Package: phutil (via r-universe)

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Title Persistence Homology Utilities

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Description A low-level package for hosting persistence data. It is part of the 'TDAverse' suite of packages, which is designed to provide a collection of packages for enabling machine learning and data science tasks using persistent homology. Implements a class for hosting persistence data, a number of coercers from and to already existing and used data structures from other packages and functions to compute distances between persistence diagrams. A formal definition and study of bottleneck and Wasserstein distances can be found in Bubenik, Scott and Stanley (2023) <doi:10.1007/s41468-022-00103-8>. Their implementation in 'phutil' relies on the 'C++' Hera library developed by Kerber, Morozov and Nigmetov (2017) <doi:10.1145/3064175>.

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`arch_spirals` *A sample of persistence diagrams from the arch spiral*

Description

A collection of 24 samples of size 120 on the arch spiral from which a persistence diagram is computed using the `TDA::ripsDiag()` function with `maxdimension = 2` and `maxscale = 6`. Each diagram has been generated using the `tdaunif::sample_arch_spiral()` function with the following parameters: `n = 120`, `arms = 2`` and sd = 0.05‘. The seed was fixed to 28415.

Usage

```
arch_spirals
```

Format

A list of length 24, where each element is an object of class 'persistence'.

`distances` *Distances between two persistence diagrams*

Description

This collection of functions computes the distance between two persistence diagrams of the same homology dimension. The diagrams must be represented `persistence`-class objects or as 2-column matrices. Matrices are assumed to have the same homological degree, and the first and second columns to contain the birth values and the death values, respectively.

Usage

```
bottleneck_distance(
  x,
  y,
  tol = sqrt(.Machine$double.eps),
  validate = TRUE,
  dimension = 0L
)

wasserstein_distance(
  x,
  y,
  tol = sqrt(.Machine$double.eps),
  p = 1,
  validate = TRUE,
  dimension = 0L
)

kantorovich_distance(
  x,
  y,
  tol = sqrt(.Machine$double.eps),
  p = 1,
  validate = TRUE,
  dimension = 0L
)
```

Arguments

`x`	Either a matrix of shape $n \times 2$ or an object of class `persistence` specifying the first persistence diagram.
`y`	Either a matrix of shape $m \times 2$ or an object of class `persistence` specifying the second persistence diagram.

`tol` A numeric value specifying the relative error. Defaults to `sqrt(.Machine$double.eps)`. For the Bottleneck distance, it can be set to `0.0` in which case the exact Bottleneck distance is computed, while an approximate Bottleneck distance is computed if `tol > 0.0`. For the Wasserstein distance, it must be strictly positive.

`validate` A boolean value specifying whether to validate the input persistence diagrams. Defaults to `TRUE`. If `FALSE`, the function will not check if the input persistence diagrams are valid. This can be useful for performance reasons, but it is recommended to keep it `TRUE` for safety.

`dimension` An integer value specifying the homology dimension for which to compute the distance. Defaults to `0L`. This is only used if `x` and `y` are objects of class `persistence`.

`p` A numeric value specifying the power for the Wasserstein distance. Defaults to `1.0`.

Details

A matching $\varphi : D_1 \to D_2$ between persistence diagrams is a bijection of multisets, where both diagrams are assumed to have all points on the diagonal with infinite multiplicity. The *p-Wasserstein distance* between D_1 and D_2 is defined as the infimum over all matchings of the expression

$$W_p(D_1, D_2) = \inf_{\varphi : D_1 \to D_2} \left(\sum_{x \in D_1} \|x - \varphi(x)\|^p \right)^{\frac{1}{p}}$$

that can be thought of as the Minkowski distance between the diagrams viewed as vectors on the shared coordinates defined by the matching φ. The norm $\|\cdot\|$ can be arbitrary; as implemented here, it is the infinity norm $\|(x_1, x_2)\|_\infty = \max(x_1, x_2)$. In the limit $p \to \infty$, the Wasserstein distance becomes the *bottleneck distance*:

$$B(D_1, D_2) = \inf_{\varphi : D_1 \to D_2} \sup_{x \in D_1} \|x - \varphi(x)\|.$$

The Wasserstein metric is also called the Kantorovich metric in recognition of the originator of the metric.

Value

A numeric value storing either the Bottleneck or the Wasserstein distance between the two persistence diagrams.

See Also

the Hera C++ library

Examples

```
bottleneck_distance(
  persistence_sample[[1]]$pairs[[1]],
  persistence_sample[[2]]$pairs[[1]]
```

```
)

bottleneck_distance(
  persistence_sample[[1]],
  persistence_sample[[2]]
)

wasserstein_distance(
  persistence_sample[[1]]$pairs[[1]],
  persistence_sample[[2]]$pairs[[1]]
)

wasserstein_distance(
  persistence_sample[[1]],
  persistence_sample[[2]]
)
```

`noisy_circle` *Toy Data: Noisy circle*

Description

A simulated data set consisting of 100 points sampled from a circle with additive Gaussian noise using a standard deviation of 0.05.

Usage

```
noisy_circle_points

noisy_circle_ripserr

noisy_circle_tda_rips
```

Format

`noisy_circle_points`**:**
A matrix with 100 rows and 2 columns listing the coordinates of the points.

`noisy_circle_ripserr`**:**
An object of class 'PHom' as returned by the `ripserr::vietoris_rips()` function, which is a data frame with 3 variables:

- `dimension`: the dimension/degree of the feature,
- `birth`: the birth value of the feature,
- `death`: the death value of the feature.

`noisy_circle_tda_rips`**:**
A list of length 1 containing an object of class 'diagram' as returned by the `TDA::ripsDiag()$diagram` function, which is a matrix with 3 columns:

- `dimension`: the dimension/degree of the feature,
- `birth`: the birth value of the feature,
- `death`: the death value of the feature.

An object of class `PHom` (inherits from `data.frame`) with 101 rows and 3 columns.

An object of class `list` of length 1.

Details

The point cloud stored in `noisy_circle_points` has been generated using the **tdaunif** package using the `tdaunif::sample_circle()` function. Specifically, the following parameters were used: `n = 100`, `sd = 0.05` and a seed of 1234.

The persistence diagram stored in `noisy_circle_ripserr` has been computed using the **ripserr** package with the `ripserr::vietoris_rips()` function. Specifically, the following parameters were used: `max_dim = 1L`.

The persistence diagram stored in `noisy_circle_tda_rips` has been computed using the **TDA** package with the `TDA::ripsDiag()` function. Specifically, the following parameters were used: `maxdimension = 1L` and `maxscale = 1.6322`.

Source

https://tdaverse.github.io/tdaunif/reference/circles.html, https://tdaverse.github.io/ripserr/reference/vietoris_rips.html, https://www.rdocumentation.org/packages/TDA/versions/1.9.1/topics/ripsDiag

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pairwise-distances *Pairwise distances within a set of persistence diagrams*

Description

This collection of functions computes the pairwise distance matrix between all pairs in a set of persistence diagrams of the same homology dimension. The diagrams must be represented as 2-column matrices. The first column of the matrix contains the birth times and the second column contains the death times of the points.

Usage

```
bottleneck_pairwise_distances(
  x,
  tol = sqrt(.Machine$double.eps),
  validate = TRUE,
  dimension = 0L,
  ncores = 1L
)

wasserstein_pairwise_distances(
```

```
  x,
  tol = sqrt(.Machine$double.eps),
  p = 1,
  validate = TRUE,
  dimension = 0L,
  ncores = 1L
)

kantorovich_pairwise_distances(
  x,
  tol = sqrt(.Machine$double.eps),
  p = 1,
  validate = TRUE,
  dimension = 0L,
  ncores = 1L
)
```

Arguments

x	A list of either 2-column matrices or objects of class persistence specifying the set of persistence diagrams.
tol	A numeric value specifying the relative error. Defaults to `sqrt(.Machine$double.eps)`. For the Bottleneck distance, it can be set to `0.0` in which case the exact Bottleneck distance is computed, while an approximate Bottleneck distance is computed if `tol > 0.0`. For the Wasserstein distance, it must be strictly positive.
validate	A boolean value specifying whether to validate the input persistence diagrams. Defaults to `TRUE`. If `FALSE`, the function will not check if the input persistence diagrams are valid. This can be useful for performance reasons, but it is recommended to keep it `TRUE` for safety.
dimension	An integer value specifying the homology dimension for which to compute the distance. Defaults to `0L`. This is only used if `x` and `y` are objects of class `persistence`.
ncores	An integer value specifying the number of cores to use for parallel computation. Defaults to `1L`.
p	A numeric value specifying the power for the Wasserstein distance. Defaults to `1.0`.

Value

An object of class 'dist' containing the pairwise distance matrix between the persistence diagrams.

Examples

```
spl <- persistence_sample[1:10]

# Extract the list of 2-column matrices for dimension 0 in the sample
x <- lapply(spl[1:10], function(x) x$pairs[[1]])
```

```
# Compute the pairwise Bottleneck distances
Db <- bottleneck_pairwise_distances(spl)
Db <- bottleneck_pairwise_distances(x)

# Compute the pairwise Wasserstein distances
Dw <- wasserstein_pairwise_distances(spl)
Dw <- wasserstein_pairwise_distances(x)
```

`persistence` *An* `S3` *class for storing persistence data*

Description

A collection of functions to coerce persistence data into objects of class `persistence` (See **Value** section for more details on this class). It is currently possible to coerce persistence data from the following sources:

- a matrix with at least 3 columns (dimension/degree, start/birth, end/death) as returned by `ripserr::vietoris_rips()` in the form of the 'PHom' class,
- a list as returned by any `*Diag()` function in the **TDA** package.

Usage

```
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'list'
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'persistence'
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'data.frame'
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'matrix'
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'diagram'
as_persistence(x, warn = TRUE, ...)

## S3 method for class 'PHom'
as_persistence(x, ...)

## S3 method for class 'hclust'
as_persistence(x, warn = TRUE, birth = NULL, ...)

## S3 method for class 'persistence'
```

```
print(x, ...)

## S3 method for class 'persistence'
format(x, ...)

get_pairs(x, dimension, ...)

## S3 method for class 'persistence'
as.matrix(x, ...)

## S3 method for class 'persistence'
as.data.frame(x, row.names = NULL, optional = TRUE, ...)

as_diagram(x, ...)

## S3 method for class 'persistence'
as_diagram(x, list = TRUE, ...)

## S3 method for class 'PHom'
as_diagram(x, list = TRUE, ...)
```

Arguments

x	An R object containing the persistence data to be coerced into an object of class persistence. Currently supported forms are: • a $\geq$ 2-column matrix (or object coercible to one) with dimension/degree, start/birth and end/death columns; if it has only 2 columns, we assume that the dimension column is missing and we set it to 0 (i.e. we assume that the data is in the form birth and death), • a base::data.frame (or object coercible to one) with at least 3 columns containing the persistence data; if it has only 2 columns, we assume that the dimension column is missing and we set it to 0, • a list of 2-column matrices (or objects coercible to one) with the first column being the birth and the second column being the death of homological features; indexed by dimension, i.e. the i-*th* element of the list corresponds to the $(i-1)$-*th* homology dimension, • an object of class 'PHom' as returned by ripserr::vietoris_rips(), • (a list as returned by a *Diag() function in **TDA** (e.g. TDA::ripsDiag()) whose first element is) an object of class 'diagram', • an object of class stats::hclust in which case we use the entry height as the death of homological features and 0 as the birth of all features.
warn	A boolean specifying whether to issue a warning if the input persistence data contained unordered pairs. Defaults to TRUE.
...	Parameters passed to methods.
birth	A numeric value specifying the height at which to declare all leaves were born. Defaults to 0 if all heights are non-negative and -Inf otherwise.

dimension	A non-negative integer specifying the homology dimension for which to recover a matrix of persistence pairs.
row.names	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional	logical. If TRUE, setting row names and converting column names (to syntactic names: see make.names) is optional. Note that all of R's **base** package as.data.frame() methods use optional only for column names treatment, basically with the meaning of data.frame(*, check.names = !optional). See also the make.names argument of the matrix method.
list	Logical; whether to return the diagram object as the sole element of a list. Defaults to TRUE for consistency with the TDA package.

Details

Caution. When providing an *unnamed* input matrix, the matrix coercer assumes that it has at least 3 columns, with the first column being the dimension/degree, the second column being the start/birth and the third column being the end/death.

Value

An object of class persistence which is a list of 2 elements:

- pairs: A list of 2-column matrices containing birth-death pairs. The i-*th* element of the list corresponds to the $(i-1)$-*th* homology dimension. If there is no pairs for a given dimension but there are pairs in higher dimensions, the corresponding element(s) is/are filled with a 0×2 numeric matrix.
- metadata: A list of length 6 containing information about how the data was computed:
  - orderered_pairs: A boolean indicating whether the pairs in the pairs list are ordered (i.e. the first column is strictly less than the second column).
  - data: The name of the object containing the original data on which the persistence data was computed.
  - engine: The name of the package and the function of this package that computed the persistence data in the form "package_name::package_function".
  - filtration: The filtration used in the computation in a human-readable format (i.e. full names, capitals where need, etc.).
  - parameters: A list of parameters used in the computation.
  - call: The exact call that generated the persistence data.

Examples

```
as_persistence(noisy_circle_ripserr)

x <- as_persistence(noisy_circle_tda_rips)
x

as_persistence(x)

get_pairs(x, dimension = 1)
```

```
as.data.frame(x)

# back and forth between `diagram` and `persistence`
x <- tdaunif::sample_projective_plane(n = 12)
( d <- TDA::alphaComplexDiag(x, maxdimension = 2) )
( p <- as_persistence(d) )
as_diagram(p)
as_diagram(p, list = FALSE)

# distances between cities
euroclust <- hclust(eurodist, method = "ward.D")
as_persistence(euroclust)

# `hclust()` can accommodate negative distances
d <- as.dist(rbind(c(0, 3, -4), c(3, 0, 5), c(-4, 5, 0)))
hc <- hclust(d, method = "single")
ph <- as_persistence(hc, birth = -10)
get_pairs(ph, 0)
```

`persistence-set` *An 'S3' class object for storing sets of persistence diagrams*

Description

An 'S3' class object for storing sets of persistence diagrams

Usage

```
as_persistence_set(x)

## S3 method for class 'persistence_set'
format(x, ...)

## S3 method for class 'persistence_set'
print(x, ...)
```

Arguments

`x`	A list of objects of class persistence.
`...`	Additional arguments passed to the function.

Value

An object of class 'persistence_set' containing the set of persistence diagrams.

Examples

```
# Create a persistence set from a list of persistence diagrams
as_persistence_set(persistence_sample[1:10])
```

persistence_sample *Toy Data: A sample of persistence diagrams*

Description

A collection of 100 samples of size 100 on the sphere from which a persistence diagram is computed using the `TDA::ripsDiag()` function with parameters `maxdimension = 1L` and `maxscale = 1.6322`. Each diagram has been generated using the `tdaunif::sample_2sphere()` function with the following parameters: `n = 100` and `sd = 0.05`. The seed was fixed to 1234.

Usage

```
persistence_sample
```

Format

A list of length 100, where each element is an object of class 'persistence'.

trefoils *A sample of persistence diagrams from the trefoil*

Description

A collection of 24 samples of size 120 on the trefoil from which a persistence diagram is computed using the `TDA::ripsDiag()` function with `maxdimension = 2` and `maxscale = 6`. Each diagram has been generated using the `tdaunif::sample_trefoil()` function with the following parameters: `n = 120` and `sd = 0.05`. The seed was fixed to 28415.

Usage

```
trefoils
```

Format

A list of length 24, where each element is an object of class 'persistence'.

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