

# Package ‘patRoön’

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**Type** Package

**Title** Workflows for Mass-Spectrometry Based Non-Target Analysis

**Version** 2.0.0

**Description** Provides an easy-to-use interface to a mass spectrometry based non-target analysis workflow. Various (open-source) tools are combined which provide algorithms for extraction and grouping of features, extraction of MS and MS/MS data, automatic formula and compound annotation and grouping related features to components. In addition, various tools are provided for e.g. data preparation and cleanup, plotting results and automatic reporting.

**License** GPL-3

**LazyData** TRUE

**RoxygenNote** 7.1.2

**URL** <https://github.com/rickhelmus/patRoön>

**BugReports** <https://github.com/rickhelmus/patRoön/issues>

**Encoding** UTF-8

**Depends** R (>= 3.5.0)

**SystemRequirements** GNU make

**Imports** methods,  
checkmate (>= 1.8.5),  
Rcpp,  
VennDiagram,  
UpSetR,  
stats,  
utils,  
parallel,  
grid,  
graphics,  
RColorBrewer,  
data.table,  
withr,  
digest,

enviPick,  
DBI,  
RSQLite ( $\geq 2.2.4$ ),  
fst,  
processx,  
tools,  
MSnbase,  
Biobase,  
BiocParallel,  
xcms,  
cluster,  
fastcluster,  
gplots,  
heatmaply,  
dynamicTreeCut,  
dendextend,  
igraph,  
visNetwork,  
rJava,  
rcdk,  
fingerprint,  
mzR,  
circlize,  
miniUI,  
rhandsontable,  
rstudioapi,  
htmlwidgets,  
shiny,  
shinyjs,  
CAMERA,  
enviPat,  
nontarget,  
knitr,  
rmarkdown,  
flexdashboard,  
DT,  
magrittr,  
kableExtra,  
R.utils,  
magick,  
glue,  
jsonlite,  
Rdpack,  
rsm,  
future,  
future.apply,  
fs,  
yaml,

keys,  
backports

**Suggests** RDCOMClient,

metfRag,  
RAMClustR,  
KPIC,  
MetaClean,  
MetaCleanData,  
testthat,  
rlang,  
vdiffR,  
patRoonData,  
devtools,  
covr,  
DiagrammeR,  
DiagrammeRsvg,  
rsvg,  
pkgload

**LinkingTo** Rcpp

**RdMacros** Rdpack

**Collate** 'RcppExports.R'

'generics.R'  
'cache.R'  
'main.R'  
'workflow-step.R'  
'TP.R'  
'TP-biotransformer.R'  
'TP-library.R'  
'features.R'  
'workflow-step-set.R'  
'features-set.R'  
'feature\_groups.R'  
'feature\_groups-set.R'  
'TP-logic.R'  
'utils.R'  
'utils-adduct.R'  
'adduct.R'  
'check\_ui.R'  
'utils-components.R'  
'components.R'  
'check\_components.R'  
'check\_features.R'  
'components-camera.R'  
'components-features.R'  
'components-cliquems.R'  
'components-clust.R'  
'components-intclust.R'

'components-set.R'  
'components-nontarget.R'  
'components-nontarget-set.R'  
'components-openms.R'  
'components-ramclustr.R'  
'components-specclust.R'  
'feature\_annotatons.R'  
'formulas.R'  
'mspeaklists.R'  
'compounds.R'  
'utils-compounds.R'  
'utils-screening.R'  
'feature\_groups-screening.R'  
'feature\_groups-screening-set.R'  
'components-tps.R'  
'compounds-cluster.R'  
'compounds-metfrag.R'  
'utils-feat\_annotatons-set.R'  
'compounds-set.R'  
'utils-sirius.R'  
'compounds-sirius.R'  
'convert.R'  
'defunct.R'  
'deprecated.R'  
'utils-IPO.R'  
'doe-optimizer.R'  
'feature\_groups-bruker.R'  
'feature\_groups-comparison.R'  
'feature\_groups-envimass.R'  
'feature\_groups-filter.R'  
'feature\_groups-kpic2.R'  
'feature\_groups-openms.R'  
'feature\_groups-optimize.R'  
'feature\_groups-optimize-kpic2.R'  
'feature\_groups-optimize-openms.R'  
'feature\_groups-optimize-xcms.R'  
'feature\_groups-optimize-xcms3.R'  
'feature\_groups-sirius.R'  
'feature\_groups-tasq.R'  
'feature\_groups-xcms.R'  
'feature\_groups-xcms3.R'  
'utils-bruker.R'  
'features-bruker.R'  
'features-envipick.R'  
'features-kpic2.R'  
'features-openms.R'  
'features-optimize.R'  
'features-optimize-envipick.R'

'features-optimize-kpic2.R'  
 'features-optimize-openms.R'  
 'features-optimize-xcms.R'  
 'features-optimize-xcms3.R'  
 'features-safed.R'  
 'features-sirius.R'  
 'features-tasq.R'  
 'features-xcms.R'  
 'features-xcms3.R'  
 'formulas-bruker.R'  
 'formulas-genform.R'  
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 'utils-formulas.R'  
 'utils-mol.R'  
 'utils-mspeaklists.R'  
 'utils-optimize.R'  
 'utils-plot.R'  
 'utils-progress.R'  
 'utils-sets.R'  
 'utils-xcms.R'  
 'zzz.R'

**VignetteBuilder** knitr

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## Description

Provides an easy-to-use interface to a mass spectrometry based non-target analysis workflow. Various (open-source) tools are combined which provide algorithms for extraction and grouping of features, extraction of MS and MS/MS data, automatic formula and compound annotation and grouping related features to components. In addition, various tools are provided for e.g. data preparation and cleanup, plotting results and automatic reporting.

## Package options

The following package options (see [options](#)) can be set:

- `patRoan.cache.mode`: A character setting the current caching mode: "save" and "load" will only save/load results to/from the cache, "both" (default) will do both and "none" to completely disable caching. This option can be changed anytime, which might be useful, for instance, to temporarily disable cached results before running a function.
- `patRoan.cache.fileName`: a character specifying the name of the cache file (default is 'cache.sqlite').
- `patRoan.MP.maxProcs`: The maximum number of processes that should be initiated in parallel. A good starting point is the number of physical cores, which is the default as detected by [detectCores](#). This option is only used when `'patRoan.MP.method="classic"'`.
- `patRoan.MP.method`: Either "classic" or "future". The former is the default and uses **processx** to execute multiple commands in parallel. When "future" the [future.apply](#) package is used for parallelization, which is especially useful for e.g. cluster computing.
- `patRoan.MP.futureSched`: Sets the `future.scheduling` function argument for [future\\_lapply](#). Only used if `'patRoan.MP.method="future"'`.
- `patRoan.MP.logPath`: The path used for logging of output from commands executed by `multiprocess`. Set to FALSE to disable logging.
- `patRoan.path.pwiz`: The path in which the ProteoWizard binaries are installed. If unset an attempt is made to find this directory from the Windows registry and 'PATH' environment variable.
- `patRoan.path.GenForm`: The path to the GenForm executable. If not set (the default) the internal GenForm binary is used. Only set if you want to override the executable.
- `patRoan.path.MetFragCL`: The complete file path to the MetFrag CL 'jar' file that *must* be set when using [generateCompoundsMetFrag](#). Example: "C:/MetFrag2.4.2-CL.jar".
- `patRoan.path.MetFragCompTox`: The complete file path to the CompTox database 'csv' file. See [generateCompounds](#) for more details.
- `patRoan.path.MetFragPubChemLite`: The complete file path to the PubChem database 'csv' file. See [generateCompounds](#) for more details.

- `patRoan.path.SIRIUS`: The directory in which SIRIUS is installed. Unless the binaries can be located via the 'PATH' environment variable, this *must* be set when using [generateFormulasSIRIUS](#) or [generateCompoundsSIRIUS](#). Example: "C:/sirius-win64-3.5.1".
- `patRoan.path.OpenMS`: The path in which the OpenMS binaries are installed. Usually the location is added to the 'PATH' environment variable when OpenMS is installed, in which case this option can be left empty.
- `patRoan.path.pngquant`: The path of the pngquant binary that is used when optimizing '.png' plots generated by [reportHTML](#) (with `optimizePng` set to `TRUE`). If the binary can be located through the 'PATH' environment variable this option can remain empty. Note that some of the functionality of `reportHTML` only locates the binary through the 'PATH' environment variable, hence, it is recommended to set up 'PATH' instead.
- `patRoan.path.obabel`: The path in which the OpenBabel binaries are installed. Usually the location is added to the 'PATH' environment variable when OpenBabel is installed, in which case this option can be left empty.
- `patRoan.path.Biotransformer`: The full file path to the biotransformer '.jar' command line utility. This needs to be set when [generateTPsBioTransformer](#) is used. For more details see <https://bitbucket.org/djoumbou/biotransformer/src/master>.

#### Author(s)

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#### See Also

Useful links:

- <https://github.com/rickhelmus/patRoan>
- Report bugs at <https://github.com/rickhelmus/patRoan/issues>

---

adduct-class

*Generic adduct class*

---

#### Description

Objects from this class are used to specify adduct information in an algorithm independent way.



## Usage

```
adduct(...)  
  
## S4 method for signature 'adduct'  
show(object)  
  
## S4 method for signature 'adduct'  
as.character(x, format = "generic", err = TRUE)
```

## Arguments

|           |   |
|-----------|---|
| x, object | An adduct object.   |
| format    | A character that specifies the source format.<br>"generic" is an internally used generic format that supports full textual conversion. Examples: "[M+H]+", "[2M+H]+", "[M+3H]3+".<br>"sirius" Is the format used by SIRIUS. It is similar to generic but does not allow multiple charges/molecules. See the SIRIUS manual for more details.<br>"genform" and "metfrag" support fixed types of adducts which can be obtained with the GenFormAdducts and MetFragAdducts functions, respectively.<br>"openms" is the format used by the MetaboliteAdductDecharger tool.<br>"cliquems" is the format used by <b>cliqueMS</b> . |
| err       | If TRUE then an error will be thrown if conversion fails, otherwise returns NA.   |
| ...       | Any of add, sub, molMult and/or charge. See Slots.  |

## Methods (by generic)

- show: Shows summary information for this object.
- as.character: Converts an adduct object to a specified character format.

## Slots

add,sub A character with one or more formulas to add/subtract.

molMult How many times the original molecule is present in this molecule (e.g. for a dimer this would be '2'). Default is '1'.

charge The final charge of the adduct (default '1').

## See Also

[as.adduct](#) for easy creation of adduct objects and [adduct utilities](#) for other adduct functionality.

## Examples

```
adduct("H") # [M+H]+  
adduct(sub = "H", charge = -1) # [M-H]-  
adduct(add = "K", sub = "H2", charge = -1) # [M+K-H2]+  
adduct(add = "H3", charge = 3) # [M+H3]3+  
adduct(add = "H", molMult = 2) # [2M+H]+
```

```
as.character(adduct("H")) # returns "[M+H]+"
```

---

adduct-utils

*Adduct utilities*


---

## Description

Several utility functions to work with adducts.

## Usage

```
GenFormAdducts()
```

```
MetFragAdducts()
```

```
as.adduct(x, format = "generic", isPositive = NULL, charge = NULL)
```

```
calculateIonFormula(formula, adduct)
```

```
calculateNeutralFormula(formula, adduct)
```

## Arguments

|            |   |
|------------|---|
| x          | The object that should be converted. Should be a character string, a numeric MetFrag adduct identifier (adduct_mode column obtained with MetFragAdducts) or an <a href="#">adduct</a> object (in which case no conversion occurs).  |
| format     | A character that specifies the source format.<br><p>"generic" is an internally used generic format that supports full textual conversion. Examples: "[M+H]+", "[2M+H]+", "[M+3H]3+".</p> <p>"sirius" Is the format used by SIRIUS. It is similar to generic but does not allow multiple charges/molecules. See the SIRIUS manual for more details.</p> <p>"genform" and "metfrag" support fixed types of adducts which can be obtained with the GenFormAdducts and MetFragAdducts functions, respectively.</p> <p>"openms" is the format used by the MetaboliteAdductDecharger tool.</p> <p>"cliquems" is the format used by <b>cliqueMS</b>.</p> |
| isPositive | A logical that specifies whether the adduct should be positive. Should only be set when format="metfrag" and x is a numeric identifier.   |
| charge     | The final charge. Only needs to be set when format="openms".  |
| formula    | A character vector with formulae to convert.  |
| adduct     | An <a href="#">adduct</a> object (or something that can be converted to it with <a href="#">as.adduct</a> ). Examples: "[M-H]-", "[M+Na]+"  |

## Details

GenFormAdducts returns a table with information on adducts supported by GenForm.

MetFragAdducts returns a table with information on adducts supported by MetFrag.

as.adduct Converts an object in to an [adduct](#) object.

calculateIonFormula Converts one or more neutral formulae to adduct ions.

calculateNeutralFormula Converts one or more adduct ions to neutral formulae.

## Examples

```
as.adduct("[M+H]+")
as.adduct("[M+H2]2+")
as.adduct("[2M+H]+")
as.adduct("[M-H]-")
as.adduct("+H", format = "genform")
as.adduct(1, isPositive = TRUE, format = "metfrag") # MetFrag adduct ID 1 --> returns [M+H]+

calculateIonFormula("C2H40", "[M+H]+") # C2H50
calculateNeutralFormula("C2H50", "[M+H]+") # C2H40
```

---

analysis-information    *Analysis information*

---

## Description

Required information for analyses that should be processed and utilities to automatically generate this information.

## Usage

```
generateAnalysisInfo(
  paths,
  groups = "",
  blanks = "",
  concs = NULL,
  formats = MSFileFormats()
)

generateAnalysisInfoFromEnviMass(path)
```

## Arguments

|                |   |
|----------------|---|
| paths          | A character vector containing one or more file paths that should be used for finding the analyses.  |
| groups, blanks | An (optional) character vector containing replicate groups and references, respectively (will be recycled). If groups is an empty character string ("") the analysis name will be set as replicate group. |

|         |   |
|---------|---|
| concs   | An optional numeric vector containing concentration values for each analysis. Can be NA if unknown. If the length of concs is less than the number of analyses the remainders will be set to NA. Set to NULL to not include concentration data. |
| formats | A character vector of analyses file types. Valid values are: Bruker, mzXML and mzML.  |
| path    | The path of the enviMass project.   |

## Details

Several properties need to be known about analyses that should be processed during various workflow steps such as [finding features](#), averaging intensities of feature groups and blank subtraction. This information should be made available with an 'analysis info' object, which is a `data.frame` containing the following columns:

- path the full path to the analysis.
- analysis the filename **without** extension. Must be **unique**, even if the path is different.
- group name of *replicate group*. A replicate group is used to group analyses together that are replicates of each other. Thus, the group column for all analyses considered to be belonging to the same replicate group should have an equal (but unique) value. Used for *e.g.* averaging and [filter](#).
- blank: all analyses within this replicate group are used by [filter](#) for blank subtraction. Multiple entries can be entered by separation with a comma.
- conc a numeric value specifying the 'concentration' of the analysis. This can be actually any kind of quantitative value such as exposure time, dilution factor or anything else which may be used to form a linear relationship.

Most functionality requires the data files to be in either the '.mzXML' or '.mzML' format. Functionality that utilizes Bruker DataAnalysis (*e.g.* [findFeaturesBruker](#)) may only work with data files in the proprietary '.d' format. Therefore, when tools with varying requirements are mixed (a common scenario), the data files also need to be present in the required formats. To deal with this situation the data files with varying formats should all be placed in the same path that was used to specify the location of the analysis.

Whether analysis data files are present in multiple formats or not, each analysis should only be entered *once*. The analysis column is used as a basename to automatically find back the data file with the required format, hence, analysis names should be specified as the file name without its file extension.

The group column is *mandatory* and needs to be filled in for each analysis. The blank column should also be present, however, these may contain empty character strings ("") for analyses where no blank subtraction should occur. The conc column is only required when obtaining regression information is desired with the [as.data.table](#) method.

`generateAnalysisInfo` is an utility function that automatically generates an analysis information object. It will collect all datafiles from given file paths and convert the filenames into valid analysis names (*i.e.* without extensions such as '.d' and '.mzML'). Duplicate analyses, which may appear when datafiles with different file extension ('.d', '.mzXML' and/or '.mzML') are present, will be automatically removed.

`generateAnalysisInfoFromEnviMass` loads analysis information from an **enviMass** project. Note: this functionality has only been tested with older versions of **enviMass**.

**Description**

Miscellaneous utility functions which interface with Bruker DataAnalysis

**Usage**

```
showDataAnalysis()

setDAMethod(anaInfo, method, close = TRUE)

revertDAAnalyses(anaInfo, close = TRUE, save = close)

recalibrateDAFiles(anaInfo, close = TRUE, save = close)

getDACalibrationError(anaInfo)

addDAEIC(
  analysis,
  path,
  mz,
  mzWindow = 0.005,
  ctype = "EIC",
  mtype = "MS",
  polarity = "both",
  bgsubtr = FALSE,
  fragpath = "",
  name = NULL,
  hideDA = TRUE,
  close = FALSE,
  save = close
)

addAllDAEICs(
  fGroups,
  mzWindow = 0.005,
  ctype = "EIC",
  bgsubtr = FALSE,
  name = TRUE,
  onlyPresent = TRUE,
  hideDA = TRUE,
  close = FALSE,
  save = close
)
```

## Arguments

|             |   |
|-------------|---|
| anaInfo     | <a href="#">Analysis info table</a>   |
| method      | The full path of the DataAnalysis method.   |
| close, save | If TRUE then Bruker files are closed and saved after processing with DataAnalysis, respectively. Setting close=TRUE prevents that many analyses might be opened simultaneously in DataAnalysis, which otherwise may use excessive memory or become slow. By default save is TRUE when close is TRUE, which is likely what you want as otherwise any processed data is lost. |
| analysis    | Analysis name (without file extension).   |
| path        | path of the analysis.   |
| mz          | $m/z$ (Da) value used for the chromatographic trace (if applicable).  |
| mzWindow    | $m/z$ window (in Da) used for the chromatographic trace (if applicable).  |
| ctype       | Type of the chromatographic trace. Valid options are: "EIC" (extracted ion chromatogram), "TIC" (total ion chromatogram, only for addDAEIC) and "BPC" (Base Peak Chromatogram).   |
| mtype       | MS filter for chromatographic trace. Valid values are: "all", "MS", "MSMS", "allMSMS" and "BBCID".  |
| polarity    | Polarity filter for chromatographic trace. Valid values: "both", "positive" and "negative".   |
| bgsubtr     | If TRUE then background subtraction ('Spectral' algorithm) will be performed.   |
| fragpath    | Precursor $m/z$ used for MS/MS traces ("" for none).  |
| name        | For addDAEIC: the name for the chromatographic trace. For addAllEICs: TRUE to automatically set EIC names. Set to NULL for none.  |
| hideDA      | Hides DataAnalysis while adding the chromatographic trace (faster).   |
| fGroups     | The <a href="#">featureGroups</a> object for which EICs should be made.   |
| onlyPresent | If TRUE then EICs are only generated for analyses where the feature was detected.   |

## Details

These functions communicate directly with Bruker DataAnalysis to provide various functionality, such as calibrating and exporting data and adding chromatographic traces. For this the **RDCOM-Client** package is required to be installed.

showDataAnalysis makes a hidden DataAnalysis window visible again. Most functions using DataAnalysis will hide the window during processing for efficiency reasons. If the window remains hidden (*e.g.* because there was an error) this function can be used to make it visible again. This function can also be used to start DataAnalysis if it is not running yet.

setDAMethod Sets a given DataAnalysis method ('.m' file) to a set of analyses. **NOTE:** as a workaround for a bug in DataAnalysis, this function will save(!), close and re-open any analyses that are already open prior to setting the new method. The close argument only controls whether the file should be closed after setting the method (files are always saved).

revertDAAnalyses Reverts a given set of analyses to their unprocessed raw state.

recalibrateDAFiles Performs automatic mass recalibration of a given set of analyses. The current method settings for each analyses will be used.

getDacalibrationError is used to obtain the standard deviation of the current mass calibration (in ppm).

addDAEIC adds an Extracted Ion Chromatogram (EIC) or other chromatographic trace to a given analysis which can be used directly with DataAnalysis.

addAllDAEICs adds Extracted Ion Chromatograms (EICs) for all features within a [featureGroups](#) object.

### Value

getDacalibrationError returns a data.frame with a column of all analyses (named analysis) and their mass error (named error).

### See Also

[analysis-information](#)

---

check-GUI

*Interactive GUI utilities to check workflow data*

---

### Description

These functions provide interactive utilities to explore and review workflow data using a [shiny](#) graphical user interface (GUI). In addition, unsatisfactory data (*e.g.* noise identified as a feature and unrelated feature groups in a component) can easily be selected for removal.

### Usage

```
## S4 method for signature 'components'
checkComponents(
  components,
  fGroups,
  session = "checked-components.yml",
  rtWindow = 30,
  clearSession = FALSE
)

importCheckFeaturesSession(
  sessionIn,
  sessionOut,
  fGroups,
  rtWindow = 6,
  mzWindow = 0.002,
  overWrite = FALSE
)
```

```
## S4 method for signature 'featureGroups'
checkFeatures(
  fGroups,
  session = "checked-features.yml",
  rtWindow = 30,
  clearSession = FALSE
)

getMCTrainData(fGroups, session)

predictCheckFeaturesSession(fGroups, session, model = NULL, overWrite = FALSE)
```

## Arguments

|                       |   |
|-----------------------|---|
| components            | The <a href="#">components</a> to be checked.   |
| fGroups               | A <a href="#">featureGroups</a> object.<br>This should be the 'new' object for <code>importCheckFeaturesSession</code> for which the session needs to be imported.  |
| session               | The session file name.  |
| rtWindow              | For <code>checkFeatures</code> and <code>checkComponents</code> : the retention time (in seconds) that will be subtracted/added to respectively the minimum and maximum retention time of the plotted feature groups. Thus, setting this value to a positive value will 'zoom out' on the retention time axis.<br>For <code>importCheckFeaturesSession</code> : the retention time window (seconds) used to relate 'old' with 'new' feature groups. |
| clearSession          | If TRUE the session will be completely cleared before starting the GUI. This effectively removes all selections for data removal.   |
| sessionIn, sessionOut | The file names for the input and output sessions.   |
| mzWindow              | The <i>m/z</i> window (in Da) used to relate 'old' with 'new' feature groups.   |
| overWrite             | Set to TRUE to overwrite the output session file if it already exists. If FALSE, the function will stop with an error message.  |
| model                 | The model that was created with <b>MetaClean</b> and that should be used to predict pass/fail data. If NULL, the example model of the <b>MetaCleanData</b> package is used.   |

## Details

The data selected for removal is stored in *sessions*. These are 'YAML' files to allow easy external manipulation. The sessions can be used to restore the selections that were made for data removal when the GUI tool is executed again. Furthermore, functionality is provided to import and export sessions. To actually remove the data the [filter](#) method should be used with the session file as input.

`checkComponents` is used to review components and their feature groups contained within. A typical use case is to verify that peaks from features that were annotated as related adducts and/or isotopes are correctly aligned.



importCheckFeaturesSession is used to import a session file that was generated from a different [featureGroups](#) object. This is useful to avoid re-doing manual interpretation of chromatographic peaks when, for instance, feature group data is re-created with different parameters.

checkFeatures is used to review chromatographic information for feature groups. Its main purpose is to assist in reviewing the quality of detected feature (groups) and easily select unwanted data such as features with poor peak shapes or noise.

getMCTrainData converts a session created by checkFeatures to a data.frame that can be used by the **MetaClean** to train a new model. The output format is comparable to that from [getPeakQualityMetrics](#).

predictCheckFeaturesSession Uses ML data from **MetaClean** to predict the quality (Pass/Fail) of feature group data, and converts this to a session which can be reviewed with checkFeatures and used to remove unwanted feature groups by [filter](#).

**Note**

checkComponents: Some componentization algorithms (e.g. [generateComponentsNontarget](#) and [generateComponentsTPs](#)) may output components where the same feature group in a component is present multiple times, for instance, when multiple TPs are matched to the same feature group. If such a feature group is selected for removal, then *all* of its result in the component will be marked for removal.

getMCTrainData only uses session data for selected feature groups. Selected features for removal are ignored, as this is not supported by **MetaClean**.

**References**

Chetnik K, Petrick L, Pandey G (2020). “MetaClean: a machine learning-based classifier for reduced false positive peak detection in untargeted LC-MS metabolomics data.” *Metabolomics*, **16**(11). doi: [10.1007/s11306020017383](https://doi.org/10.1007/s11306020017383).

---

|            |                                |
|------------|--------------------------------|
| clearCache | <i>Clearing of cached data</i> |
|------------|--------------------------------|

---

**Description**

Remove (part of) the cache database used to store (intermediate) processing results.

**Usage**

```
clearCache(what = NULL, file = NULL)
```

**Arguments**

|      |  |
|------|--|
| what | This argument describes what should be done. When what = NULL this function will list which tables are present along with an indication of their size (database rows). If what = "all" then the complete file will be removed. Otherwise, what should be a character string (a regular expression) that is used to match the table names that should be removed. |
| file | The cache file. If NULL then the value of the patRoos.cache.fileName option is used.   |

## Details

This function will either remove one or more tables within the cache sqlite database or simply wipe the whole cache file. Removing tables will VACUUM the database, which may take some time for large cache files.

---

component-generation    *Grouping feature groups in components*

---

## Description

Functionality to automatically group related feature groups (*e.g.* isotopes, adducts and homologues) to assist and simplify compound annotation.

## Usage

```
## S4 method for signature 'featureGroups'
generateComponents(fGroups, algorithm, ...)

## S4 method for signature 'featureGroups'
generateComponentsCAMERA(
  fGroups,
  ionization = NULL,
  onlyIsotopes = FALSE,
  minSize = 2,
  relMinReplicates = 0.5,
  extraOpts = NULL
)

## S4 method for signature 'featureGroupsSet'
generateComponentsCAMERA(fGroups, ionization = NULL, ...)

## S4 method for signature 'featureGroups'
generateComponentsCliqueMS(
  fGroups,
  ionization = NULL,
  maxCharge = 1,
  maxGrade = 2,
  ppm = 10,
  adductInfo = NULL,
  absMzDev = 0.005,
  minSize = 2,
  relMinAdductAbundance = 0.75,
  adductConflictsUsePref = TRUE,
  NMConflicts = c("preferential", "mostAbundant", "mostIntense"),
  prefAdducts = c("[M+H]+", "[M-H]-"),
  extraOptsCli = NULL,
```

```
    extraOptsIso = NULL,
    extraOptsAnn = NULL,
    parallel = TRUE
)

## S4 method for signature 'featureGroupsSet'
generateComponentsCliqueMS(fGroups, ionization = NULL, ...)

## S4 method for signature 'featureGroups'
generateComponentsIntClust(
  fGroups,
  method = "complete",
  metric = "euclidean",
  normFunc = max,
  average = TRUE,
  maxTreeHeight = 1,
  deepSplit = TRUE,
  minModuleSize = 1
)

## S4 method for signature 'featureGroups'
generateComponentsNontarget(
  fGroups,
  ionization = NULL,
  rtRange = c(-120, 120),
  mzRange = c(5, 120),
  elements = c("C", "H", "O"),
  rtDev = 30,
  absMzDev = 0.002,
  absMzDevLink = absMzDev * 2,
  traceHack = all(R.Version()[c("major", "minor")] >= c(3, 4)),
  ...
)

## S4 method for signature 'featureGroupsSet'
generateComponentsNontarget(fGroups, ionization = NULL, ...)

## S4 method for signature 'featureGroups'
generateComponentsOpenMS(
  fGroups,
  ionization = NULL,
  chargeMin = 1,
  chargeMax = 1,
  chargeSpan = 3,
  qTry = "heuristic",
  potentialAdducts = NULL,
  minRTOverlap = 0.66,
  retWindow = 1,
```

```

    absMzDev = 0.005,
    minSize = 2,
    relMinAdductAbundance = 0.75,
    adductConflictsUsePref = TRUE,
    NMConflicts = c("preferential", "mostAbundant", "mostIntense"),
    prefAdducts = c("[M+H]+", "[M-H]-"),
    extraOpts = NULL
)

## S4 method for signature 'featureGroupsSet'
generateComponentsOpenMS(
  fGroups,
  ionization = NULL,
  chargeMin = 1,
  chargeMax = 1,
  chargeSpan = 3,
  qTry = "heuristic",
  potentialAdducts = NULL,
  ...
)

defaultOpenMSAdducts(ionization)

## S4 method for signature 'featureGroups'
generateComponentsRAMClustR(
  fGroups,
  ionization = NULL,
  st = NULL,
  sr = NULL,
  maxt = 12,
  hmax = 0.3,
  normalize = "TIC",
  absMzDev = 0.002,
  relMzDev = 5,
  minSize = 2,
  relMinReplicates = 0.5,
  RCExperimentVals = list(design = list(platform = "LC-MS"), instrument =
    list(ionization = ionization, MSlevs = 1)),
  extraOptsRC = NULL,
  extraOptsFM = NULL
)

## S4 method for signature 'featureGroupsSet'
generateComponentsRAMClustR(fGroups, ionization = NULL, ...)

## S4 method for signature 'featureGroups'
generateComponentsSpecClust(
  fGroups,

```

```

    MSPeakLists,
    method = "complete",
    specSimParams = getDefSpecSimParams(),
    maxTreeHeight = 1,
    deepSplit = TRUE,
    minModuleSize = 1
)

## S4 method for signature 'featureGroups'
generateComponentsTPs(
  fGroups,
  fGroupsTPs = fGroups,
  ignoreParents = FALSE,
  TPs = NULL,
  MSPeakLists = NULL,
  formulas = NULL,
  compounds = NULL,
  minRTDiff = 20,
  specSimParams = getDefSpecSimParams()
)

## S4 method for signature 'featureGroupsSet'
generateComponentsTPs(
  fGroups,
  fGroupsTPs = fGroups,
  ignoreParents = FALSE,
  TPs = NULL,
  MSPeakLists = NULL,
  formulas = NULL,
  compounds = NULL,
  minRTDiff = 20,
  specSimParams = getDefSpecSimParams()
)

```

## Arguments

|                         |  |
|-------------------------|--|
| <code>fGroups</code>    | <code>featureGroups</code> object for which components should be generated.<br>For <code>generateComponentsTPs</code> : also see the <code>fGroupsTPs</code> argument.   |
| <code>algorithm</code>  | A character string describing the algorithm that should be used: "ramclustr", "camera", "nontarget", "intclust", "openms", "cliquems", "specclust", "tp"   |
| <code>...</code>        | Any parameters to be passed to the selected component generation algorithm.<br>For sets workflows: further arguments directly passed to the non-sets method.   |
| <code>ionization</code> | Which ionization polarity was used to generate the data: should be "positive" or "negative". If the <code>featureGroups</code> object has adduct annotations, and <code>ionization=NULL</code> , the ionization will be detected automatically.<br>( <b>sets workflow</b> ) This parameter is not supported for sets workflows, as the ionization will always be detected automatically. |

|  |  |
|--|--|
| onlyIsotopes                             | Logical value. If TRUE only isotopes are considered when generating components (faster). Corresponds to quick argument of <code>CAMERA::annotate</code> .  |
| minSize                                  | The minimum size of a component. Smaller components than this size will be removed. For <code>RAMClustR</code> : sets the <code>minModuleSize</code> argument to <code>ramclustR</code> . See note below.  |
| relMinReplicates                         | Feature groups within a component are only kept when they contain data for at least this (relative) amount of replicate analyses. For instance, '0.5' means that at least half of the replicates should contain data for a particular feature group in a component. In this calculation replicates that are fully absent within a component are not taken in to account. See note below.   |
| extraOpts                                | Named character vector with extra arguments directly passed to <code>CAMERA::annotate</code> ( <code>generateComponentsCAMERA</code> ) or as extra command line parameters to <code>MetaboliteAdductDecharger</code> ( <code>generateComponentsCAMERA</code> ). Set to NULL to ignore.   |
| maxCharge, maxGrade, ppm                 | Arguments passed to <code>cliqueMS::getIsotopes</code> and/or <code>cliqueMS::getAnnotation</code> .   |
| adductInfo                               | Sets the <code>adinfo</code> argument to <code>cliqueMS::getAnnotation</code> . If NULL then the default adduct information from <code>cliqueMS</code> is used ( <i>i.e.</i> the <code>positive.adinfo/negative.adinfo</code> package datasets).   |
| relMinAdductAbundance                    | The minimum relative abundance ('0-1') that an adduct should be assigned to features within the same feature group. See the Feature components section for more details.   |
| adductConflictsUsePref                   | If set to TRUE, and not all adduct assignments to the features within a feature group are equal and at least one of those adducts is a preferential adduct ( <code>prefAdducts</code> argument), then only the features with (the lowest ranked) preferential adduct are considered. In all other cases or when <code>adductConflictsUsePref=FALSE</code> only features with the most frequently assigned adduct is considered. See the Feature components section for more details. |
| NMConflicts                              | The strategies to employ when not all neutral masses within a component are equal. Valid options are: "preferential", "mostAbundant" and "mostIntense". Multiple strategies are possible, and will be executed in the given order until one succeeds. See the Feature components section for more details.   |
| prefAdducts                              | A character vector with one or more <i>preferential adducts</i> . See the Feature components section for more details.   |
| extraOptsCli, extraOptsIso, extraOptsAnn | Named list with further arguments to be passed to <code>cliqueMS::getCliques</code> , <code>cliqueMS::getIsotopes</code> and <code>cliqueMS::getAnnotation</code> , respectively. Set to NULL to ignore.   |
| parallel                                 | If set to TRUE then code is executed in parallel through the <code>futures</code> package. Please see the parallelization section in the handbook for more details.  |
| method                                   | Clustering method that should be applied (passed to <code>fastcluster::hclust</code> ).  |
| metric                                   | Distance metric used to calculate the distance matrix (passed to <code>daisy</code> ).   |
| normFunc, average                        | Passed to <code>as.data.table</code> to perform normalization and averaging of data.   |

|   |   |
|---|---|
| maxTreeHeight, deepSplit, minModuleSize | Arguments used by <a href="#">cutreeDynamicTree</a> .   |
| rtRange                                 | A numeric vector containing the minimum and maximum retention time (in seconds) between homologues. Series are always considered from low to high $m/z$ , thus, a negative minimum retention time allows detection of homologous series with increasing $m/z$ and decreasing retention times. These values set the minrt and maxrt arguments of <a href="#">homol.search</a> .  |
| mzRange                                 | A numeric vector specifying the minimum and maximum $m/z$ increment of a homologous series. Sets the minmz and maxmz arguments of <a href="#">homol.search</a> .  |
| elements                                | A character vector with elements to be considered for detection of repeating units. Sets the elements argument of <a href="#">homol.search</a> function.  |
| rtDev, absMzDev, relMzDev               | Maximum deviation for retention time or absolute/relative $m/z$ .<br>For generateComponentsRAMClustR: Sets the mzabs.error and ppm.error arguments to <a href="#">do.findmain</a> .<br>For generateComponentsNontarget: Sets the rttol and mztol arguments of <a href="#">homol.search</a> .<br>For generateComponentsOpenMS: Sets the algorithm:MetaboliteFeatureDeconvolution:mass_max option.  |
| absMzDevLink                            | Maximum absolute $m/z$ deviation when linking series. This should usually be a bit higher than absMzDev to ensure proper linkage.   |
| traceHack                               | Currently <a href="#">homol.search</a> does not work with R '>3.3.3'. This flag, which is enabled by default on these R versions, implements a (messy) workaround ( <a href="#">more details here</a> ).  |
| chargeMin, chargeMax                    | The minimum/maximum charge to consider. Corresponds to the algorithm:MetaboliteFeatureDeconvolution:charge options.   |
| chargeSpan                              | The maximum charge span for a single analyte. Corresponds to algorithm:MetaboliteFeatureDeconvolution:charge_span option.   |
| qTry                                    | Sets how charges are determined. Corresponds to algorithm:MetaboliteFeatureDeconvolution:q_try option. Valid options are "heuristic" and "all" (the "feature" option from OpenMS is currently not supported).   |
| potentialAdducts                        | The adducts to consider. Should be a numeric vector with probabilities for each adduct, e.g. potentialAdducts=c("[M+H]+" = 0.8, "[M+Na]+" = 0.2). Note that the sum of probabilities should always be '1'. Furthermore, note that additions of multiple adducts should be controlled by the chargeMin/chargeMax arguments (and <i>not</i> with potentialAdducts), e.g. if chargeMax=2 then both [M+H]+ and [2M+H]2+ may be considered. Please see the algorithm:MetaboliteFeatureDeconvolution:metabolite_adducts option of <a href="#">MetaboliteAdductDecharger</a> for more details. If NULL then the default is chosen with defaultOpenMSAdducts (which is <i>not</i> the same as OpenMS).<br>( <b>sets workflow</b> ) Should be a list where each entry specifies the potential adducts for a set. Should either be named with the sets names or follow the same order as sets(fGroups). Example: potentialAdducts=list(positive=c("[M+H]+" = 0.8, "[M+Na]+" = 0.2), negative=c("[M-H]-" = 0.8, "[M-H2O-H]-" = 0.2)) |

|  |   |
|--|---|
| <code>minRTOverlap, retWindow</code>       | Sets feature retention tolerances when grouping features. Sets the "algorithm:MetaboliteFeatureDeco" and <code>algorithm:MetaboliteFeatureDeconvolution:min_rt_overlap</code> options.  |
| <code>st, sr, maxt, hmax, normalize</code> | Arguments to tune the behaviour of feature group clustering. See their documentation from <a href="#">ramclustR</a> . When <code>st</code> is NULL it will be automatically calculated as the half of the median for all chromatographic peak widths.   |
| <code>RCEperimentVals</code>               | A named list containing two more lists: design and instrument. These are used to construct the <code>ExpDes</code> argument passed to <a href="#">ramclustR</a> .   |
| <code>extraOptsRC, extraOptsFM</code>      | Named list with further arguments to be passed to <a href="#">ramclustR</a> and <code>do.findmain</code> . Set to NULL to ignore.   |
| <code>MSPeakLists</code>                   | The <a href="#">MSPeakLists</a> object for the given feature groups that should be used for MS spectral similarity calculations. For <code>generateComponentsTPs</code> it can be NULL, in which case no calculations are performed.  |
| <code>specSimParams</code>                 | A named list with parameters that influence the calculation of MS spectra similarities. See the <a href="#">spectral similarity parameters</a> documentation for more details.  |
| <code>fGroupsTPs</code>                    | A <a href="#">featureGroups</a> object containing the feature groups that are expected to be transformation products. If a distinction between parents and TPs is not yet known, <code>fGroupsTPs</code> should equal the <code>fGroups</code> argument. Otherwise, <code>fGroups</code> should only contain the parent feature groups, and both <code>fGroups</code> and <code>fGroupsTPs</code> <i>must</i> be a subset of the same <a href="#">featureGroups</a> object. |
| <code>ignoreParents</code>                 | If TRUE then feature groups present in both <code>fGroups</code> and <code>fGroupsTPs</code> are not considered as TPs.   |
| <code>TPs</code>                           | A <a href="#">transformationProducts</a> object. Set to NULL to perform linking without this data.  |
| <code>formulas, compounds</code>           | A <a href="#">formulas/compounds</a> object to calculate annotation similarities between parents and TPs. If NULL then this data is not calculated. For more details see the <a href="#">Linking parents and transformation products</a> section below.   |
| <code>minRTDiff</code>                     | Minimum retention time (in seconds) difference between the parent and a TP to determine whether a TP elutes prior/after the parent (to calculate <code>retDir</code> values, see Details in <a href="#">componentsTPs</a> )   |

## Details

Several algorithms are provided to group feature groups that are related in some (chemical) way to each other. These components generally include adducts, isotopes, in-source fragments and homologues. The linking of this data is generally useful to provide more information for compound annotation and reduce the data size and thus complexity.

`generateComponents` is a generic function that will generate components using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `generateComponentsRAMClustR` and `generateComponentsNontarget`. While these functions may be called directly, `generateComponents` provides a generic interface and is therefore usually preferred.



`generateComponentsCAMERA` provides an interface to **CAMERA** which is used to generate components from known adducts, isotopes and in-source fragments. The specified `featureGroups` object is automatically converted to an `xcmsSet` object using `getXCMSSet`.

`generateComponentsCliqueMS` uses **cliqueMS** to generate components using the `cliqueMS::getCliques` function. The grouping of features in each component ('clique') is based on high similarity of chromatographic elution profiles. All features in each component are then annotated with the `cliqueMS::getIsotopes` and `cliqueMS::getAnnotation` functions.

`generateComponentsIntClust` generates components based on intensity profiles of feature groups. Hierarchical clustering is performed on normalized (and optionally replicate averaged) intensity data and the resulting dendrogram is automatically cut with `cutreeDynamicTree`. The distance matrix is calculated with `daisy` and clustering is performed with `fastcluster::hclust`. The clustering of the resulting components can be further visualized and modified using the methods defined for `componentsIntClust`.

`generateComponentsNontarget` uses the **nontarget R package** to generate components by unsupervised detection of homologous series. In the first step the `homol.search` function is used to detect all homologues within each replicate group (analyses within each replicate group are averaged prior to detection). Then, homologous series across replicate groups are merged in case of full overlap or when merging of partial overlapping series causes no conflicts.

`generateComponentsOpenMS` uses the **MetaboliteAdductDecharger** utility (see <http://www.openms.de>) to generate components. Features that show highly similar chromatographic elution profiles are grouped, and subsequently annotated with their adducts.

`defaultOpenMSAdducts` returns the default adducts and their probabilities when the OpenMS algorithm is used for componentization. See the `potentialAdducts` argument for more details.

`generateComponentsRAMClustR` uses **RAMClustR** to generate components from feature groups which follow similar chromatographic retention profiles, but are not necessarily restricted to known rules (e.g. adducts or isotopes). This method uses the `ramclustR` functions for generating the components, whereas `do.findmain` is used for annotation.

`generateComponentsSpecClust` generates components based on MS/MS similarity between feature groups. The similarities are converted to a distance matrix and used as input for hierarchical clustering, and the resulting dendrogram is automatically cut with `cutreeDynamicTree`. The clustering is performed with `fastcluster::hclust`.

`generateComponentsTPs` generates components by linking feature groups of transformation products and their parents. Moreover, this method typically employs data from **generated transformation products** to find parents and their TPs. However, this data is not necessary, and components can also be made based on MS/MS similarity and/or other annotation similarities between the parent and its TPs. For more details see the Linking parents and transformation products section below.

## Value

A `components` (derived) object containing all generated components.

The algorithms based on 'feature components' return a `componentsFeatures` derived object.

`generateComponentsIntClust` and `generateComponentsSpecClust` return objects derived from `componentsSpecClust`.

`generateComponentsTPs` returns objects derived from `componentsTPs`.

## Feature components

Components resulting from `generateComponentsCliqueMS` and `generateComponentsOpenMS` are based on so called *feature components*. Unlike other algorithms, components are first made on a feature level (per analysis), instead of for complete feature groups. In the final step the feature components are converted to 'regular' components by employing a consensus approach with the following steps:

1. If an adduct assigned to a feature only occurs as a minority compared to other adduct assignments within the same feature group, it is considered as an outlier and removed accordingly (controlled by the `relMinAdductAbundance` argument).
2. For features within a feature group, only keep their adduct assignment if it occurs as the most frequent or is preferential (controlled by `adductConflictsUsePref` and `prefAdducts` arguments).
3. Components are made by combining the feature groups for which at least one of their features are jointly present in the same feature component.
4. Conflicts of neutral mass assignments within a component (*i.e.* not all are the same) are dealt with. Firstly, all feature groups with an unknown neutral mass are split in another component. Then, if conflicts still occur, the feature groups with similar neutral mass (determined by `absMzDev` argument) are grouped. Depending on the `NMConflicts` argument, the group with one or more preferential adduct(s) or that is the largest or most intense is selected, whereas others are removed from the component. In case multiple groups contain preferential adducts, and '>1' preferential adducts are available, the group with the adduct that matches first in `prefAdducts` 'wins'. In case of ties, one of the next strategies in `NMConflicts` is tried.
5. If a feature group occurs in multiple components it will be removed completely.
6. the `minSize` filter is applied.

## Sets workflows

In a [sets workflow](#) the componentization data is generated differently depending on the used algorithm:

- The componentization algorithms that support annotation of adducts/isotopes, *e.g.* **RAM-ClustR**, **CAMERA** and **OpenMS**, first perform componentization for each set independently. This is necessary, because *e.g.* adducts are specific to the MS ionization mode that was used. The resulting components are then all combined in a [componentsSet](#) object. Note that the components themselves are never merged. The components are renamed to include the set name for which they were generated (*e.g.* "CMP1" becomes "CMP1-positive").
- For componentization with **nontarget** a similar strategy is applied as above. However, the output is stored in a [componentsNTSet](#) object, which supports additional methods such as `plotGraph`.
- For the componentization based on hierarchical clustering, *i.e.* the "intclust" and "specclust" algorithms, the output format is not different than for a non-sets workflow. However, for intensity based clustering, normalization of feature intensities occurs per set. For MS/MS based clustering, spectral similarities from each sets are combined as is described for the [spectrumSimilarity](#) method for sets workflows.

- For componentization of transformation products, the output class is the same ([componentsTPs](#)). However, the component tables are amended with extra information such as overall/specific set spectrum similarities. As sets data is mixed, transformation products are able to be linked with a parent, even if they were not measured in the same set.

## Parallelization

`generateComponentsOpenMS` uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoön options](#) for configuration options.

Note that for caching purposes, the analyses files must always exist on the local host computer, even if it is not participating in computations.

## Linking parents and transformation products

With `generateComponentsTPs`, each component consists of feature groups that are considered to be transformation products for one parent (the parent that 'belongs' to the component can be retrieved with the [componentInfo](#) method). The parent feature groups are taken from the `fGroups` parameter, while the feature groups for TPs are taken from `fGroupsTPs`. If a feature group occurs in both variables, it may therefore be considered as both a parent or TP.

If transformation product data is given, *i.e.* the TPs argument is set, then a suspect screening of the TPs must be performed in advance (see [screenSuspects](#) and [convertToSuspects](#) to create the suspect list). Furthermore, if TPs were generated with [generateTPsBioTransformer](#) or [generateTPsLibrary](#) then the suspect screening must also include the parents (*e.g.* by setting `includeParents=TRUE` when calling `convertToSuspects` or by amending results by setting `amend=TRUE` to `screenSuspects`). The suspect screening is necessary for the componentization algorithm to map the feature groups of the parent or TP. If the the suspect screening yields multiple TP hits, all will be reported. Similarly, if the suspect screening contains multiple hits for a parent, a component is made for each of the parent hits.

In case no transformation product data is provided (`TPs=NULL`), the componentization algorithm simply assumes that each feature group from `fGroupsTPs` is a potential TP for every parent feature group in `fGroups`. For this reason, it is highly recommended to specify which feature groups are parents/TPs (see the `fGroupsTPs` argument description above) and *crucial* that the data is post-processed, for instance by only retaining TPs that have high annotation similarity with their parents (see the [filter](#) method for [componentsTPs](#)).

An typical way to distinguish which feature groups are parents or TPs from two different (groups of) samples is by calculating Fold Changes (see the [as.data.table](#) method for feature groups and [plotVolcano](#)). Of course, other statistical techniques from R are also suitable.

During componentization, several characteristics are calculated which may be useful for post-processing:

- `specSimilarity`: the MS/MS spectral similarity between the feature groups of the TP and its parent ('0-1').
- `specSimilarityPrec`, `specSimilarityBoth`: as `specSimilarity`, but calculated with binned data using the "precursor" and "both" method, respectively (see [MS spectral similarity parameters](#) for more details).

- **fragmentMatches** The number of MS/MS fragment formula annotations that overlap between the TP and parent. If both the formulas and compounds arguments are specified then the annotation data is pooled prior to calculation. Note that only unique matches are counted. Furthermore, note that annotations from *all* candidates are considered, even if the formula/structure of the parent/TP is known. Hence, **fragmentMatches** is mainly useful when little or no chemical information is known on the parents/TPs, *i.e.*, when **TPs=NULL** or originates from **generateTPsLogic**. Since annotations for all candidates are used, it is highly recommended that the annotation objects are first processed with the **filter** method, for instance, to select only the top ranked candidates.
- **neutralLossMatches** As **fragmentMatches**, but counting overlapping neutral loss formulae.
- **retDir** The retention time direction of the TP relative to its parent. See Details in **componentsTPs**. If TP data was specified, the expected direction is stored in **TP\_retDir**.
- **retDiff,mzDiff,formulaDiff** The retention time, *m/z* and formula difference between the parent and TP (latter only available if data TP formula is available).

### Note

For **generateComponentsCAMERA** and **generateComponentsRAMClustR**: the **minSize** and **relMinReplicates** arguments provide additional filtering functionality not provided by **CAMERA** or **RAMClustR** (except **minSize**). Note that these filters are enabled by default, hence, final results may be different than what **CAMERA/RAMClustR** normally would return.

The **shift** parameter of **specSimParams** is ignored by **generateComponentsTPs**, since it always calculates similarities with all supported options.

### Author(s)

Rick Helmus <<r.helmus@uva.nl>> and Bas van de Velde (major contributions to spectral binning and similarity calculation).

### References

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---

|                  |                        |
|------------------|------------------------|
| components-class | <i>Component class</i> |
|------------------|------------------------|

---

## Description

Contains data for feature groups that are related in some way. These *components* commonly include adducts, isotopes and homologues.

## Usage

```
## S4 method for signature 'components'
componentTable(obj)

## S4 method for signature 'components'
componentInfo(obj)

## S4 method for signature 'components'
groupNames(obj)

## S4 method for signature 'components'
length(x)

## S4 method for signature 'components'
names(x)

## S4 method for signature 'components'
show(object)

## S4 method for signature 'components,ANY,ANY,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'components,ANY,ANY'
x[[i, j]]
```

```
## S4 method for signature 'components'
x$name

## S4 method for signature 'components'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'components'
as.data.table(x)

## S4 method for signature 'components'
filter(
  obj,
  size = NULL,
  adducts = NULL,
  isotopes = NULL,
  rtIncrement = NULL,
  mzIncrement = NULL,
  checkComponentsSession = NULL,
  negate = FALSE,
  verbose = TRUE
)

## S4 method for signature 'components'
findFGroup(obj, fGroup)

## S4 method for signature 'components'
plotSpectrum(obj, index, markFGroup = NULL, xlim = NULL, ylim = NULL, ...)

## S4 method for signature 'components'
plotChroms(obj, index, fGroups, rtWindow = 5, ...)

## S4 method for signature 'components'
consensus(obj, ...)

## S4 method for signature 'componentsFeatures'
show(object)

## S4 method for signature 'componentsSet'
show(object)

## S4 method for signature 'componentsSet,ANY,ANY,missing'
x[i, j, ..., sets = NULL, drop = TRUE]

## S4 method for signature 'componentsSet'
filter(obj, ..., negate = FALSE, sets = NULL)

## S4 method for signature 'componentsSet'
```

```
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'componentsSet'
consensus(obj, ...)

## S4 method for signature 'componentsSet'
unset(obj, set)
```

## Arguments

|                |  |
|----------------|--|
| obj, object, x | The component object.  |
| i, j           | For <code>[]</code> : A numeric or character value which is used to select components/feature groups by their index or name, respectively (for the order/names see <code>names()</code> / <code>groupNames()</code> ).<br><br>For <code>[]</code> : Can also be logical to perform logical selection (similar to regular vectors). If missing all components/feature groups are selected.<br><br>For <code>[]</code> : should be a scalar value. j is optional.<br><br>For delete: The data to remove from. i are the components as numeric index, logical or character, j the feature groups as numeric index/logical (relative to component) or character. If either is NULL then data for all is removed. j may also be a function: it will be called for each component, with the component (a <code>data.table</code> ) as first argument, the component name as second argument, and any other arguments passed as <code>...</code> to delete. The return value of this function specifies the feature groups to be removed (same format as j).<br><br>... |
|                | For delete: passed to the function specified as j.<br>For <code>plotChroms</code> : Further (optional) arguments passed to the <code>plotChroms</code> method for the <code>featureGroups</code> class. Note that the <code>colourBy</code> , <code>showPeakArea</code> , <code>showFGroupRect</code> and <code>topMost</code> arguments cannot be set as these are set by this method.<br>For <code>plotSpectrum</code> : Further arguments passed to <code>plot</code> .<br>For <code>consensus</code> : components objects that should be used to generate the consensus.<br>For <code>sets workflow</code> methods: further arguments passed to the base <code>components</code> method.   |
| drop           | ignored.   |
| name           | The component name (partially matched).  |
| size           | Should be a two sized vector with the minimum/maximum size of a component. Set to NULL to ignore.  |
| adducts        | Remove any feature groups within components that do not match given adduct rules. If <code>adducts</code> is a logical then only results are kept when an adduct is assigned ( <code>adducts=TRUE</code> ) or not assigned ( <code>adducts=FALSE</code> ). Otherwise, if <code>adducts</code> contains one or more <code>adduct</code> objects (or something that can be converted to it with <code>as.adduct</code> ) then only results are kept that match the given adducts. Set to NULL to ignore this filter.   |

|                          |   |
|--------------------------|---|
| isotopes                 | Only keep results that match a given isotope rule. If isotopes is a logical then only results are kept with (isotopes=TRUE) or without (isotopes=FALSE) isotope assignment. Otherwise isotopes should be a numeric vector with isotope identifiers to keep ( <i>e.g.</i> '0' for monoisotopic results, '1' for 'M+1' results etc.). Set to NULL to ignore this filter.                |
| rtIncrement, mzIncrement | Should be a two sized vector with the minimum/maximum retention or mz increment of a homologous series. Set to NULL to ignore.  |
| checkComponentsSession   | If set then components and/or feature groups are removed that were selected for removal (see <a href="#">check-GUI</a> and the <a href="#">checkComponents</a> function). The value of checkComponentsSession should either be a path to the session file or TRUE, in which case the default session file name is used. If negate=TRUE then all non-selected data is removed instead. |
| negate                   | If TRUE then filters are applied in opposite manner.  |
| verbose                  | If set to FALSE then no text output is shown.   |
| fGroup                   | The name (thus a character) of the feature group that should be searched for.   |
| index                    | The index of the component. Can be a numeric index or a character with its name.  |
| markFGroup               | If specified ( <i>i.e.</i> not NULL) this argument can be used to mark a feature group in the plotted spectrum. The value should be a character with the name of the feature group. Setting this to NULL will not mark any peak.  |
| xlim, ylim               | Sets the plot size limits used by <a href="#">plot</a> . Set to NULL for automatic plot sizing.   |
| fGroups                  | The <a href="#">featureGroups</a> object that was used to generate the components.  |
| rtWindow                 | Retention window: see the <a href="#">plotChroms</a> method for the <a href="#">featureGroups</a> class.  |
| sets                     | ( <b>sets workflow</b> ) A character with name(s) of the sets to keep (or remove if negate=TRUE).   |
| set                      | ( <b>sets workflow</b> ) The name of the set.   |

## Details

components objects are obtained from [component generators](#).

## Value

delete returns the object for which the specified data was removed.

consensus returns a components object that is produced by merging multiple specified components objects.

## Methods (by generic)

- componentTable: Accessor method for the components slot of a components class. Each component is stored as a [data.table](#).
- componentInfo: Accessor method for the componentInfo slot of a components class.



- `groupNames`: returns a character vector with the names of the feature groups for which data is present in this object.
- `length`: Obtain total number of components.
- `names`: Obtain the names of all components.
- `show`: Show summary information for this object.
- `[`: Subset on components/feature groups.
- `[[]`: Extracts a component table, optionally filtered by a feature group.
- `$`: Extracts a component table by component name.
- `delete`: Completely deletes specified (parts of) components.
- `as.data.table`: Returns all component data in a table.
- `filter`: Provides rule based filtering for components.
- `findFGroup`: Returns the component id(s) to which a feature group belongs.
- `plotSpectrum`: Plot a *pseudo* mass spectrum for a single component.
- `plotChroms`: Plot an extracted ion chromatogram (EIC) for all feature groups within a single component.
- `consensus`: Generates a consensus from multiple components objects. At this point results are simply combined and no attempt is made to merge similar components.

## Slots

`components` List of all components in this object. Use the `componentTable` method for access.

`componentInfo` A `data.table` containing general information for each component. Use the `componentInfo` method for access.

## S4 class hierarchy

- `workflowStep`
  - `components`
    - \* `componentsCamera`
    - \* `componentsFeatures`
      - `componentsCliqueMS`
      - `componentsOpenMS`
    - \* `componentsClust`
      - `componentsIntClust`
      - `componentsSpecClust`
    - \* `componentsSet`
      - `componentsNTSet`
    - \* `componentsUnset`
    - \* `componentsNT`
      - `componentsNTUnset`
    - \* `componentsRC`
    - \* `componentsTPs`

## Sets workflows

The componentsSet class is applicable for [sets workflows](#). This class is derived from components and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class [workflowStepSet](#).
- `unset` Converts the object data for a specified set into a 'non-set' object (`componentsUnset`), which allows it to be used in 'regular' workflows. Only the components in the specified set are kept.

The following methods are changed or with new functionality:

- `filter` and the subset operator (`[]`) Can be used to select components that are only present for selected sets.

## Note

`filter` Applies only those filters for which a component has data available. For instance, filtering by adduct will only filter any results within a component if that component contains adduct information.

## See Also

[component-generation](#), [componentsNT](#) and [componentsIntClust](#)

---

`componentsClust-class` *Base class for components that are based on hierarchical clustered data.*

---

## Description

This base class is derived from [components](#) and is used to store components resulting from hierarchical clustering information, for instance, generated by [generateComponentsIntClust](#) and [generateComponentsSpecClust](#).

## Usage

```
## S4 method for signature 'componentsClust'
delete(obj, ...)
```

```
## S4 method for signature 'componentsClust'
clusters(obj)
```

```
## S4 method for signature 'componentsClust'
cutClusters(obj)
```

```
## S4 method for signature 'componentsClust'
```

```

clusterProperties(obj)

## S4 method for signature 'componentsClust'
treeCut(obj, k = NULL, h = NULL)

## S4 method for signature 'componentsClust'
treeCutDynamic(obj, maxTreeHeight, deepSplit, minModuleSize)

## S4 method for signature 'componentsClust,missing'
plot(
  x,
  pal = "Paired",
  numericLabels = TRUE,
  colourBranches = length(x) < 50,
  showLegend = length(x) < 20,
  ...
)

## S4 method for signature 'componentsClust'
plotSilhouettes(obj, kSeq, pch = 16, type = "b", ...)

```

### Arguments

|   |   |
|---|---|
| ...                                     | Further options passed to <a href="#">plot.dendrogram</a> (plot) or <a href="#">plot</a> (plotSilhouettes).   |
| k, h                                    | Desired number of clusters or tree height to be used for cutting the dendrogram, respectively. One or the other must be specified. Analogous to <a href="#">cutree</a> .                          |
| maxTreeHeight, deepSplit, minModuleSize | Arguments used by <a href="#">cutreeDynamicTree</a> .   |
| x, obj                                  | A componentsClust (derived) object.   |
| pal                                     | Colour palette to be used from <a href="#">RColorBrewer</a> .   |
| numericLabels                           | Set to TRUE to label with numeric indices instead of (long) feature group names.  |
| colourBranches                          | Whether branches from cut clusters (and their labels) should be coloured. Might be slow with large numbers of clusters, hence, the default is only TRUE when this is not the case.                |
| showLegend                              | If TRUE and colourBranches is also TRUE then a legend will be shown which outlines cluster numbers and their colours. By default TRUE for small amount of clusters to avoid overflowing the plot. |
| kSeq                                    | An integer vector containing the sequence that should be used for average silhouette width calculation.   |
| pch, type                               | Passed to <a href="#">plot</a> .  |

### Methods (by generic)

- clusters: Accessor method to the clust slot, which was generated by [hclust](#).
- cutClusters: Accessor method to the cutClusters slot. Returns a vector with cluster membership for each candidate (format as [cutree](#)).

- `clusterProperties`: Returns a list with properties on how the clustering was performed.
- `treeCut`: Manually (re-)cut the dendrogram.
- `treeCutDynamic`: Automatically (re-)cut the dendrogram using the `cutreeDynamicTree` function from **dynamicTreeCut**.
- `plot`: generates a dendrogram from a given cluster object and optionally highlights resulting branches when the cluster is cut.
- `plotSilhouettes`: Plots the average silhouette width when the clusters are cut by a sequence of k numbers. The k value with the highest value (marked in the plot) may be considered as the optimal number of clusters.

### Slots

`distm` Distance matrix that was used for clustering (obtained with `daisy`).

`clust` Object returned by `hclust`.

`cutClusters` A list with assigned clusters (same format as what `cutree` returns).

`gInfo` The `groupInfo` of the feature groups object that was used.

`properties` A list containing general properties and parameters used for clustering.

`altered` Set to TRUE if the object was altered (*e.g.* filtered) after its creation.

### S4 class hierarchy

- `components`
  - `componentsClust`
    - \* `componentsIntClust`
    - \* `componentsSpecClust`

### Note

The intensity values for components (used by `plotSpectrum`) are set to a dummy value (1) as no single intensity value exists for this kind of components.

When the object is altered (*e.g.* by filtering or subsetting it), methods that need the original clustered data such as plotting methods do not work anymore and stop with an error.

### References

Schollee JE, Bourgin M, von Gunten U, McArdell CS, Hollender J (2018). “Non-target screening to trace ozonation transformation products in a wastewater treatment train including different post-treatments.” *Water Research*, **142**, 267–278. doi: [10.1016/j.watres.2018.05.045](https://doi.org/10.1016/j.watres.2018.05.045).

### See Also

`components` and `component-generation`

---

 componentsIntClust-class

*Components based on clustered intensity profiles.*


---

## Description

This class is derived from [componentsClust](#) and is used to store hierarchical clustering information from intensity profiles of feature groups.

## Usage

```
## S4 method for signature 'componentsIntClust'
plotHeatMap(
  obj,
  interactive = FALSE,
  col = NULL,
  margins = c(6, 2),
  cexCol = 1,
  ...
)

## S4 method for signature 'componentsIntClust'
plotInt(obj, index, pch = 20, type = "b", lty = 3, col = NULL, ...)
```

## Arguments

|                 |  |
|-----------------|--|
| obj             | A componentsIntClust object.   |
| interactive     | If TRUE an interactive heatmap will be drawn (with <a href="#">heatmaply</a> ).  |
| col             | The colour used for plotting. Set to NULL for automatic colours.   |
| margins, cexCol | Passed to <a href="#">heatmap.2</a>  |
| ...             | Further options passed to <a href="#">heatmap.2</a> / <a href="#">heatmaply</a> (plotHeatMap), <a href="#">plot</a> (plotInt). |
| index           | Numeric component/cluster index.   |
| pch, type, lty  | Passed to <a href="#">lines</a> .  |

## Details

Objects from this class are generated by [generateComponentsIntClust](#)

## Value

plotHeatMap returns the same as [heatmap.2](#) or [heatmaply](#).

**Methods (by generic)**

- `plotHeatMap`: draws a heatmap using the [heatmap.2](#) or [heatmaply](#) function.
- `plotInt`: makes a plot for all (normalized) intensity profiles of the feature groups within a given cluster.

**Slots**

`clusterm` Numeric matrix with normalized feature group intensities that was used for clustering.

**S4 class hierarchy**

- [componentsClust](#)
  - [componentsIntClust](#)

**Note**

When the object is altered (*e.g.* by filtering or subsetting it), methods that need the original clustered data such as plotting methods do not work anymore and stop with an error.

**See Also**

[componentsClust](#) for other relevant methods and [component-generation](#)

---

|                    |  |
|--------------------|--|
| componentsNT-class | <i>Components class for homologous series.</i> |
|--------------------|--|

---

**Description**

This class is derived from [components](#) and is used to store results from unsupervised homolog detection with the [nontarget](#) package.

**Usage**

```
## S4 method for signature 'componentsNT'
plotGraph(obj, onlyLinked)

## S4 method for signature 'componentsNTSet'
plotGraph(obj, onlyLinked, set)

## S4 method for signature 'componentsNTSet'
unset(obj, set)
```

**Arguments**

|                         |  |
|-------------------------|--|
| <code>obj</code>        | The <code>componentsNT</code> object to plot.        |
| <code>onlyLinked</code> | If TRUE then only components with links are plotted. |
| <code>set</code>        | ( <b>sets workflow</b> ) The name of the set.        |

## Details

Objects from this class are generated by [generateComponentsNontarget](#)

## Value

plotGraph returns the result of [visNetwork](#).

## Methods (by generic)

- plotGraph: Plots an interactive network graph for linked homologous series (*i.e.* series with (partial) overlap which could not be merged). The resulting graph can be browsed interactively and allows quick inspection of series which may be related. The graph is constructed with the [igraph](#) package and rendered with [visNetwork](#).

## Slots

homol A list with homol objects for each replicate group as returned by [homol.search](#)

## Sets workflows

The componentsNTSet class is applicable for [sets workflows](#). This class is derived from componentsNT and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class [workflowStepSet](#).
- unset Converts the object data for a specified set into a 'non-set' object (componentsNTUnset), which allows it to be used in 'regular' workflows. Only the components in the specified set are kept. Furthermore, the component names are restored to non-set specific names (see [generateComponents](#) for more details).

The following methods are changed or with new functionality:

- plotGraph Currently can only create graph networks from one set (specified by the set argument).

Note that the componentsNTSet class does not have a homol slot. Instead, the [setObjects](#) method can be used to access this data for a specific set.

## References

Martin Loos (2016). nontarget: Detecting Isotope, Adduct and Homologue Relations in LC-MS Data. R package version 1.9.

Loos, M., Gerber, C., Corona, F., Hollender, J., Singer, H. (2015). Accelerated isotope fine structure calculation using pruned transition trees, Analytical Chemistry 87(11), 5738-5744.

Csardi G, Nepusz T: The igraph software package for complex network research, InterJournal, Complex Systems 1695. 2006. <https://igraph.org>

Almende B.V. and Contributors, Benoit Thieurmél and Titouan Robert (2021). visNetwork: Network Visualization using 'vis.js' Library. R package version 2.1.0. <http://datastorm-open.github.io/visNetwork/>

**See Also**

[components](#) and [component-generation](#)

---

componentsSpecClust-class

*Components based on MS/MS similarity.*

---

**Description**

This class is derived from [componentsClust](#) and is used to store components from feature groups that were clustered based on their MS/MS similarities.

**Details**

Objects from this class are generated by [generateComponentsSpecClust](#)

**S4 class hierarchy**

- [componentsClust](#)
  - [componentsSpecClust](#)

**Note**

When the object is altered (*e.g.* by filtering or subsetting it), methods that need the original clustered data such as plotting methods do not work anymore and stop with an error.

**See Also**

[componentsClust](#) for other relevant methods and [component-generation](#)

---

componentsTPs-class

*Components based on parent and transformation product (TP) linkage.*

---

**Description**

This class is derived from [components](#) and is used to store components that result from linking feature groups that are (predicted to be) parents with feature groups that (are predicted to be) transformation products. For more details, see [generateComponentsTPs](#).



**Usage**

```
## S4 method for signature 'componentsTPs'
as.data.table(x)

## S4 method for signature 'componentsTPs'
filter(
  obj,
  ...,
  retDirMatch = FALSE,
  minSpecSim = NULL,
  minSpecSimPrec = NULL,
  minSpecSimBoth = NULL,
  minFragMatches = NULL,
  minNLMatches = NULL,
  formulas = NULL,
  verbose = TRUE,
  negate = FALSE
)

## S4 method for signature 'componentsTPs'
plotGraph(obj, onlyLinked)
```

**Arguments**

|  |   |
|--|---|
| x, obj                                     | A componentsTPs object.   |
| ..., verbose                               | Further arguments passed to the base <a href="#">filter method</a> .  |
| retDirMatch                                | If set to TRUE, only keep TPs for which the retention time direction (retDir, see Details in <a href="#">componentsTPs</a> ) matches with the observed direction. TPs will never be removed if the expected/observed direction is '0' ( <i>i.e.</i> unknown or not significantly different than the parent).  |
| minSpecSim, minSpecSimPrec, minSpecSimBoth | The minimum spectral similarity of a TP compared to its parent ('0-1'). The minSpecSimPrec and minSpecSimBoth apply to binned data that is shifted with the "precursor" and "both" method, respectively (see <a href="#">MS spectral similarity parameters</a> for more details). Set to NULL to ignore.  |
| minFragMatches, minNLMatches               | Minimum number of parent/TP fragment and neutral loss matches, respectively. Set to NULL to ignore. See the Linking parents and transformation products section in <a href="#">component-generation</a> for more details.   |
| formulas                                   | A <a href="#">formulas</a> object. The formula annotation data in this object is to verify if elemental additions/subtractions from metabolic logic reactions are possible (hence, it only works with data from <a href="#">generateTPsLogic</a> ). To verify elemental additions, only TPs with at least one candidate formula that has these elements are kept. Similarly, for elemental subtractions, any of the parent candidate formulae must contain the subtraction elements. Note that TPs are currently not filtered if either the parent or the TP has no formula annotations. Set to NULL to ignore. |

|            |  |
|------------|--|
| negate     | If TRUE then filters are applied in opposite manner. |
| onlyLinked | If TRUE then only components with links are plotted. |

### Value

filter returns a filtered componentsTPs object.

plotGraph returns the result of [visNetwork](#).

### Methods (by generic)

- `as.data.table`: Returns all component data as a [data.table](#).
- `filter`: Provides various rule based filtering options to clean and prioritize TP data.
- `plotGraph`: Plots an interactive network graph for linked components. Components are linked with each other if one or more transformation products overlap. The graph is constructed with the [igraph](#) package and rendered with [visNetwork](#).

### S4 class hierarchy

- [components](#)
  - [componentsTPs](#)

### Note

The intensity values for components (used by `plotSpectrum`) are set to a dummy value (1) as no single intensity value exists for this kind of components.

### References

Csardi G, Nepusz T: The igraph software package for complex network research, InterJournal, Complex Systems 1695. 2006. <https://igraph.org>

Almende B.V. and Contributors, Benoit Thieurmél and Titouan Robert (2021). visNetwork: Network Visualization using 'vis.js' Library. R package version 2.1.0. <http://datastorm-open.github.io/visNetwork/>

### See Also

[components](#) for other relevant methods and [component-generation](#)

---

|                     |  |
|---------------------|--|
| compound-generation | <i>Automatic compound identification</i> |
|---------------------|--|

---

## Description

Functionality to automatically identify chemical compounds from feature groups.

## Usage

```
## S4 method for signature 'featureGroups'
generateCompounds(fGroups, MSPeakLists, algorithm, ...)

compoundScorings(
  algorithm = NULL,
  database = NULL,
  includeSuspectLists = TRUE,
  onlyDefault = FALSE,
  includeNoDB = TRUE
)

## S4 method for signature 'featureGroups'
generateCompoundsMetFrag(
  fGroups,
  MSPeakLists,
  method = "CL",
  timeout = 300,
  timeoutRetries = 2,
  errorRetries = 2,
  topMost = 100,
  dbRelMzDev = 5,
  fragRelMzDev = 5,
  fragAbsMzDev = 0.002,
  adduct = NULL,
  database = "pubchem",
  extendedPubChem = "auto",
  chemSpiderToken = "",
  scoreTypes = compoundScorings("metfrag", database, onlyDefault = TRUE)$name,
  scoreWeights = 1,
  preProcessingFilters = c("UnconnectedCompoundFilter", "IsotopeFilter"),
  postProcessingFilters = c("InChIKeyFilter"),
  maxCandidatesToStop = 2500,
  identifiers = NULL,
  extraOpts = NULL
)

## S4 method for signature 'featureGroupsSet'
generateCompoundsMetFrag(
```

```
fGroups,  
MSPeakLists,  
method = "CL",  
timeout = 300,  
timeoutRetries = 2,  
errorRetries = 2,  
topMost = 100,  
dbRelMzDev = 5,  
fragRelMzDev = 5,  
fragAbsMzDev = 0.002,  
adduct = NULL,  
...,  
setThreshold = 0,  
setThresholdAnn = 0  
)  
  
## S4 method for signature 'featureGroups'  
generateCompoundsSIRIUS(  
  fGroups,  
  MSPeakLists,  
  relMzDev = 5,  
  adduct = NULL,  
  elements = "CHNOP",  
  profile = "qtof",  
  formulaDatabase = NULL,  
  fingerIDDatabase = "pubchem",  
  noise = NULL,  
  errorRetries = 2,  
  cores = NULL,  
  topMost = 100,  
  topMostFormulas = 5,  
  extraOptsGeneral = NULL,  
  extraOptsFormula = NULL,  
  verbose = TRUE,  
  splitBatches = FALSE  
)  
  
## S4 method for signature 'featureGroupsSet'  
generateCompoundsSIRIUS(  
  fGroups,  
  MSPeakLists,  
  relMzDev = 5,  
  adduct = NULL,  
  ...,  
  setThreshold = 0,  
  setThresholdAnn = 0  
)
```

**Arguments**

|   |   |
|---|---|
| fGroups                                       | <a href="#">featureGroups</a> object for which compounds should be identified. This should be the same or a subset of the object that was used to create the specified MSPeakLists. In the case of a subset only the remaining feature groups in the subset are considered.   |
| MSPeakLists                                   | A <a href="#">MSPeakLists</a> object that was generated for the supplied fGroups.   |
| algorithm                                     | A character string describing the algorithm that should be used: "metfrag", "sirius"  |
| ...   | Any parameters to be passed to the selected compound generation algorithm. For sets workflows: further arguments directly passed to the non-sets method.  |
| database                                      | Compound database to use. Valid values are: "pubchem", "chemspider", "for-ident", "comptox", "pubchemlite", "kegg", "sdf", "psv" and "csv". See section below for more information. Sets the MetFragDatabaseType option.  |
| includeSuspectLists, onlyDefault, includeNoDB | A logical specifying whether scoring terms related to suspect lists, default scoring terms and non-database specific scoring terms should be included in the output, respectively.  |
| method  | Which method should be used for MetFrag execution: "CL" for MetFragCL and "R" for MetFragR. The former might be faster.   |
| timeout                                       | Maximum time (in seconds) before a metFrag query for a feature group is stopped. Also see timeoutRetries argument.  |
| timeoutRetries                                | Maximum number of retries after reaching a timeout before completely skipping the metFrag query for a feature group. Also see timeout argument.   |
| errorRetries                                  | Maximum number of retries after an error occurred. This may be useful to handle e.g. connection errors.   |
| topMost                                       | Only keep this number of candidates (per feature group) with highest score. Set to NULL to always keep all candidates, however, please note that this may result in significant usage of CPU/RAM resources for large numbers of candidates.   |
| dbRelMzDev                                    | Relative mass deviation (in ppm) for database search. Sets the 'DatabaseSearchRelativeMassDeviation' option.  |
| fragRelMzDev                                  | Relative mass deviation (in ppm) for fragment matching. Sets the 'FragmentPeakMatchRelativeMassDeviation' option.   |
| fragAbsMzDev                                  | Absolute mass deviation (in Da) for fragment matching. Sets the 'FragmentPeakMatchAbsoluteMassDeviation' option.  |
| adduct  | An <a href="#">adduct</a> object (or something that can be converted to it with <a href="#">as.adduct</a> ). Examples: "[M-H]-", "[M+Na]+". If the featureGroups object has adduct annotations then these are used if adducts=NULL.<br><b>(sets workflow)</b> The adduct argument is not supported for sets workflows, since the adduct annotations will then always be used. |
| extendedPubChem                               | If database="pubchem": whether to use the <i>extended</i> database that includes information for compound scoring ( <i>i.e.</i> number of patents/PubMed references). Note that downloading candidates from this database might take extra time. Valid values are: FALSE (never use it), TRUE (always use it) or "auto" (default, use if specified scorings demand it).       |

|   |   |
|---|---|
| chemSpiderToken                             | A character string with the <b>ChemSpider security token</b> that should be set when the ChemSpider database is used. Sets the 'ChemSpiderToken' option.  |
| scoreTypes                                  | A character vector defining the scoring types. See the Scorings section below for more information. Note that both generic and MetFrag specific names are accepted ( <i>i.e.</i> name and metfrag columns returned by compoundScorings). When a local database is used, the name should match what is given there (e.g column names when database=csv). Note that MetFrag may still report other scoring data, however, these are not used for ranking. Sets the 'MetFragScoreTypes' option.  |
| scoreWeights                                | Numeric vector containing weights of the used scoring types. Order is the same as set in scoreTypes. Values are recycled if necessary. Sets the 'MetFragScoreWeights' option.   |
| preProcessingFilters, postProcessingFilters | <p>A character vector defining pre/post filters applied before/after fragmentation and scoring (<i>e.g.</i> "UnconnectedCompoundFilter", "IsotopeFilter", "ElementExclusionFilter"). Some methods require further options to be set. For all filters and more information refer to the Candidate</p> <p>Filters section on the <b>MetFragR homepage</b>. Sets the 'MetFragPreProcessingCandidateFilter' and MetFragPostProcessingCandidateFilter options.</p>   |
| maxCandidatesToStop                         | If more than this number of candidate structures are found then processing will be aborted and no results this feature group will be reported. Low values increase the chance of missing data, whereas too high values will use too much computer resources and significantly slowdown the process. Sets the 'MaxCandidateLimitToStop' option.  |
| identifiers                                 | A list containing for each feature group a character vector with database identifiers that should be used to find candidates for a feature group (the list should be named by feature group names). If NULL all relevant candidates will be retrieved from the specified database. An example usage scenario is to obtain the list of candidate identifiers from a <a href="#">compounds</a> object obtained with <a href="#">generateCompoundsSIRIUS</a> using the <a href="#">identifiers</a> method. This way, only those candidates will be searched by MetFrag that were generated by SIRIUS+CSI:FingerID. Sets the 'PrecursorCompoundIDs' option. |
| extraOpts                                   | <p>For MetFrag: A named list containing further settings to be passed to <a href="#">run.metfrag</a>. See the <b>MetFragR</b> and <b>MetFrag CL</b> homepages for all available options.</p> <p>For SIRIUS: a character vector with any extra commandline parameters for formula prediction. See the SIRIUS manual for more details.</p> <p>Set to NULL to ignore.</p>  |
| setThreshold                                | <b>(sets workflow)</b> Minimum abundance for a candidate among all sets ('0-1'). For instance, a value of '1' means that the candidate needs to be present in all the set data.   |
| setThresholdAnn                             | <b>(sets workflow)</b> As setThreshold, but only taking into account the set data that contain annotations for the feature group of the candidate.  |
| relMzDev                                    | Maximum relative deviation between the measured and candidate formula <i>m/z</i> values (in ppm). Sets the '--ppm-max' commandline option.  |

|                                    |  |
|------------------------------------|--|
| elements                           | Elements to be considered for formulae calculation. This will heavily affects the number of candidates! Always try to work with a minimal set by excluding elements you don't expect. The minimum/maximum number of elements can also be specified, for example: a value of "C[5]H[10-15]O" will only consider formulae with up to five carbon atoms, between ten and fifteen hydrogen atoms and any amount of oxygen atoms. Sets the '--elements' commandline option. |
| profile                            | Name of the configuration profile, for example: "qtof", "orbitrap", "fticr". Sets the '--profile' commandline option.  |
| formulaDatabase                    | If not NULL, use a database for retrieval of formula candidates. Possible values are: "pubchem", "bio", "kegg", "hmdb". Sets the '--database' commandline option.  |
| fingerIDDatabase                   | Database specifically used for CSI:FingerID. If NULL, the value of the formulaDatabase parameter will be used or "pubchem" when that is also NULL. Sets the '--fingerid-db' option.  |
| noise                              | Median intensity of the noise (NULL ignores this parameter). Sets the '--noise' commandline option.  |
| cores                              | The number of cores SIRIUS will use. If NULL then the default of all cores will be used.   |
| topMostFormulas                    | Do not return more than this number of candidate formulae. Note that only compounds for these formulae will be searched. Sets the '--candidates' commandline option.   |
| extraOptsGeneral, extraOptsFormula | a character vector with any extra commandline parameters for SIRIUS. For SIRIUS versions <4.4 there is no distinction between general and formula options. Otherwise commandline options specified in extraOptsGeneral are added prior to the formula command, while options specified in extraOptsFormula are added in afterwards. See the SIRIUS manual for more details. Set to NULL to ignore.   |
| verbose                            | If TRUE then more output is shown in the terminal.   |
| splitBatches                       | If TRUE then the calculations done by SIRIUS will be evenly split over multiple SIRIUS calls (which may be run in parallel depending on the <a href="#">set package options</a> ). If splitBatches=FALSE then all feature calculations are performed from a single SIRIUS execution, which is often the fastest if calculations are performed on a single computer.  |

## Details

Several algorithms are provided to automatically identify compounds for given feature groups. To this end, each measured masses for all feature groups are searched within online database(s) (e.g. [PubChem](#)) to retrieve a list of potential candidate chemical compounds. Depending on the algorithm and its parameters, further scoring of candidates is then performed using, for instance, matching of measured and theoretical isotopic patterns, presence within other data sources such as patent databases and similarity of measured and in-silico predicted MS/MS fragments. Note that this process is often quite time consuming, especially for large feature group sets. Therefore, this is

often one of the last steps within the workflow and not performed before feature groups have been prioritized.

`generateCompounds` is a generic function that will generate compounds using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `generateCompoundsMetFrag` and `generateCompoundsSIRIUS`. While these functions may be called directly, `generateCompounds` provides a generic interface and is therefore usually preferred.

`compoundScorings` displays an overview of scorings may be applied to rank candidate compounds (see Scorings section below).

`generateCompoundsMetFrag` uses the **metfRag** package or MetFrag CL for compound identification (see <http://ipb-halle.github.io/MetFrag/>). Several online compound databases such as **PubChem** and **ChemSpider** may be chosen for retrieval of candidate structures. In addition, many options exist to score and filter resulting data, and it is highly suggested to optimize these to improve results. While MS/MS data is not mandatory, it will usually greatly improve candidate scoring. The MetFrag options `PeakList`, `IonizedPrecursorMass` and `ExperimentalRetentionTimeValue` (in minutes) fields are automatically set from feature data.

`generateCompoundsSIRIUS` uses **SIRIUS** in combination with **CSI:FingerID** for compound identification. Similar to `generateFormulasSIRIUS`, candidate formulae are generated with SIRIUS. These results are then feed to CSI:FingerID to acquire candidate structures. This method requires the availability of MS/MS data, and feature groups without it will be ignored.

## Value

`compoundScorings` returns a `data.frame` with information on which scoring terms are used, what their algorithm specific name is and other information such as to which database they apply and short remarks.

`generateCompoundsMetFrag` returns a `compoundsMF` object.

`generateCompoundsSIRIUS` returns a `compounds` object.

## Scorings

Each algorithm implements their own scoring system. Their names have been simplified and harmonized where possible and are used for reporting and in the case MetFrag is used to specify how compounds should be scored (`scoreTypes` argument). The `compoundScorings` function can be used to get an overview of both the algorithm specific and generic scoring names. For instance, the table below shows all scorings for MetFrag: (some columns are omitted)

| name                | metfrag                          | database    |
|---------------------|----------------------------------|-------------|
| score               | Score                            |             |
| fragScore           | FragmenterScore                  |             |
| metFusionScore      | OfflineMetFusionScore            |             |
| individualMoNAScore | OfflineIndividualMoNAScore       |             |
| numberPatents       | PubChemNumberPatents             | pubchem     |
| numberPatents       | Patent_Count                     | pubchemlite |
| pubMedReferences    | PubChemNumberPubMedReferences    | pubchem     |
| pubMedReferences    | ChemSpiderNumberPubMedReferences | chemspider  |
| pubMedReferences    | NUMBER_OF_PUBMED_ARTICLES        | comptox     |
| pubMedReferences    | PubMed_Count                     | pubchemlite |



|                      |  |             |
|----------------------|--|-------------|
| extReferenceCount    | ChemSpiderNumberExternalReferences               | chemspider  |
| dataSourceCount      | ChemSpiderDataSourceCount                        | chemspider  |
| referenceCount       | ChemSpiderReferenceCount                         | chemspider  |
| RSCCount             | ChemSpiderRSCCount                               | chemspider  |
| smartsInclusionScore | SmartsSubstructureInclusionScore                 |             |
| smartsExclusionScore | SmartsSubstructureExclusionScore                 |             |
| suspectListScore     | SuspectListScore                                 |             |
| retentionTimeScore   | RetentionTimeScore                               |             |
| CPDATCount           | CPDAT_COUNT                                      | comptox     |
| TOXCASTActive        | TOXCAST_PERCENT_ACTIVE                           | comptox     |
| dataSources          | DATA_SOURCES                                     | comptox     |
| pubChemDataSources   | PUBCHEM_DATA_SOURCES                             | comptox     |
| EXPOCASTPredExpo     | EXPOCAST_MEDIAN_EXPOSURE_PREDICTION_MG/KG-BW/DAY | comptox     |
| ECOTOX               | ECOTOX   | comptox     |
| NORMANSUSDAT         | NORMANSUSDAT                                     | comptox     |
| MASSBANKEU           | MASSBANKEU                                       | comptox     |
| TOX21SL              | TOX21SL  | comptox     |
| TOXCAST              | TOXCAST  | comptox     |
| KEMIMARKET           | KEMIMARKET                                       | comptox     |
| MZCLOUD              | MZCLOUD  | comptox     |
| pubMedNeuro          | PubMedNeuro                                      | comptox     |
| CIGARETTES           | CIGARETTES                                       | comptox     |
| INDOORCT16           | INDOORCT16                                       | comptox     |
| SRM2585DUST          | SRM2585DUST                                      | comptox     |
| SLTCHEMDB            | SLTCHEMDB  | comptox     |
| THSMOKE              | THSMOKE  | comptox     |
| ITNANTIBIOTIC        | ITNANTIBIOTIC                                    | comptox     |
| STOFFIDENT           | STOFFIDENT                                       | comptox     |
| KEMIMARKET_EXPO      | KEMIMARKET_EXPO                                  | comptox     |
| KEMIMARKET_HAZ       | KEMIMARKET_HAZ                                   | comptox     |
| REACH2017            | REACH2017  | comptox     |
| KEMIWW_WDUIndex      | KEMIWW_WDUIndex                                  | comptox     |
| KEMIWW_StpSE         | KEMIWW_StpSE                                     | comptox     |
| KEMIWW_SEHitsOverDL  | KEMIWW_SEHitsOverDL                              | comptox     |
| ZINC15PHARMA         | ZINC15PHARMA                                     | comptox     |
| PFASMASTER           | PFASMASTER                                       | comptox     |
| peakFingerprintScore | AutomatedPeakFingerprintAnnotationScore          |             |
| lossFingerprintScore | AutomatedLossFingerprintAnnotationScore          |             |
| agroChemInfo         | AgroChemInfo                                     | pubchemlite |
| bioPathway           | BioPathway                                       | pubchemlite |
| drugMedicInfo        | DrugMedicInfo                                    | pubchemlite |
| foodRelated          | FoodRelated                                      | pubchemlite |
| pharmacoInfo         | PharmacoInfo                                     | pubchemlite |
| safetyInfo           | SafetyInfo                                       | pubchemlite |
| toxicityInfo         | ToxicityInfo                                     | pubchemlite |
| knownUse             | KnownUse   | pubchemlite |
| disorderDisease      | DisorderDisease                                  | pubchemlite |
| identification       | Identification                                   | pubchemlite |

|               |               |             |
|---------------|---------------|-------------|
| annoTypeCount | FPSum         | pubchemlite |
| annoTypeCount | AnnoTypeCount | pubchemlite |

In addition, the `compoundScorings` function is also useful to programatically generate a set of scorings to be used by MetFrag. For instance, the following can be given to the `scoreTypes` argument to use all default scorings for PubChem: `compoundScorings("metfrag", "pubchem", onlyDefault=TRUE)$name`.

For all MetFrag scoring types refer to the Candidate Scores section on the [MetFragR homepage](#).

### Sets workflows

With a [sets workflow](#), annotation is first performed for each set. This is important, since the annotation algorithms typically cannot work with data from mixed ionization modes. The annotation results are then combined to generate a *sets consensus*:

- The annotation tables for each feature group from the set specific data are combined. Rows with overlapping candidates (determined by the first-block INCHIKEY) are merged.
- Set specific data (*e.g.* the ionic formula) is retained by renaming their columns with set specific names.
- The MS/MS fragment annotations (`fragInfo` column) from each set are combined.
- The scorings for each set are averaged to calculate overall scores.
- The candidates are re-ranked based on their average ranking among the set data (if a candidate is absent in a set it is assigned the poorest rank in that set).
- The coverage of each candidate among sets is calculated. Depending on the `setThreshold` and `setThresholdAnn` arguments, candidates with low abundance are removed.

### Parallelization

`generateCompoundsMetFrag` and `generateCompoundsSIRIUS` uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoön options](#) for configuration options.

When local database files are used with `generateCompoundsMetFrag` (*e.g.* when database is set to "pubchemlite", "csv" etc.) and `'patRoön.MP.method="future"'`, then the database file must be present on all the nodes. When `pubchemlite` or `comptox` is used, the location for these databases can be configured on the host with the respective package options (`'patRoön.path.MetFragPubChemLite'` and `'patRoön.path.MetFragCompTox'`). Note that these files must *also* be present on the local host computer, even if it is not participating in computations.

### Usage of MetFrag databases

When `database="chemspider"` setting the `chemSpiderToken` argument is mandatory.

When a local database is set (*i.e.* `sdf`, `psv`, `csv`, `comptox`, `pubchemlite`) the file location of the database should be set in the `LocalDatabasePath` value via the `extraOpts` argument or using the `patRoön.path.MetFragCompTox/patRoön.path.MetFragPubChemLite` option (only when `database="comptox"` or `database="pubchemlite"`).

Examples: `options(patRoön.path.MetFragCompTox = "C:/CompTox_17March2019_SelectMetaData.csv")` `extraOpts =`

```
list(LocalDatabasePath = "C:/myDB.csv").
```

For database="comptox" the files can be obtained from [here](https://zenodo.org/record/3364464#XnjM-XLvKUK). Furthermore, the files with additions for <https://zenodo.org/record/3364464#XnjM-XLvKUK> and <https://zenodo.org/record/3472781#XnjMAHLvKUK> metadata are also supported. Note that only recent MetFrag versions ( $\geq$  '2.4.5') support these libraries.

### Note

For annotations performed with SIRIUS it is often the fastest to keep the default `splitBatches=FALSE`. In this case, all SIRIUS output will be printed to the terminal (unless `verbose=FALSE` or `'patRoon.MP.method="future"'`). Furthermore, please note that only annotations to be performed for the same adduct are grouped in a single batch execution.

### References

Ruttkies C, Schymanski EL, Wolf S, Hollender J, Neumann S (2016). "MetFrag relaunched: incorporating strategies beyond in silico fragmentation." *Journal of Cheminformatics*, **8**(1). doi: [10.1186/s1332101601159](https://doi.org/10.1186/s1332101601159).

Duhrkop K, Fleischauer M, Ludwig M, Aksenov AA, Melnik AV, Meusel M, Dorrestein PC, Rousu J, Bocker S (2019). "SIRIUS 4: a rapid tool for turning tandem mass spectra into metabolite structure information." *Nature Methods*, **16**(4), 299–302. doi: [10.1038/s4159201903448](https://doi.org/10.1038/s4159201903448).

Duhrkop K, Bocker S (2015). "Fragmentation Trees Reloaded." In Przytycka TM (ed.), *Research in Computational Molecular Biology*, 65–79. ISBN 978-3-319-16706-0.

Duhrkop K, Shen H, Meusel M, Rousu J, Bocker S (2015). "Searching molecular structure databases with tandem mass spectra using CSI:FingerID." *Proceedings of the National Academy of Sciences*, **112**(41), 12580–12585. doi: [10.1073/pnas.1509788112](https://doi.org/10.1073/pnas.1509788112).

Bocker S, Letzel MC, Liptak Z, Pervukhin A (2008). "SIRIUS: decomposing isotope patterns for metabolite identification." *Bioinformatics*, **25**(2), 218–224. doi: [10.1093/bioinformatics/btn603](https://doi.org/10.1093/bioinformatics/btn603).

### See Also

[compounds-class](#)

---

compounds-class

*Compound annotations class*

---

### Description

Contains data for compound annotations for feature groups.

**Usage**

```
## S4 method for signature 'compounds'
defaultExclNormScores(obj)

## S4 method for signature 'compounds'
show(object)

## S4 method for signature 'compounds'
identifiers(compounds)

## S4 method for signature 'compounds'
filter(
  obj,
  minExplainedPeaks = NULL,
  minScore = NULL,
  minFragScore = NULL,
  minFormulaScore = NULL,
  scoreLimits = NULL,
  ...
)

## S4 method for signature 'compounds'
addFormulaScoring(
  compounds,
  formulas,
  updateScore = FALSE,
  formulaScoreWeight = 1
)

## S4 method for signature 'compounds'
getMCS(obj, index, groupName)

## S4 method for signature 'compounds'
plotStructure(obj, index, groupName, width = 500, height = 500)

## S4 method for signature 'compounds'
plotScores(
  obj,
  index,
  groupName,
  normalizeScores = "max",
  excludeNormScores = defaultExclNormScores(obj),
  onlyUsed = TRUE
)

## S4 method for signature 'compounds'
annotatedPeakList(
  obj,
```

```
    index,
    groupName,
    MSPeakLists,
    formulas = NULL,
    onlyAnnotated = FALSE
  )

## S4 method for signature 'compounds'
plotSpectrum(
  obj,
  index,
  groupName,
  MSPeakLists,
  formulas = NULL,
  plotStruct = FALSE,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  mincx = 0.9,
  xlim = NULL,
  ylim = NULL,
  maxMolSize = c(0.2, 0.4),
  molRes = c(100, 100),
  ...
)

## S4 method for signature 'compounds'
consensus(
  obj,
  ...,
  absMinAbundance = NULL,
  relMinAbundance = NULL,
  uniqueFrom = NULL,
  uniqueOuter = FALSE,
  rankWeights = 1,
  labels = NULL
)

## S4 method for signature 'compoundsSet'
show(object)

## S4 method for signature 'compoundsSet'
delete(obj, i, j, ...)

## S4 method for signature 'compoundsSet,ANY,missing,missing'
x[i, j, ..., sets = NULL, updateConsensus = FALSE, drop = TRUE]

## S4 method for signature 'compoundsSet'
filter(obj, ..., sets = NULL, updateConsensus = FALSE, negate = FALSE)
```

```
## S4 method for signature 'compoundsSet'
plotSpectrum(
  obj,
  index,
  groupName,
  MSPeakLists,
  formulas = NULL,
  plotStruct = FALSE,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  mincex = 0.9,
  xlim = NULL,
  ylim = NULL,
  maxMolSize = c(0.2, 0.4),
  molRes = c(100, 100),
  perSet = TRUE,
  mirror = TRUE,
  ...
)

## S4 method for signature 'compoundsSet'
addFormulaScoring(
  compounds,
  formulas,
  updateScore = FALSE,
  formulaScoreWeight = 1
)

## S4 method for signature 'compoundsSet'
annotatedPeakList(obj, index, groupName, MSPeakLists, formulas = NULL, ...)

## S4 method for signature 'compoundsSet'
consensus(
  obj,
  ...,
  absMinAbundance = NULL,
  relMinAbundance = NULL,
  uniqueFrom = NULL,
  uniqueOuter = FALSE,
  rankWeights = 1,
  labels = NULL,
  filterSets = FALSE,
  setThreshold = 0,
  setThresholdAnn = 0
)

## S4 method for signature 'compoundsSet'
```

```
unset(obj, set)
```

```
## S4 method for signature 'compoundsConsensusSet'
unset(obj, set)
```

## Arguments

`obj`, `object`, `compounds`, `x`  
The compound object.

`minExplainedPeaks`, `scoreLimits`  
Passed to the [featureAnnotations](#) method.

`minScore`, `minFragScore`, `minFormulaScore`  
Minimum overall score, in-silico fragmentation score and formula score, respectively. Set to NULL to ignore. The `scoreLimits` argument allows for more advanced score filtering.

`...`  
For `plotSpectrum`: Further arguments passed to [plot](#).  
For `delete`: passed to the function specified as `j`.  
for `filter`: passed to the [featureAnnotations](#) method.  
For `consensus`: any further (and unique) compounds objects.  
For [sets workflow](#) methods: further arguments passed to the base [compounds](#) method.

`formulas`  
The [formulas](#) object that should be used for scoring/annotation. For `plotSpectrum` and `annotatedPeakList`: set to NULL to ignore.

`updateScore`  
If set to TRUE then the score column is updated by adding the normalized 'formulaScore' (weighted by 'formulaScoreWeight'). Currently, this **only** makes sense for MetFrag results!

`formulaScoreWeight`  
Weight used to update scoring (see `updateScore` parameter).

`index`  
The numeric index of the candidate structure.  
For `plotStructure` and `getMCS`: multiple indices (*i.e.* vector with length  $\geq 2$ ) should be specified to plot/calculate the most common substructure (MCS). Alternatively, '-1' may be specified to select all candidates.  
For `plotSpectrum`: two indices can be specified to compare spectra. In this case `groupName` should specify values for the spectra to compare.

`groupName`  
The name of the feature group (or feature groups when comparing spectra) to which the candidate belongs.

`width`, `height`  
The dimensions (in pixels) of the raster image that should be plotted.

`normalizeScores`  
A character that specifies how normalization of annotation scorings occurs. Either "none" (no normalization), "max" (normalize to max value) or "minmax" (perform min-max normalization). Note that normalization of negative scores (e.g. output by SIRIUS) is always performed as min-max. Furthermore, currently normalization for compounds takes the original min/max scoring values into account when candidates were generated. Thus, for compounds scoring, normalization is not affected when candidate results were removed after they were generated (*e.g.* by use of `filter`).

|                                  |   |
|----------------------------------|---|
| excludeNormScores                | <p>A character vector specifying any compound scoring names that should <i>not</i> be normalized. Set to NULL to normalize all scorings. Note that whether any normalization occurs is set by the excludeNormScores argument.</p> <p>For compounds: By default score and individualMoNAScore are set to mimic the behavior of the MetFrag web interface.</p>  |
| onlyUsed                         | If TRUE then only scorings are plotted that actually have been used to rank data (see the scoreTypes argument to <a href="#">generateCompoundsMetFrag</a> for more details).  |
| MSPeakLists                      | The <a href="#">MSPeakLists</a> object that was used to generate the candidate  |
| onlyAnnotated                    | Set to TRUE to filter out any peaks that could not be annotated.  |
| plotStruct                       | If TRUE then the candidate structure is drawn in the spectrum. Currently not supported when comparing spectra.  |
| title                            | The title of the plot. If NULL a title will be automatically made.  |
| specSimParams                    | A named list with parameters that influence the calculation of MS spectra similarities. See the <a href="#">spectral similarity parameters</a> documentation for more details.  |
| mincex                           | The formula annotation labels are automatically scaled. The mincex argument forces a minimum cex value for readability.   |
| xlim, ylim                       | Sets the plot size limits used by <a href="#">plot</a> . Set to NULL for automatic plot sizing.   |
| maxMolSize                       | Numeric vector of size two with the maximum width/height of the candidate structure (relative to the plot size).  |
| molRes                           | Numeric vector of size two with the resolution of the candidate structure (in pixels).  |
| absMinAbundance, relMinAbundance | Minimum absolute or relative ('0-1') abundance across objects for a result to be kept. For instance, relMinAbundance=0.5 means that a result should be present in at least half of the number of compared objects. Set to 'NULL' to ignore and keep all results. Limits cannot be set when uniqueFrom is not NULL.  |
| uniqueFrom                       | Set this argument to only retain compounds that are unique within one or more of the objects for which the consensus is made. Selection is done by setting the value of uniqueFrom to a logical (values are recycled), numeric (select by index) or a character (as obtained with algorithm(obj)). For logical and numeric values the order corresponds to the order of the objects given for the consensus. Set to NULL to ignore. |
| uniqueOuter                      | If uniqueFrom is not NULL and if uniqueOuter=TRUE: only retain data that are also unique between objects specified in uniqueFrom.   |
| rankWeights                      | A numeric vector with weights of to calculate the mean ranking score for each candidate. The value will be re-cycled if necessary, hence, the default value of '1' means equal weights for all considered objects.  |
| labels                           | A character with names to use for labelling. If NULL labels are automatically generated.  |
| i, j, drop                       | Passed to the <a href="#">featureAnnotations</a> method.  |
| sets                             | ( <b>sets workflow</b> ) A character with name(s) of the sets to keep (or remove if negate=TRUE). Note: if updateConsensus=FALSE then the setCoverage column of the annotation results is not updated.  |



|                               |  |
|-------------------------------|--|
| updateConsensus               | ( <b>sets workflow</b> ) If TRUE then the annotation consensus among set results is updated. See the Sets workflows section for more details.  |
| negate                        | Passed to the <a href="#">featureAnnotations</a> method.   |
| perSet, mirror                | ( <b>sets workflow</b> ) If perSet=TRUE then the set specific mass peaks are annotated separately. Furthermore, if mirror=TRUE (and there are two sets in the object) then a mirror plot is generated. |
| filterSets                    | ( <b>sets workflow</b> ) Controls how algorithms consensus abundance filters are applied. See the Sets workflows section below.  |
| setThreshold, setThresholdAnn | ( <b>sets workflow</b> ) Thresholds used to create the annotation set consensus. See <a href="#">generateCompounds</a> .   |
| set                           | ( <b>sets workflow</b> ) The name of the set.  |

### Details

compounds objects are obtained from [compound generators](#). This class is derived from the [featureAnnotations](#) class, please see its documentation for more methods and other details.

### Value

addFormulaScoring returns a compounds object updated with formula scoring.

getMCS returns an **rdk** molecule object (IAtomContainer).

consensus returns a compounds object that is produced by merging multiple specified compounds objects.

### Methods (by generic)

- defaultExclNormScores: Returns default scorings that are excluded from normalization.
- show: Show summary information for this object.
- identifiers: Returns a list containing for each feature group a character vector with database identifiers for all candidate compounds. The list is named by feature group names, and is typically used with the identifiers option of [generateCompoundsMetFrag](#).
- filter: Provides rule based filtering for generated compounds. Useful to eliminate unlikely candidates and speed up further processing. Also see the [featureAnnotations](#) method.
- addFormulaScoring: Adds formula ranking data from a [formulas](#) object as an extra compound candidate scoring (formulaScore column). The formula score for each compound candidate is between '0-1', where *zero* means no match with any formula candidates, and *one* means that the compound candidate's formula is the highest ranked.
- getMCS: Calculates the maximum common substructure (MCS) for two or more candidate structures for a feature group. This method uses the [get.mcs](#) function from **rdk**.
- plotStructure: Plots a structure of a candidate compound using the **rdk** package. If multiple candidates are specified (*i.e.* by specifying a vector for index) then the maximum common substructure (MCS) of the selected candidates is drawn.

- `plotScores`: Plots a barplot with scoring of a candidate compound.
- `annotatedPeakList`: Returns an MS/MS peak list annotated with data from a given candidate compound for a feature group.
- `plotSpectrum`: Plots an annotated spectrum for a given candidate compound for a feature group. Two spectra can be compared by specifying a two-sized vector for the `index` and `groupName` arguments.
- `consensus`: Generates a consensus of results from multiple objects. In order to rank the consensus candidates, first each of the candidates are scored based on their original ranking (the scores are normalized and the highest ranked candidate gets value '1'). The (weighted) mean is then calculated for all scorings of each candidate to derive the final ranking (if an object lacks the candidate its score will be '0'). The original rankings for each object is stored in the rank columns.

### Slots

`setThreshold`, `setThresholdAnn` (**sets workflow**) A copy of the equally named arguments that were passed when this object was created by `generateCompounds`.

`origFGNames` (**sets workflow**) The original (order of) names of the `featureGroups` object that was used to create this object.

### S4 class hierarchy

- `featureAnnotations`
  - `compounds`
    - \* `compoundsConsensus`
    - \* `compoundsMF`
    - \* `compoundsSet`
      - `compoundsConsensusSet`
    - \* `compoundsUnset`

### Source

Subscripting of formulae for plots generated by `plotSpectrum` is based on the `chemistry2expression` function from the **ReSOLUTION** package.

### Sets workflows

The `compoundsSet` class is applicable for [sets workflows](#). This class is derived from `compounds` and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class `workflowStepSet`.
- `unset` Converts the object data for a specified set into a 'non-set' object (`compoundsUnset`), which allows it to be used in 'regular' workflows. Only the annotation results that are present in the specified set are kept (based on the set consensus, see below for implications).

The following methods are changed or with new functionality:

- `filter` and the subset operator (`[]`) Can be used to select data that is only present for selected sets. Depending on the `updateConsensus`, both either operate on set consensus or original data (see below for implications).
- `annotatedPeakList` Returns a combined annotation table with all sets.
- `plotSpectrum` Is able to highlight set specific mass peaks (`perSet` and `mirror` arguments).
- `consensus` Creates the algorithm consensus based on the original annotation data (see below for implications). Then, like the sets workflow method for `generateCompounds`, a consensus is made for all sets, which can be controlled with the `setThreshold` and `setThresholdAnn` arguments. The candidate coverage among the different algorithms is calculated for each set (e.g. coverage-positive column) and for all sets (coverage column), which is based on the presence of a candidate in all the algorithms from all sets data. The consensus method for sets workflow data supports the `filterSets` argument. This controls how the algorithm consensus abundance filters (`absMinAbundance`/`relMinAbundance`) are applied: if `filterSets=TRUE` then the minimum of all coverage set specific columns is used to obtain the algorithm abundance. Otherwise the overall coverage column is used. For instance, consider a consensus object to be generated from two objects generated by different algorithms (e.g. SIRIUS and MetFrag), which both have a positive and negative set. Then, if a candidate occurs with both algorithms for the positive mode set, but only with the first algorithm in the negative mode set, `relMinAbundance=1` will remove the candidate if `filterSets=TRUE` (because the minimum relative algorithm abundance is '0.5'), while `filterSets=FALSE` will not remove the candidate (because based on all sets data the candidate occurs in both algorithms).
- `addFormulaScoring` Adds the formula scorings to the original data and re-creates the annotation set consensus (see below for implications).

Two types of annotation data are stored in a `compoundsSet` object:

1. Annotations that are produced from a consensus between set results (see `generateCompounds`).
2. The 'original' annotation data per set, prior to when the set consensus was made. This includes candidates that were filtered out because of the thresholds set by `setThreshold` and `setThresholdAnn`. However, when `filter` or subsetting (`[]`) operations are performed, the original data is also updated.

In most cases the first data is used. However, in a few cases the original annotation data is used (as indicated above), for instance, to re-create the set consensus. It is important to realize that the original annotation data may have *additional* candidates, and a newly created set consensus may therefore have 'new' candidates. For instance, when the object consists of the sets "positive" and "negative" and `setThreshold=1` was used to create it, then `compounds[, sets = "positive", updateConsensus = TRUE]` may now have additional candidates, *i.e.* those that were not present in the "negative" set and were previously removed due to the consensus threshold filter.

#### Note

The values ranges in the `scoreLimits` slot, which are used for normalization of scores, are based on the *original* scorings when the compounds were generated (*prior* to employing the `topMost` filter to `generateCompounds`).

#### References

Guha, R. (2007). 'Chemical Informatics Functionality in R'. Journal of Statistical Software 6(18)

## See Also

The [featureAnnotations](#) base class for more relevant methods and [compound-generation](#).

---

compounds-cluster

*Hierarchical clustering of compounds*

---

## Description

Perform hierarchical clustering of structure candidates based on chemical similarity and obtain overall structural information based on the maximum common structure (MCS).

## Usage

```
## S4 method for signature 'compounds'
makeHCluster(
  obj,
  method,
  fpType = "extended",
  fpSimMethod = "tanimoto",
  maxTreeHeight = 1,
  deepSplit = TRUE,
  minModuleSize = 1
)
```

## Arguments

|  |  |
|--|--|
| <code>obj</code>   | The <a href="#">compounds</a> object to be clustered.  |
| <code>method</code>  | The clustering method passed to <a href="#">hclust</a> .   |
| <code>fpType</code>  | The type of structural fingerprint that should be calculated. See the type argument of the <a href="#">get.fingerprint</a> function of <a href="#">rdck</a> .                        |
| <code>fpSimMethod</code>   | The method for calculating similarities (i.e. not dissimilarity!). See the method argument of the <a href="#">fp.sim.matrix</a> function of the <a href="#">fingerprint</a> package. |
| <code>maxTreeHeight</code> , <code>deepSplit</code> , <code>minModuleSize</code> | Arguments used by <a href="#">cutreeDynamicTree</a> .  |

## Details

Often many possible chemical structure candidates are found for each feature group when performing [compound identification](#). Therefore, it may be useful to obtain an overview of their general structural properties. One strategy is to perform hierarchical clustering based on their chemical (dis)similarity, for instance, using the Tanimoto score. The resulting clusters can then be characterized by evaluating their *maximum common substructure* (MCS).

`makeHCluster` performs hierarchical clustering of all structure candidates for each feature group within a [compounds](#) object. The resulting dendrograms are automatically cut using the [cutreeDynamicTree](#) function from the [dynamicTreeCut](#) package. The returned [compoundsCluster](#) object can then be used, for instance, for plotting dendrograms and MCS structures and manually re-cutting specific clusters.

**Value**

makeHCluster returns an `compoundsCluster` object.

**Source**

The methodology applied here has been largely derived from ‘chemclust.R’ from the **metfRag** package and the package vignette of **rdk**.

**References**

Guha, R. (2007). ‘Chemical Informatics Functionality in R’. Journal of Statistical Software 6(18)

**See Also**

`compoundsCluster`

---

`compoundsCluster-class`

*Compounds cluster class*

---

**Description**

Objects from this class are used to store hierarchical clustering data of candidate structures within `compounds` objects.

**Usage**

```
## S4 method for signature 'compoundsCluster'
clusters(obj)
```

```
## S4 method for signature 'compoundsCluster'
cutClusters(obj)
```

```
## S4 method for signature 'compoundsCluster'
clusterProperties(obj)
```

```
## S4 method for signature 'compoundsCluster'
groupNames(obj)
```

```
## S4 method for signature 'compoundsCluster'
length(x)
```

```
## S4 method for signature 'compoundsCluster'
lengths(x, use.names = TRUE)
```

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

```
## S4 method for signature 'compoundsCluster,ANY,missing,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'compoundsCluster'
treeCut(obj, k = NULL, h = NULL, groupName)

## S4 method for signature 'compoundsCluster'
treeCutDynamic(obj, maxTreeHeight, deepSplit, minModuleSize, groupName)

## S4 method for signature 'compoundsCluster,missing'
plot(
  x,
  ...,
  groupName,
  pal = "Paired",
  colourBranches = lengths(x)[groupName] < 50,
  showLegend = lengths(x)[groupName] < 20
)

## S4 method for signature 'compoundsCluster'
getMCS(obj, groupName, cluster)

## S4 method for signature 'compoundsCluster'
plotStructure(
  obj,
  groupName,
  cluster,
  width = 500,
  height = 500,
  withTitle = TRUE
)

## S4 method for signature 'compoundsCluster'
plotSilhouettes(obj, kSeq, groupName, pch = 16, type = "b", ...)
```

## Arguments

|                             |   |
|-----------------------------|---|
| <code>obj, x, object</code> | A <code>compoundsCluster</code> object.   |
| <code>use.names</code>      | A logical value specifying whether the returned vector should be named with the feature group names.  |
| <code>i</code>              | For <code>[]</code> : A numeric or character value which is used to select feature groups by their index or name, respectively (for the order/names see <code>groupNames()</code> ). Can also be logical to perform logical selection (similar to regular vectors). If missing all feature groups are selected. |
| <code>...</code>            | Further arguments passed directly to the plotting function ( <code>plot</code> or <a href="#">plot.dendrogram</a> ).  |
| <code>drop, j</code>        | ignored.  |

|   |   |
|---|---|
| k, h                                    | Desired number of clusters or tree height to be used for cutting the dendrogram, respectively. One or the other must be specified. Analogous to <a href="#">cutree</a> .                          |
| groupName                               | A character specifying the feature group name.  |
| maxTreeHeight, deepSplit, minModuleSize | Arguments used by <a href="#">cutreeDynamicTree</a> .   |
| pal                                     | Colour palette to be used from <a href="#">RColorBrewer</a> .   |
| colourBranches                          | Whether branches from cut clusters (and their labels) should be coloured. Might be slow with large numbers of clusters, hence, the default is only TRUE when this is not the case.                |
| showLegend                              | If TRUE and colourBranches is also TRUE then a legend will be shown which outlines cluster numbers and their colours. By default TRUE for small amount of clusters to avoid overflowing the plot. |
| cluster                                 | A numeric value specifying the cluster.   |
| width, height                           | The dimensions (in pixels) of the raster image that should be plotted.  |
| withTitle                               | A logical value specifying whether a title should be added.   |
| kSeq                                    | An integer vector containing the sequence that should be used for average silhouette width calculation.   |
| pch, type                               | Passed to <a href="#">plot</a> .  |

### Details

Objects from this type are returned by the compounds method for [makeHCluster](#).

### Value

cutTree and cutTreeDynamic return the modified compoundsCluster object.

getMCS returns an **redk** molecule object (IAtomContainer).

### Methods (by generic)

- **clusters**: Accessor method to the clusters slot. Returns a list that contains for each feature group an object as returned by [hclust](#).
- **cutClusters**: Accessor method to the cutClusters slot. Returns a list that contains for each feature group a vector with cluster membership for each candidate (format as [cutree](#)).
- **clusterProperties**: Returns a list with properties on how the clustering was performed.
- **groupNames**: returns a character vector with the names of the feature groups for which data is present in this object.
- **length**: Returns the total number of clusters.
- **lengths**: Returns a vector with the number of clusters per feature group.
- **show**: Show summary information for this object.
- **[**: Subset on feature groups.
- **treeCut**: Manually (re-)cut a dendrogram that was generated for a feature group.

- `treeCutDynamic`: Automatically (re-)cut a dendrogram that was generated for a feature group using the `cutreeDynamicTree` function from `dynamicTreeCut`.
- `plot`: Plot the dendrogram for clustered compounds of a feature group. Clusters are highlighted using `dendextend`.
- `getMCS`: Calculates the maximum common substructure (MCS) for all candidate structures within a specified cluster. This method uses the `get.mcs` function from `redk`.
- `plotStructure`: Plots the maximum common substructure (MCS) for all candidate structures within a specified cluster.
- `plotSilhouettes`: Plots the average silhouette width when the clusters are cut by a sequence of k numbers. The k value with the highest value (marked in the plot) may be considered as the optimal number of clusters.

### Slots

`clusters` A list with `hclust` objects for each feature group.

`dists` A list with distance matrices for each feature group.

`SMILES` A list containing a vector with SMILES for all candidate structures per feature group.

`cutClusters` A list with assigned clusters for all candidates per feature group (same format as what `cutree` returns).

`properties` A list containing general properties and parameters used for clustering.

---

|                   |  |
|-------------------|--|
| compoundsMF-class | <i>Compounds list class for MetFrag results.</i> |
|-------------------|--|

---

### Description

This class is derived from `compounds` and contains additional specific MetFrag data.

### Usage

```
## S4 method for signature 'compoundsMF'
settings(compoundsMF)
```

### Arguments

`compoundsMF` A `compoundsMF` object.

### Details

Objects from this class are generated by `generateCompoundsMetFrag`

### Methods (by generic)

- `settings`: Accessor method for the `settings` slot.



## Slots

`settings` A list with all general configuration settings passed to MetFrag. Feature specific items (e.g. spectra and precursor masses) are not contained in this list.

## S4 class hierarchy

- [compounds](#)
  - [compoundsMF](#)

## References

Ruttkies C, Schymanski EL, Wolf S, Hollender J, Neumann S (2016). “MetFrag relaunched: incorporating strategies beyond in silico fragmentation.” *Journal of Cheminformatics*, **8**(1). doi: [10.1186/s1332101601159](#).

## See Also

[compounds](#) and [compound-generation](#)

---

convertMSFiles

*MS data conversion*

---

## Description

Conversion of MS analysis files between several open and closed data formats.

## Usage

```
MSFileFormats(algorithm = "pwiz", vendor = FALSE)
```

```
convertMSFiles(  
  files = NULL,  
  outPath = NULL,  
  dirs = TRUE,  
  anaInfo = NULL,  
  from = NULL,  
  to = "mzML",  
  overWrite = FALSE,  
  algorithm = "pwiz",  
  centroid = algorithm != "openms",  
  filters = NULL,  
  extraOpts = NULL,  
  PWizBatchSize = 1  
)
```

## Arguments

|               |   |
|---------------|---|
| algorithm     | Either "pwiz" (implemented by msConvert of ProteoWizard), "openms" (implemented by FileConverter of OpenMS) or "bruker" (implemented by DataAnalysis).  |
| vendor        | If TRUE only vendor formats are returned.   |
| files, dirs   | The files argument should be a character vector with input files. If files contains directories and dirs=TRUE then files from these directories are also considered. An alternative method to specify input files is by the anaInfo argument. If the latter is specified files may be NULL. |
| outPath       | A character vector specifying directories that should be used for the output. Will be re-cycled if necessary. If NULL, output directories will be kept the same as the input directories.   |
| anaInfo       | An <a href="#">analysis info table</a> used to retrieve input files. Either this argument or files (or both) should be set ( <i>i.e.</i> not NULL).   |
| from          | Input format (see below). These are used to find analyses when dirs=TRUE or anaInfo is set.   |
| to            | Output format: "mzXML" or "mzML".   |
| overWrite     | Should existing destination file be overwritten (TRUE) or not (FALSE)?  |
| centroid      | Set to TRUE to enable centroiding (not supported if algorithm="openms"). In addition, when algorithm="pwiz" the value may be "vendor" to perform centroiding with the vendor algorithm or "cwt" to use ProteoWizard's wavelet algorithm.  |
| filters       | When algorithm="pwiz": a character vector specifying one or more filters. The elements of the specified vector are directly passed to the --filter option (see <a href="#">here</a> )   |
| extraOpts     | A character vector specifying any extra commandline parameters passed to msConvert or FileConverter. Set to NULL to ignore. For options: see <a href="#">FileConverter</a> and <a href="#">msConvert</a> .  |
| PWizBatchSize | When algorithm="pwiz": the number of analyses to process by a single call to msConvert. Usually a value of one is most efficient. Set to zero to run all analyses all at once from a single call.   |

## Details

MSFileFormats returns a character with all supported input formats (see below).

convertMSFiles converts the data format of an analysis to another. It uses tools from [ProteoWizard](#) (msConvert command), [OpenMS](#) (FileConverter command) or Bruker DataAnalysis to perform the conversion. Supported input and output formats include 'mzXML', '.mzML' and several vendor formats, depending on which algorithm is used.

## Parallelization

convertMSFiles (except if algorithm="bruker") uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoon options](#) for configuration options.

## Conversion formats

Possible output formats (to argument) are mzXML and mzML.

Possible input formats (from argument) depend on the algorithm that was chosen and may include:

- thermo: Thermo '.RAW' files (only algorithm="pwiz").
- bruker: Bruker '.d', '.yep', '.baf' and '.fid' files (only algorithm="pwiz" or algorithm="bruker").
- agilent: Agilent '.d' files (only algorithm="pwiz").
- ab: AB Sciex '.wiff' files (only algorithm="pwiz").
- waters Waters '.RAW' files (only algorithm="pwiz").
- mzXML/mzML: Open format '.mzXML'/'mzML' files (only algorithm="pwiz" or algorithm="openms").

Note that the actual supported file formats of ProteoWizard depend on how it was installed (see [here](#)).

## References

Rost HL, Sachsenberg T, Aiche S, Bielow C, Weissner H, Aicheler F, Andreotti S, Ehrlich H, Gutenbrunner P, Kenar E, Liang X, Nahnsen S, Nilse L, Pfeuffer J, Rosenberger G, Rurik M, Schmitt U, Veit J, Walzer M, Wojnar D, Wolski WE, Schilling O, Choudhary JS, Malmstrom L, Aebersold R, Reinert K, Kohlbacher O (2016). "OpenMS: a flexible open-source software platform for mass spectrometry data analysis." *Nature Methods*, **13**(9), 741–748. doi: [10.1038/nmeth.3959](https://doi.org/10.1038/nmeth.3959).

Chambers MC, Maclean B, Burke R, Amodei D, Ruderman DL, Neumann S, Gatto L, Fischer B, Pratt B, Egertson J, Hoff K, Kessner D, Tasman N, Shulman N, Frewen B, Baker TA, Brusniak M, Paulse C, Creasy D, Flashner L, Kani K, Moulding C, Seymour SL, Nuwaysir LM, Lefebvre B, Kuhlmann F, Roark J, Rainer P, Detlev S, Hemenway T, Huhmer A, Langridge J, Connolly B, Chadick T, Holly K, Eckels J, Deutsch EW, Moritz RL, Katz JE, Agus DB, MacCoss M, Tabb DL, Mallick P (2012). "A cross-platform toolkit for mass spectrometry and proteomics." *Nature Biotechnology*, **30**(10), 918–920. doi: [10.1038/nbt.2377](https://doi.org/10.1038/nbt.2377).

## Examples

```
## Not run:
# Use FileConverter of OpenMS to convert between open mzXML/mzML format
convertMSFiles("standard-1.mzXML", to = "mzML", algorithm = "openms")

# Convert all Thermo .RAW files in the analyses/raw directory to mzML and
# store the files in analyses/mzml. During conversion files are centroided by
# the peakPicking filter and only MS 1 data is kept.
convertMSFiles("analyses/raw", "analyses/mzml", dirs = TRUE, from = "thermo",
               centroid = "vendor", filters = "msLevel 1")

## End(Not run)
```

---

|                   |                                      |
|-------------------|--------------------------------------|
| feature-filtering | <i>Filtering of grouped features</i> |
|-------------------|--------------------------------------|

---

**Description**

Basic rule based filtering of feature groups.

**Usage**

```
## S4 method for signature 'featureGroups'
filter(
  obj,
  absMinIntensity = NULL,
  relMinIntensity = NULL,
  preAbsMinIntensity = NULL,
  preRelMinIntensity = NULL,
  absMinAnalyses = NULL,
  relMinAnalyses = NULL,
  absMinReplicates = NULL,
  relMinReplicates = NULL,
  absMinFeatures = NULL,
  relMinFeatures = NULL,
  absMinReplicateAbundance = NULL,
  relMinReplicateAbundance = NULL,
  maxReplicateIntrSD = NULL,
  blankThreshold = NULL,
  retentionRange = NULL,
  mzRange = NULL,
  mzDefectRange = NULL,
  chromWidthRange = NULL,
  featQualityRange = NULL,
  groupQualityRange = NULL,
  rGroups = NULL,
  results = NULL,
  removeBlanks = FALSE,
  checkFeaturesSession = NULL,
  negate = FALSE
)

## S4 method for signature 'featureGroups'
replicateGroupSubtract(fGroups, rGroups, threshold = 0)
```

**Arguments**

absMinIntensity, relMinIntensity

Minimum absolute/relative intensity for features to be kept. The relative intensity is determined from the feature with highest intensity (of all features from all groups). Set to '0' or NULL to skip this step.

|  |   |
|--|---|
| <code>preAbsMinIntensity, preRelMinIntensity</code>                  | As <code>absMinIntensity/relMinIntensity</code> , but applied <i>before</i> any other filters. This is typically used to speed-up subsequent filter steps. However, care must be taken that a sufficiently low value is chosen that is not expected to affect subsequent filtering steps. See below why this may be important.  |
| <code>absMinAnalyses, relMinAnalyses</code>                          | Feature groups are only kept when they contain data for at least this (absolute or relative) amount of analyses. Set to NULL to ignore.   |
| <code>absMinReplicates, relMinReplicates</code>                      | Feature groups are only kept when they contain data for at least this (absolute or relative) amount of replicates. Set to NULL to ignore.   |
| <code>absMinFeatures, relMinFeatures</code>                          | Analyses are only kept when they contain at least this (absolute or relative) amount of features. Set to NULL to ignore.  |
| <code>absMinReplicateAbundance, relMinReplicateAbundance</code>      | Minimum absolute/relative abundance that a grouped feature should be present within a replicate group. If this minimum is not met all features within the replicate group are removed. Set to NULL to skip this step.   |
| <code>maxReplicateIntRSD</code>                                      | Maximum relative standard deviation (RSD) of intensity values for features within a replicate group. If the RSD is above this value all features within the replicate group are removed. Set to NULL to ignore.   |
| <code>blankThreshold</code>  | Feature groups that are also present in blank analyses (see <a href="#">analysis info</a> ) are filtered out unless their relative intensity is above this threshold. For instance, a value of '5' means that only features with an intensity five times higher than that of the blank are kept. The relative intensity values between blanks and non-blanks are determined from the mean of all non-zero blank intensities. Set to NULL to skip this step. |
| <code>retentionRange, mzRange, mzDefectRange, chromWidthRange</code> | Range of retention time (in seconds), <i>m/z</i> , mass defect (defined as the decimal part of <i>m/z</i> values) or chromatographic peak width (in seconds), respectively. Features outside this range will be removed. Should be a numeric vector with length of two containing the min/max values. The maximum can be Inf to specify no maximum range. Set to NULL to skip this step.  |
| <code>featQualityRange</code>  | Used to filter features by their peak qualities/scores (see <a href="#">calculatePeakQualities</a> ). Should be a named list with min/max ranges for each quality/score to be filtered (the <a href="#">featureQualityNames</a> function can be used to obtain valid names). Example: <code>featQualityRange=list(ModalityScore=c(0.3, Inf), SymmetryScore=c(0.5, Inf))</code> . Set to NULL to ignore.   |
| <code>groupQualityRange</code>                                       | Like <code>featQualityRange</code> , but filters on group specific or averaged qualities/scores.  |
| <code>rGroups</code>   | A character vector of replicate groups that should be kept (filter) or subtracted from ( <code>replicateGroupSubtract</code> ).   |
| <code>results</code>   | Only keep feature groups that have results in the object specified by results. Valid classes are <a href="#">featureAnnotations</a> (e.g. formula/compound annotations)   |

|                      |   |
|----------------------|---|
|                      | and <a href="#">components</a> . Can also be a list with multiple objects: in this case a feature group is kept if it has a result in <i>any</i> of the objects. Set to NULL to ignore.   |
| removeBlanks         | Set to TRUE to remove all analyses that belong to replicate groups that are specified as a blank in the <a href="#">analysis-information</a> . This is useful to simplify the analyses in the specified <a href="#">featureGroups</a> object after blank subtraction. When both blankThreshold and this argument are set, blank subtraction is performed prior to removing any analyses.  |
| checkFeaturesSession | If set then features and/or feature groups are removed that were selected for removal (see <a href="#">check-GUI</a> ). The session files are typically generated with the <a href="#">checkFeatures</a> and <a href="#">predictCheckFeaturesSession</a> functions. The value of checkFeaturesSession should either be a path to the session file or TRUE, in which case the default session file name is used. If negate=TRUE then all non-selected features/feature groups are removed instead. |
| negate               | If set to TRUE then filtering operations are performed in opposite manner.  |
| fGroups, obj         | <a href="#">featureGroups</a> object to which the filter is applied.  |
| threshold            | Minimum relative threshold (compared to mean intensity of replicate group being subtracted) for a feature group to be <i>not</i> removed. When '0' a feature group is always removed when present in the given replicate groups.  |

## Details

filter performs common rule based filtering of feature groups such as blank subtraction, minimum intensity and minimum replicate abundance. Removing of features occurs by zeroing their intensity values. Furthermore, feature groups that are left completely empty (*i.e.* all intensities are zero) will be automatically removed.

replicateGroupSubtract removes feature groups present in a given set of replicate groups (unless intensities are above a given threshold). The replicate groups that are subtracted will be removed.

## Value

A filtered [featureGroups](#) object. Feature groups that are filtered away have their intensity set to zero. In case a feature group is not present in any of the analyses anymore it will be removed completely.

## Filter order

When multiple arguments are specified to filter, multiple filters are applied in sequence. Since some of these filters may affect each other, choosing their order correctly may be important for effective data filtering. For instance, when an intensity filter removes features from blank analyses, a subsequent blank filter may not adequately perform blank subtraction. Similarly, when intensity and blank filters are executed after the replicate abundance filter it may be necessary to ensure minimum replicate abundance again as the intensity and blank filters may have removed some features within a replicate group.

With this in mind, filters (if specified) occur in the following order:

1. Features/feature groups selected for removal by the session specified by checkFeaturesSession.

2. Pre-Intensity filters (*i.e.* `preAbsMinIntensity` and `preRelMinIntensity`).
3. Chromatography and mass filters (*i.e.* `retentionRange`, `mzRange`, `mzDefectRange`, `chromWidthRange`, `featQualityRange` and `groupQualityRange`).
4. Replicate abundance filters (*i.e.* `absMinReplicateAbundance`, `relMinReplicateAbundance` and `maxReplicateIntRSD`).
5. Blank filter (*i.e.* `blankThreshold`).
6. Intensity filters (*i.e.* `absMinIntensity` and `relMinIntensity`).
7. Replicate abundance filters (2nd time, only if previous filters affected results).
8. General abundance filters (*i.e.* `absMinAnalyses`, `relMinAnalyses`, `absMinReplicates`, `relMinReplicates`, `absMinFeatures` and `relMinFeatures`).
9. Replicate group filter (*i.e.* `rGroups`), results filter (*i.e.* `results`) and blank analyses removal (*i.e.* if `removeBlanks=TRUE`).

If another filtering order is desired then `filter` should be called multiple times with only one filter argument at a time.

#### See Also

[featureGroups-class](#)

[feature-grouping](#)

---

feature-finding

*Finding features*

---

#### Description

Functions and classes for collection of features.

#### Usage

```
findFeatures(analysisInfo, algorithm, ..., verbose = TRUE)
```

```
importFeatures(analysisInfo, type, ...)
```

```
## S4 method for signature 'features'
makeSet(obj, ..., adducts, labels = NULL)
```

```
## S4 method for signature 'featuresSet'
makeSet(obj, ...)
```

```
findFeaturesBruker(
  analysisInfo,
  doFMF = "auto",
  startRange = 0,
  endRange = 0,
```

```
    save = TRUE,
    close = save,
    verbose = TRUE
)

findFeaturesEnviPick(analysisInfo, ..., parallel = TRUE, verbose = TRUE)

importFeaturesEnviMass(analysisInfo, enviProjPath)

findfeaturesKPIC2(
  analysisInfo,
  kmeans = TRUE,
  level = 1000,
  ...,
  parallel = TRUE,
  verbose = TRUE
)

importfeaturesKPIC2(picsList, analysisInfo)

findFeaturesOpenMS(
  analysisInfo,
  noiseThrInt = 1000,
  chromSNR = 3,
  chromFWHM = 5,
  mzPPM = 10,
  reEstimateMTSD = TRUE,
  traceTermCriterion = "sample_rate",
  traceTermOutliers = 5,
  minSampleRate = 0.5,
  minTraceLength = 3,
  maxTraceLength = -1,
  widthFiltering = "fixed",
  minFWHM = 1,
  maxFWHM = 30,
  traceSNRFiltering = FALSE,
  localRTRange = 10,
  localMZRange = 6.5,
  isotopeFilteringModel = "metabolites (5% RMS)",
  MZScoring13C = FALSE,
  useSmoothedInts = TRUE,
  extraOpts = NULL,
  intSearchRTWindow = 3,
  useFFMIntensities = FALSE,
  verbose = TRUE
)

findFeaturesSAFD(
```



```

    analysisInfo,
    profPath = NULL,
    mzRange = c(0, 400),
    maxNumbIter = 1000,
    maxTPeakW = 300,
    resolution = 30000,
    minMSW = 0.02,
    RThreshold = 0.75,
    minInt = 2000,
    sigIncThreshold = 5,
    S2N = 2,
    minPeakWS = 3,
    verbose = TRUE
)

findFeaturesSIRIUS(analysisInfo, verbose = TRUE)

findFeaturesXCMS(analysisInfo, method = "centWave", ..., verbose = TRUE)

importFeaturesXCMS(xs, analysisInfo)

findFeaturesXCMS3(
  analysisInfo,
  param = xcms::CentWaveParam(),
  ...,
  verbose = TRUE
)

importFeaturesXCMS3(xdata, analysisInfo)

```

### Arguments

|              |  |
|--------------|--|
| analysisInfo | <a href="#">Analysis info table</a> .  |
| algorithm    | A character string describing the algorithm that should be used: "bruker", "openms", "xcms", "xcms3", "envipick", "sirius", "kpic2", "safd"  |
| ...          | Further parameters passed to <a href="#">xcmsSet</a> ( <a href="#">findFeaturesXCMS</a> ), <a href="#">xcms::findChromPeaks</a> ( <a href="#">findFeaturesXCMS3</a> ), <a href="#">enviPickwrap</a> ( <a href="#">featurefinderEnviPick</a> ), <a href="#">getPIC/getPIC.kmeans</a> ( <a href="#">findFeaturesKPIC2</a> ) or to selected feature finding or importing algorithms ( <a href="#">findFeatures</a> and <a href="#">importFeatures</a> ).<br>For makeSet: further <a href="#">features</a> objects that should be used for the <a href="#">sets workflow</a> . |
| verbose      | If set to FALSE then no text output is shown.  |
| type         | What type of data should be imported: "xcms", "xcms3", "kpic2" or "envimass".  |
| obj          | A features object that is used (together with other objects passed to ...) to create a sets object with <a href="#">makeSet</a> .  |
| adducts      | The adduct assignments to each set. Should either be a list with <a href="#">adduct</a> objects or a character vector ( <i>e.g.</i> "[M+H]+"). The order should follow that of the objects given to the obj and ... arguments.   |

|  |  |
|--|--|
| labels   | The labels, or <i>set names</i> , for each set to be created. The order should follow that of the objects given to the <code>obj</code> and <code>...</code> arguments. If <code>NULL</code> , then labels are automatically generated from the polarity of the specified adducts argument (e.g. "positive", "negative").  |
| doFMF  | Run the 'Find Molecular Features' algorithm before loading compounds. Valid options are: "auto" (run FMF automatically if current results indicate it is necessary) and "force" (run FMF <i>always</i> , even if cached results exist). Note that checks done if <code>doFMF="auto"</code> are fairly simplistic, hence set <code>doFMF="force"</code> if feature data needs to be updated.  |
| startRange, endRange                                 | Start/End retention range (seconds) from which to collect features. A 0 (zero) for <code>endRange</code> marks the end of the analysis.  |
| close, save  | If <code>TRUE</code> then Bruker files are closed and saved after processing with <code>DataAnalysis</code> , respectively. Setting <code>close=TRUE</code> prevents that many analyses might be opened simultaneously in <code>DataAnalysis</code> , which otherwise may use excessive memory or become slow. By default <code>save</code> is <code>TRUE</code> when <code>close</code> is <code>TRUE</code> , which is likely what you want as otherwise any processed data is lost. |
| parallel   | If set to <code>TRUE</code> then code is executed in parallel through the <b>futures</b> package. Please see the parallelization section in the handbook for more details.   |
| enviProjPath   | The path of the <code>enviMass</code> project.   |
| kmeans   | If <code>TRUE</code> then <code>getPIC.kmeans</code> is used to obtain PICs, otherwise it is <code>getPIC</code> .   |
| level  | Passed to <code>getPIC</code> or <code>getPIC.kmeans</code>  |
| picsList   | A list with a <code>pics</code> objects obtained with <code>getPIC</code> or <code>getPIC.kmeans</code> for each analysis.   |
| noiseThrInt  | Noise intensity threshold. Sets <code>algorithm:common:noise_threshold_int</code> option.  |
| chromSNR   | Minimum S/N of a mass trace. Sets <code>algorithm:common:chrom_peak_snr</code> option.   |
| chromFWHM  | Expected chromatographic peak width (in seconds). Sets <code>algorithm:common:chrom_fwhm</code> option.  |
| mzPPM  | Allowed mass deviation (ppm) for trace detection. Sets <code>algorithm:mtd:mass_error_ppm</code> .   |
| reEstimateMTSD                                       | If <code>TRUE</code> then enables dynamic re-estimation of <code>m/z</code> variance during mass trace collection stage. Sets <code>algorithm:mtd:reestimate_mt_sd</code> .  |
| traceTermCriterion, traceTermOutliers, minSampleRate | Termination criterion for the extension of mass traces. See <b>FeatureFinderMetabo</b> . Sets the <code>algorithm:mtd:trace_termination_criterion</code> , <code>algorithm:mtd:trace_termination_outliers</code> and <code>algorithm:mtd:min_sample_rate</code> options, respectively.   |
| minTraceLength, maxTraceLength                       | Minimum/Maximum length of mass trace (seconds). Set negative value for <code>maxlength</code> to disable maximum. Sets <code>algorithm:mtd:min_trace_length</code> and <code>algorithm:mtd:min_trace_length</code> , respectively.   |
| widthFiltering, minFWHM, maxFWHM                     | Enable filtering of unlikely peak widths. See <b>FeatureFinderMetabo</b> . Sets <code>algorithm:epd:width_filtering</code> , <code>algorithm:epd:min_fwhm</code> and <code>algorithm:epd:max_fwhm</code> , respectively.   |

|  |   |
|--|---|
| tracesSNRFiltering   | If TRUE then apply post-filtering by signal-to-noise ratio after smoothing. Sets the <code>algorithm:epd:masstrace_snr_filtering</code> option.   |
| localRTRange, localMZRange   | Retention/MZ range where to look for coeluting/isotopic mass traces. Sets the <code>algorithm:ffm:local_rt_range</code> and <code>algorithm:ffm:local_mz_range</code> options, respectively.  |
| isotopeFilteringModel  | Remove/score candidate assemblies based on isotope intensities. See <a href="#">FeatureFinderMetabo</a> . Sets the <code>algorithm:ffm:isotope_filtering_model</code> option.   |
| MZScoring13C   | Use the <sup>13</sup> C isotope as the expected shift for isotope mass traces. See <a href="#">FeatureFinderMetabo</a> . Sets <code>algorithm:ffm:mz_scoring_13C</code> .   |
| useSmoothedInts  | If TRUE then use LOWESS intensities instead of raw intensities. Sets the <code>algorithm:ffm:use_smoothed</code> option.  |
| extraOpts  | Named list containing extra options that will be passed to <a href="#">FeatureFinderMetabo</a> . Any options specified here will override any of the above. Example: <code>extraOpts=list("-algorithm:com")</code> (corresponds to setting <code>noiseThrInt=1000</code> ). Set to NULL to ignore.  |
| intSearchRTWindow  | Retention time window (in seconds, +/- feature retention time) that is used to find the closest data point to the retention time to obtain the intensity of a feature (this is needed since OpenMS does not provide this data).   |
| useFFMIntensities  | If TRUE then peak intensities are directly loaded from <a href="#">FeatureFinderMetabo</a> output. Otherwise, intensities are loaded afterwards from the input 'mzML' files, which is potentially much slower, especially with many analyses files. However, <code>useFFMIntensities=TRUE</code> is still somewhat experimental, may be less accurate and requires a recent version of OpenMS ( $\geq 2.7$ ). |
| profPath   | A character vector with paths to the profile MS data for each analysis (will be re-cycled if necessary). See the <a href="#">Using SAFD</a> section for more details.   |
| mzRange  | The <i>m/z</i> window to be imported (passed to the <code>import_files_MS1</code> function).  |
| maxNumIter, maxTPeakW, resolution, minMSW, RThreshold, minInt, sigIncThreshold, S2N, minPeakWS | Parameters directly passed to the <code>safd_s3D</code> function.   |
| method   | The method setting used by XCMS peak finding, see <a href="#">xcms::findPeaks</a>   |
| xs   | An <a href="#">xcmsSet</a> object.  |
| param  | The method parameters used by XCMS peak finding, see <a href="#">xcms::findChromPeaks</a>   |
| xdata  | An <a href="#">XCMSnExp</a> object.   |

## Details

Several functions exist to collect features (*i.e.* retention and MS information that represent potential compounds) from a set of analyses. All 'feature finders' return an object derived from the [features](#) base class. The next step in a general workflow is to group and align these features across analyses by [feature groupers](#). Note that some feature finders have a plethora of options which sometimes may have a large effect on the quality of results. Fine-tuning parameters is therefore important, and the optimum is largely dependent upon applied analysis methodology and instrumentation.

`findFeatures` is a generic function that will find features using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `findFeaturesOpenMS` and `findFeaturesBruker`. While these functions may be called directly, `findFeatures` provides a generic interface and is therefore usually preferred.

`importFeatures` is a generic function to import feature groups produced by other software. The actual functionality is provided by specific functions such as `importFeaturesXCMS` and `importFeaturesKPIC2`.

`makeSet` is used to initiate a [sets workflow](#). See the Sets workflows section for more details.

`findFeaturesBruker` uses the 'Find Molecular Features' (FMF) algorithm of Bruker DataAnalysis vendor software to find features. The resulting 'compounds' are then transferred from DataAnalysis and stored as features.

`findFeaturesEnviPick` uses the [enviPickwrap](#) function from the **enviPick** R package to extract features.

`importFeaturesEnviMass` imports features from a project generated by the **enviMass** package. NOTE: this functionality has only been tested with older versions of **enviMass**.

`findFeaturesKPIC2` uses the **KPIC2** R package to extract features.

`importFeaturesKPIC2` converts features obtained with with the **KPIC2** package to a new [features](#) object.

`findFeaturesOpenMS` uses the **FeatureFinderMetabo** TOPP tool (see <http://www.openms.de>).

`findFeaturesSAFD` uses **SAFD** to obtain features. This functionality is still experimental. Please see the Using SAFD section below for more details.

`findFeaturesSIRIUS` uses **SIRIUS** to find features. The features are collected by running the `lcms-align` command for every analysis.

`findFeaturesXCMS` uses the [xcmsSet](#) function from the **xcms** package to find features.

`importFeaturesXCMS` converts features from an existing [xcmsSet](#) object (obtained with the **xcms** package) to a new [features](#) object.

`findFeaturesXCMS3` uses the new `xcms3` interface from the **xcms** package to find features.

`importFeaturesXCMS3` converts features from an existing [XCMSnExp](#) object (obtained with the **xcms** package) to a new [features](#) object.

## Value

An object of a class which is derived from [features](#).

`makeSet` returns a [featuresSet](#) object.

## Parallelization

`findFeaturesOpenMS`, `findFeaturesSIRIUS` and `findFeaturesSAFD` uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoön options](#) for configuration options.

Note that for caching purposes, the analyses files must always exist on the local host computer, even if it is not participating in computations.

## Sets workflows

The `makeSet` method function is used to initiate a [sets workflow](#). This method simply combines all the features from specified [features](#) objects in a new [featuresSet](#) object. The [analysis information](#) for this object is updated with all analyses, and a `set` column is added to designate the set of each analysis. Note that currently, all analyses names **must** be unique across different sets. In the last step the features are *neutralized*: the specified adducts to `makeSet` is used calculate the neutral monoisotopic mass for each feature per set. This neutralization is important to group features afterwards (see the details on sets workflows in [feature grouping](#)).

## Using SAFD

The support for SAFD is still experimental, and its interface might change in the future.

In order to use SAFD, please make sure that its `julia` packages are installed and you have verified that everything works, *e.g.* by running the test data.

This algorithm only supports profile and centroided MS data. If the use of profile data is desired, centroided data must still be available for other functionality of `patRoan`. The centroided data is specified through the 'regular' [analysis info](#) mechanism. The location to any profile data is specified through the `profPath` argument (NULL for no profile data). The base file names (*i.e.* the file name without path and extension) of both centroid and profile data must be the same. Furthermore, the format of the profile data must be `mzXML`.

## Note

The file format of analyses for `findFeaturesXCMS` and `findFeaturesXCMS3` must be `mzML` or `mzXML`.

`makeSet` Currently does not support making sets from [featuresSet](#) objects.

`findFeaturesBruker` only works with Bruker data files (`.d` extension) and requires Bruker Data-Analysis and the **RDCOMClient** package to be installed. Furthermore, `DataAnalysis` combines multiple related masses in a feature (*e.g.* isotopes, adducts) but does not report the actual (monoisotopic) mass of the feature. Therefore, it is simply assumed that the feature mass equals that of the highest intensity mass peak.

If any errors related to DCOM appear it might be necessary to terminate `DataAnalysis` (note that `DataAnalysis` might still be running as a background process). The `ProcessCleaner` application installed with `DataAnalysis` can be used for this.

`findFeaturesEnvipick` Requires analysis files to be in the `mzXML` format.

The file format of analyses for `findFeaturesOpenMS` must be '`mzML`'. This functionality has been tested with `OpenMS` version  $\geq 2.0$ . Please make sure it is installed and its binaries are added to the `PATH` environment variable or the `patRoan.path.OpenMS` option is set.

## References

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H. Paul Benton, Elizabeth J. Want and Timothy M. D. Ebbels Correction of mass calibration gaps in liquid chromatography-mass spectrometry metabolomics data *Bioinformatics*, 26:2488 (2010)

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## See Also

[features-class](#) and [analysis-information](#)

---

|                  |                             |
|------------------|-----------------------------|
| feature-grouping | <i>Grouping of features</i> |
|------------------|-----------------------------|

---

**Description**

Functions and classes for grouping of features across analyses.

**Usage**

```
## S4 method for signature 'features'
groupFeatures(obj, algorithm, ..., verbose = TRUE)

## S4 method for signature 'data.frame'
groupFeatures(obj, algorithm, ..., verbose = TRUE)

importFeatureGroups(path, type, ...)

## S4 method for signature 'featuresSet'
groupFeatures(obj, algorithm, ..., verbose = TRUE)

## S4 method for signature 'featureGroups'
makeSet(
  obj,
  ...,
  groupAlgo,
  groupArgs = NULL,
  verbose = TRUE,
  adducts = NULL,
  labels = NULL
)

## S4 method for signature 'featureGroupsSet'
makeSet(obj, ...)

importFeatureGroupsBrukerPA(
  path,
  feat,
  rtWindow = 12,
  mzWindow = 0.005,
  intWindow = 5,
  warn = TRUE
)

importFeatureGroupsEnviMass(path, feat, positive)

## S4 method for signature 'features'
groupFeaturesKPIC2(
```

```
    feat,
    rtalign = TRUE,
    loadRawData = TRUE,
    groupArgs = list(tolerance = c(0.005, 12)),
    alignArgs = list(),
    verbose = TRUE
)

## S4 method for signature 'featuresSet'
groupFeaturesKPIC2(
  feat,
  groupArgs = list(tolerance = c(0.005, 12)),
  verbose = TRUE
)

importFeatureGroupsKPIC2(picsSetGrouped, analysisInfo)

## S4 method for signature 'featureGroupsKPIC2'
delete(obj, ...)

## S4 method for signature 'features'
groupFeaturesOpenMS(
  feat,
  rtalign = TRUE,
  QT = FALSE,
  maxAlignRT = 30,
  maxAlignMZ = 0.005,
  maxGroupRT = 12,
  maxGroupMZ = 0.005,
  extraOptsRT = NULL,
  extraOptsGroup = NULL,
  verbose = TRUE
)

groupFeaturesSIRIUS(analysisInfo, verbose = TRUE)

## S4 method for signature 'features'
groupFeaturesXCMS(
  feat,
  rtalign = TRUE,
  loadRawData = TRUE,
  groupArgs = list(mzwid = 0.015),
  retcorArgs = list(method = "obiwarp"),
  verbose = TRUE
)

## S4 method for signature 'featuresSet'
groupFeaturesXCMS(feat, groupArgs = list(mzwid = 0.015), verbose = TRUE)
```



```

importFeatureGroupsXCMS(xs, analysisInfo)

## S4 method for signature 'featureGroupsXCMS'
delete(obj, ...)

## S4 method for signature 'features'
groupFeaturesXCMS3(
  feat,
  rtalign = TRUE,
  loadRawData = TRUE,
  groupParam = xcms::PeakDensityParam(sampleGroups = analysisInfo(feat)$group),
  preGroupParam = groupParam,
  retAlignParam = xcms::ObiwrapParam(),
  verbose = TRUE
)

## S4 method for signature 'featuresSet'
groupFeaturesXCMS3(
  feat,
  groupParam = xcms::PeakDensityParam(sampleGroups = analysisInfo(feat)$group),
  verbose = TRUE
)

importFeatureGroupsXCMS3(xdata, analysisInfo)

## S4 method for signature 'featureGroupsXCMS3'
delete(obj, ...)

```

## Arguments

|           |  |
|-----------|--|
| obj       | Either a <a href="#">features</a> object to be grouped, or a data.frame with <a href="#">analysis info</a> to be passed to groupFeaturesSIRIUS or a featureGroups objects passed to makeSet.   |
| algorithm | A character that specifies the algorithm to be used: either "openms", "xcms", "xcms3" or "kpic2" (features method), or "sirius" (data.frame method).   |
| ...       | Any parameters to be passed to the selected grouping/importing algorithm.<br>For makeSet: further <a href="#">featureGroups</a> objects that should be used for the <a href="#">sets workflow</a> .  |
| verbose   | if FALSE then no text output will be shown.  |
| path      | The path that should be used for importing. For importFeatureGroupsBrukerPA an exported 'bucket table' '.txt' file from Bruker ProfileAnalysis, for importFeatureGroupsBrukerTAS an exported global result table (converted to '.csv') and for importFeatureGroupsEnviMass the path of the enviMass project. |
| type      | Which file type should be imported or exported: "brukerpa" (Bruker Profile-Analysis), "brukertasq" (Bruker TASQ), envimass ( <b>enviMass</b> , only import) or "mzmine" (MZMine, only export).   |

|                               |   |
|-------------------------------|---|
| groupAlgo                     | groupAlgo The name of the feature grouping algorithm. See the algorithm argument description.   |
| groupArgs                     | A list with arguments directly passed to groupFeatures (can be named). Example: groupArgs=list(maxAlignMZ=0.002).   |
| adducts                       | The adduct assignments to each set. Should either be a list with <a href="#">adduct</a> objects or a character vector (e.g. "[M+H]+"). The order should follow that of the objects given to the obj and ... arguments. if NULL then adduct annotations are used.  |
| labels                        | The labels, or <i>set names</i> , for each set to be created. The order should follow that of the objects given to the obj and ... arguments. If NULL, then labels are automatically generated from the polarity of the specified adducts argument (e.g. "positive", "negative").                                 |
| feat                          | The <a href="#">features</a> to be grouped. importFeatureGroupsBrukerPA and importFeatureGroupsEnviMass only support features generated by <a href="#">findFeaturesBruker</a> and <a href="#">importFeaturesEnviMass</a> , respectively.  |
| rtWindow, mzWindow, intWindow | Search window values for retention time (seconds), <i>m/z</i> (Da) and intensity used to find back features within feature groups from PA (+/- the retention/mass/intensity value of a feature).  |
| warn                          | Warn about missing or duplicate features when relating them back from grouped features.   |
| positive                      | Whether data from positive (TRUE) or negative (FALSE) should be loaded.   |
| rtalign                       | Enable retention time alignment.  |
| loadRawData                   | Set to TRUE if analyses are available as mzXML or mzML files. Otherwise MS data is not loaded, and some dummy data (e.g. file paths) is used in the returned object.  |
| alignArgs                     | named character vector that may contain extra parameters to be used by <a href="#">KPIC::PICset.align</a> .   |
| picsSetGrouped                | A grouped PIC set object (e.g. as returned by <a href="#">KPIC::PICset.group</a> ).   |
| analysisInfo                  | A data.frame with <a href="#">analysis info</a> .   |
| QT                            | If enabled, use FeatureLinkerUnlabeledQT instead of FeatureLinkerUnlabeled for feature grouping.  |
| maxAlignRT, maxAlignMZ        | Used for retention alignment. Maximum retention time or <i>m/z</i> difference (seconds/Dalton) for feature pairing. Sets -algorithm:pairfinder:distance_RT:max_difference and -algorithm:pairfinder:distance_MZ:max_difference options, respectively.   |
| maxGroupRT, maxGroupMZ        | as maxAlignRT and maxAlignMZ, but for grouping of features. Sets -algorithm:distance_RT:max_difference and -algorithm:distance_MZ:max_difference options, respectively.   |
| extraOptsRT, extraOptsGroup   | Named list containing extra options that will be passed to MapAlignerPoseClustering or FeatureLinkerUnlabeledQT/FeatureLinkerUnlabeled, respectively. Any options specified here will override any of the above. Example: extraOptsGroup=list("-algorithm:distance_RT:max_difference=12"). Set to NULL to ignore. |

|                           |   |
|---------------------------|---|
| retcorArgs                | named character vector that may contain extra parameters to be used by <code>xcms::retcor</code> .                                |
| xs                        | An <code>xcmsSet</code> object.   |
| groupParam, retAlignParam | parameter object that is directly passed to <code>xcms::groupChromPeaks</code> and <code>xcms::adjustRtime</code> , respectively. |
| preGroupParam             | grouping parameters applied when features are grouped <i>prior</i> to alignment (only with peak groups alignment).                |
| xdata                     | An <code>XCMSnExp</code> object.  |

## Details

After [features have been found](#) the logical next step is to align and group them across analyses. This process is necessary to allow comparison of features between multiple analyses, which otherwise would be difficult due to small deviations in retention and mass data. Thus, algorithms of 'feature groupers' are used to collect features with similar retention and mass data. In addition, advanced retention time alignment algorithms exist to enhance grouping of features even with relative large retention time deviations (*e.g.* possibly observed from analyses collected over a long period). Like [finding of features](#), various algorithms are supported which may have many parameters that can be fine-tuned. This fine-tuning is likely to be necessary, since optimal settings often depend on applied methodology and instrumentation.

`groupFeatures` is a generic function that will group features using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `groupFeaturesOpenMS` and `groupFeaturesXCMS3`. While these functions may be called directly, `groupFeatures` provides a generic interface and is therefore usually preferred.

The `data.frame` method for `groupFeatures` is a special case that currently only supports the "sirius" algorithm.

`importFeatureGroups` is a generic function to import feature groups produced by other software. The actual functionality is provided by specific functions such as `importFeatureGroupsBrukerPA` and `importFeatureGroupsEnviMass`.

`makeSet` is used to initiate a [sets workflow](#). See the Sets workflows section for more details.

`importFeatureGroupsBrukerPA` imports grouped features generated with Bruker ProfileAnalysis (PA). To do so, a 'bucket table' should be generated using PA and exported as '.txt' file. Please note that this function only supports features generated by [findFeaturesBruker](#) and it is **crucial** that DataAnalysis files remain unchanged when features are collected and the bucket table is generated. Furthermore, please note that PA does not retain information about originating features for generated buckets. For this reason, this function tries to find back the original features and care must be taken to correctly specify search parameters (`rtWindow`, `mzWindow`, `intWindow`).

`importFeatureGroupsEnviMass` imports grouped features ('profiles') generated with **enviMass**. Note that this function *only* imports 'raw' profiles, *not* any results from further componentization steps performed in **enviMass**. Furthermore, this functionality has only been tested with older versions of **enviMass**. Finally, please note that this function only supports features imported by [importFeaturesEnviMass](#) (obviously, the same project should be used for both importing functions).

groupFeaturesKPIC2 uses the the **KPIC2** R package for grouping of features. Grouping of features and alignment of their retention times are performed with the `KPIC::PICset.group` and `KPIC::PICset.align` functions, respectively.

importFeatureGroupsKPIC2 imports grouped features from an **KPIC** object.

groupFeaturesOpenMS uses the OpenMS tools for grouping of features (see <http://www.openms.de>). Retention times may be aligned by the **MapAlignerPoseClustering** TOPP tool. Grouping is achieved by either the **FeatureLinkerUnlabeled** or **FeatureLinkerUnlabeledQT** TOPP tools.

groupFeaturesSIRIUS uses **SIRIUS** to find *and* group features. This is done by running the `lcms-align` command on every analyses at once. Note that grouping feature data from other algorithms than SIRIUS are therefore not supported.

groupFeaturesXCMS uses the **xcms** package for grouping of features. Grouping of features and alignment of their retention times are performed with the `xcms::group` and `xcms::retcor` functions, respectively. Both functions have an extensive list of parameters to modify their behaviour and may therefore be used to potentially optimize results.

importFeatureGroupsXCMS converts grouped features from an `xcmsSet` object (from the **xcms** package).

groupFeaturesXCMS3 uses the new interface from the **xcms** package for grouping of features. Grouping of features and alignment of their retention times are performed with the `xcms::groupChromPeaks` and `xcms::adjustRtime` functions, respectively. Both of these functions support an extensive amount of parameters that modify their behaviour and may therefore require optimization.

importFeatureGroupsXCMS3 converts grouped features from an `XCMSnExp` object (from the **xcms** package).

## Value

An object of a class which is derived from `featureGroups`.

`makeSet` and the `featuresSet` method of `groupFeatures` return a `featureGroupsSet` object.

## Sets workflows

With a **sets workflow** the features are first neutralized, *i.e.* their  $m/z$  values is replaced by their neutral monoisotopic mass. The latter is calculated from adduct annotations, specified either directly, or already present in the input objects. The features are then grouped by any of the `groupFeatures` algorithms. The neutralization step ensures that features measured with *e.g.* different ionization polarities can be grouped since their neutral mass will be the same. The sets workflow is initiated in either of the following two ways:

1. The `groupFeatures` method can be called with a `featuresSet` object (generated with the `featuresSet` method of `makeSet`).
2. By using the `makeSet` method for `featureGroups`. This uses the `featuresSet` method internally to first create a `featuresSet` object from all the feature data inside the input `featureGroups` objects. The (neutralized) features are then (re-)grouped with `groupFeatures`.

The advantage of the second method is that it preserves adduct annotations present in the input `featureGroups` objects (*e.g.* as set by `selections` or `adducts<-`). Furthermore, the second approach allows more advanced workflows where the input `featureGroups` are first pre-treated with *e.g.* `filter` before the sets object is made. On the other hand, the first approach is easier as it doesn't

require intermediate feature grouping steps, and is often sufficient as adduct annotations can be made afterwards with `selectIons/adducts<-`, and most filter operations do not need to be done per individual set.

With both approaches the resulting `featureGroupsSet` object will contain adduct annotations, either based on those already present from input `featureGroups` objects or as specified by the `adducts` argument to `makeSet`.

**NOTE** the `loadRawData` and arguments related to retention time alignment (e.g. `rtalign`, `retcorArgs`) are currently not supported for sets workflows when using algorithms from **KPIC2** or **XCMS**.

## Note

`makeSet` Currently does not support making sets from `featureGroupsSet` objects.

## References

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Ralf Tautenhahn, Christoph Boettcher, Steffen Neumann: *Highly sensitive feature detection for high resolution LC/MS* *BMC Bioinformatics*, 9:504 (2008)

H. Paul Benton, Elizabeth J. Want and Timothy M. D. Ebbels *Correction of mass calibration gaps in liquid chromatography-mass spectrometry metabolomics data* *Bioinformatics*, 26:2488 (2010)

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### See Also

[featureGroups-class](#)

---

|                      |  |
|----------------------|--|
| feature-optimization | <i>Optimization of feature finding and grouping parameters</i> |
|----------------------|--|

---

### Description

Automatic optimization of feature finding and grouping parameters through Design of Experiments (DoE).

### Usage

```
optimizeFeatureGrouping(  
  features,  
  algorithm,  
  ...,  
  templateParams = list(),  
  paramRanges = list(),  
  maxIterations = 50,  
  maxModelDeviation = 0.1,  
  parallel = TRUE  
)  
  
generateFGroupsOptPSet(algorithm, ...)  
  
getDefFGroupsOptParamRanges(algorithm)  
  
optimizeFeatureFinding(  
  anaInfo,  
  algorithm,  
  ...,  
  templateParams = list(),  
  paramRanges = list(),  
  isoIdent = if (algorithm == "openms") "OpenMS" else "IPO",  
  checkPeakShape = "none",
```

```

CAMERAOpts = list(),
maxIterations = 50,
maxModelDeviation = 0.1,
parallel = TRUE
)

generateFeatureOptPSet(algorithm, ...)

getDefFeaturesOptParamRanges(algorithm, method = "centWave")

```

### Arguments

|                   |   |
|-------------------|---|
| features          | A <a href="#">features</a> object with the features that should be used to optimize grouping.   |
| algorithm         | The algorithm used for finding or grouping features (see <a href="#">findFeatures</a> and <a href="#">groupFeatures</a> ).  |
| ...               | One or more lists with parameter sets (see below) (for <a href="#">optimizeFeatureFinding</a> and <a href="#">optimizeFeatureGrouping</a> ). Alternatively, named arguments that set (and possibly override) the parameters that should be returned from <a href="#">generateFeatureOptPSet</a> or <a href="#">generateFGroupsOptPSet</a> . |
| templateParams    | Template parameter set (see below).   |
| paramRanges       | A list with vectors containing absolute parameter ranges (minimum/maximum) that constrain numeric parameters chosen during experiments. See the <a href="#">getDefFeaturesOptParamRange</a> and <a href="#">getDefFGroupsOptParamRanges</a> functions for defaults. Values should be Inf when no limit should be used.                      |
| maxIterations     | Maximum number of iterations that may be performed to find optimum values. Used to restrict needless long optimization procedures. In IPO this was fixed to '50'.   |
| maxModelDeviation | See the Potential suboptimal results by optimization model section below.   |
| parallel          | If set to TRUE then code is executed in parallel through the <a href="#">futures</a> package. Please see the parallelization section in the handbook for more details.  |
| anaInfo           | <a href="#">Analysis info table</a> (passed to <a href="#">findFeatures</a> ).  |
| isoIdent          | Sets the algorithm used to identify isotopes. Valid values are: "IPO", "CAMERA" and "OpenMS". The latter can only be used when OpenMS is used to find features, and is highly recommended in this situation.  |
| checkPeakShape    | Additional peak shape checking of isotopes. Only used if isoIdent="IPO". Valid values: "none", "borderIntensity", "sinusCurve" or "normalDistr".  |
| CAMERAOpts        | A list with additional arguments passed to <a href="#">CAMERA::findIsotopes</a> when isoIdent="CAMERA".   |
| method            | Method used by XCMS to find features (only if algorithm="xcms").  |

### Details

Many different parameters exist that may affect the output quality of feature finding and grouping. To avoid time consuming manual experimentation, functionality is provided to largely automate the optimization process. The methodology, which uses design of experiments (DoE), is based on the excellent [Isotopologue Parameter Optimization \(IPO\) R package](#). The functionality of this package

is directly integrated in patRoan. Some functionality was added or changed, however, the principle algorithm workings are nearly identical.

Compared to IPO, the following functionality was added or changed:

- The code was made more generic in order to include support for other feature finding/grouping algorithms (*e.g.* OpenMS, enviPick, XCMS3).
- The methodology of FeatureFinderMetabo (OpenMS) may be used to find isotopes.
- The `maxModelDeviation` parameter was added to potentially avoid suboptimal results ([issue discussed here](#)).
- The use of multiple 'parameter sets' (discussed below) which, for instance, allow optimizing qualitative parameters more easily (see examples).
- More consistent optimization code for feature finding/grouping.
- More consistent output using S4 classes (*i.e.* `optimizationResult` class).
- Parallelization is performed via the **future** package instead of **BiocParallel**. If this is enabled (`parallel=TRUE`) then any parallelization supported by the feature finding or grouping algorithm is disabled.

## Value

The `optimizeFeatureFinding` and `optimizeFeatureGrouping` return their results in a `optimizationResult` object.

## Parameter sets

Which parameters should be optimized is determined by a *parameter set*. A set is defined by a named list containing the minimum and maximum starting range for each parameter that should be tested. For instance, the set `list(chromFWHM = c(5, 10), mzPPM = c(5, 15))` specifies that the `chromFWHM` and `mzPPM` parameters (used by OpenMS feature finding) should be optimized within a range of '5'-'10' and '5'-'15', respectively. Note that this range may be increased or decreased after a DoE iteration in order to find a better optimum. The absolute limits are controlled by the `paramRanges` function argument.

Multiple parameter sets may be specified (*i.e.* through the `...` function argument). In this situation, the optimization algorithm is repeated for each set, and the final optimum is determined from the parameter set with the best response. The `templateParams` function argument may be useful in this case to define a template for each parameter set. Actual parameter sets are then constructed by joining each parameter set with the set specified for `templateParams`. When a parameter is defined in both a regular and template set, the parameter in the regular set takes precedence.

Parameters that should not be optimized but still need to be set for the feature finding/grouping functions should also be defined in a (template) parameter set. Which parameters should be optimized is determined whether its value is specified as a vector range or a single fixed value. For instance, when a set is defined as `list(chromFWHM = c(5, 10), mzPPM = 5)`, only the `chromFWHM` parameter is optimized, whereas `mzPPM` is kept constant at '5'.

Using multiple parameter sets with differing fixed values allows optimization of qualitative values (see examples below).

The parameters specified in parameter sets are directly passed through the `findFeatures` or `groupFeatures` functions. Hence, grouping and retention time alignment parameters used by XCMS should (still) be set through the `groupArgs` and `retcorArgs` parameters.



**NOTE:** For XCMS3, which normally uses parameter classes for settings its options, the parameters must be defined in a named list like any other algorithm. The set parameters are then used passed to the constructor of the right parameter class object (e.g. [CentWaveParam](#), [ObiwarParam](#)). For grouping/alignment sets, these parameters need to be specified in nested lists called `groupParams` and `retAlignParams`, respectively (similar to `groupArgs`/`retcorArgs` for `algorithm="xcms"`). Finally, the underlying XCMS method to be used should be defined in the parameter set (*i.e.* by setting the `method` field for feature parameter sets and the `groupMethod` and `retAlignMethod` for grouping/aligning parameter sets). See the examples below for more details.

**NOTE:** Similar to IPO, the `peakwidth` and `prefilter` parameters for XCMS feature finding should be split in two different values:

- The minimum and maximum ranges for `peakwidth` are optimized by setting `min_peakwidth` and `max_peakwidth`, respectively.
- The `k` and `I` parameters contained in `prefilter` are split in `prefilter` and `value_of_prefilter`, respectively.

*Similary*, for KPIC2, the following parameters should be split:

- the `width` parameter (feature optimization) is optimized by specifying the `min_width` and `max_width` parameters.
- the `tolerance` and `weight` parameters (feature grouping optimization) are optimized by setting `mz_tolerance/rt_tolerance` and `mz_weight/rt_weight` parameters, respectively.

## Functions

The `optimizeFeatureFinding` and `optimizeFeatureGrouping` are the functions to be used to optimize parameters for feature finding and grouping, respectively. These functions are analogous to [optimizeXcmsSet](#) and [optimizeRetGroup](#) from **IPO**.

The `generateFeatureOptPSet` and `generateFGroupsOptPSet` functions may be used to generate a parameter set for feature finding and grouping, respectively. Some algorithm dependent default parameter optimization ranges will be returned. These functions are analogous to [getDefaultXcmsSetStartingParams](#) and [getDefaultRetGroupStartingParams](#) from **IPO**. However, unlike their IPO counterparts, these functions will not output default fixed values. The `generateFGroupsOptPSet` will only generate defaults for density grouping if `algorithm="xcms"`.

The `getDefFeaturesOptParamRanges` and `getDefFGroupsOptParamRanges` return the default absolute optimization parameter ranges for feature finding and grouping, respectively. These functions are useful if you want to set the `paramRanges` function argument.

## Potential suboptimal results by optimization model

After each experiment iteration an optimum parameter set is found by generating a model containing the tested parameters and their responses. Sometimes the actual response from the parameters derived from the model is actually significantly lower than expected. When the response is lower than the maximum response found during the experiment, the parameters belonging to this experimental maximum may be chosen instead. The `maxModelDeviation` argument sets the maximum deviation in response between the modelled and experimental maxima. The value is relative: '0' means that experimental values will always be favored when leading to improved responses, whereas 1 will effectively disable this procedure (and return to 'regular' IPO behaviour).

## Source

The code and methodology is a direct adaptation from the [IPO R package](#).

## References

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## Examples

```
# example data from patRoonaData package
dataDir <- patRoonaData::exampleDataPath()
anaInfo <- generateAnalysisInfo(dataDir)
anaInfo <- anaInfo[1:2, ] # only focus on first two analyses (e.g. training set)

# optimize mzPPM and chromFWHM parameters
ftOpt <- optimizeFeatureFinding(anaInfo, "openms", list(mzPPM = c(5, 10), chromFWHM = c(4, 8)))

# optimize chromFWHM and isotopeFilteringModel (a qualitative parameter)
ftOpt2 <- optimizeFeatureFinding(anaInfo, "openms",
                                list(isotopeFilteringModel = "metabolites (5% RMS)",
                                     list(isotopeFilteringModel = "metabolites (2% RMS)",
                                           templateParams = list(chromFWHM = c(4, 8)))

# perform grouping optimization with optimized features object
fgOpt <- optimizeFeatureGrouping(optimizedObject(ftOpt), "xcms",
                                list(groupArgs = list(bw = c(22, 28)),
                                      retcorArgs = list(method = "obiwarp")))

# same, but using the XCMS3 interface
fgOpt2 <- optimizeFeatureGrouping(optimizedObject(ftOpt), "xcms3",
                                 list(groupMethod = "density", groupParams = list(bw = c(22, 28)),
                                       retAlignMethod = "obiwarp"))

# plot contour of first parameter set/DoE iteration
plot(ftOpt, paramSet = 1, DoEIteration = 1, type = "contour")

# generate parameter set with some predefined and custom parameters to be
# optimized.
pSet <- generateFeatureOptPSet("openms", chromSNR = c(3, 9),
                              useSmoothedInts = FALSE)
```

---

featureAnnotations-class

*Base feature annotations class*

---

**Description**

Holds information for all feature group annotations.

**Usage**

```
## S4 method for signature 'featureAnnotations'
annotations(obj)

## S4 method for signature 'featureAnnotations'
groupNames(obj)

## S4 method for signature 'featureAnnotations'
length(x)

## S4 method for signature 'featureAnnotations,ANY,missing,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'featureAnnotations,ANY,missing'
x[[i, j]]

## S4 method for signature 'featureAnnotations'
x$name

## S4 method for signature 'featureAnnotations'
as.data.table(
  x,
  fGroups = NULL,
  fragments = FALSE,
  countElements = NULL,
  countFragElements = NULL,
  OM = FALSE,
  normalizeScores = "none",
  excludeNormScores = defaultExclNormScores(x)
)

## S4 method for signature 'featureAnnotations'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featureAnnotations'
filter(
  obj,
  minExplainedPeaks = NULL,
  scoreLimits = NULL,
  elements = NULL,
  fragElements = NULL,
  lossElements = NULL,
  topMost = NULL,
  OM = FALSE,
```

```

    negate = FALSE
  )

  ## S4 method for signature 'featureAnnotations'
  plotVenn(obj, ..., labels = NULL, vennArgs = NULL)

  ## S4 method for signature 'featureAnnotations'
  plotUpSet(
    obj,
    ...,
    labels = NULL,
    nsets = length(list(...)) + 1,
    nintersects = NA,
    upsetArgs = NULL
  )

```

## Arguments

|                                  |  |
|----------------------------------|--|
| obj, x                           | featureAnnotations object to be accessed   |
| i, j                             | For <code>[]</code> : A numeric or character value which is used to select feature groups by their index or name, respectively (for the order/names see <code>groupNames()</code> ).<br><br>For <code>:</code> : Can also be logical to perform logical selection (similar to regular vectors). If missing all feature groups are selected.<br><br>For <code>[]</code> : should be a scalar value.<br><br>For delete: The data to remove from. <code>i</code> are the feature groups as numeric index, logical or character, <code>j</code> the candidates as numeric indices (rows). If either is <code>NULL</code> then data for all is removed. <code>j</code> may also be a function: it will be called for each feature group, with the annotation table (a <code>data.table</code> ) as first argument, the feature group name as second argument, and any other arguments passed as <code>...</code> to delete. The return value of this function specifies the candidate indices (rows) to be removed (specified as an integer or logical vector). |
| ...                              | For the <code>"["</code> operator: ignored.<br>For delete: passed to the function specified as <code>j</code> .<br>Others: Any further (and unique) featureAnnotations objects.  |
| drop                             | ignored.   |
| name                             | The feature group name (partially matched).  |
| fGroups                          | The <a href="#">featureGroups</a> object that was used to generate this object. If not <code>NULL</code> it is used to add feature group information (retention and <i>m/z</i> values).  |
| fragments                        | If <code>TRUE</code> then information on annotated fragments will be included. Automatically set to <code>TRUE</code> if <code>countFragElements</code> is set.  |
| countElements, countFragElements | A character vector with elements that should be counted for each candidate's formula. For instance, <code>c("C", "H")</code> adds columns for both carbon and hydrogen   |

|                            |  |
|----------------------------|--|
|                            | amounts of each formula. Note that the neutral formula (neutral_formula column) is used to count elements of non-fragmented formulae, whereas the charged formula of fragments (ion_formula column in fragInfo data) is used for fragments. Set to NULL to not count any elements.   |
| OM                         | <p>For as.data.table: if set to TRUE several columns with information relevant for organic matter (OM) characterization will be added (e.g. elemental ratios, classification). This will also make sure that countElements contains at least C, H, N, O, P and S.</p> <p>For filter: If TRUE then several filters are applied to exclude unlikely formula candidates present in organic matter (OM). See Source section for details.</p>   |
| normalizeScores            | A character that specifies how normalization of annotation scorings occurs. Either "none" (no normalization), "max" (normalize to max value) or "minmax" (perform min-max normalization). Note that normalization of negative scores (e.g. output by SIRIUS) is always performed as min-max. Furthermore, currently normalization for compounds takes the original min/max scoring values into account when candidates were generated. Thus, for compounds scoring, normalization is not affected when candidate results were removed after they were generated (e.g. by use of filter).   |
| excludeNormScores          | <p>A character vector specifying any compound scoring names that should <i>not</i> be normalized. Set to NULL to normalize all scorings. Note that whether any normalization occurs is set by the excludeNormScores argument.</p> <p>For compounds: By default score and individualMoNAScore are set to mimic the behavior of the MetFrag web interface.</p>   |
| minExplainedPeaks          | Minimum number of explained peaks. Set to NULL to ignore.  |
| scoreLimits                | Filter results by their scores. Should be a named list that contains two-sized numeric vectors with the minimum/maximum value of a score (use -Inf/Inf for no limits). The names of each element should follow the name column of the table returned by formulaScorings\$name and compoundScorings()\$name. For instance, scoreLimits=list(numberPatents=c(10, Inf)) specifies that numberPatents should be at least '10'. Note that a result without a specified scoring is never removed. If a score term exists multiple times, i.e. due to a consensus, then a candidate is kept if at least one of the terms falls within the range. Set to NULL to skip this filter.   |
| elements                   | Only retain candidate formulae (neutral form) that match a given elemental restriction. The format of elements is a character string with elements that should be present where each element is followed by a valid amount or a range thereof. If no number is specified then '1' is assumed. For instance, elements="C1-10H2-20O0-2P", specifies that '1-10', '2-20', '0-2' and '1' carbon, hydrogen, oxygen and phosphorus atoms should be present, respectively. When length(elements)>1 formulas are tested to follow at least one of the given elemental restrictions. For instance, elements=c("P", "S") specifies that either one phosphorus or one sulfur atom should be present. Set to NULL to ignore this filter. |
| fragElements, lossElements | Specifies elemental restrictions for fragment or neutral loss formulae (charged  |

|                                 |  |
|---------------------------------|--|
|                                 | form). Candidates are retained if at least one of the fragment formulae follow (or not follow if <code>negate=TRUE</code> ) the given restrictions. See <code>elements</code> for the used format. |
| <code>topMost</code>            | Only keep a maximum of <code>topMost</code> candidates with highest score (or least highest if <code>negate=TRUE</code> ). Set to <code>NULL</code> to ignore.                                     |
| <code>negate</code>             | If <code>TRUE</code> then filters are applied in opposite manner.  |
| <code>labels</code>             | A character with names to use for labelling. If <code>NULL</code> labels are automatically generated.  |
| <code>vennArgs</code>           | A list with further arguments passed to <b>VennDiagram</b> plotting functions. Set to <code>NULL</code> to ignore.   |
| <code>nsets, nintersects</code> | See <a href="#">upset</a> .  |
| <code>upsetArgs</code>          | A list with any further arguments to be passed to <a href="#">upset</a> . Set to <code>NULL</code> to ignore.  |

### Details

This class stores annotation data for feature groups, such as molecular formulae, SMILES identifiers, compound names etc. The class of objects that are generated by formula and compound annotation ([generateFormulas](#) and [generateCompounds](#)) are based on this class.

### Value

`as.data.table` returns a [data.table](#).

`delete` returns the object for which the specified data was removed.

`filter` returns a filtered `featureAnnotations` object.

`plotVenn` (invisibly) returns a list with the following fields:

- `gList` the `gList` object that was returned by the utilized **VennDiagram** plotting function.
- `areas` The total area for each plotted group.
- `intersectionCounts` The number of intersections between groups.

The order for the `areas` and `intersectionCounts` fields is the same as the parameter order from the used plotting function (see *e.g.* [draw.pairwise.venn](#) and [draw.triple.venn](#)).

### Methods (by generic)

- `annotations`: Accessor for the `groupAnnotations` slot.
- `groupNames`: returns a character vector with the names of the feature groups for which data is present in this object.
- `length`: Obtain total number of candidates.
- `[]`: Subset on feature groups.
- `[[`: Extracts annotation data for a feature group.
- `$`: Extracts annotation data for a feature group.
- `as.data.table`: Generates a table with all annotation data for each feature group and other information such as element counts.

- `delete`: Completely deletes specified annotations.
- `filter`: Provides rule based filtering for feature group annotations. Useful to eliminate unlikely candidates and speed up further processing.
- `plotVenn`: plots a Venn diagram (using [VennDiagram](#)) outlining unique and shared candidates of up to five different featureAnnotations objects.
- `plotUpSet`: plots an UpSet diagram (using the [upset](#) function) outlining unique and shared formula candidates between different featureAnnotations objects.

## Slots

`groupAnnotations` A list with for each annotated feature group a `data.table` with annotation data. Use the `annotations` method for access.

`scoreTypes` A character with all the score types present in this object.

`scoreRanges` The minimum and maximum score values of all candidates for each feature group. Used for normalization.

## Source

Calculation of the aromaticity index (AI) and related double bond equivalents (DBE\_AI) is performed as described in Koch 2015. Formula classification is performed by the rules described in Abdulla 2013. Filtering of OM related molecules is performed as described in Koch 2006 and Kujawinski 2006. (see references).

## S4 class hierarchy

- [workflowStep](#)
  - [featureAnnotations](#)
    - \* [formulas](#)
      - [formulasConsensus](#)
      - [formulasSet](#)
      - [formulasUnset](#)
    - \* [compounds](#)
      - [compoundsConsensus](#)
      - [compoundsMF](#)
      - [compoundsSet](#)
      - [compoundsUnset](#)

## References

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Lex A, Gehlenborg N, Strobel H, Vuillemot R, Pfister H (2014). “UpSet: Visualization of Intersecting Sets.” *IEEE Transactions on Visualization and Computer Graphics*, **20**(12), 1983–1992. doi: [10.1109/tvcg.2014.2346248](https://doi.org/10.1109/tvcg.2014.2346248).

### See Also

[formulas-class](#) and [compounds-class](#)

The derived [formulas](#) and [compounds](#) classes.

---

|                     |   |
|---------------------|---|
| featureGroups-class | <i>Base class for grouped features.</i> |
|---------------------|---|

---

### Description

This class holds all the information for grouped features.

### Usage

```
## S4 method for signature 'featureGroups'  
names(x)
```

```
## S4 method for signature 'featureGroups'  
analyses(obj)
```

```
## S4 method for signature 'featureGroups'  
replicateGroups(obj)
```

```
## S4 method for signature 'featureGroups'  
groupNames(obj)
```

```
## S4 method for signature 'featureGroups'  
length(x)
```

```
## S4 method for signature 'featureGroups'
```



```
show(object)

## S4 method for signature 'featureGroups'
groupTable(object, areas = FALSE)

## S4 method for signature 'featureGroups'
analysisInfo(obj)

## S4 method for signature 'featureGroups'
groupInfo(fGroups)

## S4 method for signature 'featureGroups'
featureTable(obj)

## S4 method for signature 'featureGroups'
getFeatures(obj)

## S4 method for signature 'featureGroups'
groupFeatIndex(fGroups)

## S4 method for signature 'featureGroups'
groupQualities(fGroups)

## S4 method for signature 'featureGroups'
groupScores(fGroups)

## S4 method for signature 'featureGroups'
annotations(obj)

## S4 method for signature 'featureGroups'
adducts(obj)

## S4 replacement method for signature 'featureGroups'
adducts(obj) <- value

## S4 method for signature 'featureGroups,ANY,ANY,missing'
x[i, j, ..., rGroups, results, drop = TRUE]

## S4 method for signature 'featureGroups,ANY,ANY'
x[[i, j]]

## S4 method for signature 'featureGroups'
x$name

## S4 method for signature 'featureGroups'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featureGroups'
```

```
export(obj, type, out)

getFCParams(rGroups, ...)

## S4 method for signature 'featureGroups'
as.data.table(
  x,
  average = FALSE,
  areas = FALSE,
  features = FALSE,
  qualities = FALSE,
  regression = FALSE,
  averageFunc = mean,
  normFunc = NULL,
  FCParams = NULL
)

## S4 method for signature 'featureGroups,missing'
plot(
  x,
  colourBy = c("none", "rGroups", "fGroups"),
  onlyUnique = FALSE,
  retMin = FALSE,
  showLegend = TRUE,
  col = NULL,
  pch = NULL,
  ...
)

## S4 method for signature 'featureGroups'
plotInt(
  obj,
  average = FALSE,
  normFunc = NULL,
  xnames = TRUE,
  showLegend = FALSE,
  pch = 20,
  type = "b",
  lty = 3,
  col = NULL,
  ...
)

## S4 method for signature 'featureGroups'
plotChord(
  obj,
  addSelfLinks = FALSE,
  addRetMzPlots = TRUE,
```

```

        average = FALSE,
        outerGroups = NULL,
        addIntraOuterGroupLinks = FALSE,
        ...
    )

## S4 method for signature 'featureGroups'
plotChroms(
    obj,
    rtWindow = 30,
    mzExpWindow = 0.001,
    retMin = FALSE,
    topMost = NULL,
    topMostByRGroup = FALSE,
    EICs = NULL,
    showPeakArea = FALSE,
    showFGroupRect = TRUE,
    title = NULL,
    colourBy = c("none", "rGroups", "fGroups"),
    showLegend = TRUE,
    onlyPresent = TRUE,
    annotate = c("none", "ret", "mz"),
    showProgress = FALSE,
    xlim = NULL,
    ylim = NULL,
    ...
)

## S4 method for signature 'featureGroups'
plotVenn(obj, which = NULL, ...)

## S4 method for signature 'featureGroups'
plotUpSet(obj, which = NULL, nsets = length(which), nintersects = NA, ...)

## S4 method for signature 'featureGroups'
plotVolcano(
    obj,
    FCParams,
    showLegend = TRUE,
    averageFunc = mean,
    col = NULL,
    pch = 19,
    ...
)

## S4 method for signature 'featureGroups'
unique(x, which, relativeTo = NULL, outer = FALSE)

```

```
## S4 method for signature 'featureGroups'
overlap(fGroups, which, exclusive)

## S4 method for signature 'featureGroups'
calculatePeakQualities(
  obj,
  weights,
  flatnessFactor,
  avgFunc = mean,
  parallel = TRUE
)

## S4 method for signature 'featureGroups'
selectIons(
  fGroups,
  components,
  prefAdduct,
  onlyMonoIso = TRUE,
  chargeMismatch = "adduct"
)

## S4 method for signature 'featureGroupsSet'
sets(obj)

## S4 method for signature 'featureGroupsSet'
adducts(obj, set, ...)

## S4 replacement method for signature 'featureGroupsSet'
adducts(obj, set, reGroup = TRUE) <- value

## S4 method for signature 'featureGroupsSet'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featureGroupsSet'
show(object)

## S4 method for signature 'featureGroupsSet'
featureTable(obj)

## S4 method for signature 'featureGroupsSet,ANY,ANY,missing'
x[i, j, ..., rGroups, sets = NULL, drop = TRUE]

## S4 method for signature 'featureGroupsSet'
export(obj, type, out, set)

## S4 method for signature 'featureGroupsSet'
as.data.table(
  x,
```

```
    average = FALSE,
    areas = FALSE,
    features = FALSE,
    qualities = FALSE,
    regression = FALSE,
    averageFunc = mean,
    normFunc = NULL,
    FCPParams = NULL
)

## S4 method for signature 'featureGroupsSet'
filter(
  obj,
  ...,
  negate = FALSE,
  sets = NULL,
  absMinSets = NULL,
  relMinSets = NULL
)

## S4 method for signature 'featureGroupsSet'
plotInt(
  obj,
  average = FALSE,
  normFunc = NULL,
  xnames = !sets,
  showLegend = sets,
  pch = 20,
  type = "b",
  lty = 3,
  col = NULL,
  ...,
  sets = FALSE
)

## S4 method for signature 'featureGroupsSet'
plotVenn(obj, which = NULL, ..., sets = FALSE)

## S4 method for signature 'featureGroupsSet'
unique(x, which, ..., sets = FALSE)

## S4 method for signature 'featureGroupsSet'
overlap(fGroups, which, exclusive, sets = FALSE)

## S4 method for signature 'featureGroupsSet'
selectIons(fGroups, components, prefAdduct, ...)

## S4 method for signature 'featureGroupsSet'
```

```
unset(obj, set)
```

## Arguments

|                         |  |
|-------------------------|--|
| areas                   | <p>If set to TRUE then areas are considered instead of peak intensities.</p> <p>For <code>as.data.table</code>: ignored if <code>features=TRUE</code>, as areas of features are always reported.</p>   |
| fGroups, obj, x, object | <p>featureGroups object to be accessed.</p>  |
| value                   | <p>For <code>adducts&lt;=</code>: A character with adduct annotations assigned to each feature group. The length should equal the number of feature groups. Can be named with feature group names to customize the assignment order.</p>   |
| i, j                    | <p>For <code>[/[</code>: A numeric or character value which is used to select analyses/feature groups by their index or name, respectively (for the order/names see <code>analyses()/names()</code>).</p> <p>For <code>:</code>: Can also be logical to perform logical selection (similar to regular vectors). If missing all analyses/feature groups are selected.</p> <p>For <code>[[:</code>: should be a scalar value. If <code>j</code> is not specified, <code>i</code> selects by feature groups instead.</p> <p>For <code>delete</code>: The data to remove from. <code>i</code> are the analyses as numeric index, logical or character, <code>j</code> the feature groups as numeric index, logical or character. If either is NULL then data for all is removed. <code>j</code> may also be a function: it will be called for each feature group, with a vector of the group intensities as first argument, the group name as second argument, and any other arguments passed as <code>...</code> to <code>delete</code>. The return value of this function specifies the analyses of the features in the group to be removed (same format as <code>i</code>).</p> |
| ...                     | <p>For the <code>"["</code> operator: ignored.</p> <p>For <code>delete</code>: passed to the function specified as <code>j</code>.</p> <p>For <code>getFCParams</code>: optional named arguments that override defaults.</p> <p>For <a href="#">sets workflow</a> methods: further arguments passed to the base <a href="#">featureGroups</a> method.</p> <p>Otherwise passed to <a href="#">plot</a> (plot and plotChroms), <a href="#">lines</a> (plotInt), <a href="#">VennDiagram</a> plotting functions (plotVenn), <a href="#">chordDiagram</a> (plotChord) or <a href="#">upset</a> (plotUpSet).</p>  |
| rGroups                 | <p>For <code>:</code>: An optional character vector: if specified only keep results for the given replicate groups (equivalent to the <code>rGroups</code> argument to <a href="#">filter</a>).</p> <p>For <code>getFCParams</code>: a character vector with the names of the two replicate groups to be compared.</p>   |
| results                 | <p>Optional argument. If specified only feature groups with results in the specified object are kept. The class of results should be <a href="#">featureAnnotations</a> or <a href="#">components</a>. Multiple objects can be specified in a list: in this case a feature group is kept if it has a result in <i>any</i> of the objects (equivalent to the <code>results</code> argument to <a href="#">filter</a>).</p>  |
| drop                    | <p>ignored.</p>  |

|                |  |
|----------------|--|
| name           | The feature group name (partially matched).  |
| out            | The destination file for the exported data.  |
| average        | If TRUE then data within replicate groups are averaged.<br>For <code>as.data.table</code> : if <code>features=TRUE</code> other feature properties are also averaged.  |
| features       | If TRUE then feature specific data will be added. If <code>average=TRUE</code> this data will be averaged for each feature group.  |
| qualities      | Adds feature (group) qualities ( <code>qualities="quality"</code> ), scores ( <code>qualities="score"</code> ) or both ( <code>qualities="both"</code> ), if this data is available ( <i>i.e.</i> from <code>calculatePeakQualities</code> ). If <code>qualities=FALSE</code> then nothing is reported.  |
| regression     | Set to TRUE to add regression data for each feature group. For this a linear model is created (intensity/area [depending on <code>areas</code> argument] <i>vs</i> concentration). The model concentrations (e.g. of a set of standards) is derived from the <code>conc</code> column of the <a href="#">analysis information</a> . From this model the intercept, slope and R2 is added to the output. In addition, when <code>features=TRUE</code> , concentrations for each feature are added. Note that no regression information is added when no <code>conc</code> column is present in the analysis information or when less than two concentrations are specified ( <i>i.e.</i> the minimum amount). |
| averageFunc    | Function used for averaging.<br>for <code>as.data.table</code> : only used when <code>average=TRUE</code> or <code>FCParams != NULL</code> .   |
| normFunc       | Function that should be used for normalization of data. The function is called for all intensities/areas of a feature group and these quantities are divided by the result of the function call. For example, when <code>max</code> is used normalized intensities will be between zero and one. If all quantities are zero then the function will not be called. Set to NULL to perform no normalization.   |
| FCParams       | A parameter list to calculate Fold change data (see <code>getFCParams</code> and the Fold change calculation section).<br>For <code>as.data.table</code> : set to NULL to not perform FC calculations.   |
| colourBy       | Sets the automatic colour selection: "none" for a single colour or "rGroups"/"fGroups" for a distinct colour per replicate/feature group.  |
| onlyUnique     | If TRUE and <code>colourBy="rGroups"</code> then only feature groups that are unique to a replicate group are plotted.   |
| retMin         | Plot retention time in minutes (instead of seconds).   |
| showLegend     | Plot a legend if TRUE.   |
| col            | Colour(s) used. If <code>col=NULL</code> then colours are automatically generated.   |
| pch, type, lty | Common plotting parameters passed to <i>e.g.</i> <code>plot</code> . For <code>plot</code> : if <code>pch=NULL</code> then values are automatically assigned.  |
| xnames         | Plot analysis (or replicate group if <code>average=TRUE</code> ) names on the x axis.  |
| addSelfLinks   | If TRUE then 'self-links' are added which represent non-shared data.   |
| addRetMzPlots  | Set to TRUE to enable <i>m/z vs</i> retention time scatter plots.  |
| outerGroups    | Character vector of names to be used as outer groups. The values in the specified vector should be named by analysis names ( <code>average</code> set to FALSE) or   |

|                                      |  |
|--------------------------------------|--|
|                                      | replicate group names (average set to TRUE), for instance: <code>c(analysis1 = "group1", analysis2 = "group1", analysis3 = "group2")</code> . Set to NULL to disable outer groups.   |
| <code>addIntraOuterGroupLinks</code> | If TRUE then links will be added within outer groups.  |
| <code>rtWindow</code>                | Retention time (in seconds) that will be subtracted/added to respectively the minimum and maximum retention time of the plotted feature groups. Thus, setting this value to a positive value will 'zoom out' on the retention time axis.   |
| <code>mzExpWindow</code>             | In case the $m/z$ window to plot an EIC for a particular analysis is not known ( <i>i.e.</i> no feature was detected of the feature group to be plot and <code>onlyPresent=FALSE</code> ) then the EIC $m/z$ range is estimated from the range for the complete feature group and expanded by the offset defined by <code>mzExpWindow</code> .   |
| <code>topMost</code>                 | Only plot EICs from features within this number of top most intense analyses. If NULL then all analyses are used for plotted.  |
| <code>topMostByRGroup</code>         | If set to TRUE and <code>topMost</code> is set: only plot EICs for the top most features in each replicate group. For instance, when <code>topMost=1</code> and <code>topMostByRGroup=TRUE</code> , then EICs will be plotted for the most intense feature of each replicate group.  |
| <code>EICs</code>                    | Internal parameter for now and should be kept at NULL (default).   |
| <code>showPeakArea</code>            | Set to TRUE to display integrated chromatographic peak ranges by filling (shading) their areas.  |
| <code>showFGroupRect</code>          | Set to TRUE to mark the full retention/intensity range of all features within a feature group by drawing a rectangle around it.  |
| <code>title</code>                   | Character string used for title of the plot. If NULL a title will be automatically generated.  |
| <code>onlyPresent</code>             | If TRUE then EICs will only be generated for analyses in which a particular feature group was detected. Disabling this option might be useful to see if any features were 'missed'.  |
| <code>annotate</code>                | If set to "ret" and/or "mz" then retention and/or $m/z$ values will be drawn for each plotted feature group.   |
| <code>showProgress</code>            | if set to TRUE then a text progressbar will be displayed when all EICs are being plot. Set to "none" to disable any annotation.  |
| <code>xlim, ylim</code>              | Sets the plot size limits used by <a href="#">plot</a> . Set to NULL for automatic plot sizing.  |
| <code>which</code>                   | A character vector with replicate groups used for comparison.<br>For plotting functions: set to NULL for all replicate groups.<br>For <code>plotVenn</code> : alternatively a named list containing elements of character vectors with replicate groups to compare. For instance, <code>which=list(infl = c("influent-A", "influent-B"), effl = c("effluent-A", "effluent-B"))</code> , will compare the features in replicate groups "influent-A/B" against those in "effluent-A/B". The names of the list are used for labelling in the plot, and will be made automatically if not specified. |
| <code>nsets, nintersects</code>      | See <a href="#">upset</a> .  |



|                        |   |
|------------------------|---|
| relativeTo             | A character vector with replicate groups that should be used for unique comparison. If NULL then all replicate groups are used for comparison. Replicate groups specified in which are ignored.   |
| outer                  | If TRUE then only feature groups are kept which do not overlap between the specified replicate groups for the which parameter.  |
| exclusive              | If TRUE then all feature groups are removed that are not unique to the given replicate groups.  |
| weights                | A named numeric vector that defines the weight for each score to calculate the totalScore. The names of the vector follow the score names. Unspecified weights are defaulted to '1'. Example: weights=c(ApexBoundaryRatioScore=0.5,GaussianSimilarityScore=0.5)   |
| flatnessFactor         | Passed to <b>MetaClean</b> as the flatness.factor argument to <a href="#">calculateJaggedness</a> and <a href="#">calculateModality</a> .   |
| avgFunc                | The function used to average the peak qualities and scores for each feature group.  |
| parallel               | If set to TRUE then code is executed in parallel through the <b>futures</b> package. Please see the parallelization section in the handbook for more details.   |
| components             | The components object that was generated for the given featureGroups object. Obviously, the components must be created with algorithms that support adduct/isotope annotations, such as those from <b>RAMClustR</b> and <b>cliqueMS</b> .   |
| prefAdduct             | The 'preferred adduct' (see method description). This is often "[M+H]+" or "[M-H]-".  |
| onlyMonoIso            | Set to TRUE to only keep feature groups that were annotated as monoisotopic. Feature groups are never removed by this setting if no isotope annotations are available.  |
| chargeMismatch         | Specifies how to deal with a mismatch in charge between adduct and isotope annotations. Valid values are: "adduct" (ignore isotope annotation), "isotope" (ignore adduct annotation), "none" (ignore both annotations) and "ignore" (don't check for charge mismatches). <i>Important:</i> when OpenMS is used to find features, it already removes any detected non-monoisotopic features by default. Hence, in such case setting chargeMismatch="adduct" is more appropriate. |
| set                    | ( <b>sets workflow</b> ) The name of the set.   |
| reGroup                | Set to TRUE to re-group the features after the adduct annotations are changed. See the Sets workflow section for more details.  |
| sets                   | ( <b>sets workflow</b> ) For [ and filter: a character with name(s) of the sets to keep (or remove if negate=TRUE).<br>For plotInt: if TRUE then feature intensities are plot per set (order follows the <a href="#">analysis information</a> ).<br>For plotVenn, overlap and unique: If TRUE then the which argument changes its meaning and is used to specify the names of the sets to be compared.  |
| negate                 | If set to TRUE then filtering operations are performed in opposite manner.  |
| absMinSets, relMinSets | ( <b>sets workflow</b> ) Feature groups are only kept when they contain data for at least this (absolute or relative) amount of sets. Set to NULL to ignore.  |

## Details

The featureGroup class is the workhorse of **patRoan**: almost all functionality operate on its instantiated objects. The class holds all information from grouped features (obtained from [features](#)). This class itself is virtual, hence, objects are not created directly from it. Instead, 'feature groupers' such as [groupFeaturesXCMS](#) return a featureGroups derived object after performing the actual grouping of features across analyses.

getFCParams creates a parameter list to calculate Fold changes (see the Fold change calculation section).

## Value

delete returns the object for which the specified data was removed.

plotVenn (invisibly) returns a list with the following fields:

- gList the gList object that was returned by the utilized [VennDiagram](#) plotting function.
- areas The total area for each plotted group.
- intersectionCounts The number of intersections between groups.

The order for the areas and intersectionCounts fields is the same as the parameter order from the used plotting function (see *e.g.* [draw.pairwise.venn](#) and [draw.triple.venn](#)).

calculatePeakQualities returns a modified object amended with peak qualities and scores.

selectIons returns a featureGroups object with only the selected feature groups and amended with adduct annotations.

## Methods (by generic)

- names: Obtain feature group names.
- analyses: returns a character vector with the names of the analyses for which data is present in this object.
- replicateGroups: returns a character vector with the names of the replicate groups for which data is present in this object.
- groupNames: Same as names. Provided for consistency to other classes.
- length: Obtain number of feature groups.
- show: Shows summary information for this object.
- groupTable: Accessor for groups slot.
- analysisInfo: Obtain analysisInfo (see analysisInfo slot in [features](#)).
- groupInfo: Accessor for groupInfo slot.
- featureTable: Obtain feature information (see [features](#)).
- getFeatures: Accessor for features slot.
- groupFeatIndex: Accessor for ftindex slot.
- groupQualities: Accessor for groupQualities slot.
- groupScores: Accessor for groupScores slot.
- annotations: Accessor for annotations slot.

- `adducts`: Returns a named character with adduct annotations assigned to each feature group (if available).
- `adducts<-`: Sets adduct annotations for feature groups.
- `[`: Subset on analyses/feature groups.
- `[[]`: Extract intensity values.
- `$`: Extract intensity values for a feature group.
- `delete`: Completely deletes specified feature groups.
- `export`: Exports feature groups to a '.csv' file that is readable to Bruker ProfileAnalysis (a 'bucket table'), Bruker TASQ (an analyte database) or that is suitable as input for the Targeted peak detection functionality of **MZmine**.
- `as.data.table`: Obtain a summary table (a `data.table`) with retention, *m/z*, intensity and optionally other feature data.
- `plot`: Generates an *m/z* vs retention time plot for all feature groups. Optionally highlights unique/overlapping presence amongst replicate groups.
- `plotInt`: Generates a line plot for the (averaged) intensity of feature groups within all analyses.
- `plotChord`: Generates a chord diagram which can be used to visualize shared presence of feature groups between analyses or replicate groups. In addition, analyses/replicates sharing similar properties (*e.g.* location, age, type) may be grouped to enhance visualization between these 'outer groups'.
- `plotChroms`: Plots extracted ion chromatograms (EICs) of feature groups.
- `plotVenn`: plots a Venn diagram (using **VennDiagram**) outlining unique and shared feature groups between up to five replicate groups.
- `plotUpSet`: plots an UpSet diagram (using the `upset` function) outlining unique and shared feature groups between given replicate groups.
- `plotVolcano`: Plots Fold change data in a 'Volcano plot'.
- `unique`: Obtain a subset with unique feature groups present in one or more specified replicate group(s).
- `overlap`: Obtain a subset with feature groups that overlap between a set of specified replicate group(s).
- `calculatePeakQualities`: Calculates peak and group qualities for all features and feature groups. The peak qualities (and scores) are calculated with the `features` method of this function, and subsequently averaged per feature group. Then, **MetaClean** is used to calculate the Elution Shift and Retention Time Consistency group quality metrics (see the **MetaClean** publication cited below for more details). Similarly to the `features` method, these metrics are scored by normalizing qualities among all groups and scaling them from '0' (worst) to '1' (best). The totalScore for each group is then calculated as the weighted sum from all feature (group) scores. The `getMCTrainData` and `predictCheckFeaturesSession` functions can be used to train and apply Pass/Fail ML models from **MetaClean**.
- `selectIons`: uses `componentization` results to select feature groups with preferred adduct ion and/or isotope annotation. Typically, this means that only feature groups are kept if they are

(de-)protonated adducts and are monoisotopic. The adduct annotation assignments for the selected feature groups are copied from the components to the annotations slot. If the adduct for a feature group is unknown, its annotation is defaulted to the 'preferred' adduct, and hence, the feature group will never be removed. Furthermore, if a component does not contain an annotation with the preferred adduct, the most intense feature group is selected instead. Similarly, if no isotope annotation is available, the feature group is assumed to be monoisotopic and thus not removed. An important advantage of `selectIons` is that it may considerably simplify your dataset. Furthermore, the adduct assignments allow formula/compound annotation steps later in the workflow to improve their annotation accuracy. On the other hand, it is important the componentization results are reliable. Hence, it is highly recommended that, prior to calling `selectIons`, the settings to `generateComponents` are optimized and its results are reviewed with `checkComponents`. Finally, the `adducts<-` method can be used to manually correct adduct assignments afterwards if necessary.

## Slots

`groups` Matrix (`data.table`) with intensities for each feature group (columns) per analysis (rows). Access with `groups` method.

`analysisInfo, features` `Analysis info` and `features` class associated with this object. Access with `analysisInfo` and `featureTable` methods, respectively.

`groupInfo` `data.frame` with retention time (`rts` column, in seconds) and *m/z* (`mzs` column) for each feature group. Access with `groupInfo` method.

`ftindex` Matrix (`data.table`) with feature indices for each feature group (columns) per analysis (rows). Each index corresponds to the row within the feature table of the analysis (see `featureTable`).

`groupQualities, groupScores` A `data.table` with qualities/scores for each feature group (see the `calculatePeakQualities` method).

`annotations` A `data.table` with adduct annotations for each group (see the `selectIons` method).

`groupAlgo, groupArgs, groupVerbose` (**sets workflow**) Grouping parameters that were used when this object was created. Used by `adducts<-` and `selectIons` when these methods perform a re-grouping of features.

`annotations` (**sets workflow**) As the `featureGroups` slot, but contains the annotation data per set.

## Fold change calculation

the `as.data.table` and `plotVolcano` methods can be used to calculate/plot (log<sub>2</sub>) Fold changes (FC) between two replicate groups to easily identify significant changes. The calculation process is configured through a parameter list, which can be constructed with the `getFCParams` function. The parameter list has the following entries:

- `rGroups` the name of the two replicate groups to compare (taken from the `rGroups` argument to `getFCParams`).
- `thresholdFC`: the threshold log FC for a feature group to be classified as increasing/decreasing.
- `thresholdPV`: the threshold log P for a feature group to be significantly different.

- `zeroMethod, zeroValue`: how to handle zero values when calculating the FC: `add` adds an offset to zero values, `"fixed"` sets zero values to a fixed number and `"omit"` removes zero data. The number that is added/set by the former two options is defined by `zeroValue`.
- `PVTestFunc`: a function that is used to calculate P values (usually using `t.test`).
- `PVAdjFunc`: a function that is used to adjust P values (usually using `p.adjust`)

## S4 class hierarchy

- `workflowStep`
  - `featureGroups`
    - \* `featureGroupsSet`
      - `featureGroupsScreeningSet`
    - \* `featureGroupsUnset`
    - \* `featureGroupsScreening`
      - `featureGroupsSetScreeningUnset`
    - \* `featureGroupsBruker`
    - \* `featureGroupsConsensus`
    - \* `featureGroupsEnviMass`
    - \* `featureGroupsKPIC2`
    - \* `featureGroupsOpenMS`
    - \* `featureGroupsSIRIUS`
    - \* `featureGroupsBrukerTASQ`
    - \* `featureGroupsXCMS`
    - \* `featureGroupsXCMS3`

## Sets workflows

The `featureGroupsSet` class is applicable for [sets workflows](#). This class is derived from `featureGroups` and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- `sets` Returns the set names for this object.
- `unset` Converts the object data for a specified set into a 'non-set' object (`featureGroupsUnset`), which allows it to be used in 'regular' workflows. The adduct annotations for the selected set are used to convert all feature (group) masses to ionic  $m/z$  values. The annotations persist in the converted object.

The following methods are changed or with new functionality:

- `adducts`, `adducts<-` require the set argument. The order of the data that is returned/changed follows that of the annotations slot. Furthermore, `adducts<-` will perform a re-grouping of features when its `reGroup` parameter is set to `TRUE`. The implications for this are discussed below.
- `filter` and the subset operator (`[]`) have specific arguments to choose/filter by (feature presence in) sets. See the argument descriptions.
- `as.data.table`: normalization of intensities is performed per set.

- `export` Only allows to export data from one set. The `unset` method is used prior to exporting the data.
- `overlap`, `unique`, `plotVenn`, `plotInt` allow to handle data per set. See the `sets` argument description.
- `selectIons` Will perform a re-grouping of features. The implications of this are discussed below.

A re-grouping of features occurs if `selectIons` is called or `adducts<-` is used with `reGroup=TRUE`. Afterwards, it is very likely that feature group names are changed. Since data generated later in the workflow (*e.g.* annotation steps) rely on feature group names, these objects are **not valid** anymore, and **must** be re-generated.

### Author(s)

The code to calculate and plot Fold change data was created by Bas van de Velde.

### References

- Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.
- Conway JR, Lex A, Gehlenborg N (2017). "UpSetR: an R package for the visualization of intersecting sets and their properties." *Bioinformatics*, **33**(18), 2938-2940. doi: [10.1093/bioinformatics/btx364](https://doi.org/10.1093/bioinformatics/btx364), <http://dx.doi.org/10.1093/bioinformatics/btx364>.
- Lex A, Gehlenborg N, Strobel H, Vuilleumot R, Pfister H (2014). "UpSet: Visualization of Intersecting Sets." *IEEE Transactions on Visualization and Computer Graphics*, **20**(12), 1983–1992. doi: [10.1109/tvcg.2014.2346248](https://doi.org/10.1109/tvcg.2014.2346248).
- Chetnik K, Petrick L, Pandey G (2020). "MetaClean: a machine learning-based classifier for reduced false positive peak detection in untargeted LC-MS metabolomics data." *Metabolomics*, **16**(11). doi: [10.1007/s11306020017383](https://doi.org/10.1007/s11306020017383).

---

featureGroups-compare    *Comparing feature groups*

---

### Description

Functionality to compare feature groups and make a consensus.

### Usage

```
## S4 method for signature 'featureGroups'
comparison(..., groupAlgo, groupArgs = list(rtalign = FALSE))

## S4 method for signature 'featureGroupsComparison,missing'
plot(x, retMin = FALSE, ...)

## S4 method for signature 'featureGroupsComparison'
```

```

plotVenn(obj, which = NULL, ...)

## S4 method for signature 'featureGroupsComparison'
plotUpSet(obj, which = NULL, ...)

## S4 method for signature 'featureGroupsComparison'
plotChord(obj, addSelfLinks = FALSE, addRetMzPlots = TRUE, ...)

## S4 method for signature 'featureGroupsComparison'
consensus(
  obj,
  absMinAbundance = NULL,
  relMinAbundance = NULL,
  uniqueFrom = NULL,
  uniqueOuter = FALSE
)

## S4 method for signature 'featureGroupsSet'
comparison(..., groupAlgo, groupArgs = list(rtaalign = FALSE))

## S4 method for signature 'featureGroupsComparisonSet'
consensus(obj, ...)

```

## Arguments

|                                  |  |
|----------------------------------|--|
| ...                              | <p>For comparison: featureGroups objects that should be compared. If the arguments are named (e.g. myGroups = fGroups) then these are used for labelling, otherwise objects are automatically labelled by their <a href="#">algorithm</a>.</p> <p>For plot, plotVenn, plotChord: further options passed to plot, <a href="#">VennDiagram</a> plotting functions (e.g. <a href="#">draw.pairwise.venn</a>) and <a href="#">chordDiagram</a> respectively.</p> <p>For plotUpSet: any further arguments passed to the plotUpSet method defined for <a href="#">featureGroups</a>.</p> |
| groupAlgo                        | The <a href="#">feature grouping algorithm</a> that should be used for grouping <i>pseudo</i> features (see details). Valid values are: "xcms", xcms3, kpic2 or "openms".  |
| groupArgs                        | A list containing further parameters for <a href="#">feature grouping</a> .  |
| x, obj                           | The featureGroupsComparison object.  |
| retMin                           | If TRUE retention times are plotted as minutes (seconds otherwise).  |
| which                            | A character vector specifying one or more labels of compared feature groups. For plotVenn: if NULL then all compared groups are used.  |
| addSelfLinks                     | If TRUE then 'self-links' are added which represent non-shared data.   |
| addRetMzPlots                    | Set to TRUE to enable <i>m/z</i> vs retention time scatter plots.  |
| absMinAbundance, relMinAbundance | <p>Minimum absolute or relative ('0-1') abundance across objects for a result to be kept. For instance, relMinAbundance=0.5 means that a result should be present in at least half of the number of compared objects. Set to 'NULL' to ignore and keep all results. Limits cannot be set when uniqueFrom is not NULL.</p>  |

|             |  |
|-------------|--|
| uniqueFrom  | Set this argument to only retain feature groups that are unique within one or more of the objects for which the consensus is made. Selection is done by setting the value of uniqueFrom to a logical (values are recycled), numeric (select by index) or a character (as obtained with <code>algorithm(obj)</code> ). For logical and numeric values the order corresponds to the order of the objects given for the consensus. Set to NULL to ignore. |
| uniqueOuter | If uniqueFrom is not NULL and if uniqueOuter=TRUE: only retain data that are also unique between objects specified in uniqueFrom.  |

## Details

Feature groups objects originating from differing feature finding and/or grouping algorithms (or their parameters) may be compared to assess their output and generate a consensus.

The comparison method generates a [featureGroupsComparison](#) object from given feature groups objects, which in turn may be used for (visually) comparing presence of feature groups and generating a consensus. Internally, this function will collapse each feature groups object to *pseudo* features objects by averaging their retention times, *m/z* values and intensities, where each original feature groups object becomes an 'analysis'. All *pseudo* features are then grouped using [regular feature grouping algorithms](#) so that a comparison can be made.

`plot` generates an *m/z* vs retention time plot.

`plotVenn` plots a Venn diagram outlining unique and shared feature groups between up to five compared feature groups.

`plotUpSet` plots an UpSet diagram outlining unique and shared feature groups.

`plotChord` plots a chord diagram to visualize the distribution of feature groups.

`consensus` combines all compared feature groups and averages their retention, *m/z* and intensity data. Not yet supported for [sets workflows](#).

## Value

`comparison` returns a [featureGroupsComparison](#) object.

`plotVenn` (invisibly) returns a list with the following fields:

- `gList` the `gList` object that was returned by the utilized [VennDiagram](#) plotting function.
- `areas` The total area for each plotted group.
- `intersectionCounts` The number of intersections between groups.

The order for the `areas` and `intersectionCounts` fields is the same as the parameter order from the used plotting function (see e.g. [draw.pairwise.venn](#) and [draw.triple.venn](#)).

`consensus` returns a [featureGroups](#) object with a consensus from the compared feature groups.



---

```
featureGroupsComparison-class
      Feature groups comparison class
```

---

## Description

This class is used for comparing different [featureGroups](#) objects.

## Usage

```
## S4 method for signature 'featureGroupsComparison'
names(x)

## S4 method for signature 'featureGroupsComparison'
length(x)

## S4 method for signature 'featureGroupsComparison,ANY,missing,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'featureGroupsComparison,ANY,missing'
x[[i, j]]

## S4 method for signature 'featureGroupsComparison'
x$name
```

## Arguments

|                      |  |
|----------------------|--|
| <code>x</code>       | A <code>featureGroupsComparison</code> object.   |
| <code>i</code>       | For <code>[/[</code> : A numeric or character value which is used to select labels by their index or name, respectively (for the order/names see <code>names()</code> ). |
|                      | For <code>[</code> : Can also be logical to perform logical selection (similar to regular vectors). If missing all labels are selected.                                  |
|                      | For <code>[[</code> : should be a scalar value.  |
| <code>...</code>     | Ignored.   |
| <code>drop, j</code> | ignored.   |
| <code>name</code>    | The label name (partially matched).  |

## Details

Objects from this class are returned by [comparison](#).

**Methods (by generic)**

- names: Obtain the labels that were given to each compared feature group.
- length: Number of feature groups objects that were compared.
- [: Subset on labels that were assigned to compared feature groups.
- [[: Extract a [featureGroups](#) object by its label.
- \$: Extract a compound table for a feature group.

**Slots**

fGroupsList A list of [featureGroups](#) object that were compared

comparedFGroups A *pseudo* featureGroups object containing grouped feature groups.

---

featureGroupsScreening-class

*Class for suspect screened feature groups.*

---

**Description**

This class derives from [featureGroups](#) and adds suspect screening information.

**Usage**

```
## S4 method for signature 'featureGroupsScreening'
screenInfo(obj)

## S4 method for signature 'featureGroupsScreening'
show(object)

## S4 method for signature 'featureGroupsScreening,ANY,ANY,missing'
x[i, j, ..., rGroups, suspects = NULL, drop = TRUE]

## S4 method for signature 'featureGroupsScreening'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featureGroupsScreening'
as.data.table(x, ..., collapseSuspects = ",", onlyHits = FALSE)

## S4 method for signature 'featureGroupsScreening'
annotateSuspects(
  fGroups,
  MSPeakLists,
  formulas,
  compounds,
  absMzDev = 0.005,
  relMinMSMSIntensity = 0.05,
```

```

    simMSMSMethod = "cosine",
    checkFragments = c("mz", "formula", "compound"),
    formulasNormalizeScores = "max",
    compoundsNormalizeScores = "max",
    IDFile = system.file("misc", "IDLevelRules.yml", package = "patRoan"),
    logPath = file.path("log", "ident")
)

## S4 method for signature 'featureGroupsScreening'
filter(
  obj,
  ...,
  onlyHits = NULL,
  selectHitsBy = NULL,
  selectBestFGroups = FALSE,
  maxLevel = NULL,
  maxFormRank = NULL,
  maxCompRank = NULL,
  minAnnSimForm = NULL,
  minAnnSimComp = NULL,
  minAnnSimBoth = NULL,
  absMinFragMatches = NULL,
  relMinFragMatches = NULL,
  negate = FALSE
)

## S4 method for signature 'featureGroupsScreeningSet'
screenInfo(obj)

## S4 method for signature 'featureGroupsScreeningSet'
show(object)

## S4 method for signature 'featureGroupsScreeningSet,ANY,ANY,missing'
x[i, j, ..., rGroups, suspects = NULL, sets = NULL, drop = TRUE]

## S4 method for signature 'featureGroupsScreeningSet'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featureGroupsScreeningSet'
as.data.table(x, ..., collapseSuspects = ",", onlyHits = FALSE)

## S4 method for signature 'featureGroupsScreeningSet'
annotateSuspects(
  fGroups,
  MSPeakLists = NULL,
  formulas = NULL,
  compounds = NULL,
  ...

```

```

)

## S4 method for signature 'featureGroupsScreeningSet'
filter(
  obj,
  ...,
  onlyHits = NULL,
  selectHitsBy = NULL,
  selectBestFGroups = FALSE,
  maxLevel = NULL,
  maxFormRank = NULL,
  maxCompRank = NULL,
  minAnnSimForm = NULL,
  minAnnSimComp = NULL,
  minAnnSimBoth = NULL,
  absMinFragMatches = NULL,
  relMinFragMatches = NULL,
  negate = FALSE
)

## S4 method for signature 'featureGroupsScreeningSet'
unset(obj, set)

```

## Arguments

|                         |  |
|-------------------------|--|
| obj, object, x, fGroups | The featureGroupsScreening object.   |
| i, j, rGroups           | Used for subsetting data analyses, feature groups and replicate groups, see <a href="#">featureGroups</a> .  |
| ...                     | Further arguments passed to the base method.   |
| suspects                | An optional character vector with suspect names. If specified, only featureGroups will be kept that are assigned to these suspects.  |
| drop                    | Ignored.   |
| collapseSuspects        | If a character then any suspects that were matched to the same feature group are collapsed to a single row and suspect names are separated by the value of collapseSuspects. If NULL then no collapsing occurs, and each suspect match is reported on a single row. Note that some columns will not be reported when collapsing is enabled.  |
| onlyHits                | For as.data.table: if TRUE then only feature groups with suspect hits are reported.<br>For filter <ul style="list-style-type: none"> <li>if negate=FALSE and onlyHits=TRUE then all feature groups without suspect hits will be removed. Otherwise nothing will be done.</li> <li>if negate=TRUE then onlyHits=TRUE will select feature groups without suspect hits, onlyHits=FALSE will only retain feature groups with suspect matches and this filter is ignored if onlyHits=NULL.</li> </ul> |

|   |  |
|---|--|
| MSPeakLists, formulas, compounds  | Annotation data (MSPeakLists, formulas and compounds) obtained for this featureGroupsScreening object. All arguments can be NULL to exclude it from the annotation.  |
| absMzDev  | Maximum absolute $m/z$ deviation.  |
| relMinMSMSIntensity   | Minimum relative intensity ('0-1') threshold applied when calculating annotation similarities.   |
| simMSMSMethod   | Either "cosine" or "jaccard": used to compare MS/MS peak lists for annotation similarity calculation.  |
| checkFragments  | Which type(s) of MS/MS fragments from workflow data should be checked to evaluate the number of suspect fragment matches ( <i>i.e.</i> from the fragments_mz/fragments_formula columns in the suspect list). Valid values are: "mz", "formula", "compounds". The former uses $m/z$ values in the specified MSPeakLists object, whereas the others use the formulae that were annotated to MS/MS peaks in the given formulas or compounds objects. Multiple values are possible: in this case the maximum number of fragment matches will be reported.                            |
| compoundsNormalizeScores, formulasNormalizeScores                               | A character that specifies how normalization of annotation scorings occurs. Either<br>"max" (normalize to max value) or "minmax" (perform min-max normalization). Note that normalization of negative scores ( <i>e.g.</i> output by SIRIUS) is always performed as min-max. Furthermore, currently normalization for compounds takes the original min/max scoring values into account when candidates were generated. Thus, for compounds scoring, normalization is not affected when candidate results were removed after they were generated ( <i>e.g.</i> by use of filter). |
| IDFile  | A file path to a YAML file with rules used for estimation of identification levels. See the Suspect annotation section for more details. If not specified then a default rules file will be used.  |
| logPath   | A directory path to store logging information. If NULL then logging is disabled.   |
| selectHitsBy  | Should be "intensity" or "level". For cases where the same suspect is matched to multiple feature groups, only the suspect to the feature group with highest mean intensity (selectHitsBy="intensity") or best identification level (selectHitsBy="level") is kept. In case of ties only the first hit is kept. Set to NULL to ignore this filter. If negate=TRUE then only those hits with lowest mean intensity/poorest identification level are kept.   |
| selectBestFGroups   | If TRUE then for any cases where a single feature group is matched to several suspects only the suspect assigned to the feature group with best identification score is kept. In case of ties only the first is kept.  |
| maxLevel, maxFormRank, maxCompRank, minAnnSimForm, minAnnSimComp, minAnnSimBoth | Filter suspects by maximum identification level ( <i>e.g.</i> "3a"), formula/compound rank or with minimum formula/compound/combined annotation similarity. Set to NULL to ignore.   |
| absMinFragMatches, relMinFragMatches  | Only retain suspects with this minimum number MS/MS matches with the fragments specified in the suspect list ( <i>i.e.</i> fragments_mz/fragments_formula).  |

|        |   |
|--------|---|
|        | relMinFragMatches sets the minimum that is relative ('0-1') to the maximum number of MS/MS fragments specified in the fragments_* columns of the suspect list. Set to NULL to ignore. |
| negate | If set to TRUE then filtering operations are performed in opposite manner.  |
| sets   | <b>(sets workflow)</b> A character with name(s) of the sets to keep (or remove if negate=TRUE).   |
| set    | <b>(sets workflow)</b> The name of the set.   |

### Value

annotateSuspects returns a featureGroupsScreening object, which is a [featureGroups](#) object amended with annotation data.

filter returns a filtered featureGroupsScreening object.

### Methods (by generic)

- screenInfo: Returns a table with screening information (see screenInfo slot).
- show: Shows summary information for this object.
- [: Subset on analyses, feature groups and/or suspects.
- as.data.table: Obtain a summary table (a [data.table](#)) with retention, *m/z*, intensity and optionally other feature data. Furthermore, the output table will be merged with information from screenInfo, such as suspect names and other properties and annotation data.
- annotateSuspects: Incorporates annotation data obtained during the workflow to annotate suspects with matched known MS/MS fragments, formula/candidate ranks and automatic estimation of identification levels. See the Suspect annotation section for more details. The estimation of identification levels for each suspect is logged in the log/ident directory.
- filter: Performs rule based filtering. This method builds on the comprehensive filter functionality from the base [filter, featureGroups-method](#). It adds several filters to select *e.g.* the best ranked suspects or those with a minimum estimated identification level. **NOTE:** most filters *only* affect suspect hits, not feature groups. Set onlyHits=TRUE to subsequently remove any feature groups that lost any suspect matches due to other filter steps.

### Slots

screenInfo A ([data.table](#)) with results from suspect screening. This table will be amended with annotation data when annotateSuspects is run.

### Suspect annotation

The annotateSuspects method is used to annotate suspects after [screenSuspects](#) was used to collect suspect screening results and other workflow steps such as formula and compound annotation steps have been completed. The annotation results, which can be acquired with the as.data.table and screenInfo methods, amends the current screening data with the following columns:

- formRank, compRank The rank of the suspect within the formula/compound annotation results.

- `annSimForm,annSimComp,annSimBoth` A similarity measure between measured and annotated MS/MS peaks from annotation of formulae, compounds or both. The similarity is calculated as the spectral similarity between a peaklist with (a) all MS/MS peaks and (b) only annotated peaks. Thus, a value of one means that all MS/MS peaks were annotated. If both formula and compound annotations are available then `annSimBoth` is calculated after combining all the annotated peaks, otherwise `annSimBoth` equals the available value for `annSimForm` or `annSimComp`. The similarity calculation can be configured with the `relMinMSMSIntensity` and `simMSMSMethod` arguments to `annotateSuspects`.
- `maxFrag`s The maximum number of MS/MS fragments that can be matched for this suspect (based on the `fragments_*` columns from the suspect list).
- `maxFragMatches,maxFragMatchesRel` The absolute and relative amount of experimental MS/MS peaks that were matched from the fragments specified in the suspect list. The value for `maxFragMatchesRel` is relative to the value for `maxFrag`s. The calculation of this column is influenced by the `checkFragments` argument to `annotateSuspects`.
- `estIDLevel` Provides an *estimation* of the identification level, roughly following that of (Schymanski et al. 2014). However, please note that this value is only an estimation, and manual interpretation is still necessary to assign final identification levels. The estimation is done through a set of rules, see the Identification level rules section below.

Note that only columns are present is sufficient data is available for their calculation.

### Identification level rules

The estimation of identification levels is configured through a YAML file which specifies the rules for each level. The default file is shown below.

```
1:
  suspectFragments: 3
  retention: 12
2a:
  individualMoNAScore:
    min: 0.9
    higherThanNext: .inf
  rank:
    max: 1
    type: compound
3a:
  individualMoNAScore: 0.4
3b:
  suspectFragments: 3
3c:
  annMSMSSim:
    type: compound
    min: 0.7
4a:
  annMSMSSim:
    type: formula
    min: 0.7
```

```

        higherThanNext: 0.2
isoScore:
  min: 0.5
  higherThanNext: 0.2
rank:
  max: 1
  type: formula
4b:
  isoScore:
    min: 0.9
    higherThanNext: 0.2
  rank:
    max: 1
    type: formula
5:
  all: yes

```

Most of the file should be self-explanatory. Some notes:

- Each rule is either a field of suspectFragments (minimum number of MS/MS fragments matched from suspect list), retention (maximum retention deviation from suspect list), rank (the maximum annotation rank from formula or compound annotations), all (this level is always matched) or any of the scorings available from the formula or compound annotations.
- In case any of the rules could be applied to either formula or compound annotations, the annotation type must be specified with the type field (formula or compound).
- Identification levels should start with a number and may optionally be followed by a alphabetic character. The lowest levels are checked first.
- If relative=yes then the relative scoring will be used for testing.
- For suspectFragments: if the number of fragments from the suspect list (maxFrag column) is less then the minimum rule value, the minimum is adjusted to the number of available fragments.

A template rules file can be generated with the [genIDLevelRulesFile](#) function, and this file can subsequently be passed to `annotateSuspects`. The file format is highly flexible and (sub)levels can be added or removed if desired. Note that the default file is currently only suitable when annotation is performed with GenForm and MetFrag, for other algorithms it is crucial to modify the rules.

#### S4 class hierarchy

- [featureGroups](#)
  - [featureGroupsScreening](#)
    - \* [featureGroupsSetScreeningUnset](#)

#### Source

Cosine spectral similarity calculation was based on the code from `SpectrumSimilarity()` function of **OrgMassSpecR**.



## Sets workflows

The featureGroupsScreeningSet class is applicable for [sets workflows](#). This class is derived from featureGroupsScreening and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class [workflowStepSet](#).
- unset Converts the object data for a specified set into a 'non-set' object (featureGroupsScreeningUnset), which allows it to be used in 'regular' workflows. Only the screening results present in the specified set are kept.

The following methods are changed or with new functionality:

- annotateSuspects Suspect annotation is performed per set. Thus, formula/compound ranks, estimated identification levels etc are calculated for each set. Subsequently, these results are merged in the final screenInfo. In addition, an overall formRank and compRank column is created based on the rankings of the suspect candidate in the set consensus data. Furthermore, an overall estIDLevel is generated that is based on the 'best' estimated identification level among the sets data (*i.e.* the lowest). In case there is a tie between sub-levels (*e.g.* '3a' and '3b'), then the sub-level is stripped (*e.g.* '3').
- filter All filters related to estimated identification levels and formula/compound rankings are applied to the overall set data (see above). All others are applied to set specific data: in this case candidates are only removed if none of the set data confirms to the filter.

This class derives also from [featureGroupsSet](#). Please see its documentation for more relevant details with sets workflows.

Note that the formRank and compRank columns are *not* updated when the data is subset.

## Note

The relMinMSMSIntensity filter argument to annotateSuspects is applied *after* removing the precursor ion from the peak lists (if present). Thus, intensity scales may be different when this filter is applied when the most abundant peak resulted from the precursor ion.

filter removes suspect hits with NA values when any of the filters related to minimum or maximum values are applied (unless negate=TRUE).

## Author(s)

Rick Helmus <<r.helmus@uva.nl>>, Emma Schymanski <<emma.schymanski@uni.lu>> (contributions to identification level rules), Bas van de Velde (contributions to spectral similarity calculation).

## References

Schymanski EL, Jeon J, Gulde R, Fenner K, Ruff M, Singer HP, Hollender J (2014). "Identifying Small Molecules via High Resolution Mass Spectrometry: Communicating Confidence." *Environmental Science and Technology*, **48**(4), 2097–2098. doi: [10.1021/es5002105](https://doi.org/10.1021/es5002105).

Stein SE, Scott DR (1994). "Optimization and testing of mass spectral library search algorithms for compound identification." *Journal of the American Society for Mass Spectrometry*, **5**(9), 859–866. doi: [10.1016/1044-0305\(94\)87009-8](https://doi.org/10.1016/1044-0305(94)87009-8), [https://doi.org/10.1016/1044-0305\(94\)87009-8](https://doi.org/10.1016/1044-0305(94)87009-8).

See Also

[featureGroups](#)

---

|                     |  |
|---------------------|--|
| featureQualityNames | Returns chromatographic peak quality and score names for features and/or feature groups. |
|---------------------|--|

---

Description

Returns chromatographic peak quality and score names for features and/or feature groups.

Usage

```
featureQualityNames(feats = TRUE, group = TRUE, scores = FALSE, totScore = TRUE)
```

Arguments

- |          |   |
|----------|---|
| feat     | If TRUE then names specific to features are returned.                   |
| group    | If TRUE then names specific to groups are returned.                     |
| scores   | If TRUE the score names are returned, otherwise the quality names.      |
| totScore | If TRUE (and scores=TRUE) then the name of the total score is included. |

---

|                |                     |
|----------------|---------------------|
| features-class | Base features class |
|----------------|---------------------|

---

Description

Holds information for all features present within a set of analysis.

Usage

```
## S4 method for signature 'features'
length(x)

## S4 method for signature 'features'
show(object)

## S4 method for signature 'features'
featureTable(obj)

## S4 method for signature 'features'
analysisInfo(obj)

## S4 method for signature 'features'
```

```
analyses(obj)

## S4 method for signature 'features'
replicateGroups(obj)

## S4 method for signature 'features'
as.data.table(x)

## S4 method for signature 'features'
filter(
  obj,
  absMinIntensity = NULL,
  relMinIntensity = NULL,
  retentionRange = NULL,
  mzRange = NULL,
  mzDefectRange = NULL,
  chromWidthRange = NULL,
  qualityRange = NULL,
  negate = FALSE
)

## S4 method for signature 'features,ANY,missing,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'features,ANY,missing'
x[[i]]

## S4 method for signature 'features'
x$name

## S4 method for signature 'features'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'features'
calculatePeakQualities(obj, weights, flatnessFactor, parallel = TRUE)

## S4 method for signature 'featuresSet'
sets(obj)

## S4 method for signature 'featuresSet'
show(object)

## S4 method for signature 'featuresSet'
as.data.table(x)

## S4 method for signature 'featuresSet,ANY,missing,missing'
x[i, ..., sets = NULL, drop = TRUE]
```

```
## S4 method for signature 'featuresSet'
filter(obj, ..., negate = FALSE, sets = NULL)

## S4 method for signature 'featuresSet'
unset(obj, set)

## S4 method for signature 'featuresKPIC2'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featuresXCMS'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'featuresXCMS3'
delete(obj, i = NULL, j = NULL, ...)
```

## Arguments

**obj, x, object** features object to be accessed

**absMinIntensity, relMinIntensity** Minimum absolute/relative intensity for features to be kept. The relative intensity is determined from the feature with highest intensity (within the same analysis). Set to '0' or NULL to skip this step.

**retentionRange, mzRange, mzDefectRange, chromWidthRange** Range of retention time (in seconds),  $m/z$ , mass defect (defined as the decimal part of  $m/z$  values) or chromatographic peak width (in seconds), respectively. Features outside this range will be removed. Should be a numeric vector with length of two containing the min/max values. The maximum can be Inf to specify no maximum range. Set to NULL to skip this step.

**qualityRange** Used to filter features by their peak qualities/scores (see [calculatePeakQualities](#)). Should be a named list with min/max ranges for each quality/score to be filtered (the [featureQualityNames](#) function can be used to obtain valid names). Example: `qualityRange=list(ModalityScore=c(0.3, Inf), SymmetryScore=c(0.5, Inf))`. Set to NULL to ignore.

**negate** If set to TRUE then filtering operations are performed in opposite manner.

**i, j** For `[/[]`: A numeric or character value which is used to select analyses by their index or name, respectively (for the order/names see `analyses()`).  
  
For `[]`: Can also be logical to perform logical selection (similar to regular vectors). If missing all analyses are selected.  
  
For `[]`: should be a scalar value.  
  
For `delete`: The data to remove from. `i` are the analyses as numeric index, logical or character, `j` the features as numeric index (row) of the feature. If either is NULL then data for all is removed. `j` may also be a function: it will be called for each analysis, with the feature table (a `data.table`) as first argument, the analysis name as second argument, and any other arguments passed as ...

|                |   |
|----------------|---|
|                | to delete. The return value of this function specifies the feature indices (rows) to be removed (specified as an integer or logical vector).  |
| ...            | For delete: passed to the function specified as j.<br>For <a href="#">sets workflow</a> methods: further arguments passed to the base <a href="#">features</a> method.  |
| drop           | ignored.  |
| name           | The analysis name (partially matched).  |
| weights        | A named numeric vector that defines the weight for each score to calculate the totalScore. The names of the vector follow the score names. Unspecified weights are defaulted to '1'. Example: weights=c(ApexBoundaryRatioScore=0.5,GaussianSimilarityScore=0.5) |
| flatnessFactor | Passed to <b>MetaClean</b> as the flatness. factor argument to <a href="#">calculateJaggedness</a> and <a href="#">calculateModality</a> .  |
| parallel       | If set to TRUE then code is executed in parallel through the <b>futures</b> package. Please see the parallelization section in the handbook for more details.   |
| sets           | ( <b>sets workflow</b> ) For [ and filter: a character with name(s) of the sets to keep (or remove if negate=TRUE).   |
| set            | ( <b>sets workflow</b> ) The name of the set.   |

## Details

This class provides a way to store intensity, retention times,  $m/z$  and other data for all features in a set of analyses. The class is virtual and derived objects are created by 'feature finders' such as findFeaturesOpenMS, findFeaturesXCMS and findFeaturesBruker.

## Value

featureTable: A list containing a [data.table](#) for each analysis with feature data

analysisInfo: A data.frame containing a column with analysis name (analysis), its path (path), and other columns such as replicate group name (group) and blank reference (blank).

delete returns the object for which the specified data was removed.

calculatePeakQualities returns a modified object amended with peak qualities and scores.

## Methods (by generic)

- length: Obtain total number of features.
- show: Shows summary information for this object.
- featureTable: Get table with feature information
- analysisInfo: Get analysis information
- analyses: returns a character vector with the names of the analyses for which data is present in this object.
- replicateGroups: returns a character vector with the names of the replicate groups for which data is present in this object.
- as.data.table: Returns all feature data in a table.

- `filter`: Performs common rule based filtering of features. Note that this (and much more) functionality is also provided by the `filter` method defined for `featureGroups`. However, filtering a features object may be useful to avoid grouping large amounts of features.
- `[]`: Subset on analyses.
- `[[`: Extract a feature table for an analysis.
- `$`: Extract a feature table for an analysis.
- `delete`: Completely deletes specified features.
- `calculatePeakQualities`: Calculates peak qualities for each feature. This uses **MetaClean** R package to calculate the following metrics: Apex-Boundary Ratio, FWHM2Base, Jaggedness, Modality, Symmetry, Gaussian Similarity, Sharpness, Triangle Peak Area Similarity Ratio and Zig-Zag index. Please see the **MetaClean** publication (referenced below) for more details. For each metric, an additional score is calculated by normalizing all feature values (unless the quality metric definition has a fixed range) and scale from '0' (worst) to '1' (best). Then, a `totalScore` for each feature is calculated by the (weighted) sum of all score values.

## Slots

`features` List of features per analysis file. Use the `featureTable` method for access.

`analysisInfo` Analysis group information. Use the `analysisInfo` method for access.

## S4 class hierarchy

- `workflowStep`
  - `features`
    - \* `featuresSet`
    - \* `featuresUnset`
    - \* `featuresFromFeatGroups`
    - \* `featuresConsensus`
    - \* `featuresBruker`
    - \* `featuresEnviPick`
    - \* `featuresKPIC2`
    - \* `featuresOpenMS`
    - \* `featuresSAFD`
    - \* `featuresSIRIUS`
    - \* `featuresBrukerTASQ`
    - \* `featuresXCMS`
    - \* `featuresXCMS3`

## Sets workflows

The `featuresSet` class is applicable for [sets workflows](#). This class is derived from `features` and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- `sets` Returns the set names for this object.
- `unset` Converts the object data for a specified set into a 'non-set' object (`featuresUnset`), which allows it to be used in 'regular' workflows. The adduct annotations for the selected set (*e.g.* as passed to `makeSet`) are used to convert all feature masses to ionic  $m/z$  values.

The following methods are changed or with new functionality:

- `filter` and the subset operator (`[]`) have specific arguments to choose/filter by (feature presence in) sets. See the `sets` argument description.

### Note

For `calculatePeakQualities`: sometimes **MetaClean** may return NA for the Gaussian Similarity metric, in which case it will be set to '0'.

### References

Chetnik K, Petrick L, Pandey G (2020). "MetaClean: a machine learning-based classifier for reduced false positive peak detection in untargeted LC-MS metabolomics data." *Metabolomics*, **16**(11). doi: [10.1007/s11306020017383](https://doi.org/10.1007/s11306020017383).

### See Also

[feature-finding](#)

---

|                    |  |
|--------------------|--|
| formula-generation | <i>Automatic chemical formula generation</i> |
|--------------------|--|

---

### Description

Functionality to automatically calculate chemical formulae for all feature groups.

### Usage

```
## S4 method for signature 'featureGroups'
generateFormulas(fGroups, MSPeakLists, algorithm, ...)
```

```
## S4 method for signature 'featureGroups'
generateFormulasDA(
  fGroups,
  MSPeakLists,
  precursorMzSearchWindow = 0.002,
  MSMode = "both",
  adduct = NULL,
  featThreshold = 0,
  featThresholdAnn = 0.75,
  absAlignMzDev = 0.002,
  save = TRUE,
```

```
    close = save
  )

## S4 method for signature 'featureGroupsSet'
generateFormulasDA(
  fGroups,
  MSPeakLists,
  precursorMzSearchWindow = 0.002,
  MSMode = "both",
  adduct = NULL,
  ...,
  setThreshold = 0,
  setThresholdAnn = 0
)

## S4 method for signature 'featureGroups'
generateFormulasGenForm(
  fGroups,
  MSPeakLists,
  relMzDev = 5,
  adduct = NULL,
  elements = "CHNOP",
  hetero = TRUE,
  oc = FALSE,
  extraOpts = NULL,
  calculateFeatures = TRUE,
  featThreshold = 0,
  featThresholdAnn = 0.75,
  absAlignMzDev = 0.002,
  MSMode = "both",
  isolatePrec = TRUE,
  timeout = 120,
  topMost = 50,
  batchSize = 8
)

## S4 method for signature 'featureGroupsSet'
generateFormulasGenForm(
  fGroups,
  MSPeakLists,
  relMzDev = 5,
  adduct = NULL,
  ...,
  setThreshold = 0,
  setThresholdAnn = 0
)

## S4 method for signature 'featureGroups'
```



```

generateFormulasSIRIUS(
  fGroups,
  MSPeakLists,
  relMzDev = 5,
  adduct = NULL,
  elements = "CHNOP",
  profile = "qtof",
  database = NULL,
  noise = NULL,
  cores = NULL,
  topMost = 100,
  extraOptsGeneral = NULL,
  extraOptsFormula = NULL,
  calculateFeatures = TRUE,
  featThreshold = 0,
  featThresholdAnn = 0.75,
  absAlignMzDev = 0.002,
  verbose = TRUE,
  splitBatches = FALSE
)

## S4 method for signature 'featureGroupsSet'
generateFormulasSIRIUS(
  fGroups,
  MSPeakLists,
  relMzDev = 5,
  adduct = NULL,
  ...,
  setThreshold = 0,
  setThresholdAnn = 0
)

formulaScorings()

```

### Arguments

|                                      |  |
|--------------------------------------|--|
| <code>fGroups</code>                 | <code>featureGroups</code> object for which formulae should be generated. This should be the same or a subset of the object that was used to create the specified <code>MSPeakLists</code> (only relevant for algorithms using <code>MSPeakLists</code> ). In the case of a subset only the remaining feature groups in the subset are considered. |
| <code>MSPeakLists</code>             | An <code>MSPeakLists</code> object that was generated for the supplied <code>fGroups</code> .  |
| <code>algorithm</code>               | A character string describing the algorithm that should be used: "bruker", "genform", "sirius"   |
| <code>...</code>                     | Any parameters to be passed to the selected formula generation algorithm.<br>For sets workflows: further arguments directly passed to the non-sets method.   |
| <code>precursorMzSearchWindow</code> | Search window for $m/z$ values ( $\pm$ the feature $m/z$ ) used to find back feature data of precursor/parent ions from MS/MS spectra (this data is not readily available)   |

|                  |  |
|------------------|--|
|                  | from SmartFormula3D results).  |
| MSMode           | <p>Whether formulae should be generated only from MS data ("ms"), MS/MS data ("msms") or both ("both").</p> <p>For GenForm selecting "both" will fall back to formula calculation with only MS data in case no MS/MS data is available.</p> <p>For calculation with Bruker DataAnalysis selecting "both" will calculate formulae from MS data <i>and</i> MS/MS data and combines the results (duplicated formulae are removed). This is useful when poor MS/MS data would exclude proper candidates.</p> |
| adduct           | <p>An <a href="#">adduct</a> object (or something that can be converted to it with <a href="#">as.adduct</a>). Examples: "[M-H]-", "[M+Na]+". If the featureGroups object has adduct annotations then these are used if adducts=NULL.</p> <p><b>(sets workflow)</b> The adduct argument is not supported for sets workflows, since the adduct annotations will then always be used.</p>  |
| featThreshold    | If calculateFeatures=TRUE: minimum presence ('0-1') of a formula in all features before it is considered as a candidate for a feature group. For instance, featThreshold=0.75 dictates that a formula should be present in at least 75% of the features inside a feature group.  |
| featThresholdAnn | As featThreshold, but only considers features with annotations. For instance, featThresholdAnn=0.75 dictates that a formula should be present in at least 75% of the features with annotations inside a feature group.   |
| absAlignMzDev    | When the group formula annotation consensus is made from feature annotations, the <i>m/z</i> values of annotated MS/MS fragments may slightly deviate from those of the corresponding group MS/MS peak list. The absAlignMzDev argument specifies the maximum <i>m/z</i> window used to re-align the mass peaks.   |
| close, save      | If TRUE then Bruker files are closed and saved after processing with DataAnalysis, respectively. Setting close=TRUE prevents that many analyses might be opened simultaneously in DataAnalysis, which otherwise may use excessive memory or become slow. By default save is TRUE when close is TRUE, which is likely what you want as otherwise any processed data is lost.  |
| setThreshold     | <b>(sets workflow)</b> Minimum abundance for a candidate among all sets ('0-1'). For instance, a value of '1' means that the candidate needs to be present in all the set data.  |
| setThresholdAnn  | <b>(sets workflow)</b> As setThreshold, but only taking into account the set data that contain annotations for the feature group of the candidate.   |
| relMzDev         | Maximum relative deviation between the measured and candidate formula <i>m/z</i> values (in ppm). Sets the 'ppm' and '--ppm-max' commandline options for GenForm and SIRIUS, respectively.   |
| elements         | Elements to be considered for formulae calculation. This will heavily affects the number of candidates! Always try to work with a minimal set by excluding elements you don't expect. For generateFormulasSIRIUS, the minimum/maximum number of elements can also be specified, for example: a value of "C[5]H[10-15]O" will only consider formulae with up to five carbon atoms, between ten and  |

|                                    |   |
|------------------------------------|---|
|                                    | fifteen hydrogen atoms and any amount of oxygen atoms. Sets the 'el' and '--elements' cmdline options for GenForm and SIRIUS, respectively.   |
| hetero                             | Only consider formulae with at least one hetero atom. Sets the 'het' cmdline option.  |
| oc                                 | Only consider organic formulae ( <i>i.e.</i> with at least one carbon atom). Sets the 'oc' cmdline option.  |
| extraOpts                          | An optional character vector with any other cmdline options that will be passed to GenForm or SIRIUS. See the GenForm options section/SIRIUS manual for all available cmdline options.  |
| calculateFeatures                  | If TRUE formulae are first calculated for all features prior to feature group assignment (see details).   |
| isolatePrec                        | Settings used for isolation of precursor mass peaks and their isotopes. This isolation is highly important for accurate isotope scoring of candidates, as non-relevant mass peaks will dramatically decrease the score. The value of isolatePrec should either be a list with parameters (see the <a href="#">filter method</a> for MSPeakLists for more details), TRUE for default parameters or FALSE for no isolation ( <i>e.g.</i> when you already performed isolation with the filter method). The z parameter (charge) is automatically deduced from the adduct used for annotation (unless isolatePrec=FALSE), hence any custom z setting is ignored. |
| timeout                            | Maximum time (in seconds) that a GenForm command is allowed to execute. If this time is exceeded a warning is emitted and the command is terminated. See the notes section for more information on the need of timeouts.  |
| topMost                            | Only keep this number of candidates (per feature group) with highest score. For SIRIUS: Sets the '--candidates' cmdline option.   |
| batchSize                          | Maximum number of GenForm commands that should be run sequentially in each parallel process. Combining commands with short runtimes (such as GenForm) can significantly increase parallel performance. For more information see <a href="#">executeMultiProcess</a> . Note that this is ignored if 'patRoon.MP.method="future"'.  |
| profile                            | Name of the configuration profile, for example: "qtof", "orbitrap", "fticr". Sets the '--profile' cmdline option.   |
| database                           | If not NULL, use a database for retrieval of formula candidates. Possible values are: "pubchem", "bio", "kegg", "hmdb". Sets the '--database' cmdline option.   |
| noise                              | Median intensity of the noise (NULL ignores this parameter). Sets the '--noise' cmdline option.   |
| cores                              | The number of cores SIRIUS will use. If NULL then the default of all cores will be used.  |
| extraOptsGeneral, extraOptsFormula | a character vector with any extra cmdline parameters for SIRIUS. For SIRIUS versions <4.4 there is no distinction between general and formula options. Otherwise cmdline options specified in extraOptsGeneral are added prior to the formula command, while options specified in extraOptsFormula are added afterwards. See the SIRIUS manual for more details. Set to NULL to ignore.   |

|              |   |
|--------------|---|
| verbose      | If TRUE then more output is shown in the terminal.  |
| splitBatches | If TRUE then the calculations done by SIRIUS will be evenly split over multiple SIRIUS calls (which may be run in parallel depending on the <a href="#">set package options</a> ). If splitBatches=FALSE then all feature calculations are performed from a single SIRIUS execution, which is often the fastest if calculations are performed on a single computer. |

## Details

Several algorithms are provided to automatically generate formulae for given feature groups. All tools use the accurate mass of a feature to back-calculate candidate formulae. Depending on the algorithm and data availability, other data such as isotopic pattern and MS/MS fragments may be used to further improve formula assignment and ranking.

When DataAnalysis is used for formula generation or calculateFeatures=TRUE formulae are first calculated for each feature. The results are then combined for final assignment of candidate formulae for each feature group. If a formula was found in multiple features within the group, the reported scorings and mass errors are averaged and other numeric values are those from the feature in the analysis of the "analysis" column. The calculation of formulae on 'feature level' might result in a more thorough formula search and better removal of outliers (controlled by featThreshold and featThresholdAnn arguments). In contrast, when calculations occur on 'feature group level' (i.e. calculateFeatures=FALSE), formulae are directly assigned to each feature group (by using group averaged peak MS lists), which significantly reduces processing time is, especially with many analyses. Note that in both situations subsequent algorithms that use formula data (e.g. [addFormulaScoring](#) and [reporting](#) functions) only use formula data that was eventually assigned to feature groups. Furthermore, please note that calculation of formulae with DataAnalysis always occurs on 'feature level'.

generateFormulas is a generic function that will generate formulae using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as generateFormulasDA and generateFormulasGenForm. While these functions may be called directly, generateFormulas provides a generic interface and is therefore usually preferred.

generateFormulasDA uses Bruker DataAnalysis to generate chemical formulae. This method supports scoring based on overlap between measured and theoretical isotopic patterns (both MS and MS/MS data) and the presence of 'fitting' MS/MS fragments. The method will iterate through all features (or "Compounds" in DataAnalysis terms) and call SmartFormula (and SmartFormula3D if MS/MS data is available) to generate all formulae. Parameters affecting formula calculation have to be set in advance within the DataAnalysis method for each analysis (e.g. by [setDAMethod](#)). This method requires that features were obtained with [findFeaturesBruker](#). It is recommended, but not mandatory, that the [MSPeakLists](#) are also generated by DataAnalysis.

generateFormulasGenForm uses [GenForm](#) to generate chemical formulae. When MS/MS data is available it will be used to score candidate formulae by presence of 'fitting' fragments.

generateFormulasSIRIUS uses [SIRIUS](#) to generate chemical formulae. Similarity of measured and theoretical isotopic patterns will be used for scoring candidates. Note that SIRIUS requires availability of MS/MS data.

formulaScorings returns a data.frame with information on which scoring terms are used and what their algorithm specific name is.

**Value**

A [formulas](#) object containing all generated formulae.

**Scorings**

Each algorithm implements their own scoring system. Their names have been harmonized where possible. An overview is obtained with the `formulaScorings` function:

| name      | genform    | sirius    | bruker | description                           |
|-----------|------------|-----------|--------|---------------------------------------|
| combMatch | comb_match | -         | -      | MS and MS/MS combined match value     |
| isoScore  | MS_match   | isoScore  | -      | How well the isotopic pattern matches |
| mSigma    | -          | -         | mSigma | Deviation of the isotopic pattern     |
| MSMSScore | MSMS_match | treeScore | -      | How well MS/MS data matches           |
| score     | -          | score     | Score  | Overall MS formula score              |

**Sets workflows**

With a [sets workflow](#), annotation is first performed for each set. This is important, since the annotation algorithms typically cannot work with data from mixed ionization modes. The annotation results are then combined to generate a *sets consensus*:

- The annotation tables for each feature group from the set specific data are combined. Rows with overlapping candidates (determined by the neutral formula) are merged.
- Set specific data (*e.g.* the ionic formula) is retained by renaming their columns with set specific names.
- The MS/MS fragment annotations (fragInfo column) from each set are combined.
- The scorings for each set are averaged to calculate overall scores.
- The candidates are re-ranked based on their average ranking among the set data (if a candidate is absent in a set it is assigned the poorest rank in that set).
- The coverage of each candidate among sets is calculated. Depending on the `setThreshold` and `setThresholdAnn` arguments, candidates with low abundance are removed.

**Parallelization**

`generateFormulasGenForm` and `generateFormulasSIRIUS` uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoön options](#) for configuration options.

When futures are used for parallel processing (`patRoön.MP.method="future"`), calculations with `GenForm` are done with batch mode is disabled (see `batchSize` argument), which generally limit overall performance.

**GenForm options**

Below is a list of options (generated by running `GenForm` without commandline options) which can be set by the `extraOpts` parameter.

Formula calculation from MS and MS/MS data as described in

Meringer et al (2011) MATCH Commun Math Comput Chem 65: 259-290

Usage: GenForm ms=<filename> [msms=<filename>] [out=<filename>]  
 [exist[=mv]] [m=<number>] [ion=-e|+e|-H|+H|+Na] [cha=<number>]  
 [ppm=<number>] [msmv=ndp|nsse|nsae] [acc=<number>] [rej=<number>]  
 [thms=<number>] [thmsms=<number>] [thcomb=<number>]  
 [sort[=ppm|msmv|msmsmv|combm]] [el=<elements>] [oc]] [ff=<fuzzy formula>]  
 [vsp[=<even|odd>]] [vsm2mv[=<value>]] [vsm2ap2[=<value>]] [hcf]  
 [wm[=lin|sqrt|log]] [wi[=lin|sqrt|log]] [exp=<number>] [oei]  
 [dbeexc=<number>] [ivsm2mv=<number>] [vsm2ap2=<number>]  
 [oms[=<filename>]] [omsms[=<filename>]] [oclean[=<filename>]]  
 [analyze [loss] [intens]] [dbe] [cm] [pc] [sc]

Explanation:

ms : filename of MS data (\*.txt)  
 msms : filename of MS/MS data (\*.txt)  
 out : output generated formulas  
 exist : allow only molecular formulas for that at least one structural formula exists; overrides vsp, vsm2mv, vsm2ap2; argument mv enables multiple valencies for P and S  
 m : experimental molecular mass (default: mass of MS basepeak)  
 ion : type of ion measured (default: M+H)  
 ppm : accuracy of measurement in parts per million (default: 5)  
 msmv : MS match value based on normalized dot product, normalized sum of squared or absolute errors (default: nsae)  
 acc : allowed deviation for full acceptance of MS/MS peak in ppm (default: 2)  
 rej : allowed deviation for total rejection of MS/MS peak in ppm (default: 4)  
 thms : threshold for the MS match value  
 thmsms : threshold for the MS/MS match value  
 thcomb : threshold for the combined match value  
 sort : sort generated formulas according to mass deviation in ppm, MS match value, MS/MS match value or combined match value  
 el : used chemical elements (default: CHBrClFINOPSSi)  
 oc : only organic compounds, i.e. with at least one C atom  
 ff : overwrites el and oc and uses fuzzy formula for limits of element multiplicities  
 het : formulas must have at least one hetero atom  
 vsp : valency sum parity (even for graphical formulas)  
 vsm2mv : lower bound for valency sum - 2 \* maximum valency (>=0 for graphical formulas)  
 vsm2ap2 : lower bound for valency sum - 2 \* number of atoms + 2 (>=0 for graphical connected formulas)  
 hcf : apply Heuerding-Clerc filter  
 wm : m/z weighting for MS/MS match value  
 wi : intensity weighting for MS/MS match value  
 exp : exponent used, when wi is set to log  
 oei : allow odd electron ions for explaining MS/MS peaks

```

dbeexc : excess of double bond equivalent for ions
ivsm2mv : lower bound for valency sum - 2 * maximum valency
          for fragment ions
ivsm2ap2: lower bound for valency sum - 2 * number of atoms + 2
          for fragment ions
oms     : write scaled MS peaks to output
omsm    : write weighted MS/MS peaks to output
oclean  : write explained MS/MS peaks to output
analyze : write explanations for MS/MS peaks to output
loss    : for analyzing MS/MS peaks write losses instead of fragments
intens  : write intensities of MS/MS peaks to output
dbe     : write double bond equivalents to output
cm      : write calculated ion masses to output
pc      : output match values in percent
sc      : strip calculated isotope distributions
noref   : hide the reference information

```

### Note

If any errors related to DCOM appear it might be necessary to terminate DataAnalysis (note that DataAnalysis might still be running as a background process). The ProcessCleaner application installed with DataAnalayis can be used for this.

generateFormulasGenForm always sets the 'exist' and 'oei' GenForm commandline options.

Formula calculation with GenForm may produce an excessive number of candidates for high  $m/z$  values (e.g. above 600) and/or many elemental combinations (set by elements). In this scenario formula calculation may need a very long time. Timeouts are used to avoid excessive computational times by terminating long running commands (set by the timeout argument).

For annotations performed with SIRIUS it is often the fastest to keep the default `splitBatches=FALSE`.

In this case, all SIRIUS output will be printed to the terminal (unless `verbose=FALSE` or `'patRoon.MP.method="future"'`).

Furthermore, please note that only annotations to be performed for the same adduct are grouped in a single batch execution.

### References

Meringer M, Reinker S, Zhang J, Muller A (2011). "MS/MS Data Improves Automated Determination of Molecular Formulas by Mass Spectrometry." *MATCH Commun. Math. Comput. Chem.*, **65**(2), 259–290.

Duhrkop K, Fleischauer M, Ludwig M, Aksenov AA, Melnik AV, Meusel M, Dorrestein PC, Rousu J, Bocker S (2019). "SIRIUS 4: a rapid tool for turning tandem mass spectra into metabolite structure information." *Nature Methods*, **16**(4), 299–302. doi: [10.1038/s41592-019-0344-8](https://doi.org/10.1038/s41592-019-0344-8).

Duhrkop K, Bocker S (2015). "Fragmentation Trees Reloaded." In Przytycka TM (ed.), *Research in Computational Molecular Biology*, 65–79. ISBN 978-3-319-16706-0.

Duhrkop K, Shen H, Meusel M, Rousu J, Bocker S (2015). "Searching molecular structure databases with tandem mass spectra using CSI:FingerID." *Proceedings of the National Academy of Sciences*, **112**(41), 12580–12585. doi: [10.1073/pnas.1509788112](https://doi.org/10.1073/pnas.1509788112).

Bocker S, Letzel MC, Liptak Z, Pervukhin A (2008). “SIRIUS: decomposing isotope patterns for metabolite identification.” *Bioinformatics*, **25**(2), 218–224. doi: [10.1093/bioinformatics/btn603](https://doi.org/10.1093/bioinformatics/btn603).

### See Also

[formulas-class](#). The [GenForm manual](#) (also known as MOLGEN-MSMS).

---

|                |                                  |
|----------------|----------------------------------|
| formulas-class | <i>Formula annotations class</i> |
|----------------|----------------------------------|

---

### Description

Contains data of generated chemical formulae for given feature groups.

### Usage

```
## S4 method for signature 'formulas'
annotations(obj, features = FALSE)

## S4 method for signature 'formulas'
analyses(obj)

## S4 method for signature 'formulas'
defaultExclNormScores(obj)

## S4 method for signature 'formulas'
show(object)

## S4 method for signature 'formulas,ANY,ANY'
x[[i, j]]

## S4 method for signature 'formulas'
delete(obj, i = NULL, j = NULL, ...)

## S4 method for signature 'formulas'
as.data.table(
  x,
  fGroups = NULL,
  fragments = FALSE,
  countElements = NULL,
  countFragElements = NULL,
  OM = FALSE,
  normalizeScores = "none",
  excludeNormScores = defaultExclNormScores(x),
  average = FALSE
)
```



```
## S4 method for signature 'formulas'
annotatedPeakList(
  obj,
  index,
  groupName,
  analysis = NULL,
  MSPeakLists,
  onlyAnnotated = FALSE
)

## S4 method for signature 'formulas'
plotSpectrum(
  obj,
  index,
  groupName,
  analysis = NULL,
  MSPeakLists,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  mincex = 0.9,
  xlim = NULL,
  ylim = NULL,
  ...
)

## S4 method for signature 'formulas'
plotScores(
  obj,
  index,
  groupName,
  analysis = NULL,
  normalizeScores = "max",
  excludeNormScores = defaultExclNormScores(obj)
)

## S4 method for signature 'formulas'
consensus(
  obj,
  ...,
  absMinAbundance = NULL,
  relMinAbundance = NULL,
  uniqueFrom = NULL,
  uniqueOuter = FALSE,
  rankWeights = 1,
  labels = NULL
)

## S4 method for signature 'formulasSet'
```

```
show(object)

## S4 method for signature 'formulasSet'
delete(obj, i, j, ...)

## S4 method for signature 'formulasSet,ANY,missing,missing'
x[i, j, ..., sets = NULL, updateConsensus = FALSE, drop = TRUE]

## S4 method for signature 'formulasSet'
filter(obj, ..., sets = NULL, updateConsensus = FALSE, negate = FALSE)

## S4 method for signature 'formulasSet'
plotSpectrum(
  obj,
  index,
  groupName,
  analysis = NULL,
  MSPeakLists,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  mincex = 0.9,
  xlim = NULL,
  ylim = NULL,
  perSet = TRUE,
  mirror = TRUE,
  ...
)

## S4 method for signature 'formulasSet'
annotatedPeakList(obj, index, groupName, analysis = NULL, MSPeakLists, ...)

## S4 method for signature 'formulasSet'
consensus(
  obj,
  ...,
  absMinAbundance = NULL,
  relMinAbundance = NULL,
  uniqueFrom = NULL,
  uniqueOuter = FALSE,
  rankWeights = 1,
  labels = NULL,
  filterSets = FALSE,
  setThreshold = 0,
  setThresholdAnn = 0
)

## S4 method for signature 'formulasSet'
unset(obj, set)
```

```
## S4 method for signature 'formulasConsensusSet'
unset(obj, set)
```

### Arguments

|   |  |
|---|--|
| <code>obj, x, object</code>   | The formulas object.   |
| <code>features</code>   | If TRUE returns formula data for features, otherwise for feature groups.   |
| <code>i, j</code>   | For <code>[[</code> : If both <code>i</code> and <code>j</code> are specified then <code>i</code> specifies the analysis and <code>j</code> the feature group of the feature for which annotations should be returned. Otherwise <code>i</code> specifies the feature group for which group annotations should be returned. <code>i/j</code> can be specified as integer index or as a character name.<br>Otherwise passed to the <code>featureAnnotations</code> method.  |
| <code>...</code>  | For <code>plotSpectrum</code> : Further arguments passed to <code>plot</code> .<br>For <code>delete</code> : passed to the function specified as <code>j</code> .<br>For <code>consensus</code> : Any further (and unique) formulas objects.<br>For <code>sets workflow</code> methods: further arguments passed to the base <code>formulas</code> method.   |
| <code>fGroups, fragments, countElements, countFragElements, OM</code> | Passed to the <code>featureAnnotations</code> method.  |
| <code>normalizeScores</code>  | A character that specifies how normalization of annotation scorings occurs. Either "none" (no normalization), "max" (normalize to max value) or "minmax" (perform min-max normalization). Note that normalization of negative scores (e.g. output by SIRIUS) is always performed as min-max. Furthermore, currently normalization for compounds takes the original min/max scoring values into account when candidates were generated. Thus, for compounds scoring, normalization is not affected when candidate results were removed after they were generated (e.g. by use of <code>filter</code> ). |
| <code>excludeNormScores</code>  | A character vector specifying any compound scoring names that should <i>not</i> be normalized. Set to NULL to normalize all scorings. Note that whether any normalization occurs is set by the <code>excludeNormScores</code> argument.<br>For compounds: By default score and individualMoNAScore are set to mimic the behavior of the MetFrag web interface.   |
| <code>average</code>  | If set to TRUE an 'average formula' is generated for each feature group by combining all elements from all candidates and averaging their amounts. This obviously leads to non-existing formulae, however, this data may be useful to deal with multiple candidate formulae per feature group when performing elemental characterization. Setting this to TRUE disables reporting of most other data.  |
| <code>index</code>  | The candidate index (row). For <code>plotSpectrum</code> two indices can be specified to compare spectra. In this case <code>groupName</code> and <code>analysis</code> (if not NULL) should specify values for the spectra to compare.  |
| <code>groupName</code>  | The name of the feature group (or feature groups when comparing spectra) to which the candidate belongs.   |

|                                  |  |
|----------------------------------|--|
| analysis                         | A character specifying the analysis (or analyses when comparing spectra) for which the annotated spectrum should be plotted. If NULL then annotation results for the complete feature group will be plotted.   |
| MSPeakLists                      | The <a href="#">MSPeakLists</a> object that was used to generate the candidate   |
| onlyAnnotated                    | Set to TRUE to filter out any peaks that could not be annotated.   |
| title                            | The title of the plot. Set to NULL for an automatically generated title.   |
| specSimParams                    | A named list with parameters that influence the calculation of MS spectra similarities. See the <a href="#">spectral similarity parameters</a> documentation for more details.   |
| mincex                           | The formula annotation labels are automatically scaled. The mincex argument forces a minimum cex value for readability.  |
| xlim, ylim                       | Sets the plot size limits used by <a href="#">plot</a> . Set to NULL for automatic plot sizing.  |
| absMinAbundance, relMinAbundance | Minimum absolute or relative ('0-1') abundance across objects for a result to be kept. For instance, relMinAbundance=0.5 means that a result should be present in at least half of the number of compared objects. Set to 'NULL' to ignore and keep all results. Limits cannot be set when uniqueFrom is not NULL.   |
| uniqueFrom                       | Set this argument to only retain formulas that are unique within one or more of the objects for which the consensus is made. Selection is done by setting the value of uniqueFrom to a logical (values are recycled), numeric (select by index) or a character (as obtained with <code>algorithm(obj)</code> ). For logical and numeric values the order corresponds to the order of the objects given for the consensus. Set to NULL to ignore. |
| uniqueOuter                      | If uniqueFrom is not NULL and if uniqueOuter=TRUE: only retain data that are also unique between objects specified in uniqueFrom.  |
| rankWeights                      | A numeric vector with weights of to calculate the mean ranking score for each candidate. The value will be re-cycled if necessary, hence, the default value of '1' means equal weights for all considered objects.   |
| labels                           | A character with names to use for labelling. If NULL labels are automatically generated.   |
| sets                             | <b>(sets workflow)</b> A character with name(s) of the sets to keep (or remove if negate=TRUE). Note: if updateConsensus=FALSE then the setCoverage column of the annotation results is not updated.   |
| updateConsensus                  | <b>(sets workflow)</b> If TRUE then the annotation consensus among set results is updated. See the Sets workflows section for more details.  |
| drop                             | Passed to the <a href="#">featureAnnotations</a> method.   |
| negate                           | Passed to the <a href="#">featureAnnotations</a> method.   |
| perSet, mirror                   | <b>(sets workflow)</b> If perSet=TRUE then the set specific mass peaks are annotated separately. Furthermore, if mirror=TRUE (and there are two sets in the object) then a mirror plot is generated.   |
| filterSets                       | <b>(sets workflow)</b> Controls how algorithms consensus abundance filters are applied. See the Sets workflows section below.  |

setThreshold, setThresholdAnn  
(**sets workflow**) Thresholds used to create the annotation set consensus. See [generateFormulas](#).  
set  
(**sets workflow**) The name of the set.

## Details

formulas objects are obtained from [formula generators](#). This class is derived from the [featureAnnotations](#) class, please see its documentation for more methods and other details.

## Value

annotations returns a list containing for each feature group (or feature if features=TRUE) a [data.table](#) with an overview of all generated formulae and other data such as candidate scoring and MS/MS fragments.

consensus returns a formulas object that is produced by merging results from multiple formulas objects.

## Methods (by generic)

- annotations: Accessor method to obtain generated formulae.
- analyses: returns a character vector with the names of the analyses for which data is present in this object.
- defaultExclNormScores: Returns default scorings that are excluded from normalization.
- show: Show summary information for this object.
- [[: Extracts a formula table, either for a feature group or for features in an analysis.
- as.data.table: Generates a table with all candidate formulae for each feature group and other information such as element counts.
- annotatedPeakList: Returns an MS/MS peak list annotated with data from a given candidate formula.
- plotSpectrum: Plots an annotated spectrum for a given candidate formula of a feature or feature group. Two spectra can be compared by specifying a two-sized vector for the index, groupName and (if desired) analysis arguments.
- plotScores: Plots a barplot with scoring of a candidate formula.
- consensus: Generates a consensus of results from multiple objects. In order to rank the consensus candidates, first each of the candidates are scored based on their original ranking (the scores are normalized and the highest ranked candidate gets value '1'). The (weighted) mean is then calculated for all scorings of each candidate to derive the final ranking (if an object lacks the candidate its score will be '0'). The original rankings for each object is stored in the rank columns.

## Slots

featureFormulas A list with all generated formulae for each analysis/feature group. Use the annotations method for access.

`setThreshold`, `setThresholdAnn` (**sets workflow**) A copy of the equally named arguments that were passed when this object was created by `generateFormulas`.

`origFGNames` (**sets workflow**) The original (order of) names of the `featureGroups` object that was used to create this object.

## S4 class hierarchy

- `featureAnnotations`
  - `formulas`
    - \* `formulasConsensus`
    - \* `formulasSet`
      - `formulasConsensusSet`
    - \* `formulasUnset`

## Source

Subscripting of formulae for plots generated by `plotSpectrum` is based on the `chemistry2expression` function from the **ReSOLUTION** package.

## Sets workflows

The `formulasSet` class is applicable for **sets workflows**. This class is derived from `formulas` and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class `workflowStepSet`.
- `unset` Converts the object data for a specified set into a 'non-set' object (`formulasUnset`), which allows it to be used in 'regular' workflows. Only the annotation results that are present in the specified set are kept (based on the set consensus, see below for implications).

The following methods are changed or with new functionality:

- `filter` and the subset operator (`[]`) Can be used to select data that is only present for selected sets. Depending on the `updateConsensus`, both either operate on set consensus or original data (see below for implications).
- `annotatedPeakList` Returns a combined annotation table with all sets.
- `plotSpectrum` Is able to highlight set specific mass peaks (`perSet` and `mirror` arguments).
- `consensus` Creates the algorithm consensus based on the original annotation data (see below for implications). Then, like the sets workflow method for `generateFormulas`, a consensus is made for all sets, which can be controlled with the `setThreshold` and `setThresholdAnn` arguments. The candidate coverage among the different algorithms is calculated for each set (e.g. `coverage-positive` column) and for all sets (`coverage` column), which is based on the presence of a candidate in all the algorithms from all sets data. The consensus method for sets workflow data supports the `filterSets` argument. This controls how the algorithm consensus abundance filters (`absMinAbundance`/`relMinAbundance`) are applied: if `filterSets=TRUE` then the minimum of all coverage set specific columns is used to obtain the algorithm abundance. Otherwise the overall coverage column is used. For instance, consider a consensus

object to be generated from two objects generated by different algorithms (*e.g.* SIRIUS and GenForm), which both have a positive and negative set. Then, if a candidate occurs with both algorithms for the positive mode set, but only with the first algorithm in the negative mode set, `relMinAbundance=1` will remove the candidate if `filterSets=TRUE` (because the minimum relative algorithm abundance is '0.5'), while `filterSets=FALSE` will not remove the candidate (because based on all sets data the candidate occurs in both algorithms).

Two types of annotation data are stored in a `formulasSet` object:

1. Annotations that are produced from a consensus between set results (see `generateFormulas`).
2. The 'original' annotation data per set, prior to when the set consensus was made. This includes candidates that were filtered out because of the thresholds set by `setThreshold` and `setThresholdAnn`. However, when `filter` or `subsetting` (`[]`) operations are performed, the original data is also updated.

In most cases the first data is used. However, in a few cases the original annotation data is used (as indicated above), for instance, to re-create the set consensus. It is important to realize that the original annotation data may have *additional* candidates, and a newly created set consensus may therefore have 'new' candidates. For instance, when the object consists of the sets "positive" and "negative" and `setThreshold=1` was used to create it, then `formulas[,sets = "positive",updateConsensus = TRUE]` may now have additional candidates, *i.e.* those that were not present in the "negative" set and were previously removed due to the consensus threshold filter.

## See Also

The [featureAnnotations](#) base class for more relevant methods and [formula-generation](#).

---

generics

*Miscellaneous generics*

---

## Description

Various (S4) generic functions providing a common interface for common tasks such as plotting and filtering data. The actual functionality and function arguments are often specific for the implemented methods, for this reason, please refer to the linked method documentation for each generic.

## Usage

```
adducts(obj, ...)

adducts(obj, ...) <- value

algorithm(obj)

analysisInfo(obj)

analyses(obj)
```

```
annotatedPeakList(obj, ...)
annotations(obj, ...)
calculatePeakQualities(obj, weights = NULL, flatnessFactor = 0.05, ...)
clusterProperties(obj)
clusters(obj)
consensus(obj, ...)
convertToMFDB(TPs, out, ...)
convertToSuspects(TPs, ...)
cutClusters(obj)
defaultExclNormScores(obj)
export(obj, type, out, ...)
featureTable(obj, ...)
filter(obj, ...)
getFeatures(obj)
getMCS(obj, ...)
groupNames(obj)
makeSet(obj, ...)
plotChord(obj, addSelfLinks = FALSE, addRetMzPlots = TRUE, ...)
plotChroms(obj, ...)
plotGraph(obj, onlyLinked = TRUE, ...)
plotInt(obj, ...)
plotScores(obj, ...)
plotSilhouettes(obj, kSeq, ...)
plotSpectrum(obj, ...)
```



```

plotStructure(obj, ...)

plotVenn(obj, ...)

plotUpSet(obj, ...)

delete(obj, ...)

plotVolcano(obj, ...)

replicateGroups(obj)

setObjects(obj)

sets(obj)

treeCut(obj, k = NULL, h = NULL, ...)

treeCutDynamic(
  obj,
  maxTreeHeight = 1,
  deepSplit = TRUE,
  minModuleSize = 1,
  ...
)

unset(obj, set)

```

## Arguments

|                         |   |
|-------------------------|---|
| obj                     | The object the generic should be applied to.  |
| ...                     | Any further method specific arguments. See method documentation for details.                            |
| value                   | The replacement value.  |
| weights, flatnessFactor | See method documentation.   |
| TPs                     | The <a href="#">transformationProducts</a> derived object.  |
| out                     | Output file.  |
| type                    | The export type.  |
| addSelfLinks            | If TRUE then 'self-links' are added which represent non-shared data.                                    |
| addRetMzPlots           | Set to TRUE to enable $m/z$ vs retention time scatter plots.  |
| onlyLinked              | Only plots linked objects if TRUE.  |
| kSeq                    | An integer vector containing the sequence that should be used for average silhouette width calculation. |
| k, h                    | Desired numbers of clusters. See <a href="#">cutree</a> .   |

maxTreeHeight, deepSplit, minModuleSize  
 Arguments used by [cutreeDynamicTree](#).  
 set The name of the set.

## Details

adducts returns assigned adducts of the object.

- Methods are defined for: [featureGroups](#); [featureGroupsSet](#).

adducts<- sets adducts of the object.

- Methods are defined for: [featureGroups](#); [featureGroupsSet](#).

algorithm returns the algorithm that was used to generate the object.

- Methods are defined for: [optimizationResult](#); [workflowStep](#).

analysisInfo returns the [analysis information](#) from an object.

- Methods are defined for: [featureGroups](#); [features](#); [MSPeakListsSet](#).

analyses returns a character vector with the analyses for which data is present in this object.

- Methods are defined for: [featureGroups](#); [features](#); [formulas](#); [MSPeakLists](#).

annotatedPeakList returns an annotated MS peak list.

- Methods are defined for: [compounds](#); [compoundsSet](#); [formulas](#); [formulasSet](#).

annotations returns annotations.

- Methods are defined for: [featureAnnotations](#); [featureGroups](#); [formulas](#).

calculatePeakQualities calculates chromatographic peak qualities and scores.

- Methods are defined for: [featureGroups](#); [features](#).

clusterProperties Obtain a list with properties of the generated cluster(s).

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

clusters Obtain clustering object(s).

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

consensus combines and merges data from various algorithms to generate a consensus.

- Methods are defined for: [components](#); [componentsSet](#); [compounds](#); [compoundsSet](#); [featureGroupsComparison](#); [featureGroupsComparisonSet](#); [formulas](#); [formulasSet](#).

convertToMFDB Exports the object to a local database that can be used with MetFrag.

- Methods are defined for: .

convertToSuspects Converts an object to a suspect list.

- Methods are defined for: .

cutClusters Returns assigned cluster indices of a cut cluster.

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

defaultExclNormScores Returns default scorings that are excluded from normalization.

- Methods are defined for: [compounds](#); [formulas](#).

export exports workflow data to a given format.

- Methods are defined for: [featureGroups](#); [featureGroupsSet](#).

featureTable returns feature information.

- Methods are defined for: [featureGroups](#); [featureGroupsSet](#); [features](#).

filter provides various functionality to do post-filtering of data.

- Methods are defined for: [components](#); [componentsSet](#); [componentsTPs](#); [compounds](#); [compoundsSet](#); [featureAnnotations](#); [featureGroups](#); [featureGroupsScreening](#); [featureGroupsScreeningSet](#); [featureGroupsSet](#); [features](#); [featuresSet](#); [formulasSet](#); [MSPeakLists](#); [MSPeakListsSet](#); [transformationProductsBT](#).

getFeatures returns the object's [features](#) object.

- Methods are defined for: [featureGroups](#).

getMCS Calculates the maximum common substructure.

- Methods are defined for: [compounds](#); [compoundsCluster](#).

groupNames returns a character vector with the names of the feature groups for which data is present in this object.

- Methods are defined for: [components](#); [compoundsCluster](#); [featureAnnotations](#); [featureGroups](#); [MSPeakLists](#).

makeSet creates a set from given workflow objects.

- Methods are defined for: [featureGroups](#); [featureGroupsSet](#); [features](#); [featuresSet](#).

plotChord plots a Chord diagram to assess overlapping data.

- Methods are defined for: [featureGroups](#); [featureGroupsComparison](#).

plotChroms plots extracted ion chromatogram(s).

- Methods are defined for: [components](#); [featureGroups](#).

`plotGraph` Plots an interactive network graph.

- Methods are defined for: [componentsNT](#); [componentsNTSet](#); [componentsTPs](#).

`plotInt` plots the intensity of all contained features.

- Methods are defined for: [componentsIntClust](#); [featureGroups](#); [featureGroupsSet](#).

`plotScores` plots candidate scorings.

- Methods are defined for: [compounds](#); [formulas](#).

`plotSilhouettes` plots silhouette widths to evaluate the desired cluster size.

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

`plotSpectrum` plots a (annotated) spectrum.

- Methods are defined for: [components](#); [compounds](#); [compoundsSet](#); [formulas](#); [formulasSet](#); [MSPeakLists](#); [MSPeakListsSet](#).

`plotStructure` plots a chemical structure.

- Methods are defined for: [compounds](#); [compoundsCluster](#).

`plotVenn` plots a Venn diagram to assess unique and overlapping data.

- Methods are defined for: [featureAnnotations](#); [featureGroups](#); [featureGroupsComparison](#); [featureGroupsSet](#).

`plotUpSet` plots an UpSet diagram to assess unique and overlapping data.

- Methods are defined for: [featureAnnotations](#); [featureGroups](#); [featureGroupsComparison](#).

`delete` Deletes results.

- Methods are defined for: [components](#); [componentsClust](#); [componentsSet](#); [compoundsSet](#); [featureAnnotations](#); [featureGroups](#); [featureGroupsKPIC2](#); [featureGroupsScreening](#); [featureGroupsScreeningSet](#); [featureGroupsSet](#); [featureGroupsXCMS](#); [featureGroupsXCMS3](#); [features](#); [featuresKPIC2](#); [featuresXCMS](#); [featuresXCMS3](#); [formulas](#); [formulasSet](#).

`plotVolcano` plots a volcano plot.

- Methods are defined for: [featureGroups](#).

`replicateGroups` returns a character vector with the analyses for which data is present in this object.

- Methods are defined for: [featureGroups](#); [features](#).

`setObjects` returns the *set objects* of this object. See the documentation of [workflowStepSet](#).

- Methods are defined for: [workflowStepSet](#).

`sets` returns the names of the sets inside this object. See the documentation for [sets workflows](#).

- Methods are defined for: [featureGroupsSet](#); [featuresSet](#); [workflowStepSet](#).

`treeCut` Manually cut a cluster.

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

`treeCutDynamic` Automatically cut a cluster.

- Methods are defined for: [componentsClust](#); [compoundsCluster](#).

`unset` Converts this object to a regular non-set object. See the documentation for [sets workflows](#).

- Methods are defined for: [componentsNTSet](#); [componentsSet](#); [compoundsConsensusSet](#); [compoundsSet](#); [featureGroupsScreeningSet](#); [featureGroupsSet](#); [featuresSet](#); [formulasConsensusSet](#); [formulasSet](#); [MSPeakListsSet](#).

## Other generics

Below are methods that are defined for existing generics (*e.g.* defined in base). Please see method specific documentation for more details.

[ Subsets data within an object.

- Methods are defined for: [components](#),[ANY](#),[ANY](#),[missing](#); [componentsSet](#),[ANY](#),[ANY](#),[missing](#); [compoundsCluster](#),[ANY](#),[missing](#),[missing](#); [compoundsSet](#),[ANY](#),[missing](#),[missing](#); [featureAnnotations](#),[ANY](#),[missing](#),[missing](#); [featureGroups](#),[ANY](#),[ANY](#),[missing](#); [featureGroupsComparison](#),[ANY](#),[missing](#),[missing](#); [featureGroupsScreeningSet](#),[ANY](#),[ANY](#),[missing](#); [featureGroupsSet](#),[ANY](#),[ANY](#),[missing](#); [features](#),[ANY](#),[missing](#),[missing](#); [featuresSet](#),[ANY](#),[missing](#),[missing](#); [formulasSet](#),[ANY](#),[missing](#),[missing](#); [MSPeakLists](#),[ANY](#),[ANY](#),[missing](#); [MSPeakListsSet](#),[ANY](#),[ANY](#),[missing](#); [transformationProducts](#),[ANY](#),[missing](#),[missing](#).

[[ Extract data from an object.

- Methods are defined for: [components](#),[ANY](#),[ANY](#); [featureAnnotations](#),[ANY](#),[missing](#); [featureGroups](#),[ANY](#),[ANY](#); [featureGroupsComparison](#),[ANY](#),[missing](#); [features](#),[ANY](#),[missing](#); [formulas](#),[ANY](#),[ANY](#); [MSPeakLists](#),[ANY](#),[ANY](#); [transformationProducts](#),[ANY](#),[missing](#).

\$ Extract data from an object.

- Methods are defined for: [components](#); [featureAnnotations](#); [featureGroups](#); [featureGroupsComparison](#); [features](#); [MSPeakLists](#); [transformationProducts](#).

`as.data.table` Converts an object to a table ([data.table](#)).

- Methods are defined for: [components](#); [componentsTPs](#); [featureAnnotations](#); [featureGroups](#); [featureGroupsScreening](#); [featureGroupsScreeningSet](#); [featureGroupsSet](#); [features](#); [featuresSet](#); [formulas](#); [MSPeakLists](#); [MSPeakListsSet](#); [transformationProducts](#); [workflowStep](#).

`as.data.frame` Converts an object to a table ([data.frame](#)).

- Methods are defined for: [workflowStep](#).

length Returns the length of an object.

- Methods are defined for: [components](#); [compoundsCluster](#); [featureAnnotations](#); [featureGroups](#); [featureGroupsComparison](#); [features](#); [MSPeakLists](#); [optimizationResult](#); [transformationProducts](#).

lengths Returns the lengths of elements within this object.

- Methods are defined for: [compoundsCluster](#); [optimizationResult](#).

names Return names for this object.

- Methods are defined for: [components](#); [featureGroups](#); [featureGroupsComparison](#); [transformationProducts](#).

plot Generates a plot for an object.

- Methods are defined for: [componentsClust,missing](#); [compoundsCluster,missing](#); [featureGroups,missing](#); [featureGroupsComparison,missing](#); [optimizationResult,missing](#).

show Prints information about this object.

- Methods are defined for: [adduct](#); [components](#); [componentsFeatures](#); [componentsSet](#); [compounds](#); [compoundsCluster](#); [compoundsSet](#); [featureGroups](#); [featureGroupsScreening](#); [featureGroupsScreeningSet](#); [featureGroupsSet](#); [features](#); [featuresSet](#); [formulas](#); [formulasSet](#); [MSPeakLists](#); [MSPeakListsSet](#); [optimizationResult](#); [transformationProducts](#); [workflowStep](#); [workflowStepSet](#).

---

getPICSet,features-method

*Conversion to KPIC2 objects*

---

## Description

Converts a [features](#) object to an **KPIC** object.

## Usage

```
## S4 method for signature 'features'
getPICSet(obj, loadRawData = TRUE)

## S4 method for signature 'featuresKPIC2'
getPICSet(obj, ...)
```

## Arguments

|             |  |
|-------------|--|
| obj         | The features object that should be converted.  |
| loadRawData | Set to TRUE if analyses are available as mzXML or mzML files. Otherwise MS data is not loaded, and some dummy data ( <i>e.g.</i> file paths) is used in the returned object. |
| ...         | Ignored  |

---

getXCMSSet*Conversion to XCMS objects*

---

**Description**

Converts a [features](#) or [featureGroups](#) object to an [xcmsSet](#) or [XCMSnExp](#) object.

**Usage**

```
getXCMSSet(obj, verbose = TRUE, ...)

getXCMSnExp(obj, verbose = TRUE, ...)

## S4 method for signature 'features'
getXCMSSet(obj, verbose, loadRawData)

## S4 method for signature 'featuresXCMS'
getXCMSSet(obj, verbose = TRUE, ...)

## S4 method for signature 'featureGroups'
getXCMSSet(obj, verbose, loadRawData)

## S4 method for signature 'featureGroupsXCMS'
getXCMSSet(obj, verbose, loadRawData)

## S4 method for signature 'featuresSet'
getXCMSSet(obj, ..., set)

## S4 method for signature 'featureGroupsSet'
getXCMSSet(obj, ..., set)

## S4 method for signature 'features'
getXCMSnExp(obj, verbose, loadRawData)

## S4 method for signature 'featuresXCMS3'
getXCMSnExp(obj, verbose = TRUE, ...)

## S4 method for signature 'featureGroups'
getXCMSnExp(obj, verbose, loadRawData)

## S4 method for signature 'featureGroupsXCMS3'
getXCMSnExp(obj, verbose, loadRawData)

## S4 method for signature 'featuresSet'
getXCMSnExp(obj, ..., set)

## S4 method for signature 'featureGroupsSet'
```

```
getXCMSnExp(obj, ..., set)
```

### Arguments

|             |  |
|-------------|--|
| obj         | The object that should be converted.   |
| verbose     | If FALSE then no text output is shown.   |
| ...         | ( <b>sets workflow</b> ) Further arguments passed to non-sets method.<br>Otherwise ignored.  |
| loadRawData | Set to TRUE if analyses are available as mzXML or mzML files. Otherwise MS data is not loaded, and some dummy data ( <i>e.g.</i> file paths) is used in the returned object. |
| set         | ( <b>sets workflow</b> ) The name of the set to be exported.   |

### Sets workflows

In a [sets workflow](#), [unset](#) is used to convert the feature (group) data before the object is exported.

---

|                   |                                       |
|-------------------|---------------------------------------|
| MSPeakLists-class | <i>Class containing MS Peak Lists</i> |
|-------------------|---------------------------------------|

---

### Description

Contains all MS (and MS/MS where available) peak lists for a [featureGroups](#) object.

### Usage

```
## S4 method for signature 'MSPeakLists'
peakLists(obj)

## S4 method for signature 'MSPeakLists'
averagedPeakLists(obj)

## S4 method for signature 'MSPeakLists'
analyses(obj)

## S4 method for signature 'MSPeakLists'
groupNames(obj)

## S4 method for signature 'MSPeakLists'
length(x)

## S4 method for signature 'MSPeakLists'
show(object)

## S4 method for signature 'MSPeakLists,ANY,ANY,missing'
x[i, j, ..., reAverage = FALSE, drop = TRUE]
```



```
## S4 method for signature 'MSPeakLists,ANY,ANY'
x[[i, j]]

## S4 method for signature 'MSPeakLists'
x$name

## S4 method for signature 'MSPeakLists'
as.data.table(x, fGroups = NULL, averaged = TRUE)

## S4 method for signature 'MSPeakLists'
filter(
  obj,
  absMSIntThr = NULL,
  absMSMSIntThr = NULL,
  relMSIntThr = NULL,
  relMSMSIntThr = NULL,
  topMSPeaks = NULL,
  topMSMSPeaks = NULL,
  minMSMSPeaks = NULL,
  isolatePrec = NULL,
  deIsotopeMS = FALSE,
  deIsotopeMSMS = FALSE,
  withMSMS = FALSE,
  annotatedBy = NULL,
  retainPrecursorMSMS = TRUE,
  reAverage = FALSE,
  negate = FALSE
)

## S4 method for signature 'MSPeakLists'
plotSpectrum(
  obj,
  groupName,
  analysis = NULL,
  MSLevel = 1,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  xlim = NULL,
  ylim = NULL,
  ...
)

## S4 method for signature 'MSPeakLists'
spectrumSimilarity(
  obj,
  groupName1,
  groupName2 = NULL,
```

```

    analysis1 = NULL,
    analysis2 = NULL,
    MSLevel = 1,
    specSimParams = getDefSpecSimParams(),
    NAToZero = FALSE,
    drop = TRUE
)

## S4 method for signature 'MSPeakListsSet'
analysisInfo(obj)

## S4 method for signature 'MSPeakListsSet'
show(object)

## S4 method for signature 'MSPeakListsSet,ANY,ANY,missing'
x[i, j, ..., reAverage = FALSE, sets = NULL, drop = TRUE]

## S4 method for signature 'MSPeakListsSet'
as.data.table(x, fGroups = NULL, averaged = TRUE)

## S4 method for signature 'MSPeakListsSet'
filter(
  obj,
  ...,
  annotatedBy = NULL,
  retainPrecursorMSMS = TRUE,
  reAverage = FALSE,
  negate = FALSE,
  sets = NULL
)

## S4 method for signature 'MSPeakListsSet'
plotSpectrum(
  obj,
  groupName,
  analysis = NULL,
  MSLevel = 1,
  title = NULL,
  specSimParams = getDefSpecSimParams(),
  xlim = NULL,
  ylim = NULL,
  perSet = TRUE,
  mirror = TRUE,
  ...
)

## S4 method for signature 'MSPeakListsSet'
spectrumSimilarity(

```

```

    obj,
    groupName1,
    groupName2 = NULL,
    analysis1 = NULL,
    analysis2 = NULL,
    MSLevel = 1,
    specSimParams = getDefSpecSimParams(),
    NAToZero = FALSE,
    drop = TRUE
)

## S4 method for signature 'MSPeakListsSet'
unset(obj, set)

getDefIsolatePrecParams(...)

```

### Arguments

|  |   |
|--|---|
| obj, x, object   | The <a href="#">MSPeakLists</a> object to access.   |
| i, j   | For <code>[[</code> : A numeric or character value which is used to select analyses/feature groups by their index or name, respectively (for the order/names see <code>analyses()/groupNames()</code> ).<br><br>For <code>:</code> : Can also be logical to perform logical selection (similar to regular vectors). If missing all analyses/feature groups are selected.<br><br>For <code>[[</code> : should be a scalar value. If j is not specified, i selects by feature groups instead. |
| ...  | Further arguments passed to <a href="#">plot</a> .<br>For <a href="#">sets workflow</a> methods: further arguments passed to the base <a href="#">MSPeakLists</a> method.   |
| reAverage  | Set to TRUE to regenerate group averaged MS peak lists. <b>NOTE</b> it is very important that any annotation data relying on MS peak lists (formulae/compounds) are regenerated afterwards! Otherwise it is likely that e.g. plotting methods will use wrong MS/MS data.  |
| drop   | If set to TRUE and if the comparison is made between two spectra then <a href="#">drop</a> is used to reduce the matrix return value to a numeric vector.   |
| name   | The feature group name (partially matched).   |
| fGroups  | The <a href="#">featureGroups</a> object that was used to generate this object. If not NULL it is used to add feature group information (retention and <i>m/z</i> values).  |
| averaged   | If TRUE then feature group averaged peak list data is used.   |
| absMSIntThr, absMSMSIntThr, relMSIntThr, relMSMSIntThr | Absolute/relative intensity threshold for MS or MS/MS peak lists. NULL for none.  |
| topMSPeaks, topMSMSPeaks                               | Only consider this amount of MS or MS/MS peaks with highest intensity. NULL to consider all.  |

|                            |  |
|----------------------------|--|
| minMSMSPeaks               | If the number of peaks in an MS/MS peak list ( <b>excluding</b> the precursor peak) is lower than this it will be completely removed. Set to NULL to ignore.   |
| isolatePrec                | If not NULL then value should be a list with parameters used for isolating the precursor and its isotopes in MS peak lists (see Isolating precursor data). Alternatively, TRUE to apply the filter with default settings (as given with getDefIsolatePrecParams).  |
| deIsotopeMS, deIsotopeMSMS | Remove any isotopic peaks in MS or MS/MS peak lists. This may improve data processing steps which do not assume the presence of isotopic peaks (e.g. MetFrag for MS/MS). Note that getMzRPeakLists does not (yet) support flagging of isotopes.  |
| withMSMS                   | If set to TRUE then only results will be retained for which MS/MS data is available. if negate=TRUE then only results <i>without</i> MS/MS data will be retained.  |
| annotatedBy                | Either a <a href="#">formulas</a> or <a href="#">compounds</a> object, or a list with both. Any MS/MS peaks that are <i>not</i> annotated by any of the candidates in the specified objects are removed.   |
| retainPrecursorMSMS        | If TRUE then precursor peaks will never be filtered out from MS/MS peak lists (note that precursors are never removed from MS peak lists). The negate argument does not affect this setting.   |
| negate                     | If TRUE then filters are applied in opposite manner.   |
| groupName                  | The name of the feature group for which a plot should be made. To compare spectra, two group names can be specified.   |
| analysis                   | The name of the analysis for which a plot should be made. If NULL then data from the feature group averaged peak list is used. When comparing spectra, either NULL or the analyses for both spectra should be specified.   |
| MSLevel                    | The MS level: '1' for regular MS, '2' for MSMS.  |
| title                      | The title of the plot. If NULL a title will be automatically made.   |
| specSimParams              | A named list with parameters that influence the calculation of MS spectra similarities. See the <a href="#">spectral similarity parameters</a> documentation for more details.   |
| xlim, ylim                 | Sets the plot size limits used by <a href="#">plot</a> . Set to NULL for automatic plot sizing.  |
| groupName1, groupName2     | The names of the feature groups for which the comparison should be made. If both arguments are specified then a comparison is made with the spectra specified by groupName1 <i>vs</i> those specified by groupName2. The length of either can be '>1' to generate a comparison matrix. Alternatively, if groupName2 is NULL then all the spectra specified in groupName1 will be compared with eachother, <i>i.e.</i> resulting in a square similarity matrix. |
| analysis1, analysis2       | The name of the analysis (analyses) for the comparison. If NULL then data from the feature group averaged peak list is used. Otherwise, should be the same length as groupName1/groupName2.  |
| NAToZero                   | Set to TRUE to convert NA similarities ( <i>i.e.</i> when no similarity could be calculated) to zero values.   |
| sets                       | ( <b>sets workflow</b> ) A character with name(s) of the sets to keep (or remove if negate=TRUE).  |

`perSet, mirror` (**sets workflow**) If `perSet=TRUE` then the set specific mass peaks are annotated separately. Furthermore, if `mirror=TRUE` (and there are two sets in the object) then a mirror plot is generated.

`set` (**sets workflow**) The name of the set.

## Details

Objects for this class are returned by [MS peak lists generators](#).

The `getDefIsolatePrecParams` is used to create a parameter list for isolating the precursor and its isotopes (see Isolating precursor data).

## Value

`peakLists` returns a nested list containing MS (and MS/MS where available) peak lists per feature group and per analysis. The format is: `[[analysis]][[featureGroupName]][[MSType]][[PeakLists]]` where `MSType` is either "MS" or "MSMS" and `PeakLists` a [data.table](#) containing all *m/z* values (`mz` column) and their intensities (`intensity` column). In addition, the peak list tables may contain a `cmp` column which contains an unique alphabetical identifier to which isotopic cluster (or "compound") a mass belongs (only supported by MS peak lists generated by Bruker tools at the moment). `averagedPeakLists` returns a nested list of feature group averaged peak lists in a similar format as `peakLists`.

## Methods (by generic)

- `peakLists`: Accessor method to obtain the MS peak lists.
- `averagedPeakLists`: Accessor method to obtain the feature group averaged MS peak lists.
- `analyses`: returns a character vector with the names of the analyses for which data is present in this object.
- `groupNames`: returns a character vector with the names of the feature groups for which data is present in this object.
- `length`: Obtain total number of *m/z* values.
- `show`: Shows summary information for this object.
- `[`: Subset on analyses/feature groups.
- `[[`: Extract a list with MS and MS/MS (if available) peak lists. If the second argument (`j`) is not specified the averaged peak lists for the group specified by the first argument (`i`) will be returned.
- `$`: Extract group averaged MS peaklists for a feature group.
- `as.data.table`: Returns all MS peak list data in a table.
- `filter`: provides post filtering of generated MS peak lists, which may further enhance quality of subsequent workflow steps (*e.g.* formulae calculation and compounds identification) and/or speed up these processes. The filters are applied to all peak lists for each analysis. These peak lists are subsequently averaged to update group averaged peak lists. However, since version '1.1', the resulting feature group lists are *not* filtered afterwards.
- `plotSpectrum`: Plots a spectrum using MS or MS/MS peak lists for a given feature group. Two spectra can be compared when two feature groups are specified.
- `spectrumSimilarity`: Calculates the spectral similarity between two or more spectra.

**Slots**

- peakLists** Contains a list of all MS (and MS/MS) peak lists. Use the `peakLists` method for access.
- metadata** Metadata for all spectra used to generate peak lists. Follows the format of the `peakLists` slot.
- averagedPeakLists** A list with averaged MS (and MS/MS) peak lists for each feature group.
- avgPeakListArgs** A list with arguments used to generate feature group averaged MS(/MS) peak lists.
- origFGNames** A character with the original input feature group names.
- analysisInfo** (**sets workflow**) [Analysis information](#). Use the `analysisInfo` method for access.

**Isolating precursor data**

Formula calculation typically relies on evaluating the measured isotopic pattern from the precursor to score candidates. Some algorithms (currently only GenForm) penalize candidates if mass peaks are present in MS1 spectra that do not contribute to the isotopic pattern. Since these spectra are typically very 'noisy' due to background and co-eluting ions, an additional filtering step may be recommended prior to formula calculation. During this precursor isolation step all mass peaks are removed that are (1) not the precursor and (2) not likely to be an isotopologue of the precursor. To determine potential isotopic peaks the following parameters are used:

- **maxIsotopes** The maximum number of isotopes to consider. For instance, a value of '5' means that  $M+0$  (*i.e.* the monoisotopic peak) till  $M+5$  is considered. All mass peaks outside this range are removed.
- **mzDefectRange** A two-sized vector specifying the minimum (can be negative) and maximum  $m/z$  defect deviation compared to the precursor  $m/z$  defect. When chlorinated, brominated or other compounds with strong  $m/z$  defect in their isotopologues are to be considered a higher range may be desired. On the other hand, for natural compounds this range may be tightened. Note that the search range is propagated with increasing distance from the precursor, *e.g.* the search range is doubled for  $M+2$ , tripled for  $M+3$  etc.
- **intRange** A two-sized vector specifying the minimum and maximum relative intensity range compared to the precursor. For instance, `c(0.001, 2)` removes all peaks that have an intensity below 0.1% or above 200% of that of the precursor.
- **z** The  $z$  value (*i.e.* absolute charge) to be considered. For instance, a value of 2 would look for  $M+0.5$ ,  $M+1$  etc. Note that the `mzDefectRange` is adjusted accordingly (*e.g.* halved if  $z=2$ ).
- **maxGap** The maximum number of missing adjacent isotopic peaks ('gaps'). If the (rounded)  $m/z$  difference to the previous peak exceeds this value then this and all next peaks will be removed. Similar to  $z$ , the maximum gap is automatically adjusted for charge.

These parameters should be in a list that is passed to the `isolatePrec` argument to filter. The default values can be obtained with the `getDefaultIsolatePrecParams` function:

```
maxIsotopes=5; mzDefectRange=c(-0.01, 0.01); intRange=c(0.001, 2); z=1; maxGap=2
```

## S4 class hierarchy

- workflowStep
  - MSPeakLists
    - \* MSPeakListsSet
    - \* MSPeakListsUnset

## Source

spectrumSimilarity: The principles of spectral binning and cosine similarity calculations were loosely based on the code from `spectrumSimilarity()` function of **OrgMassSpecR**.

## Sets workflows

The MSPeakListsSet class is applicable for [sets workflows](#). This class is derived from MSPeakLists and therefore largely follows the same user interface.

The following methods are specifically defined for sets workflows:

- All the methods from base class [workflowStepSet](#).
- unset Converts the object data for a specified set into a 'non-set' object (MSPeakListsUnset), which allows it to be used in 'regular' workflows. Only the MS peaks that are present in the specified set are kept.
- analysisInfo Returns the [analysis info](#) for this object.

The following methods are changed or with new functionality:

- filter and the subset operator (`[]`) Can be used to select data that is only present for selected sets. The filter method is applied for each set individually, and afterwards the results are combined again (see [generateMSPeakLists](#)). Note that this has important implications for *e.g.* relative intensity filters (`relMSIntThr/relMSMSIntThr`), `topMSPeaks/topMSMSPeaks` and `minMSMSPeaks`. Similarly, when the `annotatedBy` filter is applied, each set specific MS peak list is filtered by the annotation results from only that set.
- plotSpectrum Is able to highlight set specific mass peaks (`perSet` and `mirror` arguments).
- spectrumSimilarity First calculates similarities for each spectral pair per set (*e.g.* all positive mode spectra are compared and then all negative mode spectra are compared). This data is then combined into an overall similarity value. How this combination is performed depends on the `setCombineMethod` field of the [specSimParams](#) argument.

## Author(s)

For spectrumSimilarity: major contributions by Bas van de Velde for spectral binning and similarity calculation.

---

MSPeakLists-generation

*Generation of MS Peak Lists*

---

## Description

Functionality to generate MS peak lists.

## Usage

```
## S4 method for signature 'featureGroups'
generateMSPeakLists(fGroups, algorithm, ...)
```

```
## S4 method for signature 'featureGroups'
generateMSPeakListsDA(
  fGroups,
  bgsubtr = TRUE,
  maxMSRtWindow = 5,
  minMSIntensity = 500,
  minMSMSIntensity = 500,
  clear = TRUE,
  close = TRUE,
  save = close,
  MSMSType = "MSMS",
  avgFGroupParams = getDefAvgPListParams()
)
```

```
## S4 method for signature 'featureGroupsSet'
generateMSPeakListsDA(fGroups, ...)
```

```
## S4 method for signature 'featureGroups'
generateMSPeakListsDAFMF(
  fGroups,
  minMSIntensity = 500,
  minMSMSIntensity = 500,
  close = TRUE,
  save = close,
  avgFGroupParams = getDefAvgPListParams()
)
```

```
## S4 method for signature 'featureGroupsSet'
generateMSPeakListsDAFMF(fGroups, ...)
```

```
## S4 method for signature 'featureGroups'
generateMSPeakListsMzR(
  fGroups,
  maxMSRtWindow = 5,
```



```

precursorMzWindow = 4,
topMost = NULL,
avgFeatParams = getDefAvgPListParams(),
avgFGroupParams = getDefAvgPListParams()
)

## S4 method for signature 'featureGroupsSet'
generateMSPeakListsMzR(fGroups, ...)

getDefAvgPListParams(...)

```

## Arguments

|                                  |  |
|----------------------------------|--|
| fGroups                          | The <a href="#">featureGroups</a> object from which MS peak lists should be extracted.   |
| algorithm                        | A character string describing the algorithm that should be used: "bruker", "brukerfmmf", "mzr"   |
| ...                              | For generateMSPeakLists: Any parameters to be passed to the selected MS peak lists generation algorithm.<br>For getDefAvgPListParams: Optional named arguments that override defaults.<br>For sets workflows: further arguments passed to the non-sets workflow method.  |
| bgsubtr                          | If TRUE background will be subtracted using the 'spectral' algorithm.  |
| maxMSRtWindow                    | Maximum chromatographic peak window used for spectrum averaging (in seconds, +/- retention time). If NULL all spectra from a feature will be taken into account. Lower to decrease processing time.  |
| minMSIntensity, minMSMSIntensity | Minimum intensity for peak lists obtained with DataAnalysis. Highly recommended to set '>0' as DA tends to report many very low intensity peaks.   |
| clear                            | Remove any existing chromatogram traces/mass spectra prior to making new ones.   |
| close, save                      | If TRUE then Bruker files are closed and saved after processing with DataAnalysis, respectively. Setting close=TRUE prevents that many analyses might be opened simultaneously in DataAnalysis, which otherwise may use excessive memory or become slow. By default save is TRUE when close is TRUE, which is likely what you want as otherwise any processed data is lost.  |
| MSMSType                         | The type of MS/MS experiment performed: "MSMS" for MRM/AutoMSMS or "BBCID" for broadband CID.  |
| precursorMzWindow                | The $m/z$ window (in Da) to find MS/MS spectra of a precursor. This is typically used for Data-Dependent like MS/MS data and should correspond to the isolation $m/z$ window ( <i>i.e.</i> +/- the precursor $m/z$ ) that was used to collect the data. For Data-Independent MS/MS experiments, where precursor ions are not isolated prior to fragmentation ( <i>e.g.</i> bbCID, MSe, all-ion, ...) the value should be NULL. |
| topMost                          | Only extract MS peak lists from a maximum of topMost analyses with highest intensity. If NULL all analyses will be used.   |

avgFeatParams, avgFGroupParams

A list with parameters used for averaging of peak lists for individual features and feature groups, respectively (see below).

## Details

Formula calculation and identification tools rely on mass spectra that belong to features of interest. For processing, MS (and MS/MS) spectra are typically reduced to a table with a column containing measured  $m/z$  values and a column containing their intensities. These 'MS peak lists' can then be used for [formula generation](#) and [compound generation](#).

MS and MS/MS peak lists are first generated for all features (or a subset, if the `topMost` argument is set). During this step multiple spectra over the feature elution profile are averaged. Subsequently, peak lists will be generated for each feature group by averaging peak lists of the features within the group. Functionality that uses peak lists will either use data from individual features or from group averaged peak lists. For instance, the former may be used by formulae calculation, while compound identification and plotting functionality typically uses group averaged peak lists.

Several functions exist to automatically extract MS peak lists for feature groups.

`generateMSPeakLists` is a generic function that will generate MS peak lists using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `generateMSPeakListsMzR` and `generateMSPeakListsDA`. While these functions may be called directly, `generateMSPeakLists` provides a generic interface and is therefore usually preferred.

`generateMSPeakListsDA` uses Bruker DataAnalysis to generate MS peak lists. Naturally, this only works with analyses in the Bruker data format ('.d'). This function leverages DataAnalysis functionality to support averaging of spectra, background subtraction and identification of isotopes. In order to obtain mass spectra TICs will be added of the MS and relevant MS/MS signals.

`generateMSPeakListsDAFMF` is similar to `generateMSPeakListsDA`, but uses compounds that were generated by the Find Molecular Features (FMF) algorithm to extract MS peak lists. This is generally much faster than `generateMSPeakListsDA`, however, it only works when features were obtained using the [findFeaturesBruker](#) function. Since all MS spectra are generated in advance by Bruker DataAnalysis, no further parameters exist to customize its operation.

`generateMSPeakListsMzR` uses the **mzR** package to extract MS peak lists. For this analyses should be either in '.mzXML' or '.mzML' format. This function averages multiple spectra over a chromatographic peak to improve accuracy.

The `getDefAvgPListParams` is used to create a parameter list for peak list averaging (discussed below).

## Value

A [MSPeakLists](#) object that can be used for formulae calculation and compound identification.

## Peak list averaging parameters

The parameters set used for averaging peak lists are set by the `avgFeatParams` and `avgFGroupParams` arguments. This should be a named list with the following values:

- `clusterMzWindow`  $m/z$  window (in Da) used for clustering  $m/z$  values when spectra are averaged. For `method="hclust"` this corresponds to the cluster height, while for `method="distance"`

this value is used to find nearby masses (+/- window). Too small windows will prevent clustering  $m/z$  values (thus erroneously treating equal masses along spectra as different), whereas too big windows may cluster unrelated  $m/z$  values from different or even the same spectrum together.

- **topMost** Only retain this maximum number of MS peaks when generating averaged spectra. Lowering this number may exclude more irrelevant (noisy) MS peaks and decrease processing time, whereas higher values may avoid excluding lower intense MS peaks that may still be of interest.
- **minIntensityPre** MS peaks with intensities below this value will be removed (applied prior to selection by **topMost**) before averaging.
- **minIntensityPost** MS peaks with intensities below this value will be removed after averaging.
- **avgFun** Function that is used to calculate average  $m/z$  values.
- **method** Method used for producing averaged MS spectra. Valid values are "hclust", used for hierarchical clustering (using the [fastcluster](#) package), and "distance", to use the between peak distance. The latter method may reduce processing time and memory requirements, at the potential cost of reduced accuracy.
- **pruneMissingPrecursorMS** For MS data only: if TRUE then peak lists without a precursor peak are removed. Note that even when this is set to FALSE, functionality that relies on MS (not MS/MS) peak lists (e.g. formulae calculation) will still skip calculation if a precursor is not found.
- **retainPrecursorMSMS** For MS/MS data only: if TRUE then always retain the precursor mass peak even if it is not amongst the **topMost** peaks. Note that MS precursor mass peaks are always kept. Furthermore, note that precursor peaks in both MS and MS/MS data may still be removed by intensity thresholds (this is unlike the [filter](#) method function).

Note that when Bruker algorithms are used these parameters only control generation of feature groups averaged peak lists: how peak lists for features are generated is controlled by `DataAnalysis`.

The `getDefAvgPListParams` function can be used to generate a default parameter list. The current defaults are:

```
clusterMzWindow=0.005; topMost=50; minIntensityPre=500; minIntensityPost=500; avgFun=mean;
method="hclust"; pruneMissingPrecursorMS=TRUE; retainPrecursorMSMS=TRUE
```

## Sets workflows

With a [sets workflow](#), the feature group averaged peak lists are made per set. This is important, because for averaging peak lists cannot be mixed, for instance, when different ionization modes were used to generate the sets. The group averaged peaklists are then simply combined and labelled in the final peak lists. However, please note that annotation and other functionality typically uses only the set specific peak lists, as this functionality cannot work with mixed peak lists.

## Source

Averaging of mass spectra algorithms used by are based on the [msProcess](#) R package (now archived on CRAN).

**Note**

generateMSPeakListsDA requires that the 'Component' column is active (Method->Parameters->Layouts->Mass List Layout) in order to add isotopologue information.

If any errors related to DCOM appear it might be necessary to terminate DataAnalysis (note that DataAnalysis might still be running as a background process). The ProcessCleaner application installed with DataAnalayis can be used for this.

**References**

A cross-platform toolkit for mass spectrometry and proteomics Chambers, Matthew C. and Maclean, Brendan and Burke, Robert and Amodei, Dario and Ruderman, Daniel L. and Neumann, Steffen and Gatto, Laurent and Fischer, Bernd and Pratt, Brian and Egertson, Jarrett and Hoff, Katherine and Kessner, Darren and Tasman, Natalie and Shulman, Nicholas and Frewen, Barbara and Baker, Tahmina A. and Brusniak, Mi-Youn and Paulse, Christopher and Creasy, David and Flashner, Lisa and Kani, Kian and Moulding, Chris and Seymour, Sean L. and Nuwaysir, Lydia M. and Lefebvre, Brent and Kuhlmann, Frank and Roark, Joe and Rainer, Paape and Detlev, Suckau and Hemenway, Tina and Huhmer, Andreas and Langridge, James and Connolly, Brian and Chadick, Trey and Holly, Krisztina and Eckels, Josh and Deutsch, Eric W. and Moritz, Robert L. and Katz, Jonathan E. and Agus, David B. and MacCoss, Michael and Tabb, David L. and Mallick, Parag Nat Biotechnol. 2012 NOct;30(10):918-920.

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Daniel Müllner (2013). fastcluster: Fast Hierarchical, Agglomerative Clustering Routines for R and Python. Journal of Statistical Software, 53(9), 1-18. URL <https://www.jstatsoft.org/v53/i09/>.

**See Also**[MSPeakLists-class](#)

---

newProject*Easily create new **patRo**on projects*

---

**Description**

The newProject function is used to quickly generate a processing R script. This tool allows the user to quickly select the targeted analyses, workflow steps and configuring some of their common parameters. This function requires to be run within a **RStudio** session. The resulting script is either added to the current open file or to a new file. The [analysis information](#) will be written to a '.csv' file so that it can easily be modified afterwards.

**Usage**

```
newProject(destPath = NULL)
```

**Arguments**

|          |   |
|----------|---|
| destPath | Set destination path value to this value (useful for debugging). Set to NULL for a default value. |
|----------|---|

---

optimizationResult-class*Class containing optimization results.*

---

**Description**

Objects from this class contain optimization results resulting from design of experiment (DoE).

**Usage**

```
## S4 method for signature 'optimizationResult'
algorithm(obj)
```

```
## S4 method for signature 'optimizationResult'
length(x)
```

```
## S4 method for signature 'optimizationResult'
lengths(x, use.names = FALSE)
```

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

```
## S4 method for signature 'optimizationResult,missing'
plot(
  x,
  paramSet,
  DoEIteration,
  paramsToPlot = NULL,
  maxCols = NULL,
  type = "contour",
  image = TRUE,
  contours = "colors",
  ...
)

## S4 method for signature 'optimizationResult'
optimizedParameters(object, paramSet = NULL, DoEIteration = NULL)

## S4 method for signature 'optimizationResult'
optimizedObject(object, paramSet = NULL)

## S4 method for signature 'optimizationResult'
scores(object, paramSet = NULL, DoEIteration = NULL)

## S4 method for signature 'optimizationResult'
experimentInfo(object, paramSet, DoEIteration)
```

### Arguments

|                |   |
|----------------|---|
| obj, x, object | An optimizationResult object.   |
| use.names      | Ignored.  |
| paramSet       | Numeric index of the parameter set ( <i>i.e.</i> the first parameter set gets index '1'). For some methods optional: if NULL the best will be selected.   |
| DoEIteration   | Numeric index specifying the DoE iteration within the specified paramSet. For some methods optional: if NULL the best will be selected.   |
| paramsToPlot   | Which parameters relations should be plot. If NULL all will be plot. Alternatively, a list containing one or more character vectors specifying each two parameters that should be plotted. Finally, if only one pair should be plotted, can be a character vector specifying both parameters. |
| maxCols        | Multiple parameter pairs are plotted in a grid. The maximum number of columns can be set with this argument. Set to NULL for no limit.  |
| type           | The type of plots to be generated: "contour", "image" or "persp". The equally named functions will be called for plotting.  |
| image          | Passed to <a href="#">contour</a> (if type="contour").  |
| contours       | Passed to <a href="#">persp</a> (if type="persp").  |
| ...            | Further arguments passed to <a href="#">contour</a> , <a href="#">image</a> or <a href="#">persp</a> (depending on type).   |

## Details

Objects from this class are returned by [optimizeFeatureFinding](#) and [optimizeFeatureGrouping](#).

## Methods (by generic)

- `algorithm`: Returns the algorithm that was used for finding features.
- `length`: Obtain total number of experimental design iterations performed.
- `lengths`: Obtain number of experimental design iterations performed for each parameter set.
- `show`: Shows summary information for this object.
- `plot`: Generates response plots for all or a selected set of parameters.
- `optimizedParameters`: Returns parameter set yielding optimal results. The `paramSet` and `DoEIteration` arguments can be NULL.
- `optimizedObject`: Returns the object (*i.e.* a [features](#) or [featureGroups](#) object) that was generated with optimized parameters. The `paramSet` argument can be NULL.
- `scores`: Returns optimization scores. The `paramSet` and `DoEIteration` arguments can be NULL.
- `experimentInfo`: Returns a list with optimization information from an DoE iteration.

## Slots

`algorithm` A character specifying the algorithm that was optimized.

`paramSets` A list with detailed results from each parameter set that was tested.

`bestParamSet` Numeric index of the parameter set yielding the best response.

## Examples

```
## Not run:
# ftOpt is an optimization object.

# plot contour of all parameter pairs from the first parameter set/iteration.
plot(ftOpt, paramSet = 1, DoEIteration = 1)

# as above, but only plot two parameter pairs
plot(ftOpt, paramSet = 1, DoEIteration = 1,
     paramsToPlot = list(c("mzPPM", "chromFWHM"), c("chromFWHM", "chromSNR")))

# plot 3d perspective plots
plot(ftOpt, paramSet = 1, DoEIteration = 1, type = "persp")

## End(Not run)
```

---

|                  |  |
|------------------|--|
| printPackageOpts | <i>Prints all the package options of patRoan and their currently set values.</i> |
|------------------|--|

---

**Description**

Prints all the package options of patRoan and their currently set values.

**Usage**

```
printPackageOpts()
```

---

|           |                                  |
|-----------|----------------------------------|
| reporting | <i>Report feature group data</i> |
|-----------|----------------------------------|

---

**Description**

Functionality to report data produced by most workflow steps such as features, feature groups, calculated chemical formulae and tentatively identified compounds.

**Usage**

```
## S4 method for signature 'featureGroups'
reportCSV(
  fGroups,
  path = "report",
  reportFeatures = FALSE,
  formulas = NULL,
  formulasNormalizeScores = "max",
  formulasExclNormScores = NULL,
  compounds = NULL,
  compoundsNormalizeScores = "max",
  compoundsExclNormScores = c("score", "individualMoNAScore", "annoTypeCount"),
  compsCluster = NULL,
  components = NULL,
  retMin = TRUE,
  clearPath = FALSE
)

## S4 method for signature 'featureGroups'
reportPDF(
  fGroups,
  path = "report",
  reportFGroups = TRUE,
  formulas = NULL,
```



```

    formulasTopMost = 5,
    formulasNormalizeScores = "max",
    formulasExclNormScores = NULL,
    reportFormulaSpectra = TRUE,
    compounds = NULL,
    compoundsNormalizeScores = "max",
    compoundsExclNormScores = c("score", "individualMoNAScore", "annoTypeCount"),
    compoundsOnlyUsedScorings = TRUE,
    compoundsTopMost = 5,
    compsCluster = NULL,
    components = NULL,
    MSPeakLists = NULL,
    retMin = TRUE,
    EICGrid = c(2, 1),
    EICRtWindow = 20,
    EICMzExpWindow = 0.001,
    EICTopMost = 1,
    EICTopMostByRGroup = TRUE,
    EICOnlyPresent = TRUE,
    clearPath = FALSE
)

```

```
## S4 method for signature 'featureGroups'
```

```

reportHTML(
  fGroups,
  path = "report",
  reportPlots = c("chord", "venn", "upset", "eics", "formulas"),
  formulas = NULL,
  formulasTopMost = 5,
  formulasNormalizeScores = "max",
  formulasExclNormScores = NULL,
  compounds = NULL,
  compoundsNormalizeScores = "max",
  compoundsExclNormScores = c("score", "individualMoNAScore", "annoTypeCount"),
  compoundsOnlyUsedScorings = TRUE,
  compoundsTopMost = 5,
  compsCluster = NULL,
  includeMFWebLinks = "compounds",
  components = NULL,
  interactiveHeat = FALSE,
  MSPeakLists = NULL,
  specSimParams = getDefSpecSimParams(),
  retMin = TRUE,
  EICRtWindow = 20,
  EICMzExpWindow = 0.001,
  EICTopMost = 1,
  EICTopMostByRGroup = TRUE,
  EICOnlyPresent = TRUE,

```

```

    selfContained = TRUE,
    optimizePng = FALSE,
    clearPath = FALSE,
    openReport = TRUE,
    noDate = FALSE
)

```

## Arguments

- fGroups** The [featureGroups](#) object that should be used for reporting data.
- path** The destination file path for files generated during reporting. Will be generated if needed.
- reportFeatures** If set to TRUE then for each analysis a '.csv' file will be generated with information about its detected features.
- formulas, compounds, compsCluster, components** Further objects ([formulas](#), [compounds](#), [compoundsCluster](#), [components](#)) that should be reported. Specify NULL to skip reporting a particular object.
- compoundsNormalizeScores, formulasNormalizeScores** A character that specifies how normalization of annotation scorings occurs. Either "none" (no normalization), "max" (normalize to max value) or "minmax" (perform min-max normalization). Note that normalization of negative scores (e.g. output by SIRIUS) is always performed as min-max. Furthermore, currently normalization for compounds takes the original min/max scoring values into account when candidates were generated. Thus, for compounds scoring, normalization is not affected when candidate results were removed after they were generated (e.g. by use of filter).
- compoundsExclNormScores, formulasExclNormScores** A character vector specifying any compound scoring names that should *not* be normalized. Set to NULL to normalize all scorings. Note that whether any normalization occurs is set by the `compoundsExclNormScores, formulasExclNormScores` argument.  
For compounds: By default score and individualMoNAScore are set to mimic the behavior of the MetFrag web interface.
- retMin** If TRUE then report retention times in minutes (otherwise seconds).
- clearPath** If TRUE then the destination path will be (recursively) removed prior to reporting.
- reportFGroups** If TRUE then feature group data will be reported.
- formulasTopMost, compoundsTopMost** Only this amount of top ranked candidate formulae/compounds are reported. Lower values may significantly speed up reporting. Set to NULL to ignore.
- reportFormulaSpectra** If TRUE then explained MS/MS spectra (if available) for candidate formulae will be reported. Specifying `formulas` and setting this argument to FALSE still allows further annotation of compound MS/MS spectra.
- compoundsOnlyUsedScorings** If TRUE then only scorings are plotted that actually have been used to rank data (see the `scoreTypes` argument to [generateCompoundsMetFrag](#) for more details).

|   |   |
|---|---|
| MSPeakLists   | A <a href="#">MSPeakLists</a> object that is <i>mandatory</i> when spectra for formulae and/or compounds will be reported.  |
| EICGrid   | An integer vector in the form <code>c(columns,rows)</code> that is used to determine the plotting grid when reporting EICs in PDF files.  |
| EICRtWindow, EICMzExpWindow, EICTopMost, EICTopMostByRGroup, EICOnlyPresent | Plotting parameters passed to <a href="#">plotChroms</a> ( <i>i.e.</i> <code>rtWindow</code> , <code>mzExpWindow</code> , <code>topMost</code> , <code>topMostByRGroup</code> and <code>onlyPresent</code> arguments).  |
| reportPlots   | A character vector specifying what should be plotted. Valid options are: "chord", "venn", "upset" (plot a chord, Venn and UpSet diagram, respectively), "eics" (plot EICs for individual feature groups) and "formulas" (plot annotated formula spectra). Set to "none" to plot none of these.  |
| includeMFWebLinks   | A character specifying to which feature groups a web link should be added in the annotation page to <a href="#">MetFragWeb</a> . Options are: "compounds" (only to those with compounds results), "MSMS" (only to those with MSMS peak lists) or "none".  |
| interactiveHeat   | If TRUE an interactive heatmap HTML widget will be generated to display hierarchical clustering results. Set to FALSE for a 'regular' static plot.  |
| specSimParams   | A named list with parameters that influence the calculation of MS spectra similarities. See the <a href="#">spectral similarity parameters</a> documentation for more details.  |
| selfContained   | If TRUE the output will be a standalone HTML file which contains all graphics and script dependencies. When FALSE, the latter will be placed in an additional directory ('report_files') which should remain present when viewing the output file. Especially on Windows, a non-self contained output might be desirable when reporting large amounts of data to prevent pandoc from running out of memory. |
| optimizePng   | If TRUE then pngquant is used to reduce the size of generated graphics. A significant reduction in disk space usage may be seen, however, at the cost additional processing time. Multiple pngquant processes will be executed in parallel, which can be configured with 'patRoos.MP.maxProcs' (parallelization will always happen with the "classic" method, see <a href="#">patRoos options</a> ).        |
| openReport  | If set to TRUE then the output report file will be opened with the system browser.  |
| noDate  | If TRUE then the current date is not added to the report. This is mainly used for testing and its main purpose is to guarantee equal report files when 'reportHTML()' is called multiple times with equal arguments.  |

## Details

These functions are usually called at the very end of the workflow. It is used to report various data on features and feature groups. In addition, these functions may be used for reporting formulae and/or compounds that were generated for the specified feature groups. Data can be reported in tabular form (*i.e.* '.csv' files) by `reportCSV` or graphically by `reportPDF` and `reportHTML`. The latter functions will plot for instance chromatograms and annotated mass spectra, which are useful to get a graphical overview of results.

All functions have a wide variety of arguments that influence the reporting process. Nevertheless, most parameters are optional and only required to be given for fine tuning. In addition, only those objects (*e.g.* formulae, compounds, clustering) that are desired to be reported need to be specified.

`reportCSV` generates tabular data (*i.e.* ‘.csv’ files) for given data to be reported. This may also be useful to allow import by other tools for post processing.

`reportPDF` will report graphical data (*e.g.* chromatograms and mass spectra) within PDF files. Compared to `reportHTML` this function may be faster and yield smaller report files, however, its functionality is a bit more basic and generated data is more ‘scattered’ around.

`reportHTML` will report graphical data (*e.g.* chromatograms and mass spectra) and summary information in an easy browsable HTML file using [rmarkdown](#), [flexdashboard](#) and [knitr](#).

## Parallelization

`reportHTML` uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoön options](#) for configuration options.

Currently, `reportHTML` only uses “classic” multiprocessing, regardless of the ‘`patRoön.MP.method`’ option.

## Note

Any formulae and compounds for feature groups which are not present within `fGroups` (*i.e.* because it has been subset afterwards) will not be reported.

## References

Creating MetFrag landing page URLs based on code from [MetFamily](#) R package.

Yihui Xie (2015) Dynamic Documents with R and knitr. 2nd edition. Chapman and Hall/CRC. ISBN 978-1498716963

Yihui Xie (2014) knitr: A Comprehensive Tool for Reproducible Research in R. In Victoria Stodden, Friedrich Leisch and Roger D. Peng, editors, Implementing Reproducible Computational Research. Chapman and Hall/CRC. ISBN 978-1466561595

## Description

With sets workflows in **patRoön** a complete non-target (or suspect) screening workflow is performed with sample analyses that were measured with different MS methods (typically positive and negative ionization).

## Details

The analyses files that were measured with a different method are grouped in *sets*. In the most typical case, there is a "positive" and "negative" set, for the positively/negatively ionized data, respectively. However, other distinctions than polarity are also possible (although currently the chromatographic method should be the same between sets). A sets workflow is typically initiated with the [makeSet](#) method. The handbook contains much more details about sets workflows.

## See Also

[workflowStepSet](#), the Sets workflows sections in other documentation pages and the **patRoom** handbook.

---

specSimParams

*MS spectral similarity calculation parameters*

---

## Description

Parameters relevant for calculation of similarities between mass spectra.

## Usage

```
getDefSpecSimParams(...)
```

## Arguments

... optional named arguments that override defaults.

## Details

For the calculation of spectral similarities the following parameters exist:

- **method** The similarity method: either "cosine" or "jaccard".
- **removePrecursor** If TRUE then precursor peaks (*i.e.* the mass peak corresponding to the feature) are removed prior to similarity calculation.
- **mzWeight, intWeight** Mass and intensity weights used for cosine calculation.
- **absMzDev** Maximum absolute  $m/z$  deviation between mass peaks, used for binning spectra.
- **relMinIntensity** The minimum relative intensity for mass peaks ('0-1'). Peaks with lower intensities are not considered for similarity calculation. The relative intensities are called after the precursor peak is removed when **removePrecursor**=TRUE.
- **minPeaks** Only consider spectra that have at least this amount of peaks (*after* the spectrum is filtered).
- **shift** If and how shifting is applied prior to similarity calculation. Valid options are: "none" (no shifting), "precursor" (all mass peaks of the second spectrum are shifted by the mass difference between the precursors of both spectra) or "both" (the spectra are first binned without shifting, and peaks still unaligned are then shifted as is done when **shift**="precursor").

- `setCombinedMethod` (**sets workflow**) Determines how spectral similarities from different sets are combined. Possible values are "mean", "min" or "max", which calculates the combined value as the mean, minimum or maximum value, respectively. NA values (*e.g.* if a set does not have peak list data to combine) are removed in advance.

These parameters are typically passed as a named list as the `specSimParams` argument to functions that do spectral similarity calculations. The `getDefSpecSimParams` function can be used to generate such parameter list with defaults.

---

|                   |                                     |
|-------------------|-------------------------------------|
| suspect-screening | <i>Target and suspect screening</i> |
|-------------------|-------------------------------------|

---

## Description

Utilities to screen for analytes with known or suspected identity.

## Usage

```
## S4 method for signature 'featureGroups'
screenSuspects(
  fGroups,
  suspects,
  rtWindow,
  mzWindow,
  adduct,
  skipInvalid,
  onlyHits
)

## S4 method for signature 'featureGroupsScreening'
screenSuspects(
  fGroups,
  suspects,
  rtWindow,
  mzWindow,
  adduct,
  skipInvalid,
  onlyHits,
  amend = FALSE
)

numericIDLevel(level)

genIDLevelRulesFile(out, inLevels = NULL, exLevels = NULL)

## S4 method for signature 'featureGroupsSet'
screenSuspects(
```

```

    fGroups,
    suspects,
    rtWindow,
    mzWindow,
    adduct,
    skipInvalid,
    onlyHits
)

## S4 method for signature 'featureGroupsScreeningSet'
screenSuspects(
  fGroups,
  suspects,
  rtWindow,
  mzWindow,
  adduct,
  skipInvalid,
  onlyHits,
  amend = FALSE
)

importFeatureGroupsBrukerTASQ(path, analysisInfo, clusterRTWindow = 12)

```

### Arguments

|                    |   |
|--------------------|---|
| fGroups            | The <a href="#">featureGroups</a> object that should be screened.   |
| suspects           | A data.frame with suspect information. See the Suspect list format section below.<br><br>( <b>sets workflow</b> ) Can also be a list with suspect lists to be used for each set (otherwise the same suspect lists is used for all sets). The list can be named with the sets names to mark which suspect list is to be used with which set (e.g. suspects=list(positive=suspsPos,negative=suspsNeg)). |
| rtWindow, mzWindow | The retention time window (in seconds) and <i>m/z</i> window that will be used for matching a suspect (+/- feature data).   |
| adduct             | An <a href="#">adduct</a> object (or something that can be converted to it with <a href="#">as.adduct</a> ). Examples: "[M-H]-", "[M+Na]+". May be NULL, see Suspect list format and Matching of suspect masses sections below.   |
| skipInvalid        | If set to TRUE then suspects with invalid data (e.g. missing names or other missing data) will be ignored with a warning. Similarly, any suspects for which mass calculation failed (when no <i>mz</i> column is present in the suspect list), for instance, due to invalid SMILES, will be ignored with a warning.   |
| onlyHits           | If TRUE then all feature groups not matched by any of the suspects will be removed.   |
| amend              | If TRUE then screening results will be <i>amended</i> to the original object.   |
| level              | The identification level to be converted.   |

|                    |   |
|--------------------|---|
| out                | The file path to the target file.   |
| inLevels, exLevels | A <a href="#">regular expression</a> for the identification levels to include or exclude, respectively. For instance, exLevels="4 5" would exclude level 4 and 5 from the output file. Set to NULL to ignore. |
| path               | The file path to an Excel export of the Global results table from TASQ, converted to '.csv' format.   |
| analysisInfo       | A table with <a href="#">analysis information</a> .   |
| clusterRTWindow    | This retention time window (in seconds) is used to group hits across analyses together. See also the details section.   |

## Details

Besides 'full non-target analysis', where compounds may be identified with little to no prior knowledge, a common strategy is to screen for compounds with known or suspected identity. This may be a generally favorable approach if possible, as it can significantly reduce the load on data interpretation.

screenSuspects is used to perform suspect screening. The input [featureGroups](#) object will be screened for suspects by  $m/z$  values and optionally retention times. Afterwards, any feature groups not matched may be kept or removed, depending whether a full non-target analysis is desired.

numericIDLevel Extracts the numeric part of a given identification level (*e.g.* "3a" becomes '3').

genIDLevelRulesFile Generates a template YAML file that is used to configure the rules for automatic estimation of identification levels. This file can then be used as input for [annotateSuspects](#).

importFeatureGroupsBrukerTASQ will convert screening results from Bruker TASQ to a [featureGroups](#) object. The feature groups across analyses are formed based on the name of suspects and their closeness in retention time. The latter is necessary because TASQ does not necessarily perform checks on retention times and may therefore assign a suspect to peaks with different retention times across analyses (or within a single analysis). Hence, suspects with equal names are hierarchically clustered on their retention times (using [fastcluster](#)) to form the feature groups. The cut-off value for this is specified by the clusterRTWindow argument. The input for this function is obtained by generating an Excel export of the 'global' results and subsequently converting the file to '.csv' format.

## Value

screenSuspects returns a [featureGroupsScreening](#) object, which is a copy of the input fGroups object amended with additional screening information.

importFeatureGroupsBrukerTASQ returns a new featureGroups object containing converted screening results from Bruker TASQ.

## Sets workflows

In a [sets workflow](#), screenSuspects performs suspect screening for each set separately, and the screening results are combined afterwards. The sets column in the screenInfo data marks in which sets the suspect hit was found.

importFeatureGroupsBrukerTASQ Is currently not supported for sets workflows.



### Suspect list format

the `suspects` argument for `screenSuspects` should be a `data.frame` with the following mandatory and optional columns:

- `name` The suspect name. Must be file-compatible. (**mandatory**)
- `rt` The retention time (in seconds) for the suspect. If specified the suspect will only be matched if its retention matches the experimental value (tolerance defined by the `rtWindow` argument). (**optional**)
- `neutralMass`, `formula`, `SMILES`, `InChI` The neutral monoisotopic mass, chemical formula, SMILES or InChI for the suspect. (data from one of these columns are **mandatory** in case no value from the `mz` column is available for a suspect)
- `mz` The ionized  $m/z$  of the suspect. (**mandatory** unless it can be calculated from one of the aforementioned columns)
- `adduct` A character that can be converted with `as.adduct`. Can be used to automatically calculate values for the `mz` column. (**mandatory** unless data from the `mz` column is available, the `adduct` argument is set or `fGroups` has adduct annotations)
- `fragments_mz`, `fragments_formula` One or more MS/MS fragments (specified as  $m/z$  or formulae, respectively). Multiple values can be specified by separating them with a semicolon (;). This data is used by `annotateSuspects` to report detected MS/MS fragments and calculate identification levels. (**optional**)

### Matching of suspect masses

How the mass of a suspect is matched with the mass of a feature depends on the available data:

- If the suspect has data from the `mz` column of the suspect list, then this data is matched with the detected feature  $m/z$ .
- Otherwise, if the suspect has data in the `adduct` column of the suspect list, this data is used to calculate its `mz` value, which is then used like above.
- In the last case, the neutral mass of the suspect is matched with the neutral mass of the feature. Hence, either the `adduct` argument needs to be specified, or the `featureGroups` input object must have adduct annotations.

### Note

Both `screenSuspects` and `importFeatureGroupsBrukerTASQ` may use the suspect names to base file names used for reporting, logging etc. Therefore, it is important that these are file-compatible names. For this purpose, `screenSuspects` will automatically try to convert long, non-unique and/or otherwise incompatible suspect names.

For `screenSuspects` in some cases you may need to install **OpenBabel** (e.g. when only InChI data is available for mass calculation).

`importFeatureGroupsBrukerTASQ` will use estimated min/max values for retention times and dummy min/max  $m/z$  values for conversion to features, since this information is not (readily) available. Hence, when plotting, for instance, extracted ion chromatograms (with `plotChroms`) the integrated chromatographic peak range shown is incorrect.

## References

OBoyle NM, Banck M, James CA, Morley C, Vandermeersch T, Hutchison GR (2011). "Open Babel: An open chemical toolbox." *Journal of Cheminformatics*, **3**(1). doi: [10.1186/17582946333](https://doi.org/10.1186/17582946333).

Daniel Müllner (2013). fastcluster: Fast Hierarchical, Agglomerative Clustering Routines for R and Python. *Journal of Statistical Software*, 53(9), 1-18. URL <https://www.jstatsoft.org/v53/i09/>.

## See Also

featureGroupsScreening

---

|               |  |
|---------------|--|
| TP-generation | <i>Generation of transformation products (TPs)</i> |
|---------------|--|

---

## Description

Functionality to automatically obtain transformation products for a given list of parent compounds.

## Usage

```
generateTPs(algorithm, ...)

generateTPsBioTransformer(
  parents,
  type = "env",
  steps = 2,
  extraOpts = NULL,
  skipInvalid = TRUE,
  fpType = "extended",
  fpSimMethod = "tanimoto",
  MP = FALSE
)

generateTPsLibrary(
  parents = NULL,
  TPLibrary = NULL,
  skipInvalid = TRUE,
  matchParentsBy = "InChIKey"
)

## S4 method for signature 'featureGroups'
generateTPsLogic(fGroups, minMass = 40, adduct = NULL, transformations = NULL)

## S4 method for signature 'featureGroupsSet'
generateTPsLogic(fGroups, minMass = 40, transformations = NULL)
```

**Arguments**

|                 |  |
|-----------------|--|
| algorithm       | A character string describing the algorithm that should be used: "biotransformer", "logic", "library"  |
| ...             | Any parameters to be passed to the selected TP generation algorithm.   |
| parents         | The parents for which transformation products should be obtained. This can be (1) a suspect list (see <a href="#">suspect screening</a> for more information), (2) the resulting output <a href="#">screenSuspects</a> or (3) a <a href="#">compounds</a> annotation object. In the former two cases, the suspect (hits) are used as parents, whereas in the latter case all candidates are used as parents.<br><br>For generateTPsLibrary: can be NULL, in this case TPs for all parents in the library are obtained. |
| type            | The type of prediction. Valid values are: "env", "ecbased", "cyp450", "phaseII", "hgut", "superbio", "allHuman". Sets the -b command line option.  |
| steps           | The number of steps for the predictions. Sets the -s command line option.  |
| extraOpts       | A character with extra command line options passed to the biotransformer.jar tool.   |
| skipInvalid     | If set to TRUE then the parents will be skipped (with a warning) for which insufficient information (e.g. SMILES) is available.  |
| fpType          | The type of structural fingerprint that should be calculated. See the type argument of the <a href="#">get.fingerprint</a> function of <b>rdck</b> .   |
| fpSimMethod     | The method for calculating similarities (i.e. not dissimilarity!). See the method argument of the <a href="#">fp.sim.matrix</a> function of the <b>fingerprint</b> package.  |
| MP              | If TRUE then multiprocessing is enabled. Since BioTransformer supports native parallelization, additional multiprocessing generally doesn't lead to significant reduction in computational times. Furthermore, enabling multiprocessing can lead to very high CPU/RAM usage.   |
| TPLibrary       | If NULL, a default <b>PubChem</b> based library is used. Otherwise, TPLibrary should be a data.frame. See section below.   |
| matchParentsBy  | A character that specifies how the input parents are matched with the data from the TP library. Valid options are: "InChIKey", "InChIKey1", "InChI", "SMILES".   |
| fGroups         | A <a href="#">featureGroups</a> object for which TPs should be calculated.   |
| minMass         | A numeric that specifies the minimum mass of calculated TPs. If below this mass it will be removed.  |
| adduct          | An <a href="#">adduct</a> object (or something that can be converted to it with <a href="#">as.adduct</a> ). Examples: "[M-H]-", "[M+Na]+". If the featureGroups object has adduct annotations then these are used if adducts=NULL.<br><br>( <b>sets workflow</b> ) The adduct argument is not supported for sets workflows, since the adduct annotations will then always be used.  |
| transformations | A data.frame with transformation reactions to be used for calculating the TPs (see section below). If NULL, a default table from Schollee <i>et al.</i> is used (see references).  |

## Details

Several algorithms are available that obtain TPs for a set of parent compounds. Depending on the algorithm, the parents can be a suspect list, all the candidates in a `compounds` object or the screening results or all feature groups from a `featureGroups` object. The resulting objects can (again depending on the used algorithm) then be used for conversion to suspect lists (`convertToSuspects`), a MetFrag database (`convertToMFDB`) or further processed to generate parent to TP links from features (`generateComponentsTPs`).

`generateTPs` is a generic function that will generate transformation products using one of the supported algorithms. The actual functionality is provided by algorithm specific functions such as `generateTPsBioTransformer` and `generateTPsLogic`. While these functions may be called directly, `generateTPs` provides a generic interface and is therefore usually preferred.

`generateTPsBioTransformer` uses `BioTransformer` to predict TPs. An important advantage of this algorithm is that it provides full structural information for TPs. However, to do so, structural information also needs to be present for the parents. Afterwards, structural similarities between the parent and its TPs are calculated, which can be used to `filter` the results. In order to use this function the `‘.jar’` command line utility should be installed and specified in the `patRoom.path.BioTransformer` option. The `‘.jar’` file can be obtained via <https://bitbucket.org/djoumbou/biotransformer/src/master>.

`generateTPsLibrary` obtains transformation products from a library. Similar to `generateTPsBioTransformer`, this algorithm relies and provides structural information for parents/TPs (SMILES). By default, a library is used that is based on data from `PubChem`. However, it is also possible to use your own library.

`generateTPsLogic` applies *metabolic logic* to predict transformation products. With this algorithm, TPs are predicted from common (environmental) chemical reactions, such as hydroxylation, demethylation etc. The generated TPs result from calculating the mass differences between a parent feature after it underwent the reaction. While this only results in little information on chemical properties of the TP, an advantage of this method is that it does not rely on structural information of the parent, which may be unknown in a full non-target analysis.

## Custom TP libraries and transformations

The `TPLibrary` argument is used to specify a custom TP library for `generateTPsLibrary`. This should be a `data.frame` where each row specifies a TP for a parent, with the following columns:

- `parent_name` and `TP_name`: The name of the parent/TP.
- `parent_SMILES` and `TP_SMILES`: The SMILES of the parent structure.
- `parent_LogP` and `TP_LogP`: The log P values for the parent/TP. (**optional**)
- `LogPDiff`: The difference between parent and TP Log P values. Ignored if *both* `parent_LogP` and `TP_LogP` are specified. (**optional**)

Other columns are allowed, and will be included in the final object. Multiple TPs for a single parent are specified by repeating the value within `parent_` columns.

Similarly, the `transformations` argument to `generateTPsLogic` is used to specify custom rules to calculate transformation products. This should be a `data.frame` with the following columns:

- `transformation`: The name of the chemical transformation

- add The elements that are added by this reaction (e.g. "O").
- sub The elements that are removed by this reaction (e.g. "H2O").
- retDir The expected retention time direction relative to the parent (assuming a reversed phase like LC separation). Valid values are: '-1' (elutes before the parent), '1' (elutes after the parent) or '0' (no significant change or unknown).

## Parallelization

generateTPsBioTransformer uses multiprocessing to parallelize computations. Please see the parallelization section in the handbook for more details and [patRoam options](#) for configuration options.

## Source

The algorithm of generateTPsLogic is directly based on the work done by Schollee *et al.* (see references).

## Note

When the parents argument is a [compounds](#) object, the candidate library identifier is used in case the candidate has no defined compoundName.

## References

- Djombou-Feunang Y, Fiamoncini J, Gil-de-la-Fuente A, Greiner R, Manach C, Wishart DS (2019). "BioTransformer: a comprehensive computational tool for small molecule metabolism prediction and metabolite identification." *Journal of Cheminformatics*, **11**(1). doi: [10.1186/s1332101803245](#).
- Wicker J, Lorschbach T, Gutlein M, Schmid E, Latino D, Kramer S, Fenner K (2015). "enviPath - The environmental contaminant biotransformation pathway resource." *Nucleic Acids Research*, **44**(D1), D502–D508. doi: [10.1093/nar/gkv1229](#).
- Guha, R. (2007). 'Chemical Informatics Functionality in R'. *Journal of Statistical Software* 6(18)
- Schollee JE, Schymanski EL, Avak SE, Loos M, Hollender J (2015). "Prioritizing Unknown Transformation Products from Biologically-Treated Wastewater Using High-Resolution Mass Spectrometry, Multivariate Statistics, and Metabolic Logic." *Analytical Chemistry*, **87**(24), 12121–12129. doi: [10.1021/acs.analchem.5b02905](#).

## See Also

The [transformationProducts](#) class and derived classes [transformationProductsBT](#) and [transformationProductsLib](#) for methods to post-process TP data.

---

transformationProducts-class

*Base transformation products (TP) class*


---

## Description

Holds information for all TPs for a set of parents.

## Usage

```
## S4 method for signature 'transformationProducts'
parents(TPs)

## S4 method for signature 'transformationProducts'
products(TPs)

## S4 method for signature 'transformationProducts'
length(x)

## S4 method for signature 'transformationProducts'
names(x)

## S4 method for signature 'transformationProducts'
show(object)

## S4 method for signature 'transformationProducts,ANY,missing,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'transformationProducts,ANY,missing'
x[[i, j]]

## S4 method for signature 'transformationProducts'
x$name

## S4 method for signature 'transformationProducts'
as.data.table(x)

## S4 method for signature 'transformationProducts'
convertToSuspects(TPs, includeParents = FALSE)
```

## Arguments

|                |  |
|----------------|--|
| TPs, x, object | transformationProducts object to be accessed   |
| i              | For <code>[[</code> : A numeric or character value which is used to select parents by their index or name, respectively (for the order/names see <code>names()</code> ). |

|                |  |
|----------------|--|
|                | For [: Can also be logical to perform logical selection (similar to regular vectors). If missing all parents are selected. |
|                | For [[: should be a scalar value.  |
| ...            | Unused.  |
| drop, j        | ignored.   |
| name           | The parent name (partially matched).   |
| includeParents | If TRUE then parents are also included in the returned suspect list.   |

## Details

This class holds all generated data for transformation products for a set of parents. The class is virtual and derived objects are created by [TP generators](#).

The TP data in objects from this class include a `retDir` column. These are numeric values that hint what the chromatographic retention order of a TP might be compared to its parent: a value of `-1` means it will elute earlier, `1` it will elute later and `0` that there is no significant difference or the direction is unknown. These values are based on a typical reversed phase separation. When [generateTPsBioTransformer](#) or [generateTPsLibrary](#) was used to generate the data, the `retDir` values are based on calculated log P values of the parent and its TPs.

## Methods (by generic)

- `parents`: Accessor method for the parents slot of a `transformationProducts` class.
- `products`: Accessor method for the products slot.
- `length`: Obtain total number of transformation products.
- `names`: Obtain the names of all parents in this object.
- `show`: Show summary information for this object.
- `[`: Subset on parents.
- `[[`: Extracts a table with TPs for a parent.
- `$`: Extracts a table with TPs for a parent.
- `as.data.table`: Returns all TP data in a table.
- `convertToSuspects`: Converts this object to a suspect list that can be used as input for [screenSuspects](#).

## Slots

`parents` A [data.table](#) with metadata for all parents that have TPs in this object. Use the `parents` method for access.

`products` A list with [data.table](#) entries with TP information for each parent. Use the `products` method for access.

**S4 class hierarchy**

- [workflowStep](#)
  - [transformationProducts](#)
    - \* [transformationProductsBT](#)
    - \* [transformationProductsLibrary](#)
    - \* [transformationProductsLogic](#)

**See Also**

Derived classes [transformationProductsBT](#) and [transformationProductsLibrary](#) for specific algorithm methods and [TP-generation](#)

---

transformationProductsBT-class

*Class to store transformation products (TPs) predicted by BioTransformer*

---

**Description**

This class is used to store prediction results that are generated with [BioTransformer](#).

**Usage**

```
## S4 method for signature 'transformationProductsBT'
convertToMFDB(TPs, out, includeParents = FALSE)

## S4 method for signature 'transformationProductsBT'
filter(
  obj,
  removeParentIsomers = FALSE,
  removeTPIsomers = FALSE,
  removeDuplicates = FALSE,
  minSimilarity = NULL,
  negate = FALSE
)
```

**Arguments**

|                     |   |
|---------------------|---|
| out                 | The file name of the the output MetFrag database.                             |
| includeParents      | Set to TRUE to include the parents in the database.                           |
| obj, TPs            | transformationProductsBTs object to be accessed                               |
| removeParentIsomers | If TRUE then TPs with an equal formula as their parent (isomers) are removed. |



**removeTPIsomers**

If TRUE then all TPs with equal formula as any sibling TPs (isomers) are removed. Unlike `removeDuplicates`, *all* TP candidates are removed (including the first match). This filter automatically sets `removeDuplicates=TRUE` to avoid complete removal of TPs with equal structure.

**removeDuplicates**

If TRUE then the TPs of a parent with duplicate structures (SMILES) are removed. Such duplicates may occur when different transformation pathways yield the same TPs. The first TP candidate with duplicate structure will be kept.

**minSimilarity**

Minimum structure similarity ('0-1') that a TP should have relative to its parent. For details on how these similarities are calculated, see the [generateTPsBioTransformer](#) function. May be useful under the assumption that parents and TPs who have a high structural similarity, also likely have a high MS/MS spectral similarity (which can be evaluated after componentization with [generateComponentsTPs](#)).

**negate**

If TRUE then filters are performed in opposite manner.

**Details**

Objects from this class are generated with [generateTPsBioTransformer](#). This class is derived from the [transformationProducts](#) base class, please see its documentation for more details.

**Value**

`filter` returns a filtered `transformationProductsBT` object.

**Methods (by generic)**

- `convertToMFDB`: Exports this object as a '.csv' file that can be used as a MetFrag local database.
- `filter`: Performs rule-based filtering of the BioTransformer predictions. Useful to simplify and clean-up the data.

**S4 class hierarchy**

- [transformationProducts](#)
  - [transformationProductsBT](#)

**References**

Djoumbou-Feunang Y, Fiamoncini J, Gil-de-la-Fuente A, Greiner R, Manach C, Wishart DS (2019). "BioTransformer: a comprehensive computational tool for small molecule metabolism prediction and metabolite identification." *Journal of Cheminformatics*, **11**(1). doi: [10.1186/s1332101803245](#).

Wicker J, Lorschbach T, Gutlein M, Schmid E, Latino D, Kramer S, Fenner K (2015). "enviPath - The environmental contaminant biotransformation pathway resource." *Nucleic Acids Research*, **44**(D1), D502–D508. doi: [10.1093/nar/gkv1229](#).

**See Also**

The base class [transformationProducts](#) for more relevant methods and [TP-generation](#)

---

transformationProductsLibrary-class

*Class to store transformation products (TPs) obtained from a library*

---

**Description**

This class is used to store prediction results that are available in a TP library.

**Usage**

```
## S4 method for signature 'transformationProductsLibrary'
convertToMFDB(TPs, out, includeParents = FALSE)
```

**Arguments**

|                |   |
|----------------|---|
| TPs            | transformationProductsLibrary object to be accessed |
| out            | The file name of the the output MetFrag database.   |
| includeParents | Set to TRUE to include the parents in the database. |

**Details**

Objects from this class are generate with [generateTPsLibrary](#). This class is derived from the [transformationProducts](#) base class, please see its documentation for more details.

**Methods (by generic)**

- `convertToMFDB`: Exports this object as a ‘.csv’ file that can be used as a MetFrag local database.

**S4 class hierarchy**

- [transformationProducts](#)
  - [transformationProductsLibrary](#)

**See Also**

The base class [transformationProducts](#) for more relevant methods and [TP-generation](#)

---

|                    |  |
|--------------------|--|
| verifyDependencies | <i>Verifies if all dependencies are installed properly and instructs the user if this is not the case.</i> |
|--------------------|--|

---

**Description**

Verifies if all dependencies are installed properly and instructs the user if this is not the case.

**Usage**

```
verifyDependencies()
```

---

|         |  |
|---------|--|
| withOpt | <i>Temporarily changes package options</i> |
|---------|--|

---

**Description**

This function is inspired by `withr::with_options`: it can be used to execute some code where package options are temporarily changed. This function uses a shortened syntax, especially when changing options for `patRoan`.

**Usage**

```
withOpt(code, ..., prefix = "patRoan.")
```

**Arguments**

|        |   |
|--------|---|
| code   | The code to be executed.                                    |
| ...    | Named arguments with options to change.                     |
| prefix | A character that will be used to prefix given option names. |

**Examples**

```
## Not run:  
# Set max parallel processes to five while performing formula calculations  
withOpt(MP.maxProcs = 5, {  
  formulas <- generateFormulas(fGroups, "genform", ...)  
})  
  
## End(Not run)
```

---

workflowStep-class      *(Virtual) Base class for all workflow objects.*

---

## Description

All workflow objects (e.g. [featureGroups](#), [compounds](#), etc) are derived from this class. Objects from this class are never created directly.

## Usage

```
## S4 method for signature 'workflowStep'
algorithm(obj)

## S4 method for signature 'workflowStep'
as.data.table(x, keep.rownames = FALSE, ...)

## S4 method for signature 'workflowStep'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

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

## Arguments

obj, x, object    An object (derived from) this class.

keep.rownames    Ignored.

...                Method specific arguments. Please see the documentation of the derived classes.

row.names, optional  
                    Ignored.

## Methods (by generic)

- `algorithm`: Returns the algorithm that was used to generate an object.
- `as.data.table`: Summarizes the data in this object and returns this as a [data.table](#).
- `as.data.frame`: This method simply calls `as.data.table` and converts the result to a classic `data.frame`.
- `show`: Shows summary information for this object.

## Slots

`algorithm` The algorithm that was used to generate this object. Use the `algorithm` method for access.

**S4 class hierarchy**

- workflowStep
  - transformationProducts
    - \* transformationProductsBT
    - \* transformationProductsLibrary
    - \* transformationProductsLogic
  - features
    - \* featuresSet
    - \* featuresUnset
    - \* featuresFromFeatGroups
    - \* featuresConsensus
    - \* featuresBruker
    - \* featuresEnviPick
    - \* featuresKPIC2
    - \* featuresOpenMS
    - \* featuresSAFD
    - \* featuresSIRIUS
    - \* featuresBrukerTASQ
    - \* featuresXCMS
    - \* featuresXCMS3
  - featureGroups
    - \* featureGroupsSet
      - featureGroupsScreeningSet
    - \* featureGroupsUnset
    - \* featureGroupsScreening
      - featureGroupsSetScreeningUnset
    - \* featureGroupsBruker
    - \* featureGroupsConsensus
    - \* featureGroupsEnviMass
    - \* featureGroupsKPIC2
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    - \* componentsFeatures
      - componentsCliqueMS
      - componentsOpenMS
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      - componentsIntClust

- componentsSpecClust
- \* componentsSet
  - componentsNTSet
- \* componentsUnset
- \* componentsNT
  - componentsNTUnset
- \* componentsRC
- \* componentsTPs
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    - formulasSet
    - formulasUnset
  - \* compounds
    - compoundsConsensus
    - compoundsMF
    - compoundsSet
    - compoundsUnset
- MSPeakLists
  - \* MSPeakListsSet
  - \* MSPeakListsUnset

---

workflowStepSet-class (Virtual) base class for sets related workflow objects

---

## Description

This class is the base for many [sets workflows](#) related classes. This class is virtual, and therefore never created directly.

## Usage

```
## S4 method for signature 'workflowStepSet'
setObjects(obj)
```

```
## S4 method for signature 'workflowStepSet'
sets(obj)
```

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

## Arguments

obj, object      An object that is derived from workflowStepSet.

## Details

The most important purpose of this class is to hold data that is specific for a set. These *set objects* are typically objects with classes from a regular non-sets workflow (e.g. [components](#), [compounds](#)), and are used by the sets workflow object to e.g. form a consensus. Since the set objects may contain additional data, such as algorithm specific slots, it may in some cases be of interest to access them directly with the `setObjects` method (described below).

## Methods (by generic)

- `setObjects`: Accessor for the `setObjects` slot.
- `sets`: Returns the names for each set in this object.
- `show`: Shows summary information for this object.

## Slots

`setObjects` A list with the *set objects* (see the Details section). The list is named with the set names.

## S4 class hierarchy

- [workflowStepSet](#)
  - [componentsSet](#)
    - \* [componentsNTSet](#)
  - [featureGroupsScreeningSet](#)
  - [compoundsSet](#)
    - \* [compoundsConsensusSet](#)
  - [formulasSet](#)
    - \* [formulasConsensusSet](#)
  - [MSPeakListsSet](#)

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