependent.

Value

Returns the input \texttt{.mp} object with an embedded annotation vector.

References

See Also

Other Annotation vectors: `av_apply()`, `av_complexity()`, `av_hardlimit_artifact()`, `av_motion_artifact()`, `av_zerocrossing()`

Examples

data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tsmp(data, window_size = w, verbose = 0)
av <- av_stop_word(mp, stop_word_loc = 150, apply = TRUE)

---

**av_zerocrossing** Computes the annotation vector that favors number of zero crossing

Description

Computes the annotation vector that favors number of zero crossing

Usage

```r
av_zerocrossing(.mp, data, apply = FALSE)
```

Arguments

- `.mp` a Matrix Profile object.
- `data` a vector or a column matrix of numeric.
- `apply` logical. (Default is FALSE). Applies the Annotation Vector over the Matrix Profile. Use with caution.

Value

Returns the input `.mp` object with an embedded annotation vector.

References


See Also

Other Annotation vectors: `av_apply()`, `av_complexity()`, `av_hardlimit_artifact()`, `av_motion_artifact()`, `av_stop_word()`
Examples

data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tspm(data, window_size = w, verbose = 0)
av <- av_zerocrossing(mp, apply = TRUE)

data <- mp_test_data$train$data[1:1000]
w <- 50
mp <- tspm(data, window_size = w, verbose = 0)
av <- av_zerocrossing(mp, apply = TRUE)

compute

Computes the Matrix Profile or Pan-Matrix Profile

Description

Main API Function

Usage

compute(
  ts,
  windows = NULL,
  query = NULL,
  sample_pct = 1,
  threshold = 0.98,
  n_jobs = 1L
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>ts</td>
<td>a matrix or a vector. The time series to analyze.</td>
</tr>
<tr>
<td>windows</td>
<td>an int or a vector. The window(s) to compute the Matrix Profile. Note that it</td>
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<td></td>
<td>may be an int for a single matrix profile computation or a vector of int for</td>
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<td></td>
<td>computing the Pan-Matrix Profile.</td>
</tr>
<tr>
<td>query</td>
<td>a matrix or a vector. Optional The query to analyze. Note that when comput-</td>
</tr>
<tr>
<td></td>
<td>ing the Pan-Matrix Profile the query is ignored!</td>
</tr>
<tr>
<td>sample_pct</td>
<td>a numeric. A number between 0 and 1 representing how many samples to compute</td>
</tr>
<tr>
<td></td>
<td>for the Matrix Profile or Pan-Matrix Profile. When it is 1, the exact algo-</td>
</tr>
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<td></td>
<td>rithm is used. (default is 1.0).</td>
</tr>
<tr>
<td>threshold</td>
<td>a numeric. Correlation threshold. See details. (Default is 0.98).</td>
</tr>
<tr>
<td>n_jobs</td>
<td>an int. The number of cpu cores to use when computing the MatrixProfile.</td>
</tr>
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<td>(default is 1).</td>
</tr>
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</table>

Details

Computes the exact or approximate Matrix Profile based on the sample percent specified. Currently, MPX and SCRIMP++ are used for the exact and approximate algorithms respectively. See details for more information about the arguments combinations.

When a single windows is given, the Matrix Profile is computed. If a query is provided, AB join is computed. Otherwise the self-join is computed. When multiple windows or none are given, the
Pan-Matrix Profile is computed. If a threshold is set (it is, by default), the upper bound will be computed and the given windows or a default range (when no windows), below the upper bound will be computed.

Value

The profile computed.

References

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Main API: analyze(), discords(), motifs(), visualize()

Examples

```r
# Matrix Profile
result <- compute(mp_toy$data[, 1], 80)

# Pan-Matrix Profile
result <- compute(mp_toy$data[, 1])
```

discords  Search for Discord

Description

Search for Discord

Usage

```r
discords(
  profile,
  exclusion_zone = profile$ez,
  k = 3L,
  neighbor_count = 10L,
  radius = 3
)
```
**Arguments**

- **profile** a MatrixProfile or PMP object.
- **exclusion_zone** an int. Number of values to exclude on both sides of the motif to avoid trivial matches. Defaults to the exclusion zone used to compute the (Pan-)Matrix Profile which is found in the profile data structure.
- **k** an int. Number of discords to find. (Default is 3).
- **neighbor_count** an int. Number of neighbors to find. (Default is 3).
- **radius** an int. Set a threshold to exclude matching neighbors with distance > current discord distance * radius. (Default is 3).

**References**

Website: [http://www.cs.ucr.edu/~eamonn/MatrixProfile.html](http://www.cs.ucr.edu/~eamonn/MatrixProfile.html)

**See Also**

Other Main API: `analyze()`, `compute()`, `motifs()`, `visualize()`

---

**dist_profile** *Calculates the distance profile using MASS algorithms*

**Description**

Mueen’s Algorithm for Similarity Search is The Fastest Similarity Search Algorithm for Time Series Subsequences under Euclidean Distance and Correlation Coefficient.

**Usage**

```r
dist_profile(
  data,
  query,
  ...,
  window_size = NULL,
  method = "v3",
  index = 1,
  k = NULL,
  weight = NULL,
  paa = 1
)
```
**Arguments**

- **data** a matrix or a vector.
- **query** a matrix or a vector. See details.
- ... Precomputed values from the first iteration. If not supplied, these values will be computed.
- **window_size** an int or NULL. Sliding window size. See details.
- **method** method that will be used to calculate the distance profile. See details.
- **index** an int. Index of query window. See details.
- **k** an int or NULL. Default is NULL. Defines the size of batch for MASS V3. Prefer to use a power of 2. If NULL, it will be set automatically.
- **weight** a vector of numeric or NULL with the same length of the window_size. This is a MASS extension to weight the query.
- **paa** a numeric. Default is 1. Factor of PAA reduction (2 == half of size). This is a MASS extension.

**Details**

This function has several ways to work:

Case 1: You have a small sized query and the data. In this case you only have to provide the first two parameters data and query. Internally the window_size will be get from the query length.

Case 2: You have one or two data vectors and want to compute the join or self-similarity. In this case you need to use the recursive solution. The parameters are data, query, window_size and index. The first iteration don’t need the index unless you are starting somewhere else. The query will be the source of a query_window, starting on index, with length of window_size.

The method defines which MASS will be used. Current supported values are: v2, v3, weighted.

**Value**

Returns the distance_profile for the given query and the last_product for STOMP algorithm and the parameters for recursive call. See details.

**References**

- Abdullah Mueen, Yan Zhu, Michael Yeh, Kaveh Kamgar, Krishnamurthy Viswanathan, Chetan Kumar Gupta and Eamonn Keogh (2015), The Fastest Similarity Search Algorithm for Time Series Subsequences under Euclidean Distance

Website: [https://www.cs.unm.edu/~mueen/FastestSimilaritySearch.html](https://www.cs.unm.edu/~mueen/FastestSimilaritySearch.html)

**Examples**

```r
w <- mp_toy_data$sub_len
ref_data <- mp_toy_data$data[, 1]
# minimum example, data and query
nn <- dist_profile(ref_data, ref_data[1:w])
```
distance_profile <- sqrt(nn$distance_profile)

# data and indexed query
nn <- dist_profile(ref_data, ref_data, window_size = w, index = 10)
distance_profile <- sqrt(nn$distance_profile)

# recursive
nn <- NULL

for (i in seq_len(10)) {
  nn <- dist_profile(ref_data, ref_data, nn, window_size = w, index = i)
}

# weighted
weight <- c(rep(1, w / 3), rep(0.5, w / 3), rep(0.8, w / 3)) # just an example

nn <- dist_profile(ref_data, ref_data, window_size = w, index = 1, method = "weighted",
  weight = weight)
distance_profile <- sqrt(nn$distance_profile)

---

fast_avg_sd  

Fast implementation of moving average and moving standard deviation

---

Description

This function does not handle NA values

Usage

fast_avg_sd(data, window_size, rcpp = FALSE)

Arguments

data  
a vector or a column matrix of numeric.

window_size  
moving sd window size

rcpp  
a logical. Uses rcpp implementation.

Value

Returns a list with avg and sd vectors
fast_movavg

**Fast implementation of moving average**

**Description**
This function does not handle NA values

**Usage**

```r
fast_movavg(data, window_size)
```

**Arguments**
- `data`: a vector or a column matrix of numeric.
- `window_size`: moving sd window size

**Value**
Returns a vector with the moving average

**Examples**

```r
data_avg <- fast_movavg(mp_toy$data[, 1], mp_toy$data$sub_len)
```

---

fast_movsd

**Fast implementation of moving standard deviation**

**Description**
This function does not handle NA values

**Usage**

```r
fast_movsd(data, window_size, rcpp = FALSE)
```

**Arguments**
- `data`: a vector or a column matrix of numeric.
- `window_size`: moving sd window size
- `rcpp`: a logical. Uses rcpp implementation.

**Value**
Returns a vector with the moving standard deviation

**Examples**

```r
data_sd <- fast_movsd(mp_toy$data[, 1], mp_toy$data$sub_len)
```
find_chains  

Find Time Series Chains

Description

Time Series Chains is a new primitive for time series data mining.

Usage

```r
find_chains(.mp)
```

Arguments

- `.mp` a MatrixProfile object.

Value

Returns the input `.mp` object with a new name `chain`. It contains: `chains`, a list of chains found with more than 2 patterns and best with the best one.

References


Website: [https://sites.google.com/site/timeserieschain/](https://sites.google.com/site/timeserieschain/)

Examples

```r
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1 / 4, verbose = 0)
mp <- find_chains(mp)
```

find_discord  

Search for Discord

Description

Search for Discord
find_discord

Usage

find_discord(.mp, ...)

## S3 method for class 'MatrixProfile'
find_discord(
  .mp,
  data,
  n_discords = 1,
  n_neighbors = 3,
  radius = 3,
  exclusion_zone = NULL,
  ...
)

## S3 method for class 'PMP'
find_discord(
  .mp,
  data,
  n_discords = 1,
  n_neighbors = 3,
  radius = 3,
  exclusion_zone = NULL,
  ...
)

Arguments

.mp a MatrixProfile object.

... further arguments to be passed to class specific function.

data the data used to build the Matrix Profile, if not embedded.

n_discords an int. Number of discords to find. (Default is 1).

n_neighbors an int. Number of neighbors to find. (Default is 3).

radius an int. Set a threshold to exclude matching neighbors with distance > current discord distance * radius. (Default is 3).

exclusion_zone if a number will be used instead of embedded value. (Default is NULL).

Value

For class MatrixProfile, returns the input .mp object with a new name discord. It contains: discord_idx, a vector of discords found

For class PMP, returns the input .mp object with a new name discord. It contains: discord_idx, a vector of discords found

Examples

# Single dimension data
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1/4, verbose = 0)
mp <- find_discord(mp)
pan <- tsmp(mp_gait_data, window_size = 20:30, mode = "pmp")
mp <- find_discord(pan)

---

find_motif

**Search for Motifs**

**Description**

Search for Motifs

**Usage**

```r
find_motif(.mp, ...)
```

## S3 method for class 'MatrixProfile'

```r
find_motif (.mp, 
data, 
n_motifs = 3, 
n_neighbors = 10, 
radius = 3, 
exclusion_zone = NULL,
...
)
```

## S3 method for class 'MultiMatrixProfile'

```r
find_motif (.mp, 
data, 
n_motifs = 3, 
mode = c("guided", "unconstrained"), 
n_bit = 4, 
exclusion_zone = NULL, 
n_dim = NULL,
...
)
```

## S3 method for class 'PMP'

```r
find_motif (.mp, 
data, 
n_motifs = 3, 
n_neighbors = 10, 
radius = 3,
```
Arguments

- `.mp` a `MatrixProfile` or `MultiMatrixProfile` object.
- `...` further arguments to be passed to class specific function.
- `data` the data used to build the Matrix Profile, if not embedded.
- `n_motifs` an int. Number of motifs to find. (Default is 3).
- `n_neighbors` an int. Number of neighbors to find. (Default is 10).
- `radius` an int. Set a threshold to exclude matching neighbors with distance > current motif distance * radius. (Default is 3).
- `exclusion_zone` if a number will be used instead of embedded value. (Default is NULL).
- `mode` a string. Guided or Unconstrained search. Allow partial match. (Default is guided).
- `n_bit` an int. Bit size for discretization. Ignored on Guided search. (Default is 4).
- `n_dim` an int. Number of dimensions to use on Guided search instead of embedded value. (Default is NULL).

Value

For class `MatrixProfile`, returns the input `.mp` object with a new name `motif`. It contains:
- `motif_idx`, a list of motif pairs found and `motif_neighbor` a list with respective motif’s neighbors.

For class `MultiMatrixProfile`, returns the input `.mp` object with a new name `motif`. It contains:
- `motif_idx`, a vector of motifs found and `motif_dim` a list the dimensions where the motifs were found.

For class `PMP`, returns the input `.mp` object with a new name `motif`. It contains:
- `motif_idx`, a list of motif pairs found and `motif_neighbor` a list with respective motif’s neighbors.

Examples

```r
# Single dimension data
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1 / 4, verbose = 0)
mp <- find_motif(mp)

# Multidimension data
w <- mp_toy_data$sub_len
data <- mp_toy_data$data[1:200, ]
mp <- tsmp(data, window_size = w, mode = "mstomp", verbose = 0)
mp <- find_motif(mp)
pan <- tsmp(mp_gait_data, window_size = 20:30, mode = "pmp")
mp <- find_motif(pan)
```
**find_snippet**

---

**Description**

Time Series Snippets tries to solve mainly the common problem of summarization "Show me some representative/typical data". As stated by the original paper, potential uses of snippets are: integrating summarizations of files directly into an operating, production of automatically generated reports, for example, summarize a sleep study and also can be used to support a host of higher-level tasks, including the comparison of massive data collections.

**Usage**

```r
find_snippet(data, s_size, n_snippets = 2L, window_size = s_size/2L)
```

**Arguments**

- `data`: a matrix or a vector.
- `s_size`: an int. Size of snippet.
- `n_snippets`: an int. Number of snippets to find. (Default is 2).
- `window_size`: an int. The size of the sliding window used to compare the data. Must be smaller than `s_size`. (Default is `s_size / 2`).

**Details**

Motifs vs. snippets: While motifs reward fidelity of conservation, snippets also rewards coverage. Informally, coverage is some measure of how much of the data is explained or represented by a given snippet.

Shapelets vs. snippets: shapelets are defined as subsequences that are maximally representative of a class. Shapelets are supervised, snippets are unsupervised. Shapelets are generally biased to be as short as possible. In contrast, we want snippets to be longer, to intuitively capture the "flavor" of the time series.

**Value**

Returns the snippet: a list of `n_snippets` snippets fraction: fraction of each snippet snippetidx: the location of each snippet within time series

**References**


Website: https://sites.google.com/site/snippetfinder/

Examples

```r
snippets <- find_snippet(mp_fluss_data$walkjogrun$data[1:300], 40, n_snippets = 2)

snippets <- find_snippet(mp_fluss_data$walkjogrun$data, 120, n_snippets = 3)
plot(snippets)
```

---

**floss**

*Fast Low-cost Online Semantic Segmentation (FLOSS)*

**Description**

Fast Low-cost Online Semantic Segmentation (FLOSS)

**Usage**

```r
floss(
  .mp,
  new_data,
  data_window,
  threshold = 1,
  exclusion_zone = NULL,
  chunk_size = NULL,
  keep_cac = TRUE
)
```

**Arguments**

- `.mp` a MatrixProfile object.
- `new_data` a matrix or vector of new observations.
- `data_window` an int. Sets the size of the buffer used to keep track of semantic changes.
- `threshold` a number. (Default is 1). Set the maximum value for evaluating semantic changes. This is data specific. It is advised to check what is 'normal' for your data.
- `exclusion_zone` if a number will be used instead of embedded value. (Default is NULL).
- `chunk_size` an int. (Default is NULL). Set the size of new data that will be added to Floss in each iteration if `new_data` is large. If NULL, the size will be 50. This is not needed if `new_data` is small, like 1 observation.
- `keep_cac` a logical. (Default is TRUE). If set to FALSE, the cac_final will contain only values within data_window.
Value
Returns the input .mp object new names: cac the corrected arc count, cac_final the combination of cac after repeated calls of floss(), floss with the location of semantic changes and floss_vals with the normalized arc count value of the semantic change positions.

References
  Website: https://sites.google.com/site/onlinesemanticsegmentation/
  Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also
Other Semantic Segmentations: floss_cac(), floss_extract(), fluss_cac(), fluss_extract(), fluss_score(), fluss()

Examples
```r
data <- mp_fluss_data$tilt_abp$data[1:1000]
new_data <- mp_fluss_data$tilt_abp$data[1001:1010]
new_data2 <- mp_fluss_data$tilt_abp$data[1011:1020]
w <- 80
mp <- tsmp(data, window_size = w, verbose = 0)
data_window <- 1000
mp <- floss(mp, new_data, data_window)
mp <- floss(mp, new_data2, data_window)
```

---

**floss_cac**

FLOSS - Corrected Arc Counts

Description
Computes the arc count with edge and 'online' correction (CAC).

Usage
```r
floss_cac(.mp, data_window, exclusion_zone = NULL)
```

Arguments
- `.mp` a MatrixProfile object.
- `data_window` an int. Sets the size of the buffer used to keep track of semantic changes.
- `exclusion_zone` if a number will be used instead of embedded value. (Default is NULL).
Details

Original paper suggest using the classic statistical-process-control heuristic to set a threshold where a semantic change may occur in CAC. This may be useful in real-time implementation as we don’t know in advance the number of domain changes to look for. Please check original paper (1).

Value

Returns the input .mp object a new name cac with the corrected arc count and cac_final the combination of cac after repeated calls of floss().

References


Website: https://sites.google.com/site/onlinesemanticsegmentation/

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Semantic Segmentations: floss_extract(), floss(), fluss_cac(), fluss_extract(), fluss_score().fluss()

Examples

data <- mp_fluss_data$tilt_abp$data[1:1000]
new_data <- mp_fluss_data$tilt_abp$data[1001:1010]
w <- 10
mp <- tsmp(data, window_size = w, verbose = 0)
data_window <- 1000
mp <- stompi_update(mp, new_data, data_window)
mp <- floss_cac(mp, data_window)

floss_extract

Description

Extract candidate points of semantic changes.

Usage

floss_extract(.mpac, threshold = 1, exclusion_zone = NULL)
\textbf{fluss}

\textbf{Arguments}

- \texttt{mpac} a TSMP object of class \texttt{ArcCount}.
- \texttt{threshold} a number. (Default is 1). Set the maximum value for evaluating semantic changes. This is data specific. It is advised to check what is 'normal' for your data.
- \texttt{exclusion\_zone} if a number will be used instead of embedded value. (Default is NULL).

\textbf{Value}

Returns the input \texttt{mp} object a new name \texttt{floss} with the location of semantic changes and \texttt{floss\_vals} with the normalized arc count value of the semantic change positions.

\textbf{References}


Website: https://sites.google.com/site/onlinesemanticsegmentation/

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

\textbf{See Also}

Other Semantic Segmentations: \texttt{floss\_cac()}, \texttt{floss()}, \texttt{fluss\_cac()}, \texttt{fluss\_extract()}, \texttt{fluss\_score()}, \texttt{fluss()}

\textbf{Examples}

```r
data <- mp_fluss_data$tilt_abp$data[1:1000]
w <- 10
mp <- tsmp(data, window_size = w, verbose = 0)
mp <- fluss_cac(mp)
mp <- fluss_extract(mp, 2)
```

\textbf{Description}

FLUSS is a Domain Agnostic Online Semantic Segmentation that uses the assumption that when few arc are crossing a given index point, means that there is a high probability of semantic change. This function is a wrap to \texttt{fluss\_cac()} and \texttt{fluss\_extract()}.
Arguments

- **.mp**: a `MatrixProfile` object.
- **num_segments**: an `int`. Number of segments to extract. Based on domain knowledge.
- **exclusion_zone**: if a number will be used instead of embedded value. (Default is `NULL`).

Value

Returns the input .mp object new names: cac, corrected arc count and fluss with the location of semantic changes.

References


Website: [https://sites.google.com/site/onlinesemanticsegmentation/](https://sites.google.com/site/onlinesemanticsegmentation/)

Website: [http://www.cs.ucr.edu/~eamonn/MatrixProfile.html](http://www.cs.ucr.edu/~eamonn/MatrixProfile.html)

See Also

Other Semantic Segmentations: `floss_cac()`, `floss_extract()`, `floss()`, `fluss_cac()`, `fluss_extract()`, `fluss_score()`

Examples

```r
data <- mp_fluss_data$tilt_abp$data[1:1000]
w <- 10
mp <- tsmp(data, window_size = w, verbose = 0)
mp <- fluss(mp, 2)
```

---

**fluss_cac**  
*FLUSS - Corrected Arc Counts*

Description

Computes the arc count with edge correction (CAC).

Usage

```r
fluss_cac(.mp, exclusion_zone = NULL)
```

Arguments

- **.mp**: a `MatrixProfile` object.
- **exclusion_zone**: if a number will be used instead of embedded value. (Default is `NULL`).
Details

Original paper suggest using the classic statistical-process-control heuristic to set a threshold where a semantic change may occur in CAC. This may be useful in real-time implementation as we don’t know in advance the number of domain changes to look for. Please check original paper (1).

Value

Returns the input .mp object a new name cac with the corrected arc count.

References


Website: https://sites.google.com/site/onlinesemanticsegmentation/
Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Semantic Segmentations: floss_cac(), floss_extract(), floss(), fluss_extract(), fluss_score(), fluss()

Examples

data <- mp_fluss_data$tilt_abp$data[1:1000]
w <- 10
mp <- tsmp(data, window_size = w, verbose = 0)
mp <- fluss_cac(mp)
fluss_score

Value

Returns the input .mp object a new name fluss with the location of semantic changes.

References


Website: https://sites.google.com/site/onlinesemanticsegmentation/
Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Semantic Segmentations: floss_cac(), floss_extract(), floss(), fluss_cac(), fluss_score(), fluss()

Examples

data <- mp_fluss_data$tilt_abp$data[1:1000]
w <- 10
mp <- tsmpl(data, window_size = w, verbose = 0)
mp <- fluss_cac(mp)
mp <- fluss_extract(mp, 2)

fluss_score

FLUSS - Prediction score calculation

Description

FLUSS - Prediction score calculation

Usage

fluss_score(gtruth, extracted, data_size)

Arguments

gtruth an int or vector of int with the ground truth index of segments.
extracted an int or vector of int with the extracted indexes from fluss_extract().
data_size an int. Size of original input data.

Value

Returns the score of predicted semantic transitions compared with the ground truth. Zero is the best, One is the worst.
References


Website: https://sites.google.com/site/onlinesemanticsegmentation/
Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other Semantic Segmentations: floss_cac(), floss_extract(), floss(), fluss_cac(), fluss_extract(), fluss()

Examples

```r
data <- mp_fluss_data$tilt_abp$data[1:1000]
w <- 10
truth <- c(945, 875)
mp <- tsmp(data, window_size = w, verbose = 0)
mp <- fluss_cac(mp)
mp <- fluss_extract(mp, 2)
score <- fluss_score(truth, mp$fluss, length(data))
```

get_data

Get the data included in a TSMP object, if any.

Description

Get the data included in a TSMP object, if any.

Usage

```r
get_data(.mp)
```

Arguments

- `.mp`  
  a TSMP object.

Value

Returns the data as `matrix`. If there is more than one series, returns a `list`.

Examples

```r
mp <- tsmp(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)
get_data(mp)
```
**mass_v3**

*Calculates the distance profile using MASS_V3 algorithm*

**Description**

Mueen’s Algorithm for Similarity Search is the fastest similarity search algorithm for time series subsequences under Euclidean distance and correlation coefficient.

**Usage**

```r
mass_v3(
    query_window,
    data,
    window_size,
    data_size,
    data_mean,
    data_sd,
    query_mean,
    query_sd,
    k = NULL,
    ...
)
```

**Arguments**

- `data`: a matrix or a vector.
- `window_size`: an int. Sliding window size.
- `data_size`: an int. The length of the reference data.
- `data_mean`: precomputed data moving average.
- `data_sd`: precomputed data moving standard deviation.
- `query_mean`: precomputed query average.
- `query_sd`: precomputed query standard deviation.
- `k`: an int or NULL. Default is NULL. Defines the size of batch. Prefer to use a power of 2.
- `...`: just a placeholder to catch unused parameters.

**Details**

This is a piecewise version of MASS that performs better when the size of the pieces are well aligned with the hardware.

**Value**

Returns the distance_profile for the given query and the last_product for STOMP algorithm.
References

- Abdullah Mueen, Yan Zhu, Michael Yeh, Kaveh Kamgar, Krishnamurthy Viswanathan, Chetan Kumar Gupta and Eamonn Keogh (2015), The Fastest Similarity Search Algorithm for Time Series Subsequences under Euclidean Distance

Website: https://www.cs.unm.edu/~mueen/FastestSimilaritySearch.html

See Also

mass_pre() to precomputation of input values.

Examples

```r
w <- mp_toy_data$sub_len
ref_data <- mp_toy_data$data[, 1]
query_data <- mp_toy_data$data[, 1]
d_size <- length(ref_data)
q_size <- length(query_data)

pre <- tsmp:::mass_pre(ref_data, query_data, w)

dp <- list()
for (i in 1:(d_size - w + 1)) {
  dp[[i]] <- tsmp:::mass_v3(
    query_data[i:(i - 1 + w)], ref_data,
    pre$window_size, pre$data_size, pre$data_mean, pre$data_sd,
    pre$query_mean[i], pre$query_sd[i]
  )
}
```

`min_mp_idx` - Get index of the minimum value from a matrix profile and its nearest neighbor

Description

Get index of the minimum value from a matrix profile and its nearest neighbor

Usage

`min_mp_idx(.mp, n_dim = NULL, valid = TRUE)`

Arguments

- `.mp` - a `MatrixProfile` object.
- `n_dim` - number of dimensions of the matrix profile
- `valid` - check for valid numbers
Value
returns a matrix with two columns: the minimum and the nearest neighbor

Examples
```
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1 / 4, verbose = 0)
min_val <- min_mp_idx(mp)
```

Description
Search for Motifs

Usage
```
motifs(
  profile,
  exclusion_zone = profile$ez,
  k = 3L,
  neighbor_count = 10L,
  radius = 3
)
```

Arguments
- **profile**: a MatrixProfile or PMP object.
- **exclusion_zone**: an int. Number of values to exclude on both sides of the motif to avoid trivial matches. Defaults to the exclusion zone used to compute the (Pan-)Matrix Profile which is found in the profile data structure.
- **k**: an int. Number of motifs to find. (Default is 3).
- **neighbor_count**: an int. Number of neighbors to find. (Default is 3).
- **radius**: an int. Set a threshold to exclude matching neighbors with distance > current discord distance * radius. (Default is 3).

References
Website: [http://www.cs.ucr.edu/~eamonn/MatrixProfile.html](http://www.cs.ucr.edu/~eamonn/MatrixProfile.html)

See Also
Other Main API: `analyze()`, `compute()`, `discords()`, `visualize()`
motifs_discords_small  Just a synthetic dataset for testing

Description

Just a synthetic dataset for testing

Usage

motifs_discords_small

Format

A vector with 875 observations

mpdist  MPdist - Distance between Time Series using Matrix Profile

Description

MPdist is a recently introduced distance measure which considers two time series to be similar if they share many similar subsequences, regardless of the order of matching subsequences. It was demonstrated in that MPdist is robust to spikes, warping, linear trends, dropouts, wandering baseline and missing values, issues that are common outside of benchmark datasets.

Usage

mpdist(
  ref_data,
  query_data,
  window_size,
  type = c("simple", "vector"),
  thr = 0.05
)

Arguments

ref_data  a matrix or a vector. The reference data
query_data  a matrix or a vector. The query data
window_size  an int. Size of the sliding window.
type  the type of result. (Default is simple). See details.
thr  threshold for MPdist. (Default is 0.05). Don’t change this unless you know what you are doing.
Details

MPdist returns the distance of two time series or a vector containing the distance between all sliding windows. If argument type is set to vector, the vector is returned.

Value

Returns the distance of two time series or a vector containing the distance between all sliding windows.

References


Website: https://sites.google.com/site/mpdistinfo/

Examples

```r
ref_data <- mp_toy_data$data[, 1]
qe_data <- mp_toy_data$data[, 2]
qd_data <- mp_toy_data$data[150:200, 1]
w <- mp_toy_data$sub_len

# distance between data of same size
deq <- mpdist(ref_data, qe_data, w)

# distance between data of different sizes
ddiff <- mpdist(ref_data, qd_data, w)

# distance vector between data of different sizes
ddvec <- mpdist(ref_data, qd_data, w, type = "vector")
```

Description

Fast implementation of MP and MPI for internal purposes, without FFT

Usage

```r
mpx(
  data,
  window_size,
  query = NULL,
  idx = TRUE,
  dist = c("euclidean", "pearson"),
  n_workers = 1
)
```
**Arguments**

- **data** a matrix or a vector. The time series to analyze.
- **window_size** window size
- **query** query
- **idx** compute the profile indexes?
- **dist** distance measure, Euclidean or Pearson?
- **n_workers** threads for multi-threading

**Value**

Returns MP and MPI

**Examples**

```
mp <- mpx(mp_toy_data$data[1:200, 1], window_size = 30)
```

---

**mp_fluss_data**  
*Original data used in the FLUSS paper*

**Description**

Contains two datasets used in FLUSS paper (1), first is TiltABP from (2), and second is WalkJogRun from PAMAP’s dataset (3)

**Usage**

`mp_fluss_data`

**Format**

A list containing:

- **data** one column matrix with the dataset’s data
- **gtruth** a vector with the ground truth of semantic change according to provided dataset
- **window** window size used in original paper

**Source**

[https://sites.google.com/site/onlinesemanticsegmentation/](https://sites.google.com/site/onlinesemanticsegmentation/)

**mp_gait_data**  

**Description**  
Original data used in the Time Series Chain demo

**Usage**  
mp_gait_data

**Format**  
A matrix with 904 rows and 1 column with the Y data from an accelerometer

**Source**  
[https://sites.google.com/site/timeserieschain/](https://sites.google.com/site/timeserieschain/)

**References**  
Description

This is the Meat dataset from UCR Archive modified for Salient discovery. The original data is mixed with Random Walks and the algorithm must pick only the originals.

Usage

mp_meat_data

Format

original is the original dataset with 60+60 observations mixed with 120 random walks:

data 240 time series with length of 448 each.
labels label of each time series, -666 means a random walk.
sub_len size of sliding window.

sub is the original dataset embedded in random walks:

data One time series with length of 107520.
labels label of each original data.
labels_idx starting point where the original data was placed.
sub_len size of sliding window.

Source

http://www.cs.ucr.edu/~eamonn/time_series_data/

References


Website: https://sites.google.com/site/salientsubs/
Description

A synthetic dataset base on TRACE dataset and used as Stress Test to STDS algorithm. The TRACE dataset used here is originally from (1), and the version distributed here is from (2).

Usage

mp_test_data

Format

A list of matrices with 215010 rows and 1 dimension:

- `train$data` training data
- `train$label` label for training data
- `test$data` test data
- `test$label` label for test data

Source

https://sites.google.com/view/weaklylabeled
http://www.cs.ucr.edu/~eamonn/time_series_data/

References


mp_toy_data  

Original data used in the mSTAMP demo

Description

A synthetic dataset with embedded MOTIFs for multidimensional discovery

Usage

mp_toy_data

Format

A list with a matrix with 550 rows and 3 dimensions and an int:

data  data with embedded MOTIFs
sub_len  size of sliding window

Source

https://sites.google.com/view/mstamp/

References

• Yeh CM, Kavantzas N, Keogh E. Matrix Profile VI: Meaningful Multidimensional Motif Discovery.

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

mstomp_par  

Multivariate STOMP algorithm Parallel version

Description

Computes the Matrix Profile and Profile Index for Multivariate Time Series.

Usage

mstomp_par(
  data,
  window_size,
  exclusion_zone =getOption("tsmp.exclusion_zone", 1/2),
  verbose =getOption("tsmp.verbose", 2),
  must_dim = NULL,
  exc_dim = NULL,
  n_workers = 2
)
mstomp_par

)

mstomp(
    data,
    window_size,
    exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
    verbose = getOption("tsmp.verbose", 2),
    must_dim = NULL,
    exc_dim = NULL
)

Arguments

data an matrix of numeric, where each column is a time series. Accepts vector (see details), list and data.frame too.
window_size an int with the size of the sliding window.
exclusion_zone an numeric. Size of the exclusion zone, based on window size (default is 1/2).
verbose an int. See details. (Default is 2).
must_dim an int or vector of which dimensions to forcibly include (default is NULL).
exc_dim an int or vector of which dimensions to exclude (default is NULL).
n_workers an int. Number of workers for parallel. (Default is 2).

Details

The Matrix Profile, has the potential to revolutionize time series data mining because of its generality, versatility, simplicity and scalability. In particular it has implications for time series motif discovery, time series joins, shapelet discovery (classification), density estimation, semantic segmentation, visualization, rule discovery, clustering etc. The MSTOMP computes the Matrix Profile and Profile Index for Multivariate Time Series that is meaningful for multidimensional MOTIF discovery. It uses the STOMP algorithm that is faster than STAMP but lacks its anytime property.

Although this functions handles Multivariate Time Series, it can also be used to handle Univariate Time Series. verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.

Value

Returns a MultiMatrixProfile object, a list with the matrix profile mp, profile index pi left and right matrix profile lmp, rmp and profile index lpi, rpi, window size w, number of dimensions n_dim, exclusion zone ez, must dimensions must and excluded dimensions exc.

If the input has only one dimension, returns the same as stomp().

Functions

• mstomp_par: Parallel version.
• mstomp: Single thread version.
References

- Yeh CM, Kavantzas N, Keogh E. Matrix Profile VI: Meaningful Multidimensional Motif Discovery.

Website: https://sites.google.com/view/mstamp/
Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other matrix profile computations: scrimp(), stamp_par(), stomp_par(), tsmp(), valmod()

Examples

```r
# using all dimensions
mp <- mstomp(mp_toy_data$data[1:150, ], 30, verbose = 0)

# using threads
mp <- mstomp_par(mp_toy_data$data[1:150, ], 30, verbose = 0)

# force using dimensions 1 and 2
mp <- mstomp(mp_toy_data$data[1:200, ], 30, must_dim = c(1, 2))
# exclude dimensions 2 and 3
mp2 <- mstomp(mp_toy_data$data[1:200, ], 30, exc_dim = c(2, 3))
```

---

**plot**

*Plot a TSMP object*

**Description**

Plot a TSMP object

**Usage**

```r
## S3 method for class 'ArcCount'
plot(
x, 
data, 
type = c("data", "matrix"), 
exclusion_zone = NULL, 
edge_limit = NULL, 
threshold = stats::quantile(x$cac, 0.1), 
main = "Arcs Discover", 
xlab = "index",
```

---
... ylab = "", ...

## S3 method for class 'Valmod'
plot(
  x,
  ylab = "distance",
  xlab = "index",
  main = "Valmod Matrix Profile",
  data = FALSE,
  ...
)

## S3 method for class 'MatrixProfile'
plot(
  x,
  ylab = "distance",
  xlab = "index",
  main = "Unidimensional Matrix Profile",
  data = FALSE,
  ...
)

## S3 method for class 'MultiMatrixProfile'
plot(
  x,
  ylab = "distance",
  xlab = "index",
  main = "Multidimensional Matrix Profile",
  ...
)

## S3 method for class 'SimpleMatrixProfile'
plot(
  x,
  ylab = "distance",
  xlab = "index",
  main = "SiMPle Matrix Profile",
  data = FALSE,
  ...
)

## S3 method for class 'Fluss'
plot(
  x,
  data,
  type = c("data", "matrix"),
main = "Fast Low-cost Unipotent Semantic Segmentation",
  xlab = "index",
  ylab = "",
...)

## S3 method for class 'Floss'
plot(
  x,
  data,
  type = c("data", "matrix"),
  main = "Fast Low-cost Online Semantic Segmentation",
  xlab = "index",
  ylab = "",
...
)

## S3 method for class 'Chain'
plot(
  x,
  data,
  type = c("data", "matrix"),
  main = "Chain Discover",
  xlab = "index",
  ylab = "",
...
)

## S3 method for class 'Discord'
plot(
  x,
  data,
  type = c("data", "matrix"),
  ncol = 3,
  main = "Discord Discover",
  xlab = "index",
  ylab = "",
...
)

## S3 method for class 'Snippet'
plot(
  x,
  data,
  ncol = 3,
  main = "Snippet Finder",
  xlab = "index",
  ylab = "",
...)
## S3 method for class 'Motif'
plot(
  x,
  data,
  type = c("data", "matrix"),
  ncol = 3,
  main = "MOTIF Discover",
  xlab = "index",
  ylab = "",
  ...
)

## S3 method for class 'MultiMotif'
plot(
  x,
  data,
  type = c("data", "matrix"),
  ncol = 3,
  main = "Multidimensional MOTIF Discover",
  xlab = "index",
  ylab = "",
  ...
)

## S3 method for class 'Salient'
plot(x, data, main = "Salient Subsections", xlab = "index", ylab = "", ...)  

## S3 method for class 'PMP'
plot(
  x,
  ylab = "distance",
  xlab = "index",
  main = "Unidimensional Matrix Profile",
  data = FALSE,
  ...
)

Arguments

x a Matrix Profile

data the data used to build the Matrix Profile, if not embedded to it.
type "data" or "matrix". Choose what will be plotted.
exclusion_zone if a number will be used instead of Matrix Profile's. (Default is NULL).
edge_limit if a number will be used instead of Matrix Profile’s exclusion zone. (Default is NULL).
threshold: the maximum value to be used to plot.
main: a string. Main title.
xlab: a string. X label.
ylab: a string. Y label.
...: further arguments to be passed to `plot()`. See `par()`.
ncol: an int. Number of columns to plot Motifs.

Value

None

Examples

```r
mp <- tsmp(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)
plot(mp)
```

---

**plot_arcs**  
*Plot arcs between indexes of a Profile Index*

Description

Sometimes may be useful to see where is the nearest neighbor graphically. This is the reasoning behind, for example, FLUSS which uses the arc count to infer a semantic change, and SiMPle which infer that arcs connect similar segments of a music. See details for a deeper explanation how to use this function.

Usage

```r
plot_arcs(
  pairs,
  alpha = NULL,
  quality = 30,
  lwd = 15,
  col = c("blue", "orange"),
  main = "Arc Plot",
  ylab = "",
  xlab = "Profile Index",
  xmin = NULL,
  xmax = NULL,
  ...
)
```
Arguments

pairs  a matrix with 2 columns.
alpha  a numeric. (Default is NULL, automatic). Alpha value for lines transparency.
quality an int. (Default is 30). Number of segments to draw the arc. Bigger value, harder to render.
lwd    an int. (Default is 15). Line width.
col    a vector of colors. (Default is c("blue","orange")). Colors for right and left arc, respectively. Accepts one color.
main   a string. (Default is "Arc Plot"). Main title.
ylab   a string. (Default is "). Y label.
xlab   a string. (Default is "Profile Index"). X label.
xmin   an int. (Default is NULL). Set the minimum value of x axis.
xmax   an int. (Default is NULL). Set the maximum value of x axis.
...    further arguments to be passed to plot(). See par().

Details

You have two options to use this function. First you can provide just the data, and the function will try its best to retrieve the pairs for plotting. Second, you can skip the first parameters and just provide the pairs, which is a matrix with two columns; the first is the starting index, the second is the end index. Two colors are used to allow you to identify the direction of the arc. If you use the rpi or lpi as input, you will see that these profile indexes have just one direction.

exclusion_zone is used to filter out small arcs that may be useless (e.g. you may be interested in similarities that are far away). edge_limit is used to filter out spurious arcs that are used connect the beginning and the end of the profile (e.g. silent audio). threshold is used to filter indexes that have distant nearest neighbor (e.g. retrieve only the best motifs).

Value

None

Examples

plot_arcs(pairs = matrix(c(5, 10, 1, 10, 20, 5), ncol = 2, byrow = TRUE))

pmp

Pan-Matrix Profile

Description

Computes the Pan-Matrix Profile (PMP) for the given time series.
Usage

pmp(
  data,
  window_sizes = seq.int(from = 10, to = length(data)/2, length.out = 20),
  plot = FALSE,
  pmp_obj = NULL,
  n_workers = 1,
  verbose = getOption("tsmp.verbose", 2)
)

Arguments

data a matrix or a vector of numeric.
window_sizes a vector of the window sizes that will be evaluated. They will be rounded to the lower integer and sorted. (Default is a sequence of 20 values from 10 to half data size).
plot a logical. If TRUE, every new computation will be plotted. (Default is FALSE).
pmp_obj a PMP object that may or not contain an upper bound value, and previous computed profiles. The function will add new profiles, not replace. (Default is NULL).
n_workers an int. Number of workers for parallel. (Default is 1).
verbose an int. See details. (Default is 2).

Details

The work closest in spirit to ours is VALMOD. The idea of VALMOD is to compute the MP for the shortest length of interest, then use the information gleaned from it to guide a search through longer subsequence lengths, exploiting lower bounds to prune off some calculations. This idea works well for the first few of the longer subsequence lengths, but the lower bounds progressively weaken, making the pruning ineffective. Thus, in the five case studies they presented, the mean value of U/L was just 1.24. In contrast, consider that our termite example in Fig. 15 has a U/L ratio of 240, more than two orders of magnitude larger. Thus, VALMOD is perhaps best seen as finding motifs with some tolerance for a slightly (~25%) too short user-specified query length, rather than a true "motif-of-all-lengths" algorithm. Also note that apart from the shortest length, VALMOD only gives some information for the other lengths, unlike pmp, which contains exact distances for all subsequences of all lengths.

When just the data is provided, the exploration will be done using the default window_sizes that is a sequence of 20 values between 10 and the half data size and the resulting object will have an upper_bound equals to Inf. If an object is provided by the argument pmp_obj, this function will add more information to the resulting object, never changing the values already computed. verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.

Talk about upper bound and window sizes

1. upper_window will be set to Inf on new objects
2. upper_window will also be used for plot, and for discovery, it must not remove any existing data from the object
2. `window_sizes` is used for plot, it must not remove any mp inside the object.  
   2.1. `window_sizes` tells the function what mp are stored, it may be updated with `as.numeric(names(pmp))`  
3. the functions must be capable to handle the data without need to sort by `window_size`, but sort may be useful later(?)

Value

Returns a PMP object.

Examples

```r
# Just compute
pan <- pmp(mp_gait_data)
# Compute the upper bound, than add new profiles
pan <- pmp_upper_bound(mp_gait_data)
pan <- pmp(mp_gait_data, pmp_obj = pan)
```

---

### pmp_upper_bound

#### Pan Matrix Profile upper bound

Finds the upper bound for Pan Matrix Profile calculation.

#### Usage

```r
pmp_upper_bound(
  data,
  threshold = getOption("tsmp.pmp_ub", 0.95),
  refine_stepsize = getOption("tsmp.pmp_refine", 0.25),
  return_pmp = TRUE,
  n_workers = 1,
  verbose = getOption("tsmp.verbose", 2)
)
```

#### Arguments

- `data` a matrix or a vector of numeric.
- `threshold` a numeric. Correlation threshold. See details. (Default is 0.95).
- `refine_stepsize` a numeric. Step size for the last upper bound search. See details. (Default is 0.25).
- `return_pmp` a logical. If TRUE, returns the computed data as a PMP object, if FALSE, returns just the upper bound value. (Default is TRUE).
- `n_workers` an int. Number of workers for parallel. (Default is 1).
- `verbose` verbose an int. See details. (Default is 2).
Details

The Pan Matrix Profile may not give any further information beyond a certain window size. This
function starts computing the matrix profile for the window size of 8 and doubles it until the min-
umum correlation value found is less than the threshold. After that, it begins to refine the upper
bound using the refine_stepsize values, until the threshold value is hit.

verbose changes how much information is printed by this function; 0 means nothing, 1 means text,
2 adds the progress bar, 3 adds the finish sound.

Value

Returns a PMP object with computed data, or just the upper bound value if return_pmp is set to
FALSE.

References

• Yet to be announced
  Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

Examples

    # return the object
    pan_matrix <- pmp_upper_bound(mp_gait_data)

    # just the upper bound
    pan_ub <- pmp_upper_bound(mp_gait_data, return_pmp = FALSE)

read

Read TSMP object from JSON file.

Description

Read TSMP object from JSON file.

Usage

read(x, ...)

Arguments

x
  a character string with the input filename.

... other arguments to be passed forward.

Examples

result <- read("input.json")
remove_class

Remove a TSMP class from an object

Description
Remove a TSMP class from an object

Usage
remove_class(x, class)

Arguments
- x: a TSMP object
- class: character string with the class name

Value
the object without the class

Examples
w <- 50
data <- mp_gait_data
mp <- tsmp(data, window_size = w, exclusion_zone = 1/4, verbose = 0)
mp <- find_chains(mp)
# Remove the "Chain" class information
mp <- remove_class(mp, "Chain")

salient_mds
Convert salient sequences into MDS space

Description
Convert salient sequences into MDS space

Usage
salient_mds(.mp, data, bit_idx = 1)

Arguments
- .mp: a Matrix Profile object.
- data: the data used to build the Matrix Profile, if not embedded.
- bit_idx: an int. The index of n_bits used for MDL discretization if more than one was used. (Default is 1).
Value

Returns X,Y values for plotting

References


Website: https://sites.google.com/site/salientsubs/

Examples

# toy example
data <- mp_toy_data$data[, 1]mp <- tsmp(data, window_size = 30, verbose = 0)mps <- salient_subsequences(mp, verbose = 0/mds_data <- salient_mds(mps)plot(mds_data, main = "Multi dimensional scale")

salient_score

Computes the F-Score of salient algorithm.

Description

This score function is useful for testing several values of n_bits for MDL discretization and checking against a known set of indexes. This increase the probability of better results on relevant subsequence extraction.

Usage

salient_score(.mp, gtruth, verbose = getOption("tsmp.verbose", 2))

Arguments

.mp a Matrix Profile object.
gtruth a vector of integers with the indexes of relevant subsequences.
verbose an int. (Default is 2).

Value

Returns a list with f_score, precision, recall and bits used in the algorithm.
References


Website: https://sites.google.com/site/salientsubs/

Examples

```r
# toy example
data <- mp_toy_data$data[, 1]
mp <- tsmp(data, window_size = 30, verbose = 0)
mps <- salient_subsequences(mp, n_bits = c(4, 6, 8), verbose = 0)
label_idx <- seq(2, 500, by = 110) # fake data
salient_score(mps, label_idx, verbose = 0)
```

Description

Framework for retrieve salient subsequences from a dataset

In order to allow a meaningful visualization in Multi-Dimensional Space (MDS), this function retrieves the most relevant subsequences using Minimal Description Length (MDL) framework.

Usage

```r
salient_subsequences(
  .mp,
  data,
  n_bits = 8,
  n_cand = 10,
  exclusion_zone = NULL,
  verbose = getOption("tsmp.verbose", 2)
)
```

Arguments

- `.mp` : a TSMP object of class MatrixProfile.
- `data` : the data used to build the Matrix Profile, if not embedded.
- `n_bits` : an int or vector of int. Number of bits for MDL discretization. (Default is 8).
- `n_cand` : an int. number of candidate when picking the subsequence in each iteration. (Default is 10).
- `exclusion_zone` : if a number will be used instead of embedded value. (Default is NULL).
- `verbose` : an int. See details. (Default is 2).
Details

verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.

Value

Returns the input .mp object with a new name salient. It contains: indexes, a vector with the starting position of each subsequence, idx_bit_size, a vector with the associated bitsize for each iteration and bits the value used as input on n_bits.

References


Website: https://sites.google.com/site/salientsubs/

Examples

```r
# toy example
data <- mp_toy_data$data[, 1]
mp <- tsmp(data, window_size = 30, verbose = 0)
mps <- salient_subsequences(mp, data, verbose = 0)

# full example
data <- mp_meat_data$sub$data
w <- mp_meat_data$sub$sub_len
mp <- tsmp(data, window_size = w, verbose = 2, n_workers = 6)
mps <- salient_subsequences(mp, data, n_bits = c(4, 6, 8), verbose = 2)
```

**Description**

Computes the best so far Matrix Profile and Profile Index for Univariate Time Series. DISCLAIMER: This algorithm still in development by its authors. Join similarity, RMP and LMP not implemented yet.
Usage

scrimp(
    ..., 
    window_size, 
    exclusion_zone = getOption("tsmp.exclusion_zone", 1/2), 
    verbose = getOption("tsmp.verbose", 2), 
    s_size = Inf, 
    pre_scrimp = 1/4, 
    pre_only = FALSE
)

Arguments

... a matrix or a vector.
window_size an int. Size of the sliding window.
exclusion_zone a numeric. Size of the exclusion zone, based on window size (default is 1/2). See details.
verbose an int. See details. (Default is 2).
s_size a numeric. for anytime algorithm, represents the size (in observations) the random calculation will occur (default is Inf).
pre_scrimp a numeric. Set the pre-scrimp step based on window_size, if 0, disables pre-scrimp. (default is 1/4).
pre_only a logical. Returns only the pre script data. (Default is FALSE).

Details

The Matrix Profile, has the potential to revolutionize time series data mining because of its generality, versatility, simplicity and scalability. In particular it has implications for time series motif discovery, time series joins, shapelet discovery (classification), density estimation, semantic segmentation, visualization, rule discovery, clustering etc. The anytime SCRIMP computes the Matrix Profile and Profile Index in such manner that it can be stopped before its complete calculation and return the best so far results allowing ultra-fast approximate solutions. verbose changes how much information is printed by this function: 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound. exclusion_zone is used to avoid trivial matches.

Value

Returns a MatrixProfile object, a list with the matrix profile mp, profile index pi left and right matrix profile lmp, rmp and profile index lpi, rpi, window size w and exclusion zone ez.

References

Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other matrix profile computations: mstomp_par(), stamp_par(), stomp_par(), tsmp(), valmod()
Examples

```r
mp <- scrimp(mp_toy$data$[1:200, 1], window_size = 30, verbose = 0)

ref_data <- mp_toy$data$[, 1]
query_data <- mp_toy$data$[, 2]
# self similarity
mp <- scrimp(ref_data, window_size = 30, s_size = round(nrow(ref_data) * 0.1))
# join similarity
mp <- scrimp(ref_data, query_data, window_size = 30, s_size = round(nrow(query_data) * 0.1))
```

---

**sdts_predict**  
Framework for Scalable Dictionary learning for Time Series (SDTS)  
prediction function

### Description

This function trains a model that uses a dictionary to predict state changes. Differently from `fluss()`, it doesn’t look for semantic changes (that may be several), but for binary states like "on" or "off". Think for example that a human annotator is pressing a switch any time he thinks that the recorded data is relevant, and releases the switch when he thinks the data is noise. This algorithm will learn the switching points (even better) and try to predict using new data.

### Usage

```r
sdts_predict(model, data, window_size)
```

### Arguments

- **model**: a model created by SDTS training function `sdts_train()`.
- **data**: a vector of numeric. Time series.
- **window_size**: an int. The average sliding window size.

### Value

Returns a vector of logical with predicted annotations.

### References


Website: [https://sites.google.com/view/weaklylabeled](https://sites.google.com/view/weaklylabeled)

### See Also

Other Scalable Dictionaries: `sdts_score()`, `sdts_train()`
Examples

# This is a fast toy example and results are useless. For a complete result, run the code inside
# 'Not run' section below.
w <- c(110, 220)
subs <- 11000:20000
tr_data <- mp_test_data$train$data[subs]
tr_label <- mp_test_data$train$label[subs]
te_data <- mp_test_data$test$data[subs]
te_label <- mp_test_data$test$label[subs]
model <- sdts_train(tr_data, tr_label, w, verbose = 0)
predict <- sdts_predict(model, te_data, round(mean(w)))
sdts_score(predict, te_label, 1)

windows <- c(110, 220, 330)
model <- sdts_train(mp_test_data$train$data, mp_test_data$train$label, windows, verbose = 0)
predict <- sdts_predict(model, mp_test_data$test$data, round(mean(windows)))
sdts_score(predict, mp_test_data$test$label, 1)

sdts_score  Computes the F-Score of a SDTS prediction

Description

Computes the F-Score of a SDTS prediction.

Usage

sdts_score(pred, gtruth, beta = 1)

Arguments

pred a vector of logical. Predicted annotation from sdts_predict()
gtruth a vector of logical. Ground truth annotation.
beta a numeric. See details. (default is 1).

Details

beta is used to balance F-score towards recall (>1) or precision (<1).

Value

Returns a list with f_score, precision and recall.
References


Website: https://sites.google.com/view/weaklylabeled

See Also

Other Scalable Dictionaries: sdts_predict(), sdts_train()

Examples

```r
# This is a fast toy example and results are useless. For a complete result, run the code inside
# 'Not run' section below.
w <- c(110, 220)
subs <- 11000:20000
tr_data <- mp_test_data$train$data[subs]
tr_label <- mp_test_data$train$label[subs]
te_data <- mp_test_data$test$data[subs]
te_label <- mp_test_data$test$label[subs]
model <- sdts_train(tr_data, tr_label, w, verbose = 0)
predict <- sdts_predict(model, te_data, round(mean(w)))
sdts_score(predict, te_label, 1)

windows <- c(110, 220, 330)
model <- sdts_train(mp_test_data$train$data, mp_test_data$train$label, windows)
predict <- sdts_predict(model, mp_test_data$test$data, round(mean(windows)))
sdts_score(predict, mp_test_data$test$label, 1)
```

sdts_train

Framework for Scalable Dictionary learning for Time Series (SDTS)
training function

Description

This function trains a model that uses a dictionary to predict state changes. Differently from fluss(), it doesn’t look for semantic changes (that may be several), but for binary states like “on” or “off”. Think for example that a human annotator is pressing a switch any time he thinks that the recorded data is relevant, and releases the switch when he thinks the data is noise. This algorithm will learn the switching points (even better) and try to predict using new data.

Usage

```r
sdts_train(
  data,
  label,
  window_size,
```
beta = 1,
pat_max = Inf,
parallel = FALSE,
verbose = getOption("tsmp.verbose", 2)
)

Arguments

- **data**: a vector of numeric. Time series.
- **label**: a vector of logical. Annotations.
- **window_size**: an int or a vector of int. Sliding window sizes.
- **beta**: a numeric. See details. (default is 1).
- **pat_max**: an int. Max number of shape features captured. (default is Inf).
- **parallel**: a logical. Use parallel computation inside (default is FALSE).
- **verbose**: an int. See details. (Default is 2).

Details

beta is used to balance F-score towards recall (>1) or precision (<1). verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.

Value

Returns a list with the learned dictionary score (estimated score), score_hist (history of scores), pattern (shape features), thold (threshold values).

References


Website: https://sites.google.com/view/weaklylabeled

See Also

Other Scalable Dictionaries: sdts_predict(), sdts_score()

Examples

# This is a fast toy example and results are useless. For a complete result, run the code inside
# 'Not run' section below.
w <- c(110, 220)
subs <- 11000:20000
tr_data <- mp_test_data$train$data[subs]
tr_label <- mp_test_data$train$label[subs]
te_data <- mp_test_data$test$data[subs]
te_label <- mp_test_data$test$label[subs]
model <- sdts_train(tr_data, tr_label, w, verbose = 0)
simple_fast

Description

Compute the join similarity for Sound data

Usage

simple_fast(  
...,
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  verbose = getOption("tsmp.verbose", 2)
)

set_data

Set/changes the data included in TSMP object.

Description

This may be useful if you want to include the data lately or remove the included data (set as NULL).

Usage

set_data(.mp, data)

Arguments

.data                a TSMP object.
.data                a matrix (for one series) or a list of matrices (for two series).

Value

Returns silently the original TSMP object with changed data.

Examples

mp <- tsmp(mp_toy$data[1:200, 1], window_size = 30, verbose = 0)
mp <- set_data(mp, NULL)
Arguments

... a matrix of numeric, where each column is a time series. Accepts list and data.frame too. If a second time series is supplied it will be a join matrix profile.

window_size an int with the size of the sliding window.

exclusion_zone a numeric. Size of the exclusion zone, based on window size (default is 1/2).

verbose an int. See details. (Default is 2).

Details

verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.

Value

Returns a SimpleMatrixProfile object, a list with the matrix profile mp, profile index pi, number of dimensions n_dim, window size w and exclusion zone ez.

References


Website: https://sites.google.com/view/simple-fast
Website: https://sites.google.com/site/ismir2016simple/home

Examples

w <- 30
data <- mp_toy_data$data # 3 dimensions matrix
result <- simple_fast(data, window_size = w, verbose = 0)
Usage

```r
stamp_par(
  ..., 
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  verbose = getOption("tsmp.verbose", 2),
  s_size = Inf,
  n_workers = 2,
  weight = NULL
)
```

```r
stamp(
  ..., 
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  verbose = getOption("tsmp.verbose", 2),
  s_size = Inf,
  weight = NULL
)
```

Arguments

- `...`: a matrix or a vector. If a second time series is supplied it will be a join matrix profile.
- `window_size`: an int. Size of the sliding window.
- `exclusion_zone`: a numeric. Size of the exclusion zone, based on window size (default is 1/2). See details.
- `verbose`: an int. See details. (Default is 2).
- `s_size`: a numeric. for anytime algorithm, represents the size (in observations) the random calculation will occur (default is Inf).
- `n_workers`: an int. Number of workers for parallel. (Default is 2).
- `weight`: a vector of numeric or NULL with the same length of the window size. This is a MASS extension to weight the query.

Details

The Matrix Profile, has the potential to revolutionize time series data mining because of its generality, versatility, simplicity and scalability. In particular it has implications for time series motif discovery, time series joins, shapelet discovery (classification), density estimation, semantic segmentation, visualization, rule discovery, clustering etc. The anytime STAMP computes the Matrix Profile and Profile Index in such manner that it can be stopped before its complete calculation and return the best so far results allowing ultra-fast approximate solutions. `verbose` changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound. `exclusion_zone` is used to avoid trivial matches; if a query data is provided (join similarity), this parameter is ignored.
Value

Returns a MatrixProfile object, a list with the matrix profile mp, profile index pi left and right matrix profile lmp, rmp and profile index lpi, rpi, window size w and exclusion zone ez.

Functions

- stamp_par: Parallel version.
- stamp: Single thread version.

References


Website: [http://www.cs.ucr.edu/~eamonn/MatrixProfile.html](http://www.cs.ucr.edu/~eamonn/MatrixProfile.html)

See Also

Other matrix profile computations: `mstomp_par()`, `scrimp()`, `stomp_par()`, `tsmp()`, `valmod()`

Examples

```r
mp <- stamp(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)

# using threads
mp <- stamp_par(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)

ref_data <- mp_toy_data$data[, 1]
query_data <- mp_toy_data$data[, 2]
# self similarity
mp <- stamp(ref_data, window_size = 30, s_size = round(nrow(ref_data) * 0.1))
# join similarity
mp <- stamp(ref_data, query_data, window_size = 30, s_size = round(nrow(query_data) * 0.1))
```

stompi_update

Real-time STOMP algorithm

Description

Real-time STOMP algorithm
Usage

stompi_update(.mp, new_data, history_size = FALSE)

Arguments

- **.mp**: a TSMP object of class MatrixProfile.
- **new_data**: new data to append to original data.
- **history_size**: an int or FALSE. (Default is FALSE). Keep only this amount of data in the object. The value is for the data, not the matrix profile. Notice that the lmp and lpi will be inconsistent when repeatedly updating limiting the history size and thus will affect the mp and pi.

Value

Returns the input .mp updated with the new information.

Examples

```r
mp <- tsmp(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)
mpi <- stompi_update(mp, mp_toy_data$data[201:300, 1])
mp <- tsmp(mp_toy_data$data[1:300, 1], window_size = 30, verbose = 0)
all.equal(mp, mpi, check.attributes = FALSE)
```

---

stomp_par  

Univariate STOMP algorithm

Description

Computes the Matrix Profile and Profile Index for Univariate Time Series.

Usage

```r
stomp_par(
  ..., 
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  verbose = getOption("tsmp.verbose", 2),
  n_workers = 2
)
```

```r
stomp(
  ..., 
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  verbose = getOption("tsmp.verbose", 2)
)
```
**Arguments**

- ... a matrix or a vector. If a second time series is supplied it will be a join matrix profile.
- window_size: an int. Size of the sliding window.
- exclusion_zone: a numeric. Size of the exclusion zone, based on window size (default is 1/2). See details.
- verbose: an int. See details. (Default is 2).
- n_workers: an int. Number of workers for parallel. (Default is 2).

**Details**

The Matrix Profile, has the potential to revolutionize time series data mining because of its generality, versatility, simplicity and scalability. In particular it has implications for time series motif discovery, time series joins, shapelet discovery (classification), density estimation, semantic segmentation, visualization, rule discovery, clustering etc. verbose changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound. exclusion_zone is used to avoid trivial matches; if a query data is provided (join similarity), this parameter is ignored.

**Value**

Returns a MatrixProfile object, a list with the matrix profile mp, profile index pi left and right matrix profile lmp, rmp and profile index lpi, rpi, window size w and exclusion zone ez.

**Functions**

- stomp_par: Parallel version.
- stomp: Single thread version.

**References**

- Website: [http://www.cs.ucr.edu/~eamonn/MatrixProfile.html](http://www.cs.ucr.edu/~eamonn/MatrixProfile.html)

**See Also**

Other matrix profile computations: mstomp_par(), scrimp(), stamp_par(), tsmp(), valmod()

**Examples**

```r
mp <- stomp(mp_toy_data$data[1:200, 1], window_size = 30, verbose = 0)
#' # using threads
mp <- stomp_par(mp_toy_data$data[1:400, 1], window_size = 30, verbose = 0)
ref_data <- mp_toy_data$data[, 1]
```
```r
tquery_data <- mp_toy_data$data[, 2]
# self similarity
mp <- stomp(ref_data, window_size = 30)
# join similarity
mp2 <- stomp(ref_data, query_data, window_size = 30)
```

---

**tsmp**

*Computes the Matrix Profile and Profile Index*

**Description**

This is a wrap function that makes easy to use all available algorithms to compute the Matrix Profile and Profile Index for multiple purposes.

**Usage**

```r
tsmp(
  ...,  
  window_size,
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2),
  mode = c("stomp", "stamp", "simple", "mstomp", "scrimp", "valmod", "pmp"),
  verbose = getOption("tsmp.verbose", 2),
  n_workers = 1,
  s_size = Inf,
  must_dim = NULL,
  exc_dim = NULL,
  heap_size = 50,
  paa = 1,
  .keep_data = TRUE
)
```

**Arguments**

- `...` a matrix or a vector. If a second time series is supplied it will be a join matrix profile (except for `mstomp()`).
- `window_size` an int with the size of the sliding window. Use a vector for Valmod.
- `exclusion_zone` a numeric. Size of the exclusion zone, based on window size (default is 1/2). See details.
- `mode` the algorithm that will be used to compute the matrix profile. (Default is `stomp`). See details.
- `verbose` an int. (Default is 2). See details.
- `n_workers` an int. Number of workers for parallel. (Default is 1).
- `s_size` a numeric. for anytime algorithm, represents the size (in observations) the random calculation will occur (default is Inf). See details.
must_dim: an int or vector of which dimensions to forcibly include (default is NULL). See details.
exc_dim: an int or vector of which dimensions to exclude (default is NULL). See details.
heap_size: an int. (Default is 50). Size of the distance profile heap buffer.
paa: an int. (Default is 1). Factor of PAA reduction (2 == half of size).
.keep_data: a logical. (Default is TRUE). Keeps the data embedded to resultant object.

Details

The Matrix Profile, has the potential to revolutionize time series data mining because of its generality, versatility, simplicity and scalability. In particular it has implications for time series motif discovery, time series joins, shapelet discovery (classification), density estimation, semantic segmentation, visualization, rule discovery, clustering etc.

The first algorithm invented was the stamp() that using mass() as an ultra-fast Algorithm for Similarity Search allowed to compute the Matrix Profile in reasonable time. One of its main feature was its Anytime property which using a randomized approach could return a "best-so-far" matrix that could give us the correct answer (using for example 1/10 of all iterations) almost every time.

The next algorithm was stomp() that currently is the most used. Researchers noticed that the dot products do not need to be recalculated from scratch for each subsequence. Instead, we can reuse the values calculated for the first subsequence to make a faster calculation in the next iterations. The idea is to make use of the intersections between the required products in consecutive iterations. This approach reduced the time to compute the Matrix Profile to about 3% compared to stamp(), but on the other hand, we lost the Anytime property.

Currently there is a new algorithm that I’ll not explain further here. It is called scrimp(), and is as fast as stomp(), and have the Anytime property. This algorithm is implemented in this package, but still waiting for an article publication.

Further, there is the mstomp() that computes a multidimensional Matrix Profile that allows to meaningful MOTIF discovery in Multivariate Time Series. And simple_fast() that also handles Multivariate Time Series, but focused in Music Analysis and Exploration.

The valmod() uses a new pruning algorithm allowing a similarity search with a range of sliding window sizes.

The pmp() is a new concept that creates several profiles from a range of windows.

Some parameters are global across the algorithms:

... One or two time series (except for mstomp()). The second time series can be smaller than the first.
window_size: The sliding window.
exclusion_zone: Is used to avoid trivial matches; if a query data is provided (join similarity), this parameter is ignored.
verbose: Changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound.
n_workers: number of threads for parallel computing (except simple_fast, scrimp and valmod).
If the value is 2 or more, the '_par' version of the algorithm will be used.
s_size is used only in Anytime algorithms: stamp() and scrimp(). must_dim and exc_dim are used only in mstomp(). heap_size is used only for valmod() mode can be any of the following: stomp, stamp, simple, mstomp, scrimp, valmod, pmp.
Value

Returns the matrix profile mp and profile index pi. It also returns the left and right matrix profile lmp, rmp and profile index lpi, rpi that may be used to detect Time Series Chains. \texttt{mstomp()} returns a multidimensional Matrix Profile.

References

- Yeh CM, Kavantzas N, Keogh E. Matrix Profile VI: Meaningful Multidimensional Motif Discovery.

Website: \url{https://sites.google.com/view/simple-fast}
Website: \url{https://sites.google.com/site/ismir2016simple/home}
Website: \url{http://www.cs.ucr.edu/~eamonn/MatrixProfile.html}

See Also

Other matrix profile computations: \texttt{mstomp_par()}, \texttt{scrimp()}, \texttt{stamp_par()}, \texttt{stomp_par()}, \texttt{valmod()}

Examples

```r
# default with \texttt{[stomp()]} 
mp <- tsmp(mp_toy_data$data[,1:200, 1], window_size = 30, verbose = 0)

# Anytime STAMP 
mp <- tsmp(mp_toy_data$data[,1:200, 1], window_size = 30, mode = "stamp", s_size = 50, verbose = 0)

# \texttt{[mstomp()]} 
mp <- tsmp(mp_toy_data$data[,1:200, ], window_size = 30, mode = "mstomp", verbose = 0)

# \texttt{[simple_fast()]} 
mp <- tsmp(mp_toy_data$data[,1:200, ], window_size = 30, mode = "simple", verbose = 0)

# parallel with \texttt{[stomp_par()]} 
mp <- tsmp(mp_test_data$train$data[,1:1000, 1], window_size = 30, n_workers = 2, verbose = 0)
```
Description

Computes the Matrix Profile and Profile Index for a range of query window sizes

Usage

```r
valmod(
  ..., 
  window_min, 
  window_max, 
  heap_size = 50, 
  exclusion_zone = getOption("tsmp.exclusion_zone", 1/2), 
  lb = TRUE, 
  verbose = getOption("tsmp.verbose", 2)
)
```

Arguments

- `...`: a matrix or a vector. If a second time series is supplied it will be a join matrix profile.
- `window_min`: an int. Minimum size of the sliding window.
- `window_max`: an int. Maximum size of the sliding window.
- `heap_size`: an int. (Default is 50). Size of the distance profile heap buffer.
- `exclusion_zone`: a numeric. Size of the exclusion zone, based on window size (default is 1/2). See details.
- `lb`: a logical. (Default is TRUE). If FALSE all window sizes will be calculated using STOMP instead of pruning. This is just for academic purposes.
- `verbose`: an int. See details. (Default is 2).

Details

This algorithm uses an exact algorithm based on a novel lower bounding technique, which is specifically designed for the motif discovery problem. `verbose` changes how much information is printed by this function; 0 means nothing, 1 means text, 2 adds the progress bar, 3 adds the finish sound. `exclusion_zone` is used to avoid trivial matches; if a query data is provided (join similarity), this parameter is ignored.

Paper that implements `skimp()` suggests that `window_max / window_min > than 1.24 begins to weakening pruning in `valmod()`.
Value

Returns a Valmod object, a list with the matrix profile `mp`, profile index `pi` left and right matrix profile `lmp`, `rmp` and profile index `lpi`, `rpi`, best window size `w` for each index and exclusion zone `ez`. Additionally: `evolution_motif` the best motif distance per window size, and non-length normalized versions of `mp`, `pi` and `w`: `mpnn`, `pinn` and `wnn`.

References

  
  Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also

Other matrix profile computations: `mstomp_par()`, `scrimp()`, `stamp_par()`, `stomp_par()`, `tsmp()`

Examples

```r
mp <- valmod(mp_toy_data$data[1:200, 1], window_min = 30, window_max = 40, verbose = 0)

ref_data <- mp_toy_data$data[, 1]
query_data <- mp_toy_data$data[, 2]
# self similarity
mp <- valmod(ref_data, window_min = 30, window_max = 40)
# join similarity
mp <- valmod(ref_data, query_data, window_min = 30, window_max = 40)
```

### visualize

**Plots an object generated from one of the algorithms. In some cases multiple plots will be generated**

### Description

Plots an object generated from one of the algorithms. In some cases multiple plots will be generated

### Usage

```r
visualize(profile)
```

### Arguments

- `profile` a MatrixProfile or PMP object.
write

References
Website: http://www.cs.ucr.edu/~eamonn/MatrixProfile.html

See Also
Other Main API: analyze(), compute(), discords(), motifs()

Examples
result <- compute(mp_toy_data$data[, 1], 80)
visualize(result)

write
Write a TSMP object to JSON file.

Description
Write a TSMP object to JSON file.

Usage
write(x, ...)

### S3 method for class 'MatrixProfile'
write(x, file, ...)

### S3 method for class 'PMP'
write(x, file, ...)

Arguments

x a MatrixProfile or PMP object. If not, the base::write() function will be called.
...
other arguments to be passed forward.
file a character string with the output filename.

Examples
result <- compute(mp_toy_data$data[, 1], 80)
write(result, file = file.path(tempdir(), "output.json"))
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