# Package 'CluMSID'

January 23, 2026

**Type** Package

**Title** Clustering of MS2 Spectra for Metabolite Identification

**Version** 1.27.0

**Maintainer** Tobias Depke <depke@mailbox.org>

**Description** CluMSID is a tool that aids the identification of features
in untargeted LC-MS/MS analysis by the use of MS2 spectra similarity
and unsupervised statistical methods. It offers functions for a complete
and customisable workflow from raw data to visualisations and is
interfaceable with the xmcs family of preprocessing packages.

**License** MIT + file LICENSE

**Encoding** UTF-8

**URL** https://github.com/tdepke/CluMSID

**BugReports** https://github.com/tdepke/CluMSID/issues

**LazyData** true

**Depends** R (>= 3.6)

**biocViews** Metabolomics, Preprocessing, Clustering

**Imports** mzR, S4Vectors, dbscan, RColorBrewer, ape, network, GGally,
ggplot2, plotly, methods, utils, stats, sna, grDevices,
graphics, Biobase, gplots, MSnbase

**RoxygenNote** 6.1.1

**Suggests** knitr, rmarkdown, testthat, dplyr, readr, stringr, magrittr,
CluMSIDdata, metaMS, metaMSdata, xcms

**VignetteBuilder** knitr

**git_url** https://git.bioconductor.org/packages/CluMSID

**git_branch** devel

**git_last_commit** 4f5bb4a

**git_last_commit_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2026-01-23

**Author**  Tobias Depke [aut, cre],
        Raimo Franke [ctb],
        Mark Broenstrup [ths]

# Contents

---

| accessors | *Accessor functions for individual slots of* MS2spectrum *and* pseudospectrum *objects* |
|---|---|

---

### Description

Accessor functions for individual slots of MS2spectrum and pseudospectrum objects

## Usage

```
accessID(x)

accessAnnotation(x)

accessPrecursor(x)

accessRT(x)

accessPolarity(x)

accessSpectrum(x)

accessNeutralLosses(x)
```

## Arguments

x                     An object of class `MS2spectrum` or `pseudospectrum`

## Value

The value of the respective slot of the object (`id`, `annotation`, `precursor`, `rt`, `spectrum`, `neutral_losses`)

## Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessID(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessAnnotation(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessPrecursor(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessRT(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
```

```
    package = "CluMSIDdata"))

accessPolarity(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessSpectrum(annotatedSpeclist[[1]])

load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

accessNeutralLosses(annotatedSpeclist[[1]])
```

---

addAnnotations                        *Adding external annotations to list of* MS2spectrum *objects*

---

### Description

addAnnotations is used to add annotations that have been assigned externally, e.g. by library
search, to a list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList.

### Usage

```
addAnnotations(featlist, annolist, annotationColumn = 4)
```

### Arguments

| | |
|---|---|
| featlist | A list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList |
| annolist | A list of annotations, either as a data.frame or csv file. The order of features must be the same as in featlist. Please see the package vignette for a detailed example! |
| annotationColumn | |
| | The column of annolist were the annotation is found. Default is 4, which is the case if [writeFeaturelist](#) followed by manual addition of annotations, e.g. in Excel, is used to generate annolist. |

### Value

A list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList with ex-
ternal annotations added to the annotation slot of each MS2spectrum object.

## Examples

```
load(file = system.file("extdata",
     "featlist.RData",
     package = "CluMSIDdata"))

addAnnotations(featlist, system.file("extdata",
               "post_anno.csv",
               package = "CluMSIDdata"),
               annotationColumn = 4)
```

---

as.MS2spectrum *Convert spectra from* **MSnbase** *classes*

---

## Description

Convert spectra from **MSnbase** classes

## Usage

```
as.MS2spectrum(x)
```

## Arguments

x               An object of class [Spectrum](#) or [Spectrum2](#)

## Value

An object of class [MS2spectrum](#)

## Examples

```
#Load a "Spectrum2" object from MSnbase
library(MSnbase)
sp <- itraqdata[["X1"]]
#Convert this object to "MS2spectrum" class
new_sp <- as.MS2spectrum(sp)
#Or alternatively:
new_sp <- as(sp, "MS2spectrum")
```

---

cossim                          *Calculate cosine similarity between two spectra*

---

### Description

cossim() calculates the cosine of the spectral constrast angle as a measure for the similarity of two spectra.

### Usage

```
cossim(x, y, type = c("spectrum", "neutral_losses"),
    mzTolerance = 1e-05)

## S4 method for signature 'MS2spectrum,MS2spectrum'
cossim(x, y, type = c("spectrum",
    "neutral_losses"), mzTolerance = 1e-05)

## S4 method for signature 'pseudospectrum,pseudospectrum'
cossim(x, y,
    type = c("spectrum", "neutral_losses"), mzTolerance = 1e-05)
```

### Arguments

| | |
|---|---|
| x, y | MS2 spectra, either as matrix, MS2spectrum or pseudospectrum objects. x and y must have the same class. |
| type | Whether similarity between spectra ("spectrum", default) or neutral loss patterns ("neutral_losses") is to be compared |
| mzTolerance | The m/z tolerance used for merging. If two fragment peaks are within tolerance, they are regarded as the same. Defaults to 1e-5, i.e. 10ppm. |

### Value

The cosine similarity of x and y

### Methods (by class)

- x = MS2spectrum, y = MS2spectrum: cossim method for MS2spectrum objects
- x = pseudospectrum, y = pseudospectrum: cossim method for pseudospectrum objects

### Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

cossim(annotatedSpeclist[[1]], annotatedSpeclist[[2]])
```

---

distanceMatrix    *Create distance matrix from list of spectra*

---

### Description

distanceMatrix() creates a distance matrix from a list of MS2 spectra, MS1 pseudospectra or neutral loss patterns by pairwise comparison using the specified distance function. This distance matrix is the basis for CluMSID's data mining functions.

### Usage

```
distanceMatrix(speclist, distFun = "cossim", type = c("spectrum",
    "neutral_losses"), mz_tolerance = 1e-05)
```

### Arguments

| | |
|---|---|
| speclist | A list of MS2spectrum or pseudospectrum objects as generated by extractMS2spectra or extractPseudospectra. |
| distFun | The distance function to be used. At the moment, only cossim is implemented. |
| type | "spectrum" (default) for MS2 spectra or MS1 pseudospectra or "neutral_losses" for neutral loss patterns. |
| mz_tolerance | The *m/z* tolerance to be used for merging, default is 1e-5, i.e. +/- 10ppm. If the mass-to-charge ratios of two peaks differ less than *mz_tolerance*, they are assumed to have the same *m/z* |

### Value

A numeric length(speclist) by length(speclist) matrix containing pairwise distances (1 - similarity) between all features in speclist. Row and column names are taken from the id slot or, if present, pasted from the id and annotation slots of the MS2spectrum or pseudospectrum objects.

### Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

distanceMatrix(annotatedSpeclist[1:20])
```

| extractMS2spectra | *Extract MS2 spectra from raw data files* |
|---|---|

### Description

extractMS2spectra() is used to extract MS2 spectra from raw data files, e.g. mzXML files.

### Usage

```
extractMS2spectra(MSfile, min_peaks = 2, recalibrate_precursor = FALSE,
    RTlims = NULL)
```

### Arguments

| | |
|---|---|
| MSfile | An LC-MS/MS raw data file in one of the non-proprietary formats that can be parsed by mzR, e.g. mzXML or mzML. |
| min_peaks | Minimum number of peaks in MS2 spectrum, defaults to 2. Spectra with less than min_peaks fragment peaks will be ignored and not extracted. |
| recalibrate_precursor | |
| | Logical, defaults to FALSE. Applicable only for files that were exported to mzXML using a deprecated version of Bruker Compass Xport (< 3.0.13). If set to TRUE, the precursor m/z will be recalculated from the respective fragment m/z in the MS2 spectrum. For details, see Depke et al. 2017. |
| RTlims | Retention time interval for the extraction of spectra. Provide as numeric vector of length 2. Spectra with retention time < RTlims[1] or > RTlims[2] will be ignored. |

### Value

A list with objects of class MS2spectrum, containing MS2 spectra extracted from the raw data.

### Examples

```
my_spectra <- extractMS2spectra(MSfile = system.file("extdata",
                                "PoolA_R_SE.mzXML",
                                package = "CluMSIDdata"),
                                min_peaks = 4, RTlims = c(0,10))
```

extractPseudospectra     *Extract pseudospectra*

## Description

extractPseudospectra() is used to extract MS1 pseudospectra from **CAMERA** output.

## Usage

```
extractPseudospectra(x, min_peaks = 1, intensity_columns = NULL)
```

## Arguments

x          **CAMERA** output that contains information on pseudospectra. Can either be of class data.frame or [xsAnnotate](#). It is recommended to use either xsAnnotate objects or data.frames generated from XCMSonline results tables but other data.frames are possible.

min_peaks      Minimum number of peaks in pseudospectrum, defaults to 1. See [extractMS2spectra](#).

intensity_columns

         Numeric, defaults to NULL. If a data.frame is used as input which has not been generated from an XCMSonline results table, the indices of the columns that contain the peak intensities in the different samples have to be indicated as intensity_columns.

## Value

A list of pseudospectra, stored as objects of class [pseudospectrum](#), analogous to the output of [extractMS2spectra](#).

## Examples

```
pstable <- readr::read_delim(file = system.file("extdata",
                             "TD035_XCMS.annotated.diffreport.tsv",
                             package = "CluMSIDdata"), delim = "\t")

pseudospeclist <- extractPseudospectra(pstable, min_peaks = 2)
```

---

featureList *Generate a* data.frame *with feature information from list of* MS2spectrum *objects*

---

### Description

featureList generates a data.frame that contains feature ID, precurosur *m/z* and retention time for all features contained in a list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList. featureList is used internally by writeFeaturelist.

### Usage

```
featureList(featlist)
```

### Arguments

featlist    A list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList

### Details

Although originally designed for lists of MS2spectrum objects, the function also works with lists of pseudospectrum objects. In this case, NA is given for precursor *m/z*.

### Value

A data.frame that contains feature ID, precurosur *m/z* (if available) and retention time

### Examples

```
load(file = system.file("extdata",
    "featlist.RData",
    package = "CluMSIDdata"))

pre_anno <- featureList(featlist)
```

---

findFragment *Find spectra that contain a specific fragment*

---

### Description

findFragment is used to find spectra that contain a specific fragment ion. Its sister function is findNL, which finds specific neutral losses. Both functions work analogous to getSpectrum.

### Usage

```
findFragment(featlist, mz, tolerance = 1e-05)
```

## Arguments

| | |
|---|---|
| featlist | a list that contains only objects of class MS2spectrum |
| mz | The mass-to-charge ratio of the fragment ion of interest. |
| tolerance | The *m/z* tolerance for the fragment ion search. Default is 1E-05, i.e. +/- 10ppm. |

## Value

If the respective fragment is only found in one spectrum, the output is an object of class MS2spectrum; if it is found in more than one spectrum, the output is a list of MS2spectrum objects.

## Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))
putativeAQs <- findFragment(annotatedSpeclist, 159.068)
```

---

findNL                          *Find spectra that contain a specific neutral loss*

---

## Description

findNL is used to find spectra that contain a specific neutral loss. Its sister function is findFragment, which finds specific fragment ions. Both functions work analogous to getSpectrum.

## Usage

```
findNL(featlist, mz, tolerance = 1e-05)
```

## Arguments

| | |
|---|---|
| featlist | a list that contains only objects of class MS2spectrum |
| mz | The mass-to-charge ratio of the neutral loss of interest. |
| tolerance | The *m/z* tolerance for the neutral loss search. Default is 1E-05, i.e. +/- 10ppm. |

## Value

If the respective neutral loss is only found in one spectrum, the output is an object of class MS2spectrum; if it is found in more than one spectrum, the output is a list of MS2spectrum objects.

## Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))
findNL(annotatedSpeclist, 212.009)
```

---

getSimilarities        *Match one spectrum against a set of spectra*

---

### Description

getSimilarities calculates the similarities of one spectrum or neutral loss pattern to a set of other spectra or neutral loss patterns.

### Usage

```
getSimilarities(spec, speclist, type = c("spectrum", "neutral_losses"),
    hits_only = FALSE)
```

### Arguments

spec
: The spectrum to be compared to other spectra. Can be either an object of class MS2spectrum or a two-column numerical matrix that contains fragment mass-to-charge ratios in the first and intensities in the second column.

speclist
: The set of spectra to which spec is to be compared. Must be a list where every entry is an object of class MS2spectrum. Can be generated from an mzXML file with extractMS2spectra and mergeMS2spectra or constructed using new("MS2spectrum", ...) for every list entry (see vignette for details).

type
: Specifies whether MS2 spectra or neutral loss patterns are to be compared. Must be either 'spectrum' (default) or 'neutral_losses'.

hits_only
: Logical that indicates whether the result should contain only similarities greater than zero.

### Value

A named vector with similarities of spec to all spectra or neutral loss patterns in speclist.

### Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))
getSimilarities(annotatedSpeclist[[137]],
                annotatedSpeclist, hits_only = TRUE)
```

---

getSpectrum                    *Access individual spectra from a list of spectra by various slot entries*

---

### Description

As accessing S4 objects within lists is not trivial, getSpectrum can be used to access individual or several MS2spectrum objects by their slot entries.

### Usage

```
getSpectrum(featlist, slot, what, mz.tol = 1e-05, rt.tol = 30)
```

### Arguments

| | |
|---|---|
| featlist | a list that contains only objects of class MS2spectrum |
| slot | The slot to be searched (invalid slot arguments will produce errors). Possible values are:<br>• 'id'<br>• 'annotation'<br>• 'precursor' (*m/z* of precursor ion)<br>• 'rt' (retention time of precursor) |
| what | the search term or number, must be character for 'id' and 'annotation' and numeric for 'precursor' and 'rt' See vignette for examples. |
| mz.tol | the tolerance used for precursor ion *m/z* searches, defaults to 1E-05 (+/-10ppm) |
| rt.tol | the tolerance used for precursor ion retention time searches, defaults to 30s; high values can be used to specify retention time ranges (see vignette for example) |

### Value

If the only one spectrum matches the search criteria, the output is an object of class MS2spectrum; if more than one spectrum matches, the output is a list of MS2spectrum objects.

### Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

getSpectrum(annotatedSpeclist, "annotation", "pyocyanin")

getSpectrum(annotatedSpeclist, "id", "M244.17T796.4")

getSpectrum(annotatedSpeclist, "precursor", 286.18, mz.tol = 1E-03)

six_eight <- getSpectrum(annotatedSpeclist, "rt", 420, rt.tol = 60)
```

---

HCplot                        *Generate cluster dendrogram or heatmap from spectral similarity data*

---

### Description

HCplot() performs hierarchical clustering of spectral similarity data using average linkage as agglomeration criterion like [HCtbl](#) and generates either a circular dendrogram or a combination of dendrogram and heatmap.

### Usage

```
HCplot(distmat, h = 0.95, type = c("dendrogram", "heatmap"), ...)
```

### Arguments

| | |
|---|---|
| distmat | A distance matrix as generated by [distanceMatrix](#). |
| h | Height where the tree is to be cut, defaults to 0.95. See [cutree](#) for details. |
| type | Specifies which visualisation is to be generated: "dendrogram" (default) for a circular dendrogram or "heatmap" for a combination of dendrogram and heatmap. |
| ... | Additional graphical parameters passed to plot.phylo (for type = "dendrogram") or gplots::heatmap.2 (for type = "heatmap") |

### Value

A plot as specified by type.

### Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

HCplot(distmat[1:50,1:50], h = 0.8, type = "heatmap")
```

---

HCtbl                        *Hierarchical clustering of spectral similarity data*

---

### Description

HCtbl() performs hierarchical clustering of spectral similarity data using average linkage as agglomeration criterion.

### Usage

```
HCtbl(distmat, h = 0.95)
```

## Arguments

| distmat | A distance matrix as generated by [distanceMatrix](#). |
|---------|--------------------------------------------------------|
| h | Height where the tree is to be cut, defaults to `0.95`. See [cutree](#) for details. |

## Value

A `data.frame` with name and cluster ID for each feature in `distmat`.

## See Also

[HCplot](#)

## Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

my_HCtbl <- HCtbl(distmat[1:50,1:50], h = 0.8)
```

---

MDSplot                  *Multidimensional scaling of spectral similarity data*

---

## Description

`MDSplot()` is used to generate multidimensional scaling plots from spectral similarity data. An interactive visualisation can be produced using **plotly**.

## Usage

```
MDSplot(distmat, interactive = FALSE, highlight_annotated = FALSE, ...)
```

## Arguments

| distmat | A distance matrix as generated by [distanceMatrix](#). |
|---------|--------------------------------------------------------|
| interactive | Logical, defaults to `FALSE`. If `TRUE`, an interactive visualisation is generated using **plotly**. |
| highlight_annotated | |
| | Logical, defaults to `FALSE`. If `TRUE`, points for features for which an annotation was added before using [distanceMatrix](#) are highlighted by red colour, while other points are grey in the MDS plot. |
| ... | Additional arguments passed to geom_point(), e.g. `pch`, `size` or `alpha`. |

## Value

An MDS plot generated with the help of [cmdscale](#), [ggplot](#) and, if interactive, [ggplotly](#).

## Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

MDSplot(distmat, highlight_annotated = TRUE)
```

---

| mergeMS2spectra | *Merge MS2 spectra with or without external peak table* |

---

## Description

mergeMS2spectra is used to merge MS2 spectra that come from the same precursor. It does so either by grouping spectra of the same precursor *m/z* that fall into a defined retention time window (rt_tolerance) or by grouping spectra to peaks from an externally supplied peak table. Please see the vignette for more details.

## Usage

```
mergeMS2spectra(ms2list, mz_tolerance = 1e-05, rt_tolerance = 30,
    peaktable = NULL, exclude_unmatched = FALSE)
```

## Arguments

| | |
|---|---|
| ms2list | A list of MS2spectrum objects to be merged. |
| mz_tolerance | The *m/z* tolerance to be used for merging, default is 1e-5, i.e. +/- 10ppm. If the mass-to-charge ratios of two peaks differ less than *mz_tolerance*, they are assumed to have the same *m/z* |
| rt_tolerance | The retention time tolerance used for merging features. If used without a peak table, rt_tolerance is the maximum retention time difference between to subsequent spectra of the same precursor *m/z* with which they are still assumed to belong to the same feature If used with an external peak table, rt_tolerance is the maximum retention time difference between a spectrum and a peak in the peak table with which the spectrum is still considered to belong to that peak. |
| peaktable | An external peak table, e.g. from XCMS, that serves as a template for grouping spectra. The peaktable must be a three-column data.frame with feature ID, *m/z* and retention time for each peak/feature. |
| exclude_unmatched | |
| | If an external peak table is used: Should spectra that do not match to any peak/feature in the peak table be exclude from the resulting list? |

## Value

A merged list of [MS2spectrum](#) objects.

## Examples

```
my_spectra <- extractMS2spectra(MSfile = system.file("extdata",
                                "PoolA_R_SE.mzXML",
                                package = "CluMSIDdata"),
                                min_peaks = 4, RTlims = c(0,5))

my_merged_spectra <- mergeMS2spectra(my_spectra, rt_tolerance = 20)
```

---

mergeSpecList            *Merge list of spectra*

---

### Description

mergeSpecList() is an accessory function used only inside mergeMS2spectra.

### Usage

```
mergeSpecList(speclist, tolerance = 1e-05)
```

### Arguments

speclist        A list of MS2spectrum objects to be merged.

tolerance       The m/z tolerance to be used for merging.

### Value

A list of the same length as speclist containing merged spectra as MS2spectrum objects. If multiple spectra contribute to one consensus spectrum, than this consensus spectrum is contained in the list multiple times at the respective positions of the contributing spectra.

---

mergeTolerance           *Merge spectra with m/z tolerance*

---

### Description

mergeTolerance() merges two spectra by identifying common peaks with a given m/z tolerance. It can be used with Reduce() to merge more than two spectra.

### Usage

```
mergeTolerance(x, y, tolerance = 1e-05)
```

**Arguments**

| | |
|---|---|
| x, y | MS2 spectra as objects of class `matrix` with m/z in the first column and intensity in the second. |
| tolerance | The m/z tolerance used for merging. If two peaks are within tolerance, they are regarded as the same. Defaults to `1e-5`, i.e. 10ppm. |

**Value**

A matrix with m/z in the first column and separate columns for intensities in the respective spectra. If peaks were merged, their m/z corresponds to the mean of the two original m/z.

---

| MS2spectrum-class | *A custom S4 class for MS2 spectra, neutral loss patterns and respective metainformation* |
|---|---|

---

**Description**

A custom S4 class for MS2 spectra, neutral loss patterns and respective metainformation

**Usage**

```
## S4 method for signature 'MS2spectrum'
show(object)

## S4 method for signature 'MS2spectrum'
precursorMz(object)

## S4 method for signature 'MS2spectrum'
rtime(object)

## S4 method for signature 'MS2spectrum'
intensity(object)

## S4 method for signature 'MS2spectrum'
mz(object)

## S4 method for signature 'MS2spectrum,ANY'
peaksCount(object)
```

**Arguments**

| | |
|---|---|
| object | An object of class [MS2spectrum](#) |

**Value**

Prints information from the object slots with exception of 'spectrum' and 'neutral_losses' where only a summary is given.

## Methods (by generic)

- `show`: A show generic for `MS2spectra`.

- `precursorMz`: Method for `MSnbase::precursorMz` for `MS2spectrum` objects. Accesses `precursor` slot and returns precursor *m/z* as a numeric.

- `rtime`: Method for `MSnbase::rtime` for `MS2spectrum` objects. Accesses `rt` slot and returns retention time as a numeric.

- `intensity`: Method for `MSnbase::intensity` for `MS2spectrum` objects. Accesses `spectrum` slot and returns the intensity column as a numeric vector.

- `mz`: Method for `MSnbase::mz` for `MS2spectrum` objects. Accesses `spectrum` slot and returns the *m/z* column as a numeric vector.

- `peaksCount`: Method for `MSnbase::mz` for `MS2spectrum` objects. Accesses `spectrum` slot and returns the number of peaks as a numeric.

## Slots

`id` a character string similar to the ID used by XCMSonline or the ID given in a predefined peak list

`annotation` a character string containing a user-defined annotation, defaults to empty

`precursor` (median) *m/z* of the spectrum's precursor ion

`rt` (median) retention time of the spectrum's precursor ion

`polarity` the ionisation polarity, `"positive"` or `"negative"`

`spectrum` the actual MS2 spectrum as two-column matrix (column 1 is (median) *m/z*, column 2 is (median) intensity of the product ions)

`neutral_losses` a neutral loss pattern generated by subtracting the product ion mass-to-charge ratios from the precursor *m/z* in a matrix format analogous to the `spectrum` slot

---

networkplot                 *Correlation network from spectral similarity data*

---

## Description

`networkplot()` is used to generate correlation networks from spectral similarity data. An interactive visualisation can be produced using **plotly**.

## Usage

```
networkplot(distmat, interactive = FALSE, show_labels = FALSE,
    label_size = 1.5, highlight_annotated = FALSE,
    min_similarity = 0.1, exclude_singletons = FALSE)
```

## Arguments

| | |
|---|---|
| distmat | A distance matrix as generated by [distanceMatrix](#). |
| interactive | Logical, defaults to FALSE. If TRUE, an interactive visualisation is generated using **plotly**. |
| show_labels | Logical, defaults to FALSE. If TRUE, feature IDs are printed as labels in the network plot. Argument has no effect if interactive is TRUE (because in this case, labels are displayed on mouse-over). |
| label_size | Numeric, defaults to 1.5. If show_labels is TRUE and interactive is FALSE, label_size defines the size of labels in the plot. |
| highlight_annotated | |
| | Logical, defaults to FALSE. If TRUE, points for features for which an annotation was added before using [distanceMatrix](#) are highlighted by red colour, while other points are grey in the network plot. |
| min_similarity | Numeric, defaults to 0.1. The minimum spectral contrast angle (see[cossim](#)) that is considered a spectral similarity and hence a connection in the network. |
| exclude_singletons | |
| | Logical, defaults to FALSE. If TRUE, features that have no connection to any other feature will not be displayed in the network plot. |

## Value

A network plot generated with the help of [network](#), [ggnet2](#) and, if interactive, [ggplotly](#). Edge weights correspond to spectral similarities.

## Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

networkplot(distmat[1:50,1:50], show_labels = TRUE,
                exclude_singletons = TRUE)
```

---

neutrallossPatterns             *Generate neutral loss patterns from MS2 spectra*

---

## Description

neutrallossPatterns generates neutral loss patterns from MS2 spectra and adds them to [MS2spectrum](#) objects in the slot neutral_losses.

## Usage

```
neutrallossPatterns(x)
```

## Arguments

x                 an object of class `MS2spectrum` that contains an MS2 spectrum in the `spectrum` slot

## Value

an object of class `MS2spectrum` with a neutral loss pattern in the `neutral_losses` slot

---

OPTICSplot            *Visualisation of density-based clustering of spectral similarity data*

---

### Description

`OPTICSplot()` performs density-based clustering of spectral similarity data using the OPTICS algorithm like `OPTICStbl` and creates a reachability distance plot.

### Usage

```
OPTICSplot(distmat, eps = 10000, minPts = 3, eps_cl = 0.5, ...)
```

### Arguments

distmat    A distance matrix as generated by `distanceMatrix`.

eps        OPTICS parameters, see `optics`.

minPts     OPTICS parameters, see `optics`.

eps_cl     The reachability distance used for cluster determination, see `extractDBSCAN`.

...        Additional graphical parameters to be passed to `plot()`

### Details

The function internally uses `optics` and `extractDBSCAN` from the **dbscan** package.

### Value

A reachability distance plot as visualisation of OPTICS clustering, see code`extractDBSCAN`.

### See Also

OPTICStbl

### Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

OPTICSplot(distmat[1:50,1:50], eps_cl = 0.7)
```

---

## OPTICStbl · *Density-based clustering of spectral similarity data*

---

### Description

OPTICStbl() performs density-based clustering of spectral similarity data using the OPTICS algorithm.

### Usage

```
OPTICStbl(distmat, eps = 10000, minPts = 3, eps_cl = 0.5)
```

### Arguments

distmat          A distance matrix as generated by [distanceMatrix](.).

eps, minPts      OPTICS parameters, see [optics](.).

eps_cl           The reachability distance used for cluster determination, see [extractDBSCAN](.).

### Details

The function internally uses [optics](.) and [extractDBSCAN](.) from the **dbscan** package.

### Value

A data.frame with feature name, cluster ID and OPTICS order for each feature in distmat.

### See Also

OPTICSplot

### Examples

```
load(file = system.file("extdata",
    "distmat.RData",
    package = "CluMSIDdata"))

my_OTPICStbl <- OPTICStbl(distmat[1:50,1:50], eps_cl = 0.7)
```

pseudospectrum-class | *A custom S4 class for MS1 pseudospectra and respective metainformation*

## Description

A custom S4 class for MS1 pseudospectra and respective metainformation

## Slots

id a the "pcgroup" number assigned by **CAMERA**

annotation a character string containing a user-defined annotation, defaults to empty

rt (median) retention time of the ions contained in the pseudospectrum

spectrum the actual MS1 pseudospectrum as two-column matrix (column 1 is (median) *m/z*, column 2 is (median) intensity of the ions)

specplot | *Create a basic plot of MS2 spectra*

## Description

specplot creates a very basic plot of MS2 spectra from MS2spectrum or pseudospectrum objects.

## Usage

```
specplot(spec, ...)
```

## Arguments

spec            An object of class MS2spectrum or pseudospectrum

...             Additional graphical parameters to be passed to plot()

## Value

A plot of the MS2 spectrum saved in the spectrum slot of spec.

## Examples

```
load(file = system.file("extdata",
    "annotatedSpeclist.RData",
    package = "CluMSIDdata"))

specplot(annotatedSpeclist[[1]])
```

---

splitPolarities                    *Separate spectra with different polarities from the same run*

---

### Description

Using splitPolarities, spectra with different polarities from the same run can be separated, e.g. when processing spectra recorded with polarity-switching.

### Usage

```
splitPolarities(ms2list, polarity = c("positive", "negative"))
```

### Arguments

ms2list         A list of MS2spectrum objects as produced by extractMS2spectra.

polarity        The polarity of spectra to be analysed, must be "positive" or "negative".

### Value

A list of MS2spectrum objects that contains only spectra with the given polarity.

### Examples

```
my_spectra <- extractMS2spectra(MSfile = system.file("extdata",
                                "PoolA_R_SE.mzXML",
                                package = "CluMSIDdata"),
                                min_peaks = 4, RTlims = c(0,5))

my_positive_spectra <- splitPolarities(my_spectra, "positive")
```

---

writeFeaturelist                   *Write feature information from list of* MS2spectrum *objects*

---

### Description

writeFeaturelist uses featureList to generate a data.frame that contains feature ID, precursor *m/z* and retention time for all features contained in a list of MS2spectrum objects as produced by extractMS2spectra and mergeSpecList and writes it to a csv file.

### Usage

```
writeFeaturelist(featlist, filename = "pre_anno.csv")
```

## Arguments

| | |
|---|---|
| `featlist` | A list of `MS2spectrum` objects as produced by `extractMS2spectra` and `mergeSpecList` |
| `filename` | The desired file name of the csv file, default is `"pre_anno.csv"` |

## Details

Although originally designed for lists of `MS2spectrum` objects, the function also works with lists of `pseudospectrum` objects. In this case, NA is given for precursor *m/z*.

## Value

A csv file that contains feature ID, precurosur *m/z* and retention time. The file has a header but no row names and is separated by `','`.

## Examples

```
load(file = system.file("extdata",
    "featlist.RData",
    package = "CluMSIDdata"))

writeFeaturelist(featlist, filename = "pre_anno.csv")
```

# Index