

# Package ‘RAMClustR’

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**Type** Package

**Title** Mass Spectrometry Metabolomics Feature Clustering and Interpretation

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**Date** 2023-10-20

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**Imports** dynamicTreeCut, fastcluster, httr, jsonlite, e1071, gplots, pcaMethods, stringr, utils, webchem, ggplot2, methods

**Suggests** knitr, rmarkdown, xcms, testthat, patrick, MSnbase, InterpretMSSpectrum (>= 1.3.8), BiocManager, xml2, stringi, readxl, curl, rentrez

**License** GPL (>= 2)

**Description** A feature clustering algorithm for non-targeted mass spectrometric metabolomics data. This method is compatible with gas and liquid chromatography coupled mass spectrometry, including indiscriminant tandem mass spectrometry data <DOI:10.1021/ac501530d>.

**URL** <https://github.com/cbroeckl/RAMClustR>

**Encoding** UTF-8

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**VignetteBuilder** knitr

**NeedsCompilation** no

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---

 adap.to.rc

*adap.to.rc*


---

### Description

use pubchem rest and view APIs to retrieve structures, CIDs (if a name or inchikey is given), synonyms, and optionally vendor data, when available.

## Usage

```
adap.to.rc(  
  seq = "seq.csv",  
  spec.abund = "signal.csv",  
  msp = "spectra.msp",  
  annotations = "annotations.xlsx",  
  mzdec = 1,  
  min.score = 700,  
  manual.name = FALSE,  
  qc.tag = "qc",  
  blank.tag = "blank",  
  factor.names = c()  
)
```

## Arguments

seq	file name/path to sequence file - expect filenames in column 1 and sample names in column 2. filenames should match those in spec.abund
spec.abund	file name/path to adap-big export of signal intensities. .csv file expected
msp	file name/path to .msp file created by adap-big
annotations	file name/path to annotations .xlsx file. generally 'simple_export.xlsx'
mzdec	mz decimals to report for internal storage/reporting. generally we want 0 for adap kdb
min.score	700 (out of 1000) by default
manual.name	when looking up inchikey/names, should manual input be used to fill ambiguous names? generally recommend TRUE
qc.tag	a character string by which to recognize a sample as a qc sample. i.e. 'QC' or 'qc'.
blank.tag	a character string by which to recognize a sample as a blank sample. i.e. 'blank' or 'Blank'.
factor.names	factor names

## Details

useful for moving from chemical name to digital structure representation. greek letters are assumed to be 'UTF-8' encoded, and are converted to latin text before searching. if you are reading in your compound name list, do so with 'encoding' set to 'UTF-8'.

## Value

returns a ramclustR structured object suitable for down stream processing steps.

## Author(s)

Corey Broeckling

---

add_params	<i>add_params</i>
------------	-------------------

---

**Description**

add rc.feature.replace.na params in ramclustObj

**Usage**

```
add_params(ramclustObj, params, param_name)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
params	vector containing parameters to add
param_name	name of the parameter/step

**Value**

ramclustR object with rc.feature.replace.na params added.

---

annotate	<i>evaluate ramSearch, MSFinder mssearch, MSFinder Structure, MS-Finder Formula, and findmain output to annotate spectra of ramclustR object</i>
----------	--

---

**Description**

After running RAMSearch (msp) and MSFinder on .mat or .msp files, import the spectral search results

**Usage**

```
annotate(
  ramclustObj = NULL,
  standardize.names = FALSE,
  min.msms.score = 0.8,
  database.priority = NULL,
  database.priority.factor = 0.1,
  find.inchikey = TRUE,
  taxonomy.inchi = NULL,
  taxonomy.inchi.factor = 0.1,
  use.ri = TRUE,
  sri = 300,
  ri.na.factor = 0.6,
  reset = TRUE
)
```

**Arguments**

<code>ramclustObj</code>	R object - the ramclustR object which was used to write the .mat or .msp files
<code>standardize.names</code>	logical: if TRUE, use inchikey for standardized chemical name lookup ( <a href="http://cts.fiehnlab.ucdavis.edu/">http://cts.fiehnlab.ucdavis.edu/</a> )
<code>min.msms.score</code>	numerical: what is the minimum MSFinder similarity score acceptable. default = 6.5
<code>database.priority</code>	character. Formula assignment prioritization based on presence in one or more (structure) databases. Can be set to a single or multiple database names. must match database names as they are listed in MSFinder precisely. Can also be set to 'all' (note that MSFinder reports all databases matched, not just databases in MSFinder parameters). If any database is set, the best formula match to any of those databases is selected, rather than the best formula match overall. If NULL, this will be set to include all selected databases (from <code>ramclustObj\$msfinder.dbs</code> , retrieved from search output during <code>import.msfinder.formulas()</code> , when available) or 'all'.
<code>database.priority.factor</code>	numeric, between 0 and 1. 0.1 by default. The proportion by which scores for structures not in priority database are assessed
<code>find.inchikey</code>	logical. default = TRUE. use chemical translation service to try to look up inchikey for chemical name.
<code>taxonomy.inchi</code>	vector or data frame. Only when <code>rescore.structure = TRUE</code> . user can supply a vector of inchikeys. If used, structures which match first block of inchikey retain full score, while all other structures are penalized.
<code>taxonomy.inchi.factor</code>	numeric, between 0 and 1. 0.1 by default. The proportion by which scores for structures not in taxonomy.inchi vector are assessed
<code>use.ri</code>	logical. default = TRUE. If retention index is available in ramclustObj (set by <code>'rc.calibrate.ri'</code> ) and in library spectra from MSFinder, use RI similarity to rescore.
<code>sri</code>	numeric. sigma value for retention index. controls decay rate of retention index curve. decay rate between 0 and 1 exported, and multiplied by spectrum score, totalscore.
<code>ri.na.factor</code>	numeric. between 0 and 1. 0.5 by default. how should spectrum scores be treated when no retention index is available? NA values are replaced by retention index similarities of ri.na.factor when <code>use.ri = TRUE</code> .
<code>reset</code>	logical. If TRUE, removes any previously assigned annotations.

**Details**

this function imports the output from the MSFinder program to annotate the ramclustR object

**Value**

an updated ramclustR object, with the at `$msfinder.formula`, `$msfinder.formula.score`, `$ann`, and `$ann.conf` slots updated to annotated based on output from 1. ramsearch output, 2. msfinder

mssearch, 3. msfinder predicted structure, 4. msfinder predicted formula, and 5. interpretMSSpectrum inferred molecular weight, with listed order as priority.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

Tsugawa H, Kind T, Nakabayashi R, Yukihira D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem*. 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

<http://cts.fiehnlab.ucdavis.edu/static/download/CTS2-MS2015.pdf>

---

annotation.summary      *annotation.summary()*

---

**Description**

Write a .csv file containing a summary of the annotations in the ramclustR object.

**Usage**

```
annotation.summary(ramclustObj = NULL, outfile = NULL)
```

**Arguments**

ramclustObj	R object - the ramclustR object which was used to write the .mat or .msp files
outfile	file path/name of output csv summary file. if NULL (default) will be exported to spectra/annotaionSummary.csv

**Details**

this function exports a csv file summarizing annotation evidence for each compound

**Value**

nothing

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

*assign.z**assign.z*

---

**Description**

infer charge state of features in ramclustR object.

**Usage**

```
assign.z(  
  ramclustObj = NULL,  
  chargestate = c(1:5),  
  mzError = 0.02,  
  nEvents = 2,  
  minPercentSignal = 10,  
  assume1 = TRUE  
)
```

**Arguments**

ramclustObj	ramclustR object to annotate
chargestate	integer vector. vector of integers of charge states to look for. default = c(1:5)
mzError	numeric. the error allowed in charge state m/z filtering. absolute mass units
nEvents	integer. the number of isotopes necessary to assign a charge state > 1. default = 2.
minPercentSignal	numeric. the ratio of isotope signal (all isotopes) divided by total spectrum signal * 100 must be greater than minPercentSignal to evaluate charge state. Value should be between 0 and 100.
assume1	logical. when TRUE, m/z values for which no isotopes are found are assumed to be at z = 1.

**Details**

Annotation of ramclustR spectra. looks at isotope spacing for clustered features to infer charge state for each feature and a max charge state for each compound



**Value**

returns a ramclustR object. new slots holding:

zmax. vector with length equal to number of compounds. max charge state detected for that compound

fm. vector of inferred 'm', m/z value \* z value

fz. vector of inferred 'z' values based on analysis of isotopes in spectrum.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

change.annotation	<i>evaluate ramSearch, MSFinder mssearch, MSFinder Structure, MSFinder Formula, and findmain output to annotate spectra of ramclustR object</i>
-------------------	---

---

**Description**

After running RAMSearch (msp) and MSFinder on .mat or .msp files, import the spectral search results

**Usage**

```
change.annotation(  
  ramclustObj = NULL,  
  msfinder.dir = "C:/MSFinder/MSFINDER ver 3.22",  
  standardize.names = FALSE,  
  min.msms.score = 3.5,  
  database.priority = "all",  
  any.database.priority = TRUE,  
  reset = TRUE  
)
```

## Arguments

<code>ramclustObj</code>	R object - the ramclustR object which was used to write the .mat or .msp files
<code>msfinder.dir</code>	full path to MSFinder directory - used for naming refinement
<code>standardize.names</code>	logical: if TRUE, use inchikey for standardized chemical name lookup ( <a href="http://cts.fiehnlab.ucdavis.edu/">http://cts.fiehnlab.ucdavis.edu/</a> )
<code>min.msms.score</code>	numerical: what is the minimum MSFinder similarity score acceptable. default = 3.5
<code>database.priority</code>	character. Formula assignment prioritization based on presence in one or more databases. Can be set to a single or multiple database names. must match database names as they are listed in MSFinder precisely. Can also be set to 'all' (note that MSFinder reports all databases matched, not just selected databases). If any database is set, the best formula match to that (those) database(s) is selected, rather than the best formula match overall.
<code>any.database.priority</code>	logical. First priority in formula assignment is based on any of the 'database.priority' values. Secondary priority from all other databases (determined in original MSFinder search) if TRUE. If false, formula assignment score from MSFinder used independent of structure search results.
<code>reset</code>	logical. If TRUE, removes any previously assigned annotations.

## Details

this function imports the output from the MSFinder program to annotate the ramclustR object

## Value

an updated ramclustR object, with the at `$msfinder.formula`, `$msfinder.formula.score`, `$ann`, and `$ann.conf` slots updated to annotated based on output from 1. ramsearch output, 2. msfinder mssearch, 3. msfinder predicted structure, 4. msfinder predicted formula, and 5. interpretMSSpectrum inferred molecular weight, with listed order as priority.

## Author(s)

Corey Broeckling

## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

Tsugawa H, Kind T, Nakabayashi R, Yukihiro D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem.* 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

<http://cts.fiehnlab.ucdavis.edu/static/download/CTS2-MS2015.pdf>

---

checks

*checks*

---

### Description

check if MS data contains mz and rt, and if MSMS data is present feature names and sample names are identical

### Usage

```
checks(  
  ms1_featureDefinitions = NULL,  
  ms1_featureValues = NULL,  
  ms2_featureValues = NULL,  
  feature_names = NULL  
)
```

### Arguments

`ms1_featureDefinitions`  
dataframe with metadata with columns: mz, rt, feature names containing MS data

`ms1_featureValues`  
dataframe with rownames = sample names, colnames = feature names containing MS data

`ms2_featureValues`  
dataframe with rownames = sample names, colnames = feature names containing MSMS data

`feature_names` feature names extracted from the data

---

`check_arguments_filter.blanks`

*check\_arguments\_filter.blanks*

---

### Description

check provided arguments

**Usage**

```
check_arguments_filter.blanks(ramclustObj, sn)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
sn	numeric defines the ratio for 'signal'. i.e. sn = 3 indicates that signal intensity must be 3 fold higher in sample than in blanks, on average, to be retained.

---

```
check_arguments_filter.cv
```

```
check_arguments_filter.cv
```

---

**Description**

check provided arguments

**Usage**

```
check_arguments_filter.cv(ramclustObj, qc.tag)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
qc.tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type")). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.

---

```
check_arguments_replace.na
```

```
check_arguments_replace.na
```

---

**Description**

check provided arguments

**Usage**

```
check_arguments_replace.na(
  ramclustObj,
  replace.int,
  replace.noise,
  replace.zero
)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
replace.int	default = 0.1. proportion of minimum feature value to replace NA (or zero) values with
replace.noise	default = 0.1. proportion of replace.int value by which noise is added via 'jitter'
replace.zero	logical if TRUE, any zero values are replaced with noise as if they were NA values

---

compd.summary	<i>compd.summary</i>
---------------	----------------------

---

**Description**

a bit of reporting for compounds, quick access summary and plot (if available)

**Usage**

```
compd.summary(ramclustObj = NULL, compd = 1)
```

**Arguments**

ramclustObj	ramclustR object to annotate
compd	integer. compound number to report. i.e. 459.

**Details**

Reports name, annotation, retention time, number of features in spectrum, median and mean signal intensity, and if interpretMSSpectrum (do.findmain) has been run, plots an annotated MS level spectrum.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

compute\_do.sets      *compute\_do.sets*

---

**Description**

compute data frame to use in ramclustObj

**Usage**

```
compute_do.sets(ramclustObj)
```

**Arguments**

ramclustObj      ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

**Value**

vector which is used to select data frame to use in ramclustObj

---

compute\_SpecAbundAve      *compute\_SpecAbundAve*

---

**Description**

further aggregate by sample names for 'SpecAbundAve' dataset

**Usage**

```
compute_SpecAbundAve(ramclustObj = NULL)
```

**Arguments**

ramclustObj      ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

**Value**

ramclustR object with aggregate by sample names for 'SpecAbundAve' dataset

---

compute_wt_mean	<i>compute_wt_mean</i>
-----------------	------------------------

---

**Description**

compute weighted.mean intensity of feature in ms/msms level data

**Usage**

```
compute_wt_mean(data, global.min, fmz, ensure.no.na)
```

**Arguments**

data	feature in ms/msms level data
global.min	minimum intensity in ms/msms level data
fmz	feature retention time
ensure.no.na	logical: if TRUE, any 'NA' values in msint and/or msmsint are replaced with numerical values based on 10 percent of feature min plus noise. Used to ensure that spectra are not written with NA values.

**Value**

weighted.mean intensity of feature in ms/msms level data

---

create_ramclustObj	<i>create_ramclustObj</i>
--------------------	---------------------------

---

**Description**

create ramclustr Object

**Usage**

```
create_ramclustObj(
  ExpDes = NULL,
  input_history = NULL,
  MSdata = NULL,
  MSMSdata = NULL,
  frt = NULL,
  fmz = NULL,
  st = NULL,
  phenoData = NULL,
  feature_names = NULL,
  sample_names = NULL,
  xcmsOrd = NULL,
  ensure.no.na = TRUE
)
```

**Arguments**

ExpDes	either an R object created by R ExpDes object: data used for record keeping and labelling msp spectral output
input_history	input history
MSdata	dataframe containing MS Data
MSMSdata	dataframe containing MSMS Data
frt	feature retention time, in whatever units were fed in
fmz	feature retention time
st	numeric: sigma t - time similarity decay value
phenoData	dataframe containing phenoData
feature_names	feature names extracted from the data
sample_names	sample names extracted from the data
xcmsOrd	original xcms order of features, for back-referencing when necessary
ensure.no.na	logical: if TRUE, any 'NA' values in msint and/or msmsint are replaced with numerical values based on 10 percent of feature min plus noise. Used to ensure that spectra are not written with NA values.

**Value**

an ramclustR object. this object is formatted as an hclust object with additional slots for holding feature and compound data.

---

defineExperiment      *defineExperiment*

---

**Description**

Create an Experimental Design R object for record-keeping and msp output

**Usage**

```
defineExperiment(csv = FALSE, force.skip = FALSE)
```

**Arguments**

csv	logical or filepath. If csv = TRUE , csv template called "ExpDes.csv" will be written to your working directory. you will fill this in manually, ensuring that when you save you retain csv format. ramclustR will then read this file in and and format appropriately. If csv = FALSE, a pop up window will appear (in windows, at least) asking for input. If a character string with full path (and file name) to a csv file is given, this will allow you to read in a previously edited csv file.
force.skip	logical. If TRUE, ramclustR creates a pseudo-filled ExpDes object to enable testing of functionality. Not recommended for real data, as your exported spectra will be improperly labelled.



**Value**

an Exp Des R object which will be used for record keeping and writing spectra data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

define_samples	<i>define_samples</i>
----------------	-----------------------

---

**Description**

define samples in each set

**Usage**

```
define_samples(ramclustObj, tag)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.

**Value**

samples found using the tag

do.findmain

*do.findmain***Description**

Cluster annotation function: inference of 'M' - molecular weight of the compound giving rise to each spectrum - using the InterpretMSSpectrum::findMain function

**Usage**

```
do.findmain(
  ramclustObj = NULL,
  cmpd = NULL,
  mode = "positive",
  mzabs.error = 0.005,
  ppm.error = 10,
  ads = NULL,
  nls = NULL,
  scoring = "auto",
  plot.findmain = TRUE,
  writeMat = TRUE,
  writeMS = TRUE,
  use.z = TRUE
)
```

**Arguments**

ramclustObj	ramclustR object to annotate.
cmpd	integer: vector defining compound numbers to annotated. if NULL (default), all compounds
mode	character: "positive" or "negative"
mzabs.error	numeric: absolute mass deviation allowed, default = 0.01
ppm.error	numeric: ppm mass error _added_ to mzabs.error, default = 10
ads	character: vector of allowed adducts, i.e. c("[M+H]+"). if NULL, default positive mode values of H+, Na+, K+, and NH4+, as monomer, dimer, and trimer, are assigned. Negative mode include "[M-H]-", "[M+Na-2H]-", "[M+K-2H]-", "[M+CH2O2-H]-" as monomer, dimer, and trimer.
nls	character: vector of allowed neutral losses, i.e. c("[M+H-H2O]+"). if NULL, an extensive list derived from CAMERA's will be used.
scoring	character: one of 'imss', 'ramclustr', or 'auto'. default = 'auto'. see details.
plot.findmain	logical: should pdf polts be generated for evaluation? default = TRUE. PDF saved to working.directory/spectra
writeMat	logical: should individual .mat files (for MSFinder) be generated in a 'mat' subdirectory in the 'spectra' folder? default = TRUE.

writeMS	logical: should individual .ms files (for Sirius) be generated in a 'ms' subdirectory in the 'spectra' folder? default = TRUE. Note that no import functions are yet written for Sirius output.
use.z	logical: if you have previously run the 'assign.z' function from ramclustR, there will be a slot reflecting the feature mass after accounting for charge (fm) - if TRUE this is used instead of feature m/z (fmz) in interpreting MS data and exporting spectra for annotation.

## Details

a partially annotated ramclustR object. base structure is that of a standard R heirarchical clustering output, with additional slots described in ramclustR documentation (?ramclustR). New slots added after using the interpretMSSpectrum functionality include those described below.

## Value

\$M: The inferred molecular weight of the compound giving rise to the each spectrum

\$M.ppm: The ppm error of all the MS signals annotated, high error values should be considered 'red flags'.

\$M.ann: The annotated spectrum supporting the interpretation of M

\$use.findmain: Logical vector indicating whether findmain scoring (TRUE) or ramclustR scoring (FALSE) was used to support inference of M. By default, findmain scoring is used. When ramclustR scoring differs from findmain scoring, the scoring metric which predicts higher M is selected.

\$M.ramclustr: M selected using ramclustR scoring

\$M.ppm.ramclustr: ppm error of M selected using ramclustR scoring. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

\$M.ann.ramclustr: annotated spectrum supporting M using ramclustR scoring

\$M.nann.ramclustr: number of masses annotated using ramclustR scoring. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

\$M.space.ramclustr: the 'space' of scores between the best and second best ramclustR scores. Calculated as a ratio. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

\$M.findmain: M selected using findmain scoring

\$M.ppm.findmain: ppm error of M selected using findmain scoring. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

\$M.ann.findmain: annotated spectrum supporting M using findmain scoring

\$M.nann.findmain: number of masses annotated using findmain scoring. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

\$M.space.findmain: the 'space' of scores between the best and second best findmain scores. Calculated as a ratio. Used to resolve conflicts between ramclustR and findmain M assignment when scoring = auto.

## Author(s)

Corey Broeckling

## References

- Jaeger C, ... Lisee J. Compound annotation in liquid chromatography/high-resolution mass spectrometry based metabolomics: robust adduct ion determination as a prerequisite to structure prediction in electrospray ionization mass spectra. *Rapid Commun Mass Spectrom.* 2017 Aug 15;31(15):1261-1266. doi: 10.1002/rcm.7905. PubMed PMID: 28499062.
- Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem.* 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.
- Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem.* 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

export.msfinder.formulas

*export MSFinder formula prediction results in tabular format.*

---

## Description

After running MSFinder, results have been imported to the ramclustR object. This function exports as a .csv file for ease of viewing.

## Usage

```
export.msfinder.formulas(  
  ramclustObj = NULL,  
  export.all = FALSE,  
  output.directory = NULL  
)
```

## Arguments

ramclustObj     R object - the ramclustR object which was used to write the .mat or .msp files

export.all     logical: default = FALSE. If TRUE, export all columns, if FALSE, only columns 1: "exactmass"

output.directory     valid path: default = NULL. If NULL, results are exported to spectra/mat directory.

## Details

this function exports a .csv file containing all returned MSFinder molecular formula hypotheses. this file is saved (by default) to the working directory spectra/mat/ directory

**Value**

an updated ramclustR object, with the RC\$ann and RC\$ann.conf slots updated to annotated based on output from 1. ramsearch output, 2. msfinder mssearch, 3. msfinder predicted structure, 4. msfinder predicted formula, and 5. interpretMSSpectrum inferred molecular weight, with listed order as priority.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

Tsugawa H, Kind T, Nakabayashi R, Yukihira D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem*. 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

---

exportDataset

*exportDataset*

---

**Description**

export one of 'SpecAbund', 'SpecAbundAve', 'MSdata' or 'MSMSdata' from an RC object to csv

**Usage**

```
exportDataset(  
  ramclustObj = NULL,  
  which.data = "SpecAbund",  
  label.by = "ann",  
  appendFactors = TRUE  
)
```

**Arguments**

ramclustObj	ramclustR object to export from
which.data	name of dataset to export. SpecAbund, SpecAbundAve, MSdata, or MSMSdata
label.by	either 'ann' or 'cmpd', generally. name of ramclustObj slot used as csv header for each column (compound)
appendFactors	logical. If TRUE (default) the factor data frame is appended to the left side of the dataset.

**Details**

Useful for exporting the processed signal intensity matrix to csv for analysis elsewhere.

**Value**

nothing is returned. file exported as csv to 'datasets/\*.csv'

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

filter\_blanks

*filter\_blanks*

---

**Description**

filter blanks

**Usage**

```
filter_blanks(ramclustObj, keep, d1)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
keep	union of which signal is at least 3x larger, output of filter_signal()
d1	MS Data

**Value**

ramclustObj object with feature.filter.blanks

---

filter\_good\_features    *filter\_good\_features*

---

**Description**

filter to keep only 'good' features

**Usage**

```
filter_good_features(ramclustObj, keep)
```

**Arguments**

ramclustObj    ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)  
keep            features to keep. output of find\_good\_features().

**Value**

ramclustR object filtered to keep only 'good' features

---

filter\_signal            *filter\_signal*

---

**Description**

filter signal

**Usage**

```
filter_signal(ms.qc.mean, ms.blank.mean, sn)
```

**Arguments**

ms.qc.mean        ms qc mean signal intensities  
ms.blank.mean    ms blank mean signal intensities  
sn                numeric defines the ratio for 'signal'. i.e. sn = 3 indicates that signal intensity must be 3 fold higher in sample than in blanks, on average, to be retained.

**Value**

union of which signal is at least 3x larger

---

findfeature	<i>findfeature</i>
-------------	--------------------

---

### Description

see if any features match a given mass, and whether they are plausibly M0

### Usage

```
findfeature(
  ramclustObj = NULL,
  mz = NULL,
  mztol = 0.02,
  rt = NULL,
  rttol = 2,
  iso.rttol = 2,
  zmax = 6,
  m.check = TRUE
)
```

### Arguments

ramclustObj	R object: the ramclustR object to explore
mz	numeric: mz value to search for
mztol	numeric: absolute mass tolerance around mz
rt	numeric: optional rt value to search for (generally in seconds, though use whatever units your data is in)
rttol	numeric: absolute retention time tolerance around rt.
iso.rttol	numeric: when examining isotope patterns, feature retention time tolerance around features matching mz +/- mztol
zmax	integer: maximum charge state to consider. default is 6.
m.check	logical: check whether the matching masses are plausibly M0. That is, we look for ions 1 proton mass (from charge state 1:zmax) below the target m/z at the same time that have intensities consistent with target ion being a non-M0 isotope.

### Details

a convenience function to perform a targeted search of all features for a mass of interest. Also performs a crude plausibility check as to whether the matched feature could be M0, based on the assumption of approximately 1 carbon per 17 m/z units and natural isotopic abundance of 1.1

### Value

returns a table to the console listing masses which match, their retention time and intensity, and whether it appears to be plausible as M0



**Author(s)**

Corey Broeckling

---

findmass	<i>findmass</i>
----------	-----------------

---

**Description**

see if any features match a given mass, and whether they are plausibly M0

**Usage**

```
findmass(  
  ramclustObj = NULL,  
  mz = NULL,  
  mztol = 0.02,  
  rttol = 2,  
  zmax = 6,  
  m.check = TRUE  
)
```

**Arguments**

ramclustObj	R object: the ramclustR object to explore
mz	numeric: mz value to search for
mztol	numeric: absolute mass tolerance around mz
rttol	numeric: when examining isotope patterns, feature retention time tolerance around features matching mz +/- mztol
zmax	integer: maximum charge state to consider. default is 6.
m.check	logical: check whether the matching masses are plausibly M0. That is, we look for ions 1 proton mass (from charge state 1:zmax) below the target m/z at the same time that have intensities consistent with target ion being a non-M0 isotope.

**Details**

a convenience function to perform a targeted search of all features for a mass of interest. Also performs a crude plausibility check as to whether the matched feature could be M0, based on the assumption of approximately 1 carbon per 17 m/z units and natural isotopic abundance of 1.1

**Value**

returns a table to the console listing masses which match, their retention time and intensity, and whether it appears to be plausible as M0

**Author(s)**

Corey Broeckling

---

 find\_good\_features     *find\_good\_features*


---

**Description**

find 'good' features, acceptable CV at either MS or MSMS level results in keeping

**Usage**

```
find_good_features(ramclustObj, do.sets, max.cv, qc)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
do.sets	select data frame to use.
max.cv	numeric maximum allowable cv for any feature. default = 0.5
qc	QC samples found by define_samples

**Value**

ramclustR object  
features to keep

---

 fooddb2msfinder     *foodb2msfinder*


---

**Description**

convenience function for converting FoodDB database export format to MSFinder custom database import format. Before running this, please have downloaded .csv files from FoodDB with the appropriate Display Field Headers (see details)

**Usage**

```
fooddb2msfinder(
  foodb.files = NULL,
  out.dir = NULL,
  out.name = "FoodDB_for_MSFinder.txt"
)
```

**Arguments**

foodb.files	default = NULL, if path is set, will read automatically. If NULL, directory selection by user.
out.dir	default = NULL. Can set to existing directory with full path name. If NULL, directory selection by user.
out.name	default = "FoodDB_for_MSFinder.txt".

**Details**

Input file(s) should be csv formatted, with required headers of 'Name', 'Smiles', 'Inchikey', 'Chemical formula', and 'Mono mass' - case sensitive. Output will be in tab delimited text format in directory of choice.

**Value**

Nothing is returned - output file written to directory set by 'out.dir' and name set by 'out.name'

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

get.taxon.cids	<i>get.taxon.cids</i>
----------------	-----------------------

---

**Description**

use pubchem rest to retrieve pubchem CIDS known to be found in a given species. NCBI taxid should be used as input. i.e. Homo sapiens subsp. 'Denisova' is taxid 741158

**Usage**

```
get.taxon.cids(  
  taxid = NULL,  
  taxstring = NULL,  
  sub.taxa.n = 1000,  
  get.inchikey = TRUE  
)
```

**Arguments**

taxid	integer NCBI taxid for the taxon to search.
taxstring	taxonomy string for the taxon of interest.
sub.taxa.n	integer value for the number of subtaxa to consider. Note that if the sub.taxa.n value is less than the available number of subtaxa, only the first sub.taxa.n values, as reported by rentrez, are returned. If you require specific subtaxa, you should call those taxids explicitly to ensure those results are returned.
get.inchikey	logical whether to get the InChIKeys as well (default TRUE).

**Details**

this function enables return of a list of pubchem CIDs which can be used for prioritizing annotations. If a genus level taxid is selected, setting the sub.taxa.n option > 0 will return metabolites associated with that taxid and all (assuming n is large enough) subtaxa. i.e. setting taxid to 9605 (genus = 'Homo') will return metabolites associated with Homo sapiens, Homo heidelbergensis, Homo sapiens subsp. 'Denisova', etc.

**Value**

returns a vector of integer pubchem cids (and optionally inchikeys if get.inchikey was set to TRUE)

**Author(s)**

Corey Broeckling

---

getData

*getData*

---

**Description**

retrieve and parse sample names, retrieve metabolite data. returns as list of two data frames

**Usage**

```
getData(  
  ramclustObj = NULL,  
  which.data = "SpecAbund",  
  delim = "-",  
  cmpdlabel = "cmpd",  
  filter = FALSE  
)
```

**Arguments**

ramclustObj	ramclustR object to retrieve data from
which.data	character; which dataset (SpecAbund or SpecAbundAve) to reference
delim	character; "-" by default - the delimiter for parsing sample names to factors
cmpdlabel	= "cmpd"; label the data with the annotation. can also be set to 'ann' for column names assigned as annotatins.
filter	= TRUE; logical, if TRUE, checks for \$cmpd.use slot generated by rc.cmpd.cv.filter() function, and only gets acceptable compounds.

**Details**

convenience function for parsing sample names and returning a dataset.

**Value**

returns a list of length 3: \$design is the experimental sample factors after parsing by the delim, \$data is the dataset, \$full.data is merged \$des and \$data data.frames.

**Author(s)**

Corey Broeckling

---

getSmilesInchi	<i>getSmilesInchi</i>
----------------	-----------------------

---

**Description**

use PubChem API to look up full smiles and inchi notation for each inchikey

**Usage**

```
getSmilesInchi(ramclustObj = NULL, inchikey = NULL, ignore.stereo = TRUE)
```

**Arguments**

ramclustObj	ramclustR object to look up smiles and inchi for each inchikey (without a smiles/inchi). Must provide one of ramclustObj or inchikey.
inchikey	character vector of inchikey strings. Must provide one of ramclustObj or inchikey.
ignore.stereo	logical. default = TRUE. If the Pubchem databases does not have the full inchikey string, should we search by the first (non-stereo) block of the inchikey? When true, returns the first pubchem match to the inchikey block one string. If the full inchikey is present, that is used preferentially.

**Details**

The \$inchikey slot is used to look up parameters from pubchem. PubChem CID, a pubchem URL, smiles (canonical) and inchi are returned. if smiles and inchi slots are already present (from MS-Finder, for example) pubchem smiles and inchi are used to fill in missing values only, not replace.

**Value**

returns a ramclustR object. new vector of \$smiles and \$inchi with length equal to number of compounds.

**Author(s)**

Corey Broeckling

**References**

Kim S, Thiessen PA, Bolton EE, Bryant SH. PUG-SOAP and PUG-REST: web services for programmatic access to chemical information in PubChem. Nucleic Acids Res. 2015;43(W1):W605-11.

---

get\_ExpDes

*get\_ExpDes*

---

**Description**

get Experimental Design

**Usage**

```
get_ExpDes(csv.in)
```

**Arguments**

csv.in            Experimental Design read from csv

**Value**

list containing design and instrument

---

```
get_instrument_platform
      get_instrument_platform
```

---

**Description**

get instrument platform

**Usage**

```
get_instrument_platform(design)
```

**Arguments**

design                    data frame containing Experimental Design

**Value**

instrument platform

---

```
import.adap.kdb            import.adap.kdb
```

---

**Description**

use pubchem rest and view APIs to retrieve structures, CIDs (if a name or inchikey is given), synonyms, and optionally vendor data, when available.

**Usage**

```
import.adap.kdb(
  ramclustObj = NULL,
  annotations = NULL,
  min.score = 700,
  annotate = TRUE,
  manual.name = TRUE
)
```

**Arguments**

ramclustObj	ramclustR object to be annotated.
annotations	file name/path to annotations .xlsx file. generally 'simple_export.xlsx'
min.score	700 (out of 1000) by default
annotate	logical. TRUE by default. for now please leave default
manual.name	when looking up inchikey/names, should manual input be used to fill ambiguous names? generally recommend TRUE

**Details**

useful for moving from chemical name to digital structure representation. greek letters are assumed to be 'UTF-8' encoded, and are converted to latin text before searching. if you are reading in your compound name list, do so with 'encoding' set to 'UTF-8'.

**Value**

returns a ramclustR structured object suitable for down stream processing steps.

**Author(s)**

Corey Broeckling

---

import.msfinder.formulas

*import.msfinder.formulas*

---

**Description**

After running MSFinder on .mat or .msp files, import the formulas that were predicted and their scores

**Usage**

```
import.msfinder.formulas(ramclustObj = NULL, mat.dir = NULL, msp.dir = NULL)
```

**Arguments**

ramclustObj	R object - the ramclustR object which was used to write the .mat or .msp files
mat.dir	optional path to .mat directory
msp.dir	optional path to .msp directory

**Details**

this function imports the output from the MSFinder program to support annotation of the ramclustR object

**Value**

new slot at \$msfinder.formula.details

**Author(s)**

Corey Broeckling



## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

Tsugawa H, Kind T, Nakabayashi R, Yukihiro D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem*. 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

---

```
import.msfinder.mssearch
```

```
import.MSFinder.mssearch
```

---

## Description

After running MSFinder on .mat or .msp files, import the spectral search results

## Usage

```
import.msfinder.mssearch(  
  ramclustObj = NULL,  
  mat.dir = NULL,  
  msp.dir = NULL,  
  dir.extension = ".mssearch"  
)
```

## Arguments

ramclustObj	R object - the ramclustR object which was used to write the .mat or .msp files
mat.dir	optional path to .mat directory
msp.dir	optional path to .msp directory
dir.extension	optional directory name code specifying subset of results to use. Useful if running MSFinder from the command line for both spectral searching and interpretation.

## Details

this function imports the output from the MSFinder program to annotate the ramclustR object

## Value

an updated ramclustR object, with new slots at \$msfinder.mssearch.details and \$msfinder.mssearch.scores

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 27560453.

Tsugawa H, Kind T, Nakabayashi R, Yukihiro D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem*. 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

---

`import.msfinder.structures``write.methods`

---

**Description**

write RAMClustR processing methods and citations to text file

**Usage**`import.msfinder.structures(ramclustObj = NULL, mat.dir = NULL, msp.dir = NULL)`**Arguments**

<code>ramclustObj</code>	R object - the ramclustR object which was used to write the .mat or .msp files
<code>mat.dir</code>	directory in which to look for mat file MSFinder output - by default the /spectra/mat in the working directory
<code>msp.dir</code>	directory in which to look for msp file MSFinder output - by default the /spectra/msp in the working directory

**Details**

this function exports a file called `ramclustr_methods.txt` which contains the processing history, parameters used, and relevant citations.

**Value**

an annotated ramclustR object  
nothing - new file written to working director

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

import.sirius	<i>import.sirius</i>
---------------	----------------------

---

**Description**

After running Sirius on .ms files, import the annotation results

**Usage**

```
import.sirius(ramclustObj = NULL, ms.dir = NULL, ion.mode = NULL)
```

**Arguments**

ramclustObj	R object - the ramclustR object which was used to write the .mat or .msp files
ms.dir	optional path to .mat directory. default = "spectra/ms/out" subdirectory in working directory
ion.mode	specify either "N" for negative ionization mode or "P" for positive ionization mode

**Details**

this function imports the output from the Sirius program to annotate the ramclustR object

**Value**

an updated ramclustR object, with new slots at \$msfinder.sirius

**Author(s)**

Corey Broeckling

## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

impRamSearch

*impRamSearch*

---

## Description

import ramsearch output for annotating an RC object

## Usage

```
impRamSearch(ramclustObj = NULL, ramsearchout = "spectra/results.rse")
```

## Arguments

ramclustObj     ramclustR object to annotate  
ramsearchout   path to .rse file to import

## Details

Annotation of ramclustR exported .msp spectra is accomplished using RAMSearch. Exported ramsearch annotations (.rse) can be imported with this function

## Value

returns a ramclustR object. new slots holding .rse data

## Author(s)

Corey Broeckling

## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

```
manual.annotation.template  
    manual.annotation.template
```

---

### Description

export a .csv formatted template for manually editing MSFinder annotations

### Usage

```
manual.annotation.template(  
  ramclustObj = NULL,  
  outfile = "manual.annotation.template.csv"  
)
```

### Arguments

ramclustObj     ramclustR object to annotate  
outfile         output file directory and name. default = 'manual.annotation.template.csv'

### Details

While unsupervised annotation is rapid and objective, subjective knowledge can be used to improve annotations. This function writes a template file containing compound name, computationally assigned inchikey, and an empty column for your manually inferred inchikey. Upon completion of manual annotation, you can reimport this file and update your ramclustR object to reflect your manual input.

### Author(s)

Corey Broeckling

### References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Tsugawa H, Kind T, Nakabayashi R, Yukihiro D, Tanaka W, Cajka T, Saito K, Fiehn O, Arita M. Hydrogen Rearrangement Rules: Computational MS/MS Fragmentation and Structure Elucidation Using MS-FINDER Software. *Anal Chem*. 2016 Aug 16;88(16):7946-58. doi: 10.1021/acs.analchem.6b00770. Epub 2016 Aug 4. PubMed PMID: 27419259.

mean\_signal\_intensities  
*mean\_signal\_intensities*

---

**Description**

calculate MS mean signal intensities

**Usage**

```
mean_signal_intensities(data, sample)
```

**Arguments**

data	MS/MSMS data
sample	sample found using the tag, output of define_samples()

**Value**

mean signal intensities

---

mergeRCobjects      *mergeRCobjects*

---

**Description**

merge two ramclustR objects

**Usage**

```
mergeRCobjects(  
  ramclustObj.1 = NULL,  
  ramclustObj.2 = NULL,  
  mztol = 0.02,  
  rttol = 30,  
  course.rt.adj = NULL,  
  mzwt = 2,  
  rtwt = 1,  
  intwt = 3  
)
```

**Arguments**

ramclustObj.1	ramclustR object 1: this object will be the base for the new object. That is all the features from ramclustObj.1 will be retained.
ramclustObj.2	ramclustR object 2: this object will mapped and appended to ramclustObj.1. That is only features which appear consistent with those from ramclustObj.1 will be retained.
mztol	numeric: absolute mass tolerance around mz
rttol	numeric: feature retention time tolerance. Value set by this option will be used during the initial anchor mapping phase. Two times the standard error of the rt loess correction will be used for the full mapping.
course.rt.adj	numeric: default = NULL. optional approximate retention time shift between ramclustObj.1 and ramclustObj.2. i.e if the retention time of ramclustObj.1 is on average 15 seconds longer than that of ramclustObj.2, enter '15'. if 1 is less than 2, enter a negative number. This is applied before mapping to enable a smaller 'rttol' value to be used.
mzwt	numeric: when mapping features, weighting value used for similarities between feature mass values (see rtwt, intwt)
rtwt	numeric: when mapping features, weighting value used for similarities between feature retention time values (see mzwt, intwt)
intwt	numeric: when mapping features, weighting value used for similarities between ranked signal intensity values (see rtwt, mzwt)

**Details**

Two ramclustR objects are merged with this function, mapping features between them. The first (ramclustObj.1) object use used as the template - all data in it is retained. ramclustObj.2 is mapped to ramclustObj.1 feature by feature - only mapped features are retained. A new ramclustObj is returned, with a new SpecAbund dataset with the same column number as the ramclustObj.1\$SpecAbund set.

**Value**

returns a ramclustR object. All values from ramclustObj.1 are retained. SpecAbund dataset from ramclustObj.1 is moved to RC\$SpecAbund.1, where RC is the new ramclustObj.

**Author(s)**

Corey Broeckling

---

```
normalized_data_batch_qc  
    normalized_data_batch_qc
```

---

## Description

normalize data using batch.qc

## Usage

```
normalized_data_batch_qc(  
  data = NULL,  
  batch = NULL,  
  order = NULL,  
  qc = NULL,  
  qc.inj.range = 20,  
  output.plot = FALSE  
)
```

## Arguments

data	feature in ms/msms level data
batch	integer vector with length equal to number of injections in xset or csv file or dataframe
order	integer vector with length equal to number of injections in xset or csv file or dataframe
qc	logical vector with length equal to number of injections in xset or csv file or dataframe
qc.inj.range	integer: how many injections around each injection are to be scanned for presence of QC samples when using batch.qc normalization? A good rule of thumb is between 1 and 3 times the typical injection span between QC injections. i.e. if you inject QC ever 7 samples, set this to between 7 and 21. smaller values provide more local precision but make normalization sensitive to individual poor outliers (though these are first removed using the boxplot function outlier detection), while wider values provide less local precision in normalization but better stability to individual peak areas.
output.plot	logical set to TRUE to store plots

## Value

normalized data.



---

normalized\_data\_tic     *normalized\_data\_tic*

---

**Description**

normalize data using TIC

**Usage**

```
normalized_data_tic(ramclustObj = NULL)
```

**Arguments**

ramclustObj     ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

**Value**

ramclustR object with total extracted ion normalized data.

---

order\_datasets     *order\_datasets*

---

**Description**

order the datasets first by batch and run order

**Usage**

```
order_datasets(order = NULL, batch = NULL, qc = NULL, data = NULL)
```

**Arguments**

order	integer vector with length equal to number of injections in xset or csv file or dataframe
batch	integer vector with length equal to number of injections in xset or csv file or dataframe
qc	logical vector with length equal to number of injections in xset or csv file or dataframe
data	feature in ms/msms level data

**Value**

ordered feature in ms/msms level data, order, batch, qc

---

`ramclustR`*ramclustR*

---

### Description

Main clustering function for grouping features based on their analytical behavior.

### Usage

```
ramclustR(  
  xcmsObj = NULL,  
  ms = NULL,  
  pheno_csv = NULL,  
  idsms = NULL,  
  taglocation = "filepaths",  
  MStag = NULL,  
  idMSMStag = NULL,  
  featdelim = "_",  
  timepos = 2,  
  st = NULL,  
  sr = NULL,  
  maxt = NULL,  
  deepSplit = FALSE,  
  blocksize = 2000,  
  mult = 5,  
  hmax = NULL,  
  sampNameCol = 1,  
  collapse = TRUE,  
  mspout = TRUE,  
  ExpDes = NULL,  
  normalize = "TIC",  
  qc.inj.range = 20,  
  order = NULL,  
  batch = NULL,  
  qc = NULL,  
  minModuleSize = 2,  
  linkage = "average",  
  mzdec = 3,  
  cor.method = "pearson",  
  rt.only.low.n = TRUE,  
  replace.zeros = TRUE  
)
```

### Arguments

`xcmsObj` `xcmsObject`: containing grouped feature data for clustering by `ramclustR`

ms	filepath: optional csv input. Features as columns, rows as samples. Column header mz_rt
pheno_csv	filepath: optional csv input containing phenoData
idmsms	filepath: optional idMSMS / MSe csv data. same dim and names as ms required
taglocation	character: "filepaths" by default, "phenoData[,1]" is another option. refers to xcms slot
MStag	character: character string in 'taglocation' to designat MS / MSe files e.g. "01.cdf"
idMSMStag	character: character string in 'taglocation' to designat idMSMS / MSe files e.g. "02.cdf"
featdelim	character: how feature mz and rt are delimited in csv import column header e.g. "="
timepos	integer: which position in delimited column header represents the retention time (csv only)
st	numeric: sigma t - time similarity decay value
sr	numeric: sigma r - correlational similarity decay value
maxt	numeric: maximum time difference to calculate retention similarity for - all values beyond this are assigned similarity of zero
deepSplit	logical: controls how aggressively the HCA tree is cut - see ?cutreeDynamicTree
blocksize	integer: number of features (scans?) processed in one block =1000,
mult	numeric: internal value, can be used to influence processing speed/ram usage
hmax	numeric: precut the tree at this height, default 0.3 - see ?cutreeDynamicTree
sampNameCol	integer: which column from the csv file contains sample names?
collapse	logical: reduce feature intensities to spectrum intensities?
mspout	logical: write msp formatted spectra to file?
ExpDes	either an R object created by R ExpDes object: data used for record keeping and labelling msp spectral output
normalize	character: either "none", "TIC", "quantile", or "batch.qc" normalization of feature intensities. see batch.qc overview in details.
qc.inj.range	integer: how many injections around each injection are to be scanned for presence of QC samples when using batch.qc normalization? A good rule of thumb is between 1 and 3 times the typical injection span between QC injections. i.e. if you inject QC ever 7 samples, set this to between 7 and 21. smaller values provide more local precision but make normalization sensitive to individual poor outliers (though these are first removed using the boxplot function outlier detection), while wider values provide less local precision in normalization but better stability to individual peak areas.
order	integer vector with length equal to number of injections in xset or csv file
batch	integer vector with length equal to number of injections in xset or csv file
qc	logical vector with length equal to number of injections in xset or csv file.
minModuleSize	integer: how many features must be part of a cluster to be returned? default = 2
linkage	character: heirarchical clustering linkage method - see ?hclust

mzdec	integer: number of decimal places used in printing m/z values
cor.method	character: which correlational method used to calculate 'r' - see ?cor
rt.only.low.n	logical: default = TRUE At low injection numbers, correlational relationships of peak intensities may be unreliable. by default ramclustR will simply ignore the correlational r value and cluster on retention time alone. if you wish to use correlation with at n < 5, set this value to FALSE.
replace.zeros	logical: TRUE by default. NA, NaN, and Inf values are replaced with zero, and zero values are sometimes returned from peak peaking. When TRUE, zero values will be replaced with a small amount of noise, with noise level set based on the detected signal intensities for that feature.

## Details

Main clustering function output - see citation for algorithm description or vignette('RAMClustR') for a walk through. batch.qc. normalization requires input of three vectors (1) batch (2) order (3) qc. This is a feature centric normalization approach which adjusts signal intensities first by comparing batch median intensity of each feature (one feature at a time) QC signal intensity to full dataset median to correct for systematic batch effects and then secondly to apply a local QC median vs global median sample correction to correct for run order effects.

## Value

\$featclus: integer vector of cluster membership for each feature

\$frt: feature retention time, in whatever units were fed in (xcms uses seconds, by default)

\$fmz: feature retention time, reported in number of decimal points selected in ramclustR function

\$xcmsOrd: the original XCMS (or csv) feature order for cross referencing, if need be

\$clrt: cluster retention time

\$clrtsd: retention time standard deviation of all the features that comprise that cluster

\$nfeat: number of features in the cluster

\$nsing: number of 'singletons' - that is the number of features which clustered with no other feature

\$ExpDes: the experimental design object used when running ramclustR. List of two dataframes.

\$cmpd: compound name. C#### are assigned in order of output by dynamicTreeCut. Compound with the most features is classified as C0001...

\$ann: annotation. By default, annotation names are identical to 'cmpd' names. This slot is a placeholder for when annotations are provided

\$MSdata: the MSdataset provided by either xcms or csv input

\$MSMSdata: the (optional) MSe/idMSMS dataset provided by either xcms or csv input

\$SpecAbund: the cluster intensities after collapsing features to clusters

\$SpecAbundAve: the cluster intensities after averaging all samples with identical sample names

- 'spectra' directory is created in the working directory. In this directory a .msp is (optionally) created, which contains the spectra for all compounds in the dataset following clustering. if MSe/idMSMS data are provided, they are listed with the same compound name as the MS spectrum, with the collision energy provided in the ExpDes object provided to distinguish low from high CE spectra.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

**Examples**

```
## Choose input file with feature column names `mz_rt` (expected by default).
## Column with sample name is expected to be first (by default).
## These can be adjusted with the `featdelim` and `sampNameCol` parameters.
wd <- getwd()
filename <- system.file("extdata", "peaks.csv", package = "RAMClustR", mustWork = TRUE)
print(filename)
head(data.frame(read.csv(filename)), c(6L, 5L))

## If the file contains features from MS1, assign those to the `ms` parameter.
## If the file contains features from MS2, assign those to the `idmsms` parameter.
## If you ran `xcms` for the feature detection, the assign the output to the `xcmsObj` parameter.
## In this example we use a MS1 feature table stored in a `csv` file.
setwd(tempdir())
ramclustobj <- ramclustR(ms = filename, st = 5, maxt = 1, blocksize = 1000)

## Investigate the deconvoluted features in the `spectra` folder in MSP format
## or inspect the `ramclustobj` for feature retention times, annotations etc.
print(ramclustobj$ann)
print(ramclustobj$nfeat)
print(ramclustobj$SpecAbund[, 1:6])
setwd(wd)
```

---

rc.calibrate.ri

*rc.calibrate.ri*

---

**Description**

extractor for xcms objects in preparation for clustering

**Usage**

```
rc.calibrate.ri(ramclustObj = NULL, calibrant.data = "", poly.order = 3)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
calibrant.data	character vector defining the file path/name to a csv file containing columns including 'rt', and 'ri'. Alternatively, a data.frame with those column names (case sensitive)
poly.order	integer default = 3. polynomial order used to fit rt vs ri data, and calculate ri for all feature and metabolite rt values. poly.order should be appreciably smaller than the number of calibrant points.

**Details**

This function generates a new slot in the ramclustR object for retention index. Calibration is performed using a polynomial fit of order poly.order. It is the user's responsibility to ensure that the number and span of calibrant points is sufficient to calibrate the full range of feature and compound retention times. i.e. if the last calibration point is at 1000 seconds, but the last eluting peak is at 1300 seconds, the calibration will be very poor for the late eluting compound.

**Value**

ramclustR object with retention index assigned for features (\$fri) and compounds (\$cri).

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem.* 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.cmpd.filter.blanks *rc.cmpd.filter.blanks*

---

**Description**

used to remove compounds which are found at similar intensity in blank samples. Only applied after clustering. see also rc.feature.filter.blanks for filtering at the feature level (only done before clustering).

**Usage**

```
rc.cmpd.filter.blanks(  
  ramclustObj = NULL,  
  qc.tag = "QC",  
  blank.tag = "blank",  
  sn = 3,  
  remove.blanks = TRUE  
)
```

**Arguments**

ramclustObj	ramclustObj containing SpecAbund dataframe.
qc.tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.
blank.tag	see 'qc.tag', but for blanks to use as background.
sn	numeric defines the ratio for 'signal'. i.e. sn = 3 indicates that signal intensity must be 3 fold higher in sample than in blanks, on average, to be retained.
remove.blanks	logical. TRUE by default. this removes any recognized blanks samples from the SpecAbund sets after they are used to filter contaminant compounds

**Details**

This function removes compounds which contain signal in QC samples comparable to blanks.

**Value**

ramclustR object with normalized data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.cmpd.filter.cv      *rc.cmpd.filter.cv*

---

### Description

extractor for xcms objects in preparation for clustering

### Usage

```
rc.cmpd.filter.cv(ramclustObj = NULL, qc.tag = "QC", max.cv = 0.5)
```

### Arguments

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
qc.tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.
max.cv	numeric maximum allowable cv for any feature. default = 0.3

### Details

This function offers normalization by total extracted ion signal. it is recommended to first run 'rc.feature.filter.blanks' to remove non-sample derived signal.

### Value

ramclustR object with total extracted ion normalized data.

### Author(s)

Corey Broeckling

### References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.



---

```
rc.cmpd.get.classyfire  
  getClassyFire
```

---

**Description**

use classyfire web API to look up full ClassyFire hierarchy for each inchikey

**Usage**

```
rc.cmpd.get.classyfire(  
  ramclustObj = NULL,  
  inchikey = NULL,  
  get.all = TRUE,  
  max.wait = 10,  
  posts.per.minute = 5  
)
```

**Arguments**

ramclustObj	ramclustR object to ClassyFy. Must supply one of either ramclustObj or inchikey (see below)
inchikey	vector of text inchikeys to ClassyFy. Must supply one of either ramclustObj or inchikey.
get.all	logical; if TRUE, when inchikey classyfire lookup fails, submits for classification. Can be slow. max.wait (below) sets max time to spend on each compound before moving on. default = FALSE.
max.wait	numeric; maximum time (seconds) to wait per compound when 'get.all' = TRUE.
posts.per.minute	integer; a limit set when 'get.all' is true. ClassyFire server accepts no more than 5 posts per minute when calculating new ClassyFire results. Slows down submission process to keep server from denying access.

**Details**

The \$inchikey slot is used to look up the

**Value**

returns a ramclustR object. new dataframe in \$classyfire slot with rows equal to number of compounds.

**Author(s)**

Corey Broeckling

## References

Djombou Feunang Y, Eisner R, Knox C, Chepelev L, Hastings J, Owen G, Fahy E, Steinbeck C, Subramanian S, Bolton E, Greiner R, and Wishart DS. ClassyFire: Automated Chemical Classification With A Comprehensive, Computable Taxonomy. *Journal of Cheminformatics*, 2016, 8:61. DOI: 10.1186/s13321-016-0174-y

---

rc.cmpd.get.pubchem    *rc.cmpd.get.pubchem*

---

## Description

use pubchem rest and view APIs to retrieve structures, CIDs (if a name or inchikey is given), synonyms, and optionally vendor data, when available.

## Usage

```
rc.cmpd.get.pubchem(  
  ramclustObj = NULL,  
  search.name = NULL,  
  cmpd.names = NULL,  
  cmpd.cid = NULL,  
  cmpd.inchikey = NULL,  
  cmpd.smiles = NULL,  
  use.parent.cid = FALSE,  
  manual.entry = FALSE,  
  get.vendors = FALSE,  
  priority.vendors = c("Sigma Aldrich", "Alfa Chemistry", "Acros Organics", "VWR",  
    "Alfa Aesar", "molport", "Key Organics", "BLD Pharm"),  
  get.properties = TRUE,  
  all.props = FALSE,  
  get.synonyms = TRUE,  
  find.short.lipid.name = TRUE,  
  find.short.synonym = TRUE,  
  max.name.length = 30,  
  assign.short.name = TRUE,  
  get.bioassays = TRUE,  
  get.pathways = TRUE,  
  write.csv = TRUE  
)
```

## Arguments

ramclustObj	RAMClust Object input. if used, ramclustObj\$CID, ramclustObj\$inchikey, and ramclustObj\$ann are used as input, in that order, and ramclustObj is returned with \$pubchem slot appended.
search.name	character. optional name to assign to pubchem search to name output .csv files.

cmpd.names	character vector. i.e. c("caffeine", "theobromine", "glucose")
cmpd.cid	numeric integer vector. i.e. c(2519, 5429, 107526)
cmpd.inchikey	character vector. i.e. c("RYYVLZVUVIJVGH-UHFFFAOYSA-N", "YAPQBXQYLJRXSA-UHFFFAOYSA-N", "GZCGUPFRVQAUEE-SLPGGIOYSA-N")
cmpd.smiles	character vector. i.e. c("CN1C=NC2=C1C(=O)N(C(=O)N2C)C", "CN1C=NC2=C1C(=O)NC(=O)N2C")
use.parent.cid	logical. If TRUE, the CID for each supplied name/inchikey is used to retrieve its parent CID (i.e. the parent of sodium palmitate is palmitic acid). The parent CID is used to retrieve all other names, properties.
manual.entry	logical. if TRUE, user input is enabled for compounds not matched by name. A browser window will open with the pubchem search results in your default browser.
get.vendors	logical. if TRUE, vendor data is returned for each compound with a matched CID. Includes vendor count and vendor product URL, if available
priority.vendors	character vector. i.e. c("MyFavoriteCompany", "MySecondFavoriteCompany"). If these vendors are found, the URL returned is from priority vendors. Priority is given by order input by user.
get.properties	logical. if TRUE, physicochemical property data are returned for each compound with a matched CID.
all.props	logical. If TRUE, all pubchem properties ( <a href="https://pubchemdocs.ncbi.nlm.nih.gov/pug-rest\$_Toc494865567">https://pubchemdocs.ncbi.nlm.nih.gov/pug-rest\$_Toc494865567</a> ) are returned. If false, only a subset (faster).
get.synonyms	= TRUE. logical. if TRUE, retrieve pubchem synonyms. returned to \$synonyms slot
find.short.lipid.name	= TRUE. logical. If TRUE, and get.synonyms = TRUE, looks for lipid short hand names in synonyms list (i.e. PC(36:6)). returned to \$short.name slot. Short names are assigned only if assign.short.names = TRUE.
find.short.synonym	= TRUE. logical. If TRUE, and get.synonyms = TRUE, looks for lipid short synonyms, with prioritization for names with fewer numeric characters (i.e. database accession numbers or CAS numbers). returned to \$short.name slot. Short names are assigned only if assign.short.names = TRUE.
max.name.length	= 20. integer. If names are longer than this value, short names will be searched for, else, retain original name.
assign.short.name	= TRUE. If TRUE, short names from find.short.lipid.name and/or find.short.synonym = TRUE, short names are assigned the be the default annotation name (\$ann slot), and original annotations are moved to \$long.name slot.
get.bioassays	logical. If TRUE, return a table summarizing existing bioassay data for that CID.
get.pathways	logical. If TRUE, return a table of metabolic pathways for that CID.
write.csv	logical. If TRUE, write csv files of all returned pubchem data.

**Details**

useful for moving from chemical name to digital structure representation. greek letters are assumed to be 'UTF-8' encoded, and are converted to latin text before searching. if you are reading in your compound name list, do so with 'encoding' set to 'UTF-8'.

**Value**

returns a list with one or more of \$pubchem (compound name and identifiers) - one row in dataframe per CID; \$properties contains physicochemical properties - one row in dataframe per CID; \$vendors contains the number of vendors for a given compound and selects a vendor based on 'priority.vendors' supplied, or randomly choses a vendor with a HTML link - one row in dataframe per CID; \$bioassays contains a summary of bioassay activity data from pubchem - zero to many rows in dataframe per CID

**Author(s)**

Corey Broeckling

---

rc.cmpd.get.smiles.inchi  
*getSmilesInchi*

---

**Description**

use PubChem API to look up full smiles and inchi notation for each inchikey

**Usage**

```
rc.cmpd.get.smiles.inchi(  
  ramclustObj = NULL,  
  inchikey = NULL,  
  ignore.stereo = TRUE  
)
```

**Arguments**

ramclustObj	ramclustR object to look up smiles and inchi for each inchikey (without a smiles/inchi). Must provide one of ramclustObj or inchikey.
inchikey	character vector of inchikey strings. Must provide one of ramclustObj or inchikey.
ignore.stereo	logical. default = TRUE. If the Pubchem databases does not have the full inchikey string, should we search by the first (non-stereo) block of the inchikey? When true, returns the first pubchem match to the inchikey block one string. If the full inchikey is present, that is used preferentially.

**Details**

The \$inchikey slot is used to look up parameters from pubchem. PubChem CID, a pubchem URL, smiles (canonical) and inchi are returned. if smiles and inchi slots are already present (from MS-Finder, for example) pubchem smiles and inchi are used to fill in missing values only, not replace.

**Value**

returns a ramclustR object. new vector of \$smiles and \$inchi with length equal to number of compounds.

**Author(s)**

Corey Broeckling

**References**

Kim S, Thiessen PA, Bolton EE, Bryant SH. PUG-SOAP and PUG-REST: web services for programmatic access to chemical information in PubChem. *Nucleic Acids Res.* 2015;43(W1):W605-11.

---

rc.cmpd.replace.na      *rc.cmpd.replace.na*

---

**Description**

replaces any NA (and optionally zero) values with small signal (20

**Usage**

```
rc.cmpd.replace.na(  
  ramclustObj = NULL,  
  replace.int = 0.1,  
  replace.noise = 0.1,  
  replace.zero = TRUE  
)
```

**Arguments**

ramclustObj	ramclustObj containing SpecAbund dataset
replace.int	default = 0.2. proportion of minimum feature value to replace NA (or zero) values with
replace.noise	default = 0.2. proportion of replace.int value by which noise is added via 'jitter'
replace.zero	logical if TRUE, any zero values are replaced with noise as if they were NA values

**Details**

noise is added by finding for each feature the minimum detected value, multiplying that value by `replace.int`, then adding (`replace.int*replace.noise`) noise. `abs()` is used to ensure no negative values result.

**Value**

ramclustR object with NA and zero values removed.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.expand.sample.names

*rc.expand.sample.names*

---

**Description**

turn concatenated sample names into factors

**Usage**

```
rc.expand.sample.names(  
  ramclustObj = NULL,  
  delim = "-",  
  factor.names = TRUE,  
  quiet = FALSE  
)
```

**Arguments**

<code>ramclustObj</code>	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
<code>delim</code>	what delimiter should be used to separate names into factors? '-' by default
<code>factor.names</code>	logical or character vector. if TRUE, user will enter names one by one in console. If character vector (i.e. <code>c("trt", "time")</code> ) names are assigned to table
<code>quiet</code>	logical. if TRUE, user will not be prompted to enter names one by one in console.

**Details**

This function only works on newer format ramclustObjects with a \$phenoData slot.

This function will split sample names by a delimiter, and enable users to name factors

**Value**

ramclustR object with normalized data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.export.msp.rc      *rc.export.msp.rc*

---

**Description**

Cluster annotation function: inference of 'M' - molecular weight of the compound giving rise to each spectrum - using the InterpretMSSpectrum::findMain function

**Usage**

```
rc.export.msp.rc(ramclustObj = NULL, one.file = TRUE, mzdec = 1)
```

**Arguments**

ramclustObj	ramclustR object to annotate.
one.file	logical, should all msp spectra be written to one file? If false, each spectrum is an individual file.
mzdec	integer. Number of decimal points to export mass values with.

**Details**

exports files to a directory called 'spectra'. If one.file = FALSE, a new directory 'spectra/msp' is created to hold the individual msp files. if do.findman has been run, spectra are written as ms2 spectra, else as ms1.

**Value**

nothing, just exports files to the working directory

**Author(s)**

Corey Broeckling

---

```
rc.feature.filter.blanks
      rc.feature.filter.blanks
```

---

**Description**

used to remove features which are found at similar intensity in blank samples

**Usage**

```
rc.feature.filter.blanks(
  ramclustObj = NULL,
  qc.tag = "QC",
  blank.tag = "blank",
  sn = 3,
  remove.blanks = TRUE
)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
qc.tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.
blank.tag	see 'qc.tag', but for blanks to use as background.
sn	numeric defines the ratio for 'signal'. i.e. sn = 3 indicates that signal intensity must be 3 fold higher in sample than in blanks, on average, to be retained.
remove.blanks	logical. TRUE by default. this removes any recognized blanks samples from the MSdata and MSMSdata sets after they are used to filter contaminant features.

**Details**

This function offers normalization by run order, batch number, and QC sample signal intensity.

Each input vector should be the same length, and equal to the number of samples in the \$MSdata set.

Input vector order is assumed to be the same as the sample order in the \$MSdata set.

**Value**

ramclustR object with normalized data.



**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.feature.filter.cv    *rc.feature.filter.cv*

---

**Description**

extractor for xcms objects in preparation for clustering

**Usage**

```
rc.feature.filter.cv(ramclustObj = NULL, qc.tag = "QC", max.cv = 0.5)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
qc.tag	character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.
max.cv	numeric maximum allowable cv for any feature. default = 0.5

**Details**

This function offers normalization by total extracted ion signal. it is recommended to first run 'rc.feature.filter.blanks' to remove non-sample derived signal.

**Value**

ramclustR object with total extracted ion normalized data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

```
rc.feature.normalize.batch.qc  
    rc.feature.normalize.batch.qc
```

---

## Description

normalize data using batch.qc

## Usage

```
rc.feature.normalize.batch.qc(  
  order = NULL,  
  batch = NULL,  
  qc = NULL,  
  ramclustObj = NULL,  
  qc.inj.range = 20,  
  output.plot = FALSE  
)
```

## Arguments

order	integer vector with length equal to number of injections in xset or csv file or dataframe
batch	integer vector with length equal to number of injections in xset or csv file or dataframe
qc	logical vector with length equal to number of injections in xset or csv file or dataframe
ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
qc.inj.range	integer: how many injections around each injection are to be scanned for presence of QC samples when using batch.qc normalization? A good rule of thumb is between 1 and 3 times the typical injection span between QC injections. i.e. if you inject QC ever 7 samples, set this to between 7 and 21. smaller values provide more local precision but make normalization sensitive to individual poor outliers (though these are first removed using the boxplot function outlier detection), while wider values provide less local precision in normalization but better stability to individual peak areas.
output.plot	logical set to TRUE to store plots

## Value

ramclustR object with normalized data.

---

```
rc.feature.normalize.qc
rc.feature.normalize.qc
```

---

## Description

extractor for xcms objects in preparation for clustering

## Usage

```
rc.feature.normalize.qc(
  ramclustObj = NULL,
  order = NULL,
  batch = NULL,
  qc = NULL,
  output.plot = FALSE,
  p.cut = 0.05,
  rsq.cut = 0.1,
  p.adjust = "none"
)
```

## Arguments

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
order	integer vector with length equal to number of injections in xset or csv file
batch	integer vector with length equal to number of injections in xset or csv file
qc	logical vector with length equal to number of injections in xset or csv file or dataframe
output.plot	logical: if TRUE (default), plots are output to PDF.
p.cut	numeric when run order correction is applied, only features showing a run order vs signal with a linear p-value (after FDR correction) < p.cut will be adjusted. also requires r-squared < rsq.cut.
rsq.cut	numeric when run order correction is applied, only features showing a run order vs signal with a linear r-squared > rsq.cut will be adjusted. also requires p values < p.cut.
p.adjust	which p-value adjustment should be used? default = "none", see ?p.adjust

## Details

This function offers normalization by run order, batch number, and QC sample signal intensity.

Each input vector should be the same length, and equal to the number of samples in the \$MSdata set.

Input vector order is assumed to be the same as the sample order in the \$MSdata set.

**Value**

ramclustR object with normalized data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.feature.normalize.quantile  
*rc.feature.normalize.quantile*

---

**Description**

normalize data using quantile

**Usage**

```
rc.feature.normalize.quantile(ramclustObj = NULL)
```

**Arguments**

ramclustObj      ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

**Value**

ramclustR object with normalized data.

---

rc.feature.normalize.tic  
*rc.feature.normalize.tic*

---

**Description**

extractor for xcms objects in preparation for clustering

**Usage**

```
rc.feature.normalize.tic(ramclustObj = NULL)
```

**Arguments**

ramclustObj      ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

**Details**

This function offers normalization by total extracted ion signal. it is recommended to first run 'rc.feature.filter.blanks' to remove non-sample derived signal.

**Value**

ramclustR object with total extracted ion normalized data.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem.* 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.feature.replace.na    *rc.feature.replace.na*

---

**Description**

replaces any NA (and optionally zero) values with small signal (20

**Usage**

```
rc.feature.replace.na(  
  ramclustObj = NULL,  
  replace.int = 0.1,  
  replace.noise = 0.1,  
  replace.zero = TRUE,  
  which.data = c("MSdata", "MSMSdata")  
)
```

**Arguments**

ramclustObj      ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)

replace.int      default = 0.1. proportion of minimum feature value to replace NA (or zero) values with

replace.noise    default = 0.1. proportion of replace.int value by which noise is added via 'jitter'

replace.zero     logical if TRUE, any zero values are replaced with noise as if they were NA values

which.data       name of dataset

**Details**

noise is added by finding for each feature the minimum detected value, multiplying that value by `replace.int`, then adding (`replace.int*replace.noise`) noise. `abs()` is used to ensure no negative values result.

**Value**

ramclustR object with NA and zero values removed.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

rc.get.csv.data      *rc.get.csv.data*

---

**Description**

extractor for csv objects in preparation for normalization and clustering

**Usage**

```
rc.get.csv.data(  
  csv = NULL,  
  phenoData = NULL,  
  idmsms = NULL,  
  ExpDes = NULL,  
  sampNameCol = 1,  
  st = NULL,  
  timepos = 2,  
  featdelim = "_",  
  ensure.no.na = TRUE  
)
```

**Arguments**

csv	filepath: csv input. Features as columns, rows as samples. Column header <code>mz_rt</code>
phenoData	character: character string in 'taglocation' to designate files as either MS / DIA(MSe, MSall, AIF, etc) e.g. "01.mzML"
idmsms	filepath: optional idMSMS / MSe csv data. same dim and names as ms required

ExpDes	either an R object created by R ExpDes object: data used for record keeping and labelling msp spectral output
sampNameCol	integer: which column from the csv file contains sample names?
st	numeric: sigma t - time similarity decay value
timepos	integer: which position in delimited column header represents the retention time
featdelim	character: how feature mz and rt are delimited in csv import column header e.g. "="
ensure.no.na	logical: if TRUE, any 'NA' values in msint and/or msmsint are replaced with numerical values based on 10 percent of feature min plus noise. Used to ensure that spectra are not written with NA values.

### Details

This function creates a ramclustObj which will be used as input for clustering.

### Value

an empty ramclustR object. this object is formatted as an hclust object with additional slots for holding feature and compound data. details on these found below.

\$frt: feature retention time, in whatever units were fed in

\$fmz: feature retention time, reported in number of decimal points selected in ramclustR function

\$ExpDes: the experimental design object used when running ramclustR. List of two dataframes.

\$MSdata: the MSdataset provided by either xcms or csv input

\$MSMSdata: the (optional) DIA(MSe, MSall, AIF etc) dataset

\$xcmsOrd: original xcms order of features, for back-referencing when necessary

\$msint: weighted.mean intensity of feature in ms level data

\$msmsint: weighted.mean intensity of feature in msms level data

### Author(s)

Corey Broeckling

### References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

**Examples**

```
## Choose csv input file. Features as columns, rows as samples
## Choose csv input file phenoData
filename <- system.file("extdata", "peaks.csv", package = "RAMClustR", mustWork = TRUE)
phenoData <- system.file("extdata", "phenoData.csv", package = "RAMClustR", mustWork = TRUE)

ramclustobj <- rc.get.csv.data(csv = filename, phenoData = phenoData, st = 5)
```

---

```
rc.get.df.data      rc.get.df.data
```

---

**Description**

extractor for dataframe input in preparation for normalization and clustering

**Usage**

```
rc.get.df.data(
  ms1_featureDefinitions = NULL,
  ms1_featureValues = NULL,
  ms2_featureDefinitions = NULL,
  ms2_featureValues = NULL,
  phenoData = NULL,
  ExpDes = NULL,
  featureNamesColumnIndex = 1,
  st = NULL,
  ensure.no.na = TRUE
)
```

**Arguments**

ms1_featureDefinitions	dataframe with metadata with columns: mz, rt, feature names containing MS data
ms1_featureValues	dataframe with rownames = sample names, colnames = feature names containing MS data
ms2_featureDefinitions	dataframe with metadata with columns: mz, rt, feature names containing MSMS data
ms2_featureValues	dataframe with rownames = sample names, colnames = feature names containing MSMS data
phenoData	dataframe containing phenoData
ExpDes	either an R object created by R ExpDes object: data used for record keeping and labelling msp spectral output



featureNamesColumnIndex	integer: which column in 'ms1_featureDefinitions' contains feature names?
st	numeric: sigma t - time similarity decay value
ensure.no.na	logical: if TRUE, any 'NA' values in msint and/or msmsint are replaced with numerical values based on 10 percent of feature min plus noise. Used to ensure that spectra are not written with NA values.

## Details

This function creates a ramclustObj which will be used as input for clustering.

## Value

an empty ramclustR object. this object is formatted as an hclust object with additional slots for holding feature and compound data. details on these found below.

\$frt: feature retention time, in whatever units were fed in

\$fmz: feature retention time, reported in number of decimal points selected in ramclustR function

\$ExpDes: the experimental design object used when running ramclustR. List of two dataframes.

\$MSdata: the MSdataset provided by either xcms or csv input

\$MSMSdata: the (optional) DIA(MSe, MSall, AIF etc) dataset

\$xcmsOrd: original xcms order of features, for back-referencing when necessary

\$msint: weighted.mean intensity of feature in ms level data

\$msmsint: weighted.mean intensity of feature in msms level data

## Author(s)

Zargham Ahmad, Helge Hecht, Corey Broeckling

## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem.* 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem.* 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

## Examples

```
## Choose dataframe with metadata with columns: mz, rt, feature names containing MS data
## Choose dataframe with rownames = sample names, colnames = feature names containing MS data
## Choose dataframe containing phenoData
df1 <- readRDS(system.file("extdata", "featDefinition.rds", package = "RAMClustR", mustWork = TRUE))
df2 <- readRDS(system.file("extdata", "featValues.rds", package = "RAMClustR", mustWork = TRUE))
df3 <- readRDS(system.file("extdata", "phenoData_df.rds", package = "RAMClustR", mustWork = TRUE))
```

```
ramclustr <- rc.get.df.data(ms1_featureDefinitions=df1, ms1_featureValues=df2, phenoData=df3, st=5)
```

---

```
rc.get.xcms.data      rc.get.xcms.data
```

---

## Description

extractor for xcms objects in preparation for normalization and clustering

## Usage

```
rc.get.xcms.data(
  xcmsObj = NULL,
  taglocation = "filepaths",
  MStag = NULL,
  MSMStag = NULL,
  ExpDes = NULL,
  mzdec = 3,
  ensure.no.na = TRUE
)
```

## Arguments

xcmsObj	xcmsObject: containing grouped feature data for clustering by ramclustr
taglocation	character: "filepaths" by default, "phenoData[,1]" is another option. refers to xcms slot
MStag	character: character string in 'taglocation' to designate files as either MS / DIA(MSe, MSall, AIF, etc) e.g. "01.mzML"
MSMStag	character: character string in 'taglocation' to designate files as either MS / DIA(MSe, MSall, AIF, etc) e.g. "02.mzML"
ExpDes	either an R object created by R ExpDes object: data used for record keeping and labelling msp spectral output
mzdec	integer: number of decimal places for storing m/z values
ensure.no.na	logical: if TRUE, any 'NA' values in msint and/or msmsint are replaced with numerical values based on 10 percent of feature min plus noise. Used to ensure that spectra are not written with NA values.

## Details

This function creates a ramclustrObj which will be used as input for clustering.

**Value**

an empty ramclustR object. this object is formatted as an hclust object with additional slots for holding feature and compound data. details on these found below.

\$frt: feature retention time, in whatever units were fed in (xcms uses seconds, by default)

\$fmz: feature retention time, reported in number of decimal points selected in ramclustR function

\$ExpDes: the experimental design object used when running ramclustR. List of two dataframes.

\$MSdata: the MSdataset provided by either xcms or csv input

\$MSMSdata: the (optional) DIA(MSe, MSall, AIF etc) dataset provided by either xcms or csv input

\$xcmsOrd: original xcms order of features, for back-referencing when necessary

\$msint: weighted.mean intensity of feature in ms level data

\$msmsint: weighted.mean intensity of feature in msms level data

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

rc.qc

rc.qc

---

**Description**

summarize quality control for clustering and for quality control sample variation based on compound (\$SpecAbund) and feature (\$MSdata and \$MSMSdata, if present)

**Usage**

```
rc.qc(  
  ramclustObj = NULL,  
  qc.tag = "QC",  
  remove.qc = FALSE,  
  npc = 4,  
  scale = "pareto",  
  outfile.basename = "ramclustQC",  
  view.hist = TRUE,  
  do.plot = TRUE  
)
```

**Arguments**

ramclustObj	ramclustR object to analyze
qc.tag	qc.tag character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.
remove.qc	logical - if TRUE (default) QC injections will be removed from the returned ramclustObj (applies to \$MSdata, \$MSMSdata, \$SpecAbund, \$phenoData, as appropriate). If FALSE, QC samples remain.
npc	number of Principle components to calculate and plot
scale	"pareto" by default: PCA scaling method used
outfile.basename	base name of output files. Extensions added internally. default = "ramclustQC"
view.hist	logical. should histograms be plotted?
do.plot	logical should plots be shown/plotted?

**Details**

plots a ramclustR summary plot. first page represents the correlation of each cluster to all other clusters, sorted by retention time. large blocks of yellow along the diagonal indicate either poor clustering or a group of coregulated metabolites with similar retention time. It is an imperfect diagnostic, particularly with lipids on reverse phase LC or sugars on HILIC LC systems. Page 2: histogram of r values from page 1 - only r values one position from the diagonal are used. Pages 3:5 - PCA results, with QC samples colored red. relative standard deviation calculated as  $\text{sd}(\text{QC PC scores}) / \text{sd}(\text{all PC scores})$ . Page 6: histogram of CV values for each compound in the dataset, QC samples only.

**Value**

new RC object. Saves output summary plots to pdf and .csv summary tables to new 'QC' directory. If remove.qc = TRUE, moves QC samples to new \$QC slot from original position.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

rc.ramclustr

*rc.ramclustr***Description**

Main clustering function for grouping features based on their analytical behavior.

**Usage**

```
rc.ramclustr(
  ramclustObj = NULL,
  st = NULL,
  sr = NULL,
  maxt = NULL,
  deepSplit = FALSE,
  blocksize = 2000,
  mult = 5,
  hmax = NULL,
  collapse = TRUE,
  minModuleSize = 2,
  linkage = "average",
  cor.method = "pearson",
  rt.only.low.n = TRUE
)
```

**Arguments**

ramclustObj	ramclustR object: containing ungrouped features. constructed by rc.get.xcms.data, for example
st	numeric: sigma t - time similarity decay value
sr	numeric: sigma r - correlational similarity decay value
maxt	numeric: maximum time difference to calculate retention similarity for - all values beyond this are assigned similarity of zero
deepSplit	logical: controls how aggressively the HCA tree is cut - see ?cutreeDynamicTree
blocksize	integer: number of features (scans?) processed in one block =1000,
mult	numeric: internal value, can be used to influence processing speed/ram usage
hmax	numeric: precut the tree at this height, default 0.3 - see ?cutreeDynamicTree
collapse	logical: if true (default), feature quantitative values are collapsed into spectra quantitative values.
minModuleSize	integer: how many features must be part of a cluster to be returned? default = 2
linkage	character: heirarchical clustering linkage method - see ?hclust
cor.method	character: which correlational method used to calculate 'r' - see ?cor
rt.only.low.n	logical: default = TRUE At low injection numbers, correlational relationships of peak intensities may be unreliable. by default ramclustR will simply ignore the correlational r value and cluster on retention time alone. if you wish to use correlation with at n < 5, set this value to FALSE.

## Details

Main clustering function output - see citation for algorithm description or vignette('RAMClustR') for a walk through. batch.qc. normalization requires input of three vectors (1) batch (2) order (3) qc. This is a feature centric normalization approach which adjusts signal intensities first by comparing batch median intensity of each feature (one feature at a time) QC signal intensity to full dataset median to correct for systematic batch effects and then secondly to apply a local QC median vs global median sample correction to correct for run order effects.

## Value

\$featclus: integer vector of cluster membership for each feature

\$clrt: cluster retention time

\$clrtsd: retention time standard deviation of all the features that comprise that cluster

\$nfeat: number of features in the cluster

\$nsing: number of 'singletons' - that is the number of features which clustered with no other feature

\$cmpd: compound name. C#### are assigned in order of output by dynamicTreeCut. Compound with the most features is classified as C0001...

\$ann: annotation. By default, annotation names are identical to 'cmpd' names. This slot is a placeholder for when annotations are provided

\$SpecAbund: the cluster intensities after collapsing features to clusters

\$SpecAbundAve: the cluster intensities after averaging all samples with identical sample names

## Author(s)

Corey Broeckling

## References

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

rc.remove.qc

rc.remove.qc

---

## Description

summarize quality control for clustering and for quality control sample variation based on compound (\$SpecAbund) and feature (\$MSdata and \$MSMSdata, if present)

**Usage**

```
rc.remove.qc(ramclustObj = NULL, qc.tag = "QC")
```

**Arguments**

ramclustObj      ramclustR object to analyze

qc.tag            qc.tag character vector of length one or two. If length is two, enter search string and factor name in \$phenoData slot (i.e. c("QC", "sample.type"). If length one (i.e. "QC"), will search for this string in the 'sample.names' slot by default.

**Details**

simply moves QC samples out of the way for downstream processing. moved to a \$qc slot.

**Value**

new RC object. moves QC samples to new \$qc slot from original position.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

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---

rc.restore.qc.samples    *rc.restore.qc.samples*

---

**Description**

summarize quality control for clustering and for quality control sample variation based on compound (\$SpecAbund) and feature (\$MSdata and \$MSMSdata, if present)

**Usage**

```
rc.restore.qc.samples(ramclustObj = NULL)
```

**Arguments**

ramclustObj      ramclustR object to analyze

**Details**

moves all of \$phenoData, \$MSdata, \$MSMSdata, \$SpecAbund back to original positions from \$qc slot

**Value**

RC object

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

RCQC

*RCQC*

---

**Description**

filter RC object and summarize quality control sample variation

**Usage**

```
RCQC(
  ramclustObj = NULL,
  qctag = "QC",
  npc = 4,
  scale = "pareto",
  which.data = "SpecAbund",
  outfile = "ramclustQC.pdf"
)
```

**Arguments**

ramclustObj	ramclustR object to analyze
qctag	"QC" by default - rowname tag to identify QC samples
npc	number of Principle components to calculate and plot
scale	"pareto" by default: PCA scaling method used
which.data	which dataset to use. "SpecAbund" by default
outfile	name of output pdf file.



**Details**

plots a ramclustR summary plot. first page represents the correlation of each cluster to all other clusters, sorted by retention time. large blocks of yellow along the diagonal indicate either poor clustering or a group of coregulated metabolites with similar retention time. It is an imperfect diagnostic, particularly with lipids on reverse phase LC or sugars on HILIC LC systems. Page 2: histogram of r values from page 1 - only r values one position from the diagonal are used. Pages 3:5 - PCA results, with QC samples colored red. relative standard deviation calculated as  $\text{sd}(\text{QC PC scores}) / \text{sd}(\text{all PC scores})$ . Page 6: histogram of CV values for each compound in the dataset, QC samples only.

**Value**

new RC object, with QC samples moved to new slot. prints output summary plots to pdf.

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

Broeckling CD, Ganna A, Layer M, Brown K, Sutton B, Ingelsson E, Peers G, Prenni JE. Enabling Efficient and Confident Annotation of LC-MS Metabolomics Data through MS1 Spectrum and Time Prediction. *Anal Chem*. 2016 Sep 20;88(18):9226-34. doi: 10.1021/acs.analchem.6b02479. Epub 2016 Sep 8. PubMed PMID: 7560453.

---

remove\_blanks

*remove\_blanks*

---

**Description**

remove blanks

**Usage**

```
remove_blanks(ramclustObj, blank)
```

**Arguments**

ramclustObj	ramclustObj containing MSdata with optional MSMSdata (MSe, DIA, idMSMS)
blank	blank samples found by define_samples

**Value**

ramclustObj object with blanks removed

---

replace_na	<i>replace_na</i>
------------	-------------------

---

**Description**

add rc.feature.replace.na params in ramclustObj

**Usage**

```
replace_na(data, replace.int, replace.zero, replace.noise)
```

**Arguments**

data	selected data frame to use
replace.int	default = 0.1. proportion of minimum feature value to replace NA (or zero) values with
replace.zero	logical if TRUE, any zero values are replaced with noise as if they were NA values
replace.noise	default = 0.1. proportion of replace.int value by which noise is added via 'jitter'

**Value**

selected ramclustR data frame with NA and zero values removed.  
number of features replaced

---

write.methods	<i>write.methods</i>
---------------	----------------------

---

**Description**

write RAMClustR processing methods and citations to text file

**Usage**

```
write.methods(ramclustObj = NULL, filename = NULL)
```

**Arguments**

ramclustObj	R object - the ramclustR object which was used to write the .mat or .msp files
filename	define filename/path to write. uses 'ramclustr_methods.txt' and the working directory by default.

**Details**

this function exports a file called ramclustr\_methods.txt which contains the processing history, parameters used, and relevant citations.

**Value**

an annotated ramclustR object  
nothing - new file written to working director

**Author(s)**

Corey Broeckling

**References**

Broeckling CD, Afsar FA, Neumann S, Ben-Hur A, Prenni JE. RAMClust: a novel feature clustering method enables spectral-matching-based annotation for metabolomics data. *Anal Chem*. 2014 Jul 15;86(14):6812-7. doi: 10.1021/ac501530d. Epub 2014 Jun 26. PubMed PMID: 24927477.

---

write.msp

*write.msp*

---

**Description**

Cluster annotation function: inference of 'M' - molecular weight of the compound giving rise to each spectrum - using the InterpretMSSpectrum::findMain function

**Usage**

```
write.msp(ramclustObj = NULL, one.file = FALSE)
```

**Arguments**

ramclustObj	ramclustR object to annotate.
one.file	logical, should all msp spectra be written to one file? If false, each spectrum is an individual file.

**Details**

exports files to a directory called 'spectra'. If one.file = FALSE, a new directory 'spectra/msp' is created to hold the individual msp files. if do.findman has been run, spectra are written as ms2 spectra, else as ms1.

**Value**

nothing, just exports files to the working directory

**Author(s)**

Corey Broeckling

---

`write_csv``write_csv`

---

**Description**

write csv template called "ExpDes.csv" to your working directory. you will fill this in manually, ensuring that when you save you retain csv format. ramclustR will then read this file in and and format appropriately.

**Usage**

```
write_csv(data)
```

**Arguments**

data                      csv template to write

**Value**

read ExpDes.csv file

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