# Package 'mappeR'

February 17, 2025

**Type** Package

**Title** Construct and Visualize TDA Mapper Graphs

**Description** Topological data analysis (TDA) is a method of data analysis that uses techniques from topology to analyze high-dimensional data. Here we implement Mapper, an algorithm from this area developed by Singh, Mémoli and Carlsson (2007) which generalizes the concept of a Reeb graph <https://en.wikipedia.org/wiki/Reeb_graph>.

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**URL** https://github.com/Uiowa-Applied-Topology/mappeR

**BugReports** https://github.com/Uiowa-Applied-Topology/mappeR/issues

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`assemble_mapper_object`

*Construct mapper graph from data*

---

## Description

Construct mapper graph from data

## Usage

```
assemble_mapper_object(binclust_data, dists, binning = TRUE)
```

## Arguments

| | |
|---|---|
| `binclust_data` | A list of bins, each containing named vectors whose names are those of data points and whose values are cluster ids |
| `dists` | A distance matrix for the data that has been binned and clustered. |
| `binning` | Whether the output dataframe should sort vertices into "bins" or not. Should be true if using clustering, leave false otherwise |

### Value

A list of two dataframes, one with node data containing bin membership, datapoints per cluster, and cluster dispersion, and one with edge data containing sources, targets, and weights representing overlap strength.

---

## check_in_interval *Get a tester function for an interval.*

---

### Description

Get a tester function for an interval.

### Usage

```
check_in_interval(endpoints)
```

### Arguments

| | |
|---|---|
| endpoints | A vector of interval endpoints, namely a left and a right. Must be in order. |

### Value

A function that eats a data point and outputs TRUE if the datapoint is in the interval and FALSE if not.

---

## compute_tightness *Compute dispersion of a single cluster*

---

### Description

Compute dispersion of a single cluster

### Usage

```
compute_tightness(dists, cluster)
```

### Arguments

| | |
|---|---|
| dists | A distance matrix for points in the cluster. |
| cluster | A list containing named vectors, whose names are data point names and whose values are cluster labels |

## Details

This method computes a measure of cluster dispersion. It finds the medoid of the input data set and returns the average distance to the medoid. Formally, we say the tightness $\tau$ of a cluster $C$ is given by

$$\tau(C) = \frac{1}{(|C| - 1)} \sum_i \text{dist}(x_i, x_j)$$

where

$$x_j = \arg \min_{x_j \in C} \sum_{x_i \in C, i \neq j} \text{dist}(x_i, x_j)$$

A smaller value indicates a tighter cluster based on this metric.

## Value

A real number in $[0, 1]$ representing a measure of dispersion of a cluster.

---

`convert_to_clusters` *"Clustering" for ballmapper just means treating each bin as its own cluster.*

---

## Description

"Clustering" for ballmapper just means treating each bin as its own cluster.

## Usage

```
convert_to_clusters(bins)
```

## Arguments

| | |
|---|---|
| `bins` | A list of bins, each containing names of data from some data frame. |

## Value

A named vector whose names are data point names and whose values are cluster labels

`create_1D_mapper_object` *Run 1D mapper*

## Description

Run mapper using a one-dimensional filter, a cover of intervals, and a clustering algorithm.

## Usage

```
create_1D_mapper_object(
  data,
  dists,
  filtered_data,
  cover,
  clusterer = hierarchical_clusterer("single")
)
```

## Arguments

| | |
|---|---|
| `data` | A data frame. |
| `dists` | A distance matrix for the data frame. |
| `filtered_data` | The result of a function applied to the data frame; there should be one filter value per observation in the original data frame. |
| `cover` | A 2D array of interval left and right endpoints; rows should be intervals and columns left and right endpoints (in that order). |
| `clusterer` | A function which accepts a list of distance matrices as input, and returns the results of clustering done on each distance matrix. |

## Value

A list of two data frames, one with node data containing bin membership, data points per cluster, and cluster dispersion, and one with edge data containing sources, targets, and weights representing overlap strength.

## Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))
projx = data$x

num_bins = 10
percent_overlap = 25

cover = create_width_balanced_cover(min(projx), max(projx), num_bins, percent_overlap)

create_1D_mapper_object(data, dist(data), projx, cover)
```

`create_balls` *Make a cover of balls*

## Description

Make a cover of balls

## Usage

```
create_balls(data, dists, eps)
```

## Arguments

| | |
|---|---|
| `data` | A data frame. |
| `dists` | A distance matrix for the data frame. |
| `eps` | A positive real number. |

## Value

A list of vectors of data point names, one list element per ball. The output is such that every data point is contained in a ball of radius $\varepsilon$, and no ball center is contained in more than one ball. The centers are datapoints themselves.

## Examples

```
num_points = 5000

P.data = data.frame(
  x = sapply(1:num_points, function(x)
    sin(x) * 10) + rnorm(num_points, 0, 0.1),
  y = sapply(1:num_points, function(x)
    cos(x) ^ 2 * sin(x) * 10) + rnorm(num_points, 0, 0.1),
  z = sapply(1:num_points, function(x)
    10 * sin(x) ^ 2 * cos(x)) + rnorm(num_points, 0, 0.1)
)

P.dist = dist(P.data)
balls = create_balls(data = P.data, dists = P.dist, eps = .25)
```

## create_ball_mapper_object

*Run mapper using a trivial filter, a cover of balls, and no clustering algorithm.*

### Description

Run mapper using an $\varepsilon$-net cover (greedily generated) and the 2D inclusion function as a filter.

### Usage

```
create_ball_mapper_object(data, dists, eps)
```

### Arguments

| | |
|---|---|
| data | A data frame. |
| dists | A distance matrix for the data frame. |
| eps | A positive real number for your desired ball radius. |

### Value

A list of two data frames, one with node data containing ball size, data points per ball, ball tightness, and one with edge data containing sources, targets, and weights representing overlap strength.

### Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))
eps = .5

create_ball_mapper_object(data, dist(data), eps)
```

## create_bins

*Create bins of data*

### Description

Create bins of data

### Usage

```
create_bins(data, filtered_data, cover_element_tests)
```

### Arguments

| | |
|---|---|
| `data` | A data frame. |
| `filtered_data` | The result of a function applied to the data frame; there should be one filter value per observation in the original data frame. |
| `cover_element_tests` | A list of membership test functions for a set of cover elements. In other words, each element of `cover_element_tests` is a function that returns `TRUE` or `FALSE` when given a filter value. |

### Value

A list of level sets, each containing a vector of the names of the data inside it.

---

## `create_clusterball_mapper_object` *Run clusterball mapper*

---

### Description

Run ball mapper, but additionally cluster within the balls. Can use two different distance matrices to accomplish this.

### Usage

```
create_clusterball_mapper_object(
  data,
  dist1,
  dist2,
  eps,
  clusterer = hierarchical_clusterer("single")
)
```

### Arguments

| | |
|---|---|
| `data` | A data frame. |
| `dist1` | A distance matrix for the data frame; this will be used to ball the data. |
| `dist2` | Another distance matrix for the data frame; this will be used to cluster the data after balling. |
| `eps` | A positive real number for your desired ball radius. |
| `clusterer` | A function which accepts a list of distance matrices as input, and returns the results of clustering done on each distance matrix. |

### Value

A list of two dataframes, one with node data containing bin membership, datapoints per cluster, and cluster dispersion, and one with edge data containing sources, targets, and weights representing overlap strength.

## Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))
data.dists = dist(data)
eps = 1

create_clusterball_mapper_object(data, data.dists, data.dists, eps)
```

---

`create_mapper_object` *Create a mapper object*

---

## Description

Run the mapper algorithm on a data frame.

## Usage

```
create_mapper_object(
  data,
  dists,
  filtered_data,
  cover_element_tests,
  clusterer = NULL
)
```

## Arguments

| | |
|---|---|
| `data` | A data frame. |
| `dists` | A distance matrix for the data frame. |
| `filtered_data` | The result of a function applied to the data frame; there should be one filter value per observation in the original data frame. |
| `cover_element_tests` | A list of membership test functions for a set of cover elements. In other words, each element of `cover_element_tests` is a function that returns `TRUE` or `FALSE` when given a filter value. |
| `clusterer` | A function which accepts a list of distance matrices as input, and returns the results of clustering done on each distance matrix. Defaults to `NULL`, meaning no all data in each bin will be lumped into a single cluster. |

## Value

A list of two dataframes, one with node data and one with edge data.

## Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))
projx = data$x

num_bins = 10
percent_overlap = 25
xcover = create_width_balanced_cover(min(projx), max(projx), num_bins, percent_overlap)

check_in_interval <- function(endpoints) {
 return(function(x) (endpoints[1] - x <= 0) & (endpoints[2] - x >= 0))
}

# each of the "cover" elements will really be a function that checks if a data point lives in it
xcovercheck = apply(xcover, 1, check_in_interval)

# build the mapper object
xmapper = create_mapper_object(
  data = data,
  dists = dist(data),
  filtered_data = projx,
  cover_element_tests = xcovercheck
)
```

---

`create_single_bin` *Create a bin of data*

---

## Description

Create a bin of data

## Usage

```
create_single_bin(data, filtered_data, cover_element_test)
```

## Arguments

| | |
|---|---|
| `data` | A data frame. |
| `filtered_data` | The result of a function applied to the data frame; there should be one filter value per observation in the original data frame. |
| `cover_element_test` | A membership test function for a cover element. It should return `TRUE` or `FALSE` when given a filtered data point. |

## Value

A vector of names of points from the data frame, representing a level set.

`create_width_balanced_cover` *Generate an overlapping cover of an interval*

## Description

This is a function that generates a cover of an interval $[a, b]$ with some number of (possibly) overlapping, evenly spaced, identical width subintervals.

## Usage

```
create_width_balanced_cover(min_val, max_val, num_bins, percent_overlap)
```

## Arguments

| | |
|---|---|
| `min_val` | The left endpoint $a$. A real number. |
| `max_val` | The right endpoint $b$. A real number. |
| `num_bins` | The number of cover intervals with which to cover the interval. A positive integer. |
| `percent_overlap` | How much overlap desired between the cover intervals (the percent of the intersection of each interval with its immediate neighbor relative to its length, e.g., $[0, 2]$ and $[1, 3]$ would have $50\%$ overlap). A real number between 0 and 100, inclusive. |

## Value

A 2D numeric array.

- left_ends - The left endpoints of the cover intervals.
- right_ends - The right endpoints of the cover intervals.

## Examples

```
create_width_balanced_cover(min_val=0, max_val=100, num_bins=10, percent_overlap=15)
create_width_balanced_cover(-11.5, 10.33, 100, 2)
```

## cut_dendrogram *Cut a dendrogram in context*

### Description

Cut a dendrogram in context

### Usage

```
cut_dendrogram(dend, threshold)
```

### Arguments

| | |
|---|---|
| dend | A single dendrogram. |
| threshold | A mininum tallest branch value. |

### Details

The number of clusters is determined to be 1 if the tallest branch of the dendrogram is less than the threshold, or if the index of dispersion (standard deviation squared divided by mean) of the branch heights is below 0.015. Otherwise, we cut at the longest branch of the dendrogram to determine the number of clusters.

### Value

A named vector whose names are data point names and whose values are cluster labels.

## eccentricity_filter *Compute eccentricity of data points*

### Description

Compute eccentricity of data points

### Usage

```
eccentricity_filter(dists)
```

### Arguments

| | |
|---|---|
| dists | A distance matrix associated to a data frame. |

### Value

A vector of centrality measures, calculated per data point as the sum of its distances to every other data point, divided by the number of points.

## Examples

```
num_points = 100

P.data = data.frame(
  x = sapply(1:num_points, function(x)
    sin(x) * 10) + rnorm(num_points, 0, 0.1),
  y = sapply(1:num_points, function(x)
    cos(x) ^ 2 * sin(x) * 10) + rnorm(num_points, 0, 0.1)
)

P.dist = dist(P.data)
eccentricity = eccentricity_filter(P.dist)
```

---

# get_bin_vector *Recover bins*

---

## Description

Recover bins

## Usage

```
get_bin_vector(binclust_data)
```

## Arguments

| | |
|---|---|
| binclust_data | A list of bins, each containing named vectors whose names are those of data points and whose values are cluster ids. |

## Value

A vector of integers equal in length to the number of clusters, whose members identify which bin that cluster belongs to.

---

# get_clustered_data *Get data within a cluster*

---

## Description

Get data within a cluster

## Usage

```
get_clustered_data(binclust_data)
```

### Arguments

| | |
|---|---|
| binclust_data | A list of bins, each containing named vectors whose names are those of data points and whose values are cluster ids |

### Value

A list of strings, each a comma separated list of the toString values of the data point names.

---

## get_clusters *Perform the clustering step in mapper*

---

### Description

This function processes the binned data and global distance matrix to return freshly clustered data.

### Usage

```
get_clusters(bins, dists, clusterer)
```

### Arguments

| | |
|---|---|
| bins | A list containing "bins" of vectors of names of data points. |
| dists | A distance matrix containing pairwise distances between named data points. |
| clusterer | A function which accepts a list of distance matrices as input, and returns the results of clustering done on each distance matrix. |

### Value

The output of `clusterer` applied to a list of distance matrices, which should be a list containing named vectors (one per bin), whose names are data point names and whose values are cluster labels.

---

## get_cluster_sizes *Compute cluster sizes*

---

### Description

Compute cluster sizes

### Usage

```
get_cluster_sizes(binclust_data)
```

### Arguments

| | |
|---|---|
| binclust_data | A list of bins, each containing named vectors whose names are those of data points and whose values are cluster ids. |

### Value

A vector of integers representing the lengths of the clusters in the input data.

---

`get_cluster_tightness_vector` *Compute dispersion measures of a list of clusters*

---

### Description

Compute dispersion measures of a list of clusters

### Usage

```
get_cluster_tightness_vector(dists, binclust_data)
```

### Arguments

| | |
|---|---|
| `dists` | A distance matrix for the data points inside all the input clusters |
| `binclust_data` | A list of named vectors whose names are those of data points and whose values are cluster ids |

### Value

A vector of real numbers in $(0, \infty)$ representing a measure of dispersion of a cluster, calculated according to compute_tightness.

---

`get_edgelist_from_overlaps` *Obtain edge list from cluster intersections*

---

### Description

Obtain edge list from cluster intersections

### Usage

```
get_edgelist_from_overlaps(overlaps, num_vertices)
```

### Arguments

| | |
|---|---|
| `overlaps` | A named list of edges, whose elements contain the names of clusters in the overlap represented by that edge; output of `get_overlaps()`. |
| `num_vertices` | The number of vertices in the graph. |

### Value

A 2D array representing the edge list of a graph.

`get_edge_weights` *Calculate edge weights*

## Description

Calculate edge weights

## Usage

```
get_edge_weights(overlap_lengths, cluster_sizes, edges)
```

## Arguments

| | |
|---|---|
| `overlap_lengths` | A named vector of cluster overlap lengths, obtained by calling `length()` on the output from `[get_overlaps()]`. |
| `cluster_sizes` | A vector of cluster sizes. |
| `edges` | A 2D array of source and target nodes, representing an edge list. Should be ordered consistently with the `overlap_lengths` parameter. |

## Details

This value is calculated per edge by dividing the number of data points in the overlap by the number of points in the cluster on either end, and taking the maximum value. Formally,

$$w(\{c_i, c_j\}) = \max\left\{\frac{|c_i \cap c_j|}{|c_i|}, \frac{|c_i \cap c_j|}{|c_j|}\right\}$$

## Value

A vector of real numbers representing cluster overlap strength.

---

`get_hierarchical_clusters` *Perform single-linkage hierarchical clustering and process dendrograms in a semi-global context.*

## Description

Perform single-linkage hierarchical clustering and process dendrograms in a semi-global context.

## Usage

```
get_hierarchical_clusters(dist_mats, method)
```

### Arguments

| | |
|---|---|
| `dist_mats` | A list of distance matrices to be used for clustering. |
| `method` | A string to pass to hclust to tell it what kind of clustering to do. |

### Value

A list containing named vectors (one per dendrogram), whose names are data point names and whose values are cluster labels.

---

## `get_overlaps` *Get cluster overlaps*

---

### Description

Get cluster overlaps

### Usage

```
get_overlaps(binclust_data)
```

### Arguments

| | |
|---|---|
| `binclust_data` | A list of bins, each containing named vectors whose names are those of data points and whose values are cluster ids. |

### Value

A named list of edges, whose elements contain the names of clusters in the overlap represented by that edge.

---

## `get_raw_clusters` *Ship data off to the clustering goblins*

---

### Description

This function tells the computer to look away for a second, so the goblins come and cluster your data while it's not watching.

### Usage

```
get_raw_clusters(dist_mats, clusterer)
```

### Arguments

| | |
|---|---|
| `dist_mats` | A list of distance matrices of each bin that is to be clustered. |
| `clusterer` | A function which accepts a list of distance matrices as input, and returns the results of clustering done on each distance matrix in a list. |

### Value

The output of `clusterer(dist_mats)`, which needs to be a list containing named vectors (one per bin), whose names are data point names and whose values are cluster labels (within each bin)

---

## `get_tallest_branch` *Find the tallest branch of a dendrogram*

---

### Description

Find the tallest branch of a dendrogram

### Usage

```
get_tallest_branch(dend)
```

### Arguments

| | |
|---|---|
| `dend` | A single dendrogram. |

### Value

The height of the tallest branch (longest time between merge heights) of the input dendrogram.

---

## `hierarchical_clusterer` *Create a little dude to perform hierarchical clustering in a semi-global context using the hclust package.*

---

### Description

Create a little dude to perform hierarchical clustering in a semi-global context using the hclust package.

### Usage

```
hierarchical_clusterer(method)
```

### Arguments

| | |
|---|---|
| `method` | A string to pass to hclust to tell it what kind of clustering to do. |

## Details

This clusterer determines cutting heights for bin dendrograms generated by hclust by first considering the tallest branches across all dendrograms; if all branch heights of a given dendrogram are below a threshold (10 percent of the global tallest), that dendrogram will be considered to describe a single cluster. Additionally, if the index of dispersion of the branch heights of a dendrogram are below 0.015, we will also consider it as describing a single cluster. If neither of these are true, then we will cut the dendrogram at its longest branch.

## Value

A function that inputs a list of distance matrices and returns a list containing one vector per bin, whose element names are data point names and whose values are cluster labels (within each bin).

## Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))
projx = data$x

num_bins = 10
percent_overlap = 25

cover = create_width_balanced_cover(min(projx), max(projx), num_bins, percent_overlap)

create_1D_mapper_object(data, dist(data), projx, cover, hierarchical_clusterer("mcquitty"))
```

---

# is_in_ball *Get a tester function for a ball.*

---

## Description

Get a tester function for a ball.

## Usage

```
is_in_ball(ball)
```

## Arguments

| | |
|---|---|
| ball | A list of data points. |

## Value

A function that eats a data point and returns TRUE or FALSE depending if the point is in the ball or not.

## mapper_object_to_igraph *make igraph*

### Description

make igraph

### Usage

```
mapper_object_to_igraph(mapperobject)
```

### Arguments

| | |
|---|---|
| mapperobject | mapper object generated by mappeR |

### Value

an igraph object

### Examples

```
data = data.frame(x = sapply(1:100, function(x) cos(x)), y = sapply(1:100, function(x) sin(x)))

projy = data$y

cover = create_width_balanced_cover(min(projy), max(projy), 10, 25)

mapperobj = create_1D_mapper_object(data, dist(data), data$y, cover)

mapper_object_to_igraph(mapperobj)
```

## next_triangular *Find which triangular number you're on*

### Description

Find which triangular number you're on

### Usage

```
next_triangular(x)
```

### Arguments

| | |
|---|---|
| x | A positive integer. |

### Value

The index of the next greatest or equal triangular number to $x$.

---

`process_dendrograms` *Cut many dendrograms in context*

---

### Description

Cut many dendrograms in context

### Usage

```
process_dendrograms(dends, semi_local_clustering = TRUE)
```

### Arguments

| | |
|---|---|
| `dends` | A list of dendrograms to be cut. |
| `semi_local_clustering` | Whether you want clustering to happen in a semi-local (entire dataset visible) or strictly local (only current level set visible) context. Defaults to semi-local. |

### Details

This function uses a value of 10 percent of the tallest branch across dendrograms as a threshold for cut_dendrogram.

### Value

A list of named vectors (one per dendrogram) whose names are data point names and whose values are cluster labels.

---

`run_link` *Perform agglomerative clustering on a single distance matrix.*

---

### Description

Perform agglomerative clustering on a single distance matrix.

### Usage

```
run_link(dist, method)
```

### Arguments

| | |
|---|---|
| `dist` | A distance matrix. |
| `method` | A string to pass to hclust to determine clustering method. |

## Value

A dendrogram generated by `fastcluster`.

---

`subset_dists` *Subset a distance matrix*

---

## Description

Subset a distance matrix

## Usage

```
subset_dists(bin, dists)
```

## Arguments

| | |
|---|---|
| `bin` | A list of names of data points. |
| `dists` | A distance matrix for data points in the bin, possibly including extra points. |

## Value

A distance matrix for only the data points in the input bin.

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