Package 'ume'

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Title Ultrahigh-Resolution Mass Spectrometry Data Evaluation for Complex Organic Matter

Version 1.5.2

Description Provides tools for assigning molecular formulas from exact masses obtained by ultrahigh-resolution mass spectrometry. The methodology follows the workflow described in Leefmann et al. (2019) <doi:10.1002/rcm.8315>. The package supports the inspection, filtering and visualization of molecular formula data and includes utilities for calculating common molecular parameters (e.g., double bond equivalents, DBE). A graphical user interface is available via the 'shiny'-based 'ume' application.

URL https://gitlab.awi.de/bkoch/ume, https://ume.awi.de/, https://www.awi.de/en/ume

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Author Boris Koch [aut, cre] (ORCID: <https://orcid.org/0000-0002-8453-731X>), Tim Leefmann [ctb], Fabian Moye [ctb]

Maintainer Boris Koch <boris.koch@awi.de>

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Contents

add_known_mf . . . 3
add_missing_element_columns . . . 4
assign_formulas . . . 5
as_peaklist . . . 7
calc_data_summary . . . 8
calc_dbe . . . 10
calc_eval_params . . . 11
calc_exact_mass . . . 12
calc_ideg . . . 13
calc_iterr . . . 15
calc_ma . . . 16
calc_ma_abs . . . 17
calc_neutral_mass . . . 18
calc_nm . . . 19
calc_norm_int . . . 20
calc_number_assignment . . . 21
calc_pielou_evenness . . . 22
calc_shannon_index . . . 23
calc_simpson_index . . . 24
classify_files . . . 25
color.palette . . . 26
convert_data_table_to_molecular_formulas . . . 27
convert_molecular_formula_to_data_table . . . 29
create_ume_formula_library . . . 30
download_library . . . 32
eval_isotopes . . . 33
filter_int . . . 34
filter_mass_accuracy . . . 35
filter_mf_data . . . 36
get_isotope_info . . . 38
is_ume_peaklist . . . 38
known_mf . . . 39
lib_demo . . . 40
masses . . . 40
mf_data_demo . . . 41
nice_labels_dt . . . 43
order_columns . . . 44
peaklist_demo . . . 45
remove_blanks . . . 46
remove_empty_columns . . . 47
remove_id_columns . . . 48
remove_unknown_columns . . . 49
subset_known_mf . . . 49
tab_ume_labels . . . 50
theme_uplots . . . 51
ume_assign_formulas . . . 51

ume_filter_formulas . . . 53
uplot_cluster . . . 55
uplot_cvm . . . 56
uplot_dbe_minus_o_freq . . . 57
uplot_dbe_vs_c . . . 58
uplot_dbe_vs_o . . . 59
uplot_dbe_vs_ppm . . . 61
uplot_freq . . . 61
uplot_freq_ma . . . 62
uplot_freq_vs_ppm . . . 63
uplot_hc_vs_m . . . 65
uplot_heteroatoms . . . 66
uplot_isotope_precision . . . 67
uplot_kmd . . . 68
uplot_lcms . . . 70
uplot_ma_vs_mz . . . 71
uplot_ms . . . 72
uplot_n_mf_per_sample . . . 73
uplot_pca . . . 74
uplot_ppm_avg . . . 75
uplot_ratios . . . 76
uplot_reproducibility . . . 78
uplot_ri_vs_sample . . . 79
uplot_vk . . . 80
ustats_outlier . . . 82

Index **83**

`add_known_mf` *Add metainformation derived from ume::known_mf*

Description

Join molecular formula data and metadata about known formulas (e.g. annotate carboxylic-rich alicyclic molecules (CRAM)). The name of the molecular formula column will be set to "mf".

Usage

```
add_known_mf(mfd, mf_col = "mf", known_mf = ume::known_mf, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`mf_col`	Name of the column in mfd that has the molecular formula information (default: "mf"). Formulas have upper case element symbols and elements in the formula are ordered according to the Hill system.

known_mf	data.table with known molecular formulas (ume::known_mf).
...	Additional arguments passed to methods.

Value

A data.table containing additional columns having information on formula categories

Author(s)

Boris P. Koch

References

CRAM Hertkorn N., Benner R., Frommberger M., Schmitt-Kopplin P., Witt M., Kaiser K., Kettrup A., Hedges J.I. (2006). Characterization of a major refractory component of marine dissolved organic matter. *Geochimica et Cosmochimica Acta*, **70**, 2990-3010. doi:10.1016/j.gca.2006.03.021
Surfactants Lechtenfeld O.J., Koch B.P., Gasparovic B., Frka S., Witt M., Kattner G. (2013). The influence of salinity on the molecular and optical properties of surface microlayers in a karstic estuary. Marine Chemistry, 150, 25-38. doi:10.1016/j.marchem.2013.01.006

Ideg Flerus R., Lechtenfeld O.J., Koch B.P., McCallister S.L., Schmitt-Kopplin P., Benner R., Kaiser K., Kattner G. (2012). A molecular perspective on the ageing of marine dissolved organic matter. *Biogeosciences*, **9**, 1935-1955. doi:10.5194/bg919352012

iTerr Medeiros P.M., Seidel M., Niggemann J., Spencer R.G.M., Hernes P.J., Yager P.L., Miller W.L., Dittmar T., Hansell D.A. (2016). A novel molecular approach for tracing terrigenous dissolved organic matter into the deep ocean. *Global Biogeochemical Cycles*, **30**, 689-699. doi:10.1002/2015gb005320

See Also

Other Formula assignment: calc_eval_params(), check_formula_library(), eval_isotopes(), ume_assign_formulas()

Examples

```
add_known_mf(mfd = mf_data_demo)
```

---

add_missing_element_columns
Add Missing Isotope Columns to mfd

Description

This function ensures that missing isotope columns are added to the input data table (`mfd`), which is required for further data evaluation that considers isotope information. If any of the specified isotope columns are not already present in the data, they will be added with a default value of `0`.

The function is typically used to standardize the dataset by ensuring that all expected isotopes (e.g., nitrogen-15, carbon-13) are represented, even if they are not initially present in the data. The function works by checking for the existence of each specified isotope column and adding the missing ones.

Usage

```
add_missing_element_columns(mfd, missing_cols = "15n")
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`missing_cols`	A character vector of isotope column names that should be checked and added if missing. By default, it includes `"15n"`, but additional isotopes can be specified as needed (e.g., `"na"`, `"d"`, `"35cl"`, etc.).

Value

A `data.table` object with the missing isotope columns added, where missing columns are populated with a default value of `0`. The original `mfd` object is modified in place.

See Also

Other tools: `order_columns()`

Examples

```
# Add missing isotope columns to a demo dataset
mfd_with_isotopes <- add_missing_element_columns(mfd = mf_data_demo)

# Add a specific isotope column for Nitrogen-15 (if missing)
mfd_with_15n <- add_missing_element_columns(mfd = mf_data_demo, missing_cols = c("15n", "na"))
```

`assign_formulas` *Molecular Formula Assignment*

Description

Assigns molecular formulas to molecular masses using a predefined library. Input of the peaklist (`pl`) is internally checked `as_peaklist()`, converted to neutral masses `calc_neutral_mass()`, and assigned with molecular formulas based on the mass accuracy (`ma_dev`) provided `calc_ma_abs()`. The input can be either:

- A peaklist (`data.table`) containing m/z values or neutral masses and additional metadata .
- A numeric vector of m/z values or neutral masses without additional metadata (internally checked and standardized by `as_peaklist()`).

Usage

```
assign_formulas(pl, formula_library, verbose = FALSE, ...)
```

Arguments

`pl`	Either a peaklist (`data.table`) with at least columns `mz`, `i_magnitude`, and `file_id`, or a numeric vector of masses. For numeric input, a minimal peaklist is constructed internally.
`formula_library`	Molecular formula library: a predefined data.table used for assigning molecular formulas to a peak list and for mass calibration. The library requires a fixed format, including mass values for matching. Predefined libraries are available in the R package *ume.formulas* and further described in Leefmann et al. (2019). A standard library for marine dissolved organic matter is `ume.formulas::lib_02`. New libraries can be built using `ume::create_ume_formula_library()`.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Arguments passed on to `calc_ma_abs`, `calc_neutral_mass` `m` Measured mass `ma_dev` Mass accuracy in +/- parts per million (ppm) `mz` Numeric vector of m/z values (> 0). `pol` Character: `"neg"`, `"pos"`, or `"neutral"`.

Details

This function calculates the neutral mass of peaks in `pl` and compares it to mass values in `formula_library`, assigning molecular formulas based on mass accuracy thresholds. If 13C, 15N, or 34S isotope information is missing, additional columns are added to the output table.

Value

A `data.table` where each row represents a molecular formula assigned to a mass peak. The table contains:

- All columns of the input peaklist `pl` (e.g. `mz`, `i_magnitude`, `file_id`).
- All columns of the input `formula_library` (e.g. `mf`, element counts).
- Calculated columns:

  - `m` — neutral mass.
  - `m_cal` — exact mass of the assigned formula.
  - `del` — absolute mass error (Da).
  - `ppm` — mass error in parts per million.
  - `mf_id` — unique ID for each (file_id, mf) combination.
- Added isotope columns (`13C`, `15N`, `34S`) if missing in the library.

One peak may receive zero, one, or multiple assigned formulas depending on the mass accuracy threshold.

Author(s)

Boris P. Koch

Examples

```
# Example using demo data
assign_formulas(pl = peaklist_demo,
                formula_library = ume::lib_demo,
                pol = "neg",
                ma_dev = 0.2,
                verbose = FALSE)
```

---

as_peaklist *Check format of peaklist*

Description

Flexible entry point for UME. Accepts:

- data.frame / data.table peaklists
- numeric m/z vectors
- file paths (csv, txt, tsv, rds)

Normalizes column names, adds missing structural columns (file_id, peak_id), removes invalid rows, validates schema, and assigns the UME peaklist class. Creates a standardized `data.table` ready for formula assignment.

Usage

```
as_peaklist(pl, verbose = FALSE, track_original_names = TRUE, ...)
```

Arguments

pl	Input object representing a peaklist. Can be: • data.frame or data.table • file path to a supported tabular format • numeric vector of m/z values
verbose	logical; if TRUE, show progress messages.
track_original_names	Logical (default: TRUE). If TRUE, as_peaklist() stores a "original_colnames" attribute mapping canonical UME names (e.g. "mz") to the user's original column names (e.g. "m/z"). Internal functions that perform many := operations (e.g. assign_formulas()) may set this to FALSE to avoid attribute- related shallow-copy warnings.
...	Reserved for future extensions.

Value

A validated and normalized peaklist as a data.table with class "ume_peaklist".

See Also

Other check ume objects: check_formula_library(), check_mfd()

---

calc_data_summary *Create a Data Summary Table for Element Ratios and Parameters*

Description

Generates a data summary table that provides intensity-weighted averages for element ratios, mass accuracy, and additional parameters. Results can be grouped based on the specified grouping columns.

Usage

```
calc_data_summary(mfd, grp = "file_id", ...)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
grp	Character vector. Names of columns (e.g., sample or file identifiers) used to aggregate results.
...	Additional arguments passed to methods.

Details

This function computes a variety of weighted averages and summary statistics for mass spectrometry data using the provided peak list (`mfd`). Calculated values include weighted averages for elemental counts (e.g., Carbon, Hydrogen), elemental ratios (e.g., O/C, H/C), and additional parameters such as the base peak intensity and summed intensities. It also calculates the aromaticity index (`wa(AI)`) based on the elemental composition. If grouping columns are provided, the summary statistics are calculated for each group.

The function also joins additional indices (`ideg`, `iterr`) from related functions `calc_ideg()` and `calc_iterr()` to the final summary table.

Value

A `data.table` containing the summarized results, with columns including:

n(mf) Number of molecular formulas per group.

accuracy (median) Median accuracy in parts-per-million (ppm) for the identified peaks.

accuracy (3 sigma cut-off) Maximum ppm accuracy within a three-sigma range.

wa(mz) Weighted average m/z value.

wa(DBE) Weighted average Double Bond Equivalent (DBE).

wa(element) Weighted averages for elements (C, H, N, O, P, S) and ratios (O/C, H/C, N/C, S/C).

wa(NOSC) Weighted average nominal oxidation state of carbon.

wa(delG0_Cox) Weighted average Gibbs free energy (Cox) in kJ/mol.

wa(AI) Weighted average aromaticity index.

wa(C/N) and wa(C/S) Ratios derived from N/C and S/C.

ideg, ideg_n Indices for degree of identification, as calculated by `calc_ideg()`.

iterr, iterr_n, iterr2, iterr2_n Iteration error indices from `calc_iterr()`.

median(i_magnitude) Median intensity value.

int(basepeak) Intensity of the base peak.

int(summed) Summed intensity of all peaks.

See Also

Other calculations: `calc_dbe()`, `calc_eval_params()`, `calc_exact_mass()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_nm()`, `calc_norm_int()`, `calc_number_assignment()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
# Example using demo data, grouping by file ID
calc_data_summary(mfd = mf_data_demo, grp = c("file_id"))
```

calc_dbe *Calculate Double Bond Equivalent (DBE)*

Description

Calculates the Double Bond Equivalent (DBE) for a given neutral molecular formula. DBE is a measure of unsaturation, representing the total number of rings and pi bonds in a molecule. This function uses the `masses` data table to determine valence information for each element in the input molecular formula.

Usage

```
calc_dbe(mfd, masses = ume::masses, verbose = FALSE, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`masses`	A data.table. Defaults to `ume::masses` (based on NIST data) containing isotope information for elements, including nominal and exact mass, relative abundance, and Hill system order.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Additional arguments passed to methods.

Details

This function computes DBE based on the molecular formula specified in `mfd`. `mfd` can be a data.table or a character string or character vector of molecular formula strings.

For each isotope in the formula, DBE is calculated as the sum of (valence - 2) multiplied by the count of that isotope, divided by 2, and then adding 1. Elements with a valence of 2 are excluded from the DBE calculation.

The function will stop and print an error if any elements in `mfd` have missing valence information in `masses`.

Value

A numeric vector of the same length as the number of rows in `mfd`, where each entry represents the calculated DBE for the corresponding molecular formula. The result vector is named 'dbe'.

See Also

Other calculations: `calc_data_summary()`, `calc_eval_params()`, `calc_exact_mass()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_nm()`, `calc_norm_int()`, `calc_number_assignment()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
# Example with user-defined data
calc_dbe("C6H10O6")
calc_dbe("C6H10Br2")
calc_dbe(c("C3[13C1]H10O4", "C6H10O6"))

# Example with demo data from UME package
calc_dbe(mfd = mf_data_demo)
```

`calc_eval_params` *Calculate UME Evaluation Parameters*

Description

This function calculates and adds several evaluation parameters as additional columns to the `mfd` data table. These parameters are essential for evaluating the molecular structure and isotopic distribution, enabling further analysis. For a detailed description of the output table, see `help(mf_data_demo)`.

Usage

```
calc_eval_params(mfd, verbose = FALSE, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Additional arguments passed to methods.

Value

The original `data.table` `mfd` with additional evaluation columns:

`nm` Nominal molecular mass: Calculated if not already present.

`dbe`) Double Bond Equivalent (measure of unsaturation).

`kmd` Kendrick mass defect for CH4 versus O exchange.

`O/C`, `H/C`, `N/C`, `S/C`) Element ratios for a molecular formula.

`nsp_type`, `snp_check` Types of combinations of N, S, and P atoms in a formula.

`nosc“}{Weighted average nominal oxidation state of carbon.} \item{`**delG0_Cox**`}{Weighted average Gibbs`
A mass accuracy threshold calculated for each spectrum.

Author(s)

Boris P. Koch

References

Hughey C.A., Hendrickson C.L., Rodgers R.P., Marshall A.G., Qian K.N. (2001). Kendrick mass defect spectrum: A compact visual analysis for ultrahigh-resolution broadband mass spectra. *Analytical Chemistry*, **73**, 4676-4681. doi:10.1021/ac010560w

Koch B.P., Dittmar T. (2006). From mass to structure: an aromaticity index for high-resolution mass data of natural organic matter. *Rapid Communications in Mass Spectrometry*, **20**, 926-932. doi:10.1002/rcm.2386

LaRowe D.E., Van Cappellen P. (2011). Degradation of natural organic matter: A thermodynamic analysis. *Geochimica et Cosmochimica Acta*, **75**, 2030-2042. doi:10.1016/j.gca.2011.01.020

See Also

Other Formula assignment: `add_known_mf()`, `check_formula_library()`, `eval_isotopes()`, `ume_assign_formulas()`

Other calculations: `calc_data_summary()`, `calc_dbe()`, `calc_exact_mass()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_nm()`, `calc_norm_int()`, `calc_number_assignment()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
# Example usage with a demo molecular formula dataset
mfd_with_params <- calc_eval_params(mfd = mf_data_demo, verbose = TRUE)
```

`calc_exact_mass` *Calculate Exact Monoisotopic Mass of a Molecule*

Description

This function calculates the exact monoisotopic mass for each molecule in a given data table based on the specified isotope composition. Exact masses of elements and isotopes used in the calculation are retrieved from the `ume::masses` data, based on data from NIST (https://www.nist.gov/pml/atomic-weights-and-isotopic-compositions-relative-atomic-masses).

Usage

```
calc_exact_mass(mfd, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`...`	Additional arguments passed to methods.

Value

A numeric vector of the calculated exact monoisotopic mass.

Author(s)

Boris P. Koch

See Also

Other calculations: `calc_data_summary()`, `calc_dbe()`, `calc_eval_params()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_nm()`, `calc_norm_int()`, `calc_number_assignment()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
# Example with demo data
calc_exact_mass(mfd = mf_data_demo)
# Custom example
calc_exact_mass(data.table::data.table(c = 3, h = 8, o = 1))
```

---

calc_ideg *Calculate Degradation Index (Ideg)*

Description

This function calculates the degradation index ('Ideg') following Flerus et al. (2012). High Ideg values indicate 'older' marine DOM (i.e., a higher contribution of peaks that correlate negatively with delta14C), while low values indicate 'younger' DOM (i.e., a higher contribution of peaks that correlate positively with delta14C)./

Ideg is computed as the ratio of summed magnitudes for five negative (NEG) molecular formulas to the total summed magnitudes of five positive (POS) and five negative (NEG) molecular formulas:

$$Ideg = \frac{\sum NEG}{\sum NEG + \sum POS}$$

The index ranges from 0 to 1 and is valid only if all required formulas (n = 10) are present. Ideg depends strongly on the type of sample preparation, ionization method, and instrument settings, and should only be interpreted for relative changes within the same dataset.

Usage

```
calc_ideg(
  mfd,
  mf_col = "mf",
  magnitude_col = "i_magnitude",
  grp = "file_id",
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
mf_col	Character. The name of the column containing molecular formulas. Default is "mf".
magnitude_col	Character. The name of the column containing magnitude values (absolute or relative). Default is "i_magnitude".
grp	Character vector. Names of columns (e.g., sample or file identifiers) used to aggregate results.
...	Additional arguments passed to methods.

Value

A data.table with columns:

- grp: Grouping variable.
- ideg: Calculated degradation index (rounded to 3 decimals).
- ideg_n: Number of assigned formulas used in the calculation.

See Also

Other calculations: calc_data_summary(), calc_dbe(), calc_eval_params(), calc_exact_mass(), calc_ma(), calc_neutral_mass(), calc_nm(), calc_norm_int(), calc_number_assignment(), calc_number_occurrence(), calc_recalibrate_ms()

Examples

```
# Create a minimal dataset containing all required POS and NEG formulas
library(data.table)

demo_ideg <- data.table(
  file_id = 1,
  mf = c(
    "C17H20O9", "C19H22O10", "C20H22O10", "C20H24O11", "C21H26O11",   # NEG
    "C13H18O7", "C14H20O7", "C15H22O7", "C15H22O8", "C16H24O8"        # POS
  ),
  i_magnitude = c(
    1200, 900, 1500, 700, 800,     # NEG intensities
    2000, 1800, 2200, 1600, 1900   # POS intensities
  )
)

calc_ideg(
  mfd = demo_ideg,
  mf_col = "mf",
  magnitude_col = "i_magnitude",
  grp = "file_id"
)
```

`calc_iterr` *Calculate terrestrial indeces Iterr and Iterr2 (after Medeiros et al. 2016)*

Description

Calculate a degradation index 'Iterr' and modified index 'iterr2' after Medeiros et al. (2016). High Iterr values represent higher contribution of terrestrial material (i.e. higher contribution of peaks that correlate positively with delta13C) while low values represent less terrestrial material (i.e. higher contribution of peaks that correlate negatively with delta13C). Iterr / Iterr2 are calculated from a peak magnitude ratio of 50 or 5 POS and NEG formulas, respectively: sum(POS) / (sum(POS) + sum(NEG)) Therefore Iterr / Iterr2 range between 1 and 0. It should be noted that absolute values strongly depend on factors such as type of solid phase extraction, ionization method, instrument settings etc. Therefore values can only be interpreted as relative changes. It should also be noted that for an appropriate evaluation ALL index formulas must be present.

Usage

```
calc_iterr(
  mfd,
  mf_col = "mf",
  magnitude_col = "i_magnitude",
  grp = "file_id",
  ...
)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`mf_col`	Name of the column containing molecular formulas (string)
`magnitude_col`	Name of the column containing absolute or relative mass peak magnitudes (string).
`grp`	Character vector. Names of columns (e.g., sample or file identifiers) used to aggregate results.
`...`	Additional arguments passed to methods.

Value

Iterr and iterr2 values

Examples

```
library(data.table)

# Create a minimal dataset containing all required
```

```
# POS, NEG, POS2, and NEG2 formulas for demonstration

demo_iterr <- data.table(
  file_id = 1,
  mf = c(
    # NEG (Iterr)
    'C13H12O5','C15H14O4','C14H12O5','C14H14O5','C13H12O6',
    'C16H16O4','C15H14O5','C14H12O6','C15H16O5','C14H14O6',
    'C16H14O5','C16H16O5','C15H14O6','C15H16O6','C14H14O7',
    'C17H16O5','C16H14O6','C17H18O5','C16H16O6','C15H14O7',
    'C17H16O6','C16H14O7','C18H18O6','C17H16O7','C17H18O7',
    'C18H16O7','C18H18O7','C17H16O8','C19H18O7','C20H20O7',
    'C19H18O8','C20H18O9','C19H16O10','C21H20O9','C20H18O10',
    'C22H22O9','C21H20O10','C23H22O10','C24H24O10','C25H26O10',

    # POS (Iterr)
    'C15H19NO6','C15H21NO6','C17H21NO7','C17H23NO7','C17H22O8',
    'C16H21NO8','C17H20N2O7','C17H19NO8','C18H23NO7','C17H21NO8',
    'C18H24O8','C16H19NO9','C17H23NO8','C17H22O9','C17H24O9',
    'C18H21NO8','C17H19NO9','C18H23NO8','C18H22O9','C17H21NO9',
    'C18H24O9','C18H20N2O8','C18H21NO9','C19H24O9','C18H23NO9',
    'C18H22O10','C18H24O10','C20H24O9','C19H22O10','C20H26O9',
    'C19H24O10','C19H26O10','C20H24O10','C20H26O10','C19H24O11',
    'C20H24O11','C20H26O11','C20H26O12','C22H28O11','C21H28O12',

    # NEG2 (Iterr2)
    'C17H18O7','C18H18O7','C17H16O7','C17H16O8','C15H16O6',

    # POS2 (Iterr2)
    'C20H24O9','C20H24O10','C19H22O10','C17H21NO8','C20H26O9'
  ),

  # Assign magnitude values (arbitrary but valid)
  i_magnitude = c(
    rep(1000, 40),  # NEG
    rep(2000, 40),  # POS
    rep(1500, 5),   # NEG2
    rep(1800, 5)    # POS2
  )
)

calc_iterr(
  mfd = demo_iterr,
  mf_col = "mf",
  magnitude_col = "i_magnitude",
  grp = "file_id"
)
```

---

calc_ma *Calculate mass accuracy*

Description

Calculates relative mass accuracy (ma, in parts per million) as: (measured mass - theoretical mass) / theoretical mass * 1000000 Returned value is rounded to 4 digits.

Usage

```
calc_ma(m, m_cal, ...)
```

Arguments

m	Measured mass
m_cal	Calculated (theoretical) mass.
...	Additional arguments passed to methods.

Value

A numeric vector of mass accuracy.

See Also

Other calculations: calc_data_summary(), calc_dbe(), calc_eval_params(), calc_exact_mass(), calc_ideg(), calc_neutral_mass(), calc_nm(), calc_norm_int(), calc_number_assignment(), calc_number_occurrence(), calc_recalibrate_ms()

Examples

```
# Use of single values
calc_ma(m = 264.08641, m_cal = 264.08653)
# Use in a molecular formula table
calc_ma(m = mf_data_demo$m, m_cal = mf_data_demo$m_cal)
mf_data_demo[, .(m, m_cal, accuracy_in_ppm = calc_ma(m, m_cal))]
```

---

calc_ma_abs *Calculate absolute mass accuracy range (ma)*

Description

This function calculates the absolute mass accuracy range for a neutral mass (m) at a given a mass accuracy (ma_dev).

Usage

```
calc_ma_abs(m, ma_dev, ...)
```

Arguments

m	Measured mass
ma_dev	Mass accuracy in +/- parts per million (ppm)
...	Additional arguments passed to methods.

Value

Returns a list with two values: m_min, m_max

Examples

```
calc_ma_abs(m = 327.0134, ma_dev = 0.5)
```

---

calc_neutral_mass *Calculate neutral molecular mass*

Description

Calculates neutral molecular masses for singly charged ions with full numerical precision. No user options are modified.

The conversion used is:

- negative mode: m = mz + 1.0072763
- positive mode: m = mz - 1.0072763
- neutral: m = mz

Usage

```
calc_neutral_mass(mz, pol = c("neg", "pos", "neutral"), ...)
```

Arguments

mz	Numeric vector of m/z values (> 0).
pol	Character: "neg", "pos", or "neutral".
...	Additional arguments passed to methods.

Value

Numeric vector of neutral masses.

See Also

Other calculations: calc_data_summary(), calc_dbe(), calc_eval_params(), calc_exact_mass(), calc_ideg(), calc_ma(), calc_nm(), calc_norm_int(), calc_number_assignment(), calc_number_occurrence(), calc_recalibrate_ms()

Examples

```
calc_neutral_mass(199.32, pol = "neg")
```

`calc_nm` *Calculate Nominal Mass of a Molecule*

Description

Computes the nominal mass (integer mass) for each molecular formula in the provided data. This function uses isotope masses stored in the dataset `ume::masses`, based on values from NIST, for accurate calculation of each element's nominal mass contribution.

Usage

```
calc_nm(mfd, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`...`	Additional arguments passed to methods.

Details

The function calculates the nominal mass of each molecular formula by retrieving the relevant integer mass values of isotopes from `ume::masses`. This information is processed to create a calculation string which is then evaluated to obtain the nominal mass for each molecule.

The nominal mass is derived by summing the integer masses of each constituent element in the formula, where the integer mass for each element is multiplied by the number of atoms of that element in the molecule.

Note: This function depends on `ume::get_isotope_info()` for isotope data retrieval.

Value

A numeric vector of the calculated nominal mass.

See Also

Other calculations: `calc_data_summary()`, `calc_dbe()`, `calc_eval_params()`, `calc_exact_mass()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_norm_int()`, `calc_number_assignment()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
# Example using a demo dataset to calculate nominal mass
calc_nm(mfd = mf_data_demo)
```

`calc_norm_int` *Calculate Normalized Peak Intensities*

Description

Computes normalized peak intensities for a molecular formula dataset and adds the results as additional columns to the input `data.table` (`mfd`). It also calculates:

- the number of molecular formula assignments per peak (`n_assignments`)
- the total occurrences of each formula across the dataset (`n_occurrence`)

Normalized intensities are stored in a new column `norm_int`, and the reference intensity used for normalization is stored in `int_ref`.

Supported normalization methods:

- `"none"` – no normalization; raw peak intensities are copied to `norm_int`
- `"bp"` – normalized to the base peak intensity per spectrum
- `"sum"` – normalized by the total sum of intensities per spectrum
- `"sum_ubiq"` – normalized by the sum of intensities of ubiquitous peaks across the dataset
- `"sum_rank"` – normalized by the sum of the top `n_rank` most intense peaks per spectrum
- `"euc"` – Euclidean normalization (optional, not implemented in current version)

Usage

```
calc_norm_int(
  mfd,
  ms_id = "file_id",
  peak_id = "peak_id",
  peak_magnitude = "i_magnitude",
  normalization = c("bp", "sum", "sum_ubiq", "sum_rank", "none"),
  n_rank = 200,
  verbose = FALSE,
  ...
)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`ms_id`	Character; name of the column identifying individual spectra (default: `"file_id"`).
`peak_id`	Character; name of the column identifying unique peaks (default: `"peak_id"`).
`peak_magnitude`	Character; name of the column containing peak intensity values (default: `"i_magnitude"`).
`normalization`	Character; normalization method to apply. One of `"bp"`, `"sum"`, `"sum_ubiq"`, `"sum_rank"`, `"none"`. Default is `"bp"`.

n_rank	Integer; number of top-ranked peaks to use for "sum_rank" normalization (default: 200).
verbose	logical; if TRUE, show progress messages.
...	Additional arguments (currently unused).

Value

A data.table identical to mfd but with additional columns:

norm_int Normalized peak intensity based on selected method.

int_ref Reference intensity used for normalization (e.g., sum, base peak).

n_assignments Number of formula assignments per peak (calculated internally).

n_occurrence Number of occurrences of each formula across all spectra (calculated internally).

See Also

Other calculations: calc_data_summary(), calc_dbe(), calc_eval_params(), calc_exact_mass(), calc_ideg(), calc_ma(), calc_neutral_mass(), calc_nm(), calc_number_assignment(), calc_number_occurrence(calc_recalibrate_ms()

Examples

```
mfd_norm <- calc_norm_int(
  mfd = mf_data_demo,
  normalization = "sum_ubiq"
)
```

---

calc_number_assignment

Calculate Number of Molecular Formula Assignments per Peak

Description

This function calculates the number of molecular formula (mf) assignments for each individual peak (peak_id) within a specified mass spectrum (ms_id). It counts the occurrences of molecular formulas assigned to each peak and returns a vector of counts corresponding to the number of assignments for each unique combination of mass spectrum ID, peak ID, and molecular formula.

Usage

```
calc_number_assignment(ms_id, peak_id, mf, ...)
```

Arguments

ms_id	A vector containing the mass spectrum ID for each peak.
peak_id	A vector containing the peak ID for each peak.
mf	Character vector of molecular formula(s) (e.g., c("C10H23NO4", "C10H24N4O2S")).
...	Additional arguments passed to methods.

Value

A vector of integer counts representing the number of molecular formula assignments for each unique combination of mass spectrum ID, peak ID, and molecular formula.

See Also

Other calculations: `calc_data_summary()`, `calc_dbe()`, `calc_eval_params()`, `calc_exact_mass()`, `calc_ideg()`, `calc_ma()`, `calc_neutral_mass()`, `calc_nm()`, `calc_norm_int()`, `calc_number_occurrence()`, `calc_recalibrate_ms()`

Examples

```
ms_ids <- c("file1", "file1", "file2", "file2", "file3")
peak_ids <- c(1, 2, 2, 3, 4)
mfs <- c("C10H10N2O8", "C10H12N2O8", "C10H10N2O8", "C10H11NOS4", "C10H24N4O2S")
n_assignments <- calc_number_assignment(ms_id = ms_ids, peak_id = peak_ids, mf = mfs)
print(n_assignments)

mf_data_demo[, calc_number_assignment(file_id, peak_id, mf)]
```

---

calc_pielou_evenness *Calculate Pielou's Evenness*

Description

This function calculates Pielou's evenness index, a measure of the distribution of abundances across molecular formulas. Evenness ranges from 0 (one molecular formula dominates) to 1 (all formulas are equally abundant).

Evenness is derived using the Shannon index:

$$E = \frac{H}{\log(S)}$$

where:

- H is the Shannon diversity index.
- S is the number of unique molecular formulas.

If there is only one molecular formula, evenness is defined as 1.

Usage

```
calc_pielou_evenness(mf, magnitude)
```

Arguments

`mf`	Character vector. A list of unique molecular formulas.
`magnitude`	Numeric vector. A list of respective intensities (abundances) for each molecular formula. Must be non-negative and have the same length as `mf`.

Value

A single numeric value representing Pielou's evenness.

Examples

```
calc_pielou_evenness(
  mf = c("C10H20O5", "C12H18O3", "C18H30O6"),
  magnitude = c(1982375, 2424, 312410)
)
```

`calc_shannon_index` *Calculate the Shannon Diversity Index*

Description

The Shannon diversity index is calculated to quantify the diversity of molecular formulas based on their relative abundances. This index considers both the richness (number of unique formulas) and the evenness (distribution of abundances). Higher values indicate greater diversity.

The Shannon index is defined as:

$$H = -\sum(p_i \cdot \ln(p_i))$$

where:

- p_i is the relative abundance of the i-th molecular formula.

Zero-abundance formulas are excluded from the calculation.

Usage

```
calc_shannon_index(mf, magnitude)
```

Arguments

`mf`	Character vector. A list of unique molecular formulas.
`magnitude`	Numeric vector. A list of respective abundances (intensities) for each molecular formula. Must be non-negative and have the same length as `mf`.

Value

A single numeric value representing the Shannon diversity index. Returns 0 if `magnitude` is all zeros.

Examples

```
calc_shannon_index(
  mf = c("C10H20O5", "C12H18O3", "C18H30O6"),
  magnitude = c(1982375, 2424, 312410)
)
```

`calc_simpson_index` *Calculate the Simpson Diversity Index*

Description

The Simpson diversity index is calculated to measure the probability that two randomly selected individuals (e.g., molecular formulas) belong to the same category. It quantifies the dominance or evenness within a dataset.

The Simpson index is defined as:

$$D = \sum(p_i^2)$$

where:

- p_i is the relative abundance of the i-th molecular formula.

The index ranges between 0 and 1:

- A value near 0 indicates high diversity (even distribution of abundances).
- A value of 1 indicates no diversity (one molecular formula dominates).

Usage

```
calc_simpson_index(mf, magnitude)
```

Arguments

`mf`	Character vector. A list of unique molecular formulas.
`magnitude`	Numeric vector. A list of respective abundances (intensities) for each molecular formula. Must be non-negative and have the same length as `mf`.

Value

A single numeric value representing the Simpson diversity index. Returns 0 if `magnitude` is all zeros.

Examples

```
calc_simpson_index(
  mf = c("C10H20O5", "C12H18O3", "C18H30O6"),
  magnitude = c(1982375, 2424, 312410)
)
```

`classify_files` *Classify FTMS files into categories based on filename patterns*

Description

Classifies entries into categories (blank, standard, pool, sample, ...) based on pattern rules applied to a specific search column. The identifiers returned in each category are also configurable.

Usage

```
classify_files(
  fi,
  search_col = "link_rawdata",
  id_col = "file_id",
 patterns = list(blank = c("blk", "blank", "MQ"), standard = c("srfa", "standard"), pool
    = c("pool")),
  include_blank_check = TRUE,
  return = c("list", "table")
)
```

Arguments

`fi`	`data.table`. Must contain the columns specified in `search_col` and `id_col`.
`search_col`	Character. Name of the column used for pattern matching. Defaults to `"link_rawdata"`.
`id_col`	Character. Name of the column whose values are returned for each category. Defaults to `"file_id"`.
`patterns`	Named list of character vectors. Each list entry is a category name, and its value is a vector of patterns.
`include_blank_check`	Logical; if TRUE and `blank_check` exists, it is used to assign `"blank"`.
`return`	Either `"list"` (default) or `"table"`.

- `"list"` → named list of ID vectors
- `"table"` → `fi` with added column `category_analysis`

Details

Default behavior:

- `"blank"`: `blank_check == "blank"` or pattern `"blk"`
- `"standard"`: pattern `"srfa"`
- `"pool"`: pattern `"pool"`
- `"sample"`: everything unmatched

Pattern matching is case-insensitive.

Value

Named list or a classified `data.table`.

Examples

```
# Minimal demo data
fi <- data.table::data.table(
  file_id       = 1:6,
  filename      = c("NS_blk_01.raw", "SRFA_20.raw", "Pool_A.raw",
                    "Sample_01.raw", "Sample_02.raw", "MQ_blank.raw"),
  blank_check   = c("blank", NA, NA, NA, NA, "blank"),  # optional column
  link_rawdata  = c("NS_blk_01.raw", "SRFA_20.raw", "Pool_A.raw",
                    "Sample_01.raw", "Sample_02.raw", "MQ_blank.raw")
)

# 1) Default behavior: return named list of file_ids by category
classify_files(fi)

# 2) Use a different column for pattern matching
classify_files(fi, search_col = "filename")

# 3) Return another ID field (here: file_id → stays the same for demo)
classify_files(fi, id_col = "file_id")

# 4) Return the full table with new category column
classify_files(fi, return = "table")
```

---

color.palette *Create a Custom Interpolated Color Palette*

Description

Constructs a continuous color palette from a sequence of base colors. Intermediate colors are interpolated between each pair of adjacent colors, optionally using a custom number of interpolation steps.

Usage

```
color.palette(steps, n.steps.between = NULL, ...)
```

Arguments

`steps`	A character vector of base colors (e.g., hex codes or color names). These colors define the breakpoints in the palette.
`n.steps.between`	An optional integer vector specifying how many interpolated colors should be added **between** each pair of entries in `steps`. Must have length `length(steps) - 1`. If `NULL` (default), no intermediate colors are added beyond the endpoints.
`...`	Additional arguments passed to methods.

Details

This helper is primarily used for UME visualizations (e.g., color bars in density plots), but it can be used independently for any plotting task.

Value

A function of class `"colorRampPalette"` that generates interpolated color vectors when called with a single integer argument `n`.

For example, `pal <- color.palette(c("blue", "white", "red")); pal(100)` returns a vector of 100 smoothly interpolated colors.

Examples

```
# Generate a simple blue-white-red palette
pal <- color.palette(c("blue", "white", "red"))
pal(10)

# Add additional steps between colors
pal2 <- color.palette(c("blue", "white", "red"), n.steps.between = c(5, 10))
pal2(20)
```

---

convert_data_table_to_molecular_formulas

Convert Data Table with Element Counts to Molecular Formulas

Description

Creates a character vector of molecular formulas and adds it as a column to the input `data.table`. The molecular formula string follows the **Hill system order** for element arrangement. If keep_element_sums == TRUE, a data.table is returned that also provides the sum of atoms of each element in the molecular formula.

Usage

```
convert_data_table_to_molecular_formulas(
  mfd,
  isotope_formulas = FALSE,
  keep_element_sums = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
isotope_formulas	Logical. If TRUE the output table will have an additional molecular formula string that includes isotope information (e.g. "[12C5][13C1][1H12][16O6]")
keep_element_sums	description. If TRUE the output table will have additional columns containing the total count of atoms of an element (e.g. S_tot).
verbose	logical; if TRUE, show progress messages.
...	Additional arguments passed to methods.

Details

This function extracts element or isotope counts from a table with columns for each element of a molecular formula, including those with isotopic notation. It ensures that only valid elements are included based on a reference table (masses).

The function internally uses the ume::masses table that contains element and isotopic symbols.

Value

The original table mfd as data.table having additional columns:

mf Standardized molecular formula following the Hill order.

mf_iso If isotope_formulas = TRUE: Standardized molecular formula considering all isotopes of an element.

C_tot If keep_element_sums = TRUE: The total count of all atoms that are carbon isotopes (similar for all other elements.

Notes

- The function correctly handles isotopic notations such as [13C] and [18O2].
- The output follows the **Hill order**, meaning **C, H first**, followed by other elements in alphabetical order.
- Single-element counts (e.g., C1H4 → CH4) are formatted without explicit 1.

See Also

Other molecular formula functions: convert_molecular_formula_to_data_table()

Examples

```
convert_data_table_to_molecular_formulas(mf_data_demo[, .(`12C`, `1H`, `14N`, `16O`, `31P`, `32S`)])
```

`convert_molecular_formula_to_data_table` *Convert Molecular Formulas to a Data Table of Element Counts*

Description

Parses a character vector of molecular formulas and returns a `data.table` where each row represents a molecular formula, and each column corresponds to an element, showing the count of atoms of that element. The resulting table follows the **Hill system order** for element arrangement.

Usage

```
convert_molecular_formula_to_data_table(
  mf,
  masses = ume::masses,
  table_format = c("wide", "long")
)
```

Arguments

`mf`	Character vector of molecular formula(s) (e.g., `c("C10H23NO4", "C10H24N4O2S")`).
`masses`	A data.table. Defaults to `ume::masses` (based on NIST data) containing isotope information for elements, including nominal and exact mass, relative abundance, and Hill system order.
`table_format`	A string (two options) that controls the output table format: `wide` (DEFAULT, dcast) or `long` (normalized, melt)

Details

This function extracts element counts from molecular formulas, including those with isotopic notation. It ensures that only valid elements are included based on a reference table (`masses`) and flags invalid entries. Duplicate molecular formulas are identified and processed only once, with a warning issued.

The function internally creates an enriched `masses` table to account for isotopic symbols and standard element notation.

Value

A `data.table` with:

mf Standardized molecular formula following the Hill order.

mf_iso Original input molecular formula.

mass Exact molecular mass calculated from element masses.

elements Columns for each element present in the formulas, showing the atom count.

Warnings

- If duplicate formulas are detected, only unique ones are processed, and a warning is issued.
- If invalid element symbols are found, the function stops with an error message.
- If a molecular formula contains duplicate isotopes/elements, an error is triggered.

Notes

- The function correctly handles isotopic notations such as `[13C]` and `[18O2]`.
- The output follows the **Hill order**, meaning **C, H first**, followed by other elements in alphabetical order.
- Single-element counts (e.g., `C1H4` → `CH4`) are formatted without explicit `1`.

See Also

Other molecular formula functions: `convert_data_table_to_molecular_formulas()`

Examples

```
# Example usage
molecular_formulas <- c("C10H23NO4", "C10H24N4O2S", "C6[13C2]H12[18O2]ONaCl")
convert_molecular_formula_to_data_table(molecular_formulas)
```

---

create_ume_formula_library

Create a molecular formula library for UME

Description

Generates all combinations of element / isotope counts between `min_formula` and `max_formula`, filtered by mass, DBE, element ratios, and heuristic rules (Kind & Fiehn 2007).

Usage

```
create_ume_formula_library(
  max_formula,
  min_formula = "C1H1",
  lib_version = 99,
  masses = ume::masses,
  max_mass = 152,
  ratio_filter = TRUE,
  heu_filter = TRUE,
  max_oc = 1.2,
  max_hc = 3.1,
  max_nc = 1.3,
  max_pc = 0.3,
```

```
  max_sc = 0.8,
  verbose = FALSE
)
```

Arguments

max_formula	Character. Maximum element/isotope counts, e.g. "C20H40O10" or "C1000\[13C1\]H2000".
min_formula	Character. Minimum element/isotope counts (default "C1H1").
lib_version	Integer. Library version identifier (default 99).
masses	A data.table. Defaults to ume::masses (based on NIST data) containing isotope information for elements, including nominal and exact mass, relative abundance, and Hill system order.
max_mass	Numeric. Maximum allowed exact mass.
ratio_filter	Logical. Apply O/C, H/C, N/C, P/C, S/C filters.
heu_filter	Logical. Apply Kind - Fiehn heuristic rules.
max_oc	Maximum oxygen / carbon ratio in a molecule; (UM_orig: 1.5; 7 rules: 1.2)
max_hc	Maximum hydrogen / carbon ratio in a molecule; (UM_orig: ; 7 rules: 1.2)
max_nc	Maximum nitrogen / carbon ratio in a molecule; (UM_orig: 0.5; 7 rules: 1.3)
max_pc	Maximum phosphorus / carbon ratio in a molecule; (UM_orig: 3; 7 rules: 0.3)
max_sc	Maximum sulfur / carbon ratio in a molecule; (UM_orig: 4; 7 rules: 0.8)
verbose	Logical. Print progress messages.

Value

A data.table containing the generated molecular formula library. The returned object has class "ume_library" and includes one row per molecular formula, with columns for:

- elemental and isotopic counts (e.g., 12C, 13C, 1H, 16O, ...)
- double bond equivalent (dbe)
- exact mass (mass)
- molecular formula string (mf)
- a unique versioned key (vkey)

Additional metadata is stored as attributes:

- "lib_version": numeric version identifier
- "min_formula": user-supplied minimum formula
- "max_formula": user-supplied maximum formula
- "max_mass": maximum allowed exact mass
- "filters": list describing applied ratio and heuristic filters
- "call": the matched function call

The object inherits from both "ume_library" and "data.table".

References

Kind T., Fiehn O. (2007). Seven Golden Rules for heuristic filtering of molecular formulas obtained by accurate mass spectrometry. *BMC Bioinformatics*, **8**, 105. doi:10.1186/147121058105

`download_library` *Download and Load a UME Formula Library from Zenodo*

Description

Downloads one of the UME formula libraries from Zenodo **only when explicitly called by the user**.

Unlike earlier versions, this CRAN-compliant implementation:

- **never writes to the user's filespace unless** `dest` **is explicitly provided**
- **does NOT create ~/.ume/** or any other default directory
- **does NOT perform automatic caching**
- In non-interactive environments (CRAN checks), the function **returns NULL**

Usage

```
download_library(
  library = "lib_05.rds",
  doi = "10.5281/zenodo.17606457",
  dest = NULL,
  overwrite = FALSE
)
```

Arguments

`library`	Character. One of `"lib_02.rds"` or `"lib_05.rds"`.
`doi`	Character. Zenodo DOI.
`dest`	Optional file path where the library should be saved. If `NULL`, the library is **loaded into memory only**.
`overwrite`	Logical. Redownload even if `dest` exists?

Value

A `data.table` or `NULL` (in non-interactive mode).

`eval_isotopes` *Evaluate isotope information*

Description

Add isotope information to the parent mass and optionally remove isotopoloques from mfd table. Required for further data evaluation that considers isotope information.

Usage

```
eval_isotopes(mfd, remove_isotopes = TRUE, verbose = FALSE, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`remove_isotopes`	If set to TRUE (default), all entries for isotopologues are removed from mfd. The main isotope information for each parent ion is still maintained in the "intxy"-columns.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Additional arguments passed to methods.

Value

A data.table with additional columns such as "int_13c" containing stable isotope abundance information.

Author(s)

Boris P. Koch

See Also

Other Formula assignment: `add_known_mf()`, `calc_eval_params()`, `check_formula_library()`, `ume_assign_formulas()`

Examples

```
eval_isotopes(mfd = mf_data_demo)
```

`filter_int` *Filter by (relative) peak magnitude*

Description

This function filters molecular formulas by (relative) peak abundances.

Usage

```
filter_int(mfd, norm_int_min = NULL, norm_int_max = NULL, verbose = FALSE, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`norm_int_min`	Lower threshold (>=) of (normalized) peak magnitude
`norm_int_max`	Upper threshold (<=) of (normalized) peak magnitude
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Arguments passed on to `calc_norm_int` `ms_id` Character; name of the column identifying individual spectra (default: `"file_id"`). `peak_id` Character; name of the column identifying unique peaks (default: `"peak_id"`). `peak_magnitude` Character; name of the column containing peak intensity values (default: `"i_magnitude"`). `normalization` Character; normalization method to apply. One of `"bp"`, `"sum"`, `"sum_ubiq"`, `"sum_rank"`, `"none"`. Default is `"bp"`. `n_rank` Integer; number of top-ranked peaks to use for `"sum_rank"` normalization (default: 200).

Value

data.table; subset of original molecular formula table

See Also

Other Formula subsetting: `filter_mass_accuracy()`, `filter_mf_data()`, `remove_blanks()`, `subset_known_mf()`, `ume_assign_formulas()`, `ume_filter_formulas()`

Examples

```
filter_int(mfd = calc_norm_int(mfd = mf_data_demo,
normalization = "sum_rank", n_rank = 100), norm_int_min = 1)
```

`filter_mass_accuracy` *Automated filter for mass accuracy*

Description

This function automatically sets a filter for mass accuracy for each individual spectrum.

Usage

```
filter_mass_accuracy(
  mfd,
  ma_col = "ppm",
  file_col = "file_id",
  msg = FALSE,
  ...
)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`ma_col`	Name of the column that contains mass accuracy values in ppm (string)
`file_col`	Name of the column that contains file name
`msg`	logical. Deprecated synonym for `verbose`.
`...`	Additional arguments passed to methods.

Value

data.table; subset of original molecular formula table

See Also

Other Formula subsetting: `filter_int()`, `filter_mf_data()`, `remove_blanks()`, `subset_known_mf()`, `ume_assign_formulas()`, `ume_filter_formulas()`

`filter_mf_data` *Filter molecular formula data by mass spectrometric metadata*

Description

This function filters molecular formulas by isotope numbers, element ratios, etc.

Usage

```
filter_mf_data(
  mfd,
  c_iso_check = FALSE,
  n_iso_check = FALSE,
  s_iso_check = FALSE,
  ma_dev = 3,
  dbe_max = 999,
  dbe_o_min = -999,
  dbe_o_max = 999,
  mz_min = 1,
  mz_max = 9999,
  n_min = 0,
  n_max = 999,
  s_min = 0,
  s_max = 999,
  p_min = 0,
  p_max = 999,
  oc_min = 0,
  oc_max = 999,
  hc_min = 0,
  hc_max = 999,
  nc_min = 0,
  nc_max = 99,
  verbose = FALSE,
  ...
)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`c_iso_check`	(TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope
`n_iso_check`	(TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope

s_iso_check	(TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope
ma_dev	Deviation range of mass accuracy in +/- ppm (default: 3 ppm)
dbe_max	Maximum number for DBE
dbe_o_min	Minimum number for DBE minus O atoms
dbe_o_max	Maximum number for DBE minus O atoms
mz_min	Minimum of mass to charge value
mz_max	Maximum of mass to charge value
n_min	Minimum number of nitrogen atoms
n_max	Maximum number of nitrogen atoms
s_min	Minimum number of nitrogen atoms
s_max	Maximum number of nitrogen atoms
p_min	Minimum number of nitrogen atoms
p_max	Maximum number of nitrogen atoms
oc_min	Minimum atomic ratio of oxygen / carbon
oc_max	Maximum atomic ratio of oxygen / carbon
hc_min	Minimum atomic ratio of hydrogen / carbon
hc_max	Maximum atomic ratio of hydrogen / carbon
nc_min	Minimum atomic ratio of nitrogen / carbon
nc_max	Maximum atomic ratio of nitrogen / carbon
verbose	logical; if TRUE, show progress messages.
...	Additional arguments passed to methods.

Value

data.table; subset of original molecular formula table

Author(s)

Boris P. Koch

See Also

Other Formula subsetting: filter_int(), filter_mass_accuracy(), remove_blanks(), subset_known_mf(), ume_assign_formulas(), ume_filter_formulas()

Examples

```
filter_mf_data(mfd = mf_data_demo, dbe_o_max = 10)
```

get_isotope_info *Retrieve NIST element and isotope data*

Description

Checks if element/isotope columns are present in `mfd` and lookup of NIST isotope information (based on masses). Can be applied to a formula library and any table having molecular formula data. If only an element name is identified, the symbol and data of the lightest isotope of the element will be returned. For example, the column name "C" will return "12C" isotope data.

Usage

```
get_isotope_info(mfd, masses = ume::masses, verbose = FALSE, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`masses`	A data.table. Defaults to `ume::masses` (based on NIST data) containing isotope information for elements, including nominal and exact mass, relative abundance, and Hill system order.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Additional arguments passed to methods.

Value

A data.table containing information on all isotopes identified in mfd and a column "orig_name" having the original names of the isotope / element columns in `mfd`. Results are ordered according to Hill system.

Examples

```
get_isotope_info(mfd = mf_data_demo, verbose = TRUE)
```

is_ume_peaklist *Check whether an object is a UME peaklist*

Description

Check whether an object is a UME peaklist

Usage

```
is_ume_peaklist(x)
```

Arguments

x	Any object

Value

TRUE/FALSE

---

known_mf *Collection of known formulas, for which additional information is available.*

Description

Known formulas; contains formulas for which additional knowledge is available. This can be also calibration lists. Due to size reasons the table is restricted to what is covered by standard UME formula library (mz<=700, elements CHONSP considered). The original version is part of the UME database and transferred to UME using UTF-8 encoding. CRAM molecular formulas are taken from the supplementary material that is provided by Hertkorn et al. (2006).

Usage

```
known_mf
```

Format

A data.table with ~300,000 rows and 14 variables:

mz Mass to charge ratio (numeric)

mf molecular formula

Source

taken from www.awi.de

See Also

Other ume data: lib_demo, masses, mf_data_demo, nice_labels_dt, peaklist_demo, tab_ume_labels

Examples

```
data(known_mf)
```

lib_demo *Demo formula library (200 - 300 Da, neutral mass)*

Description

Contains a small molecular formula library for demonstration and validation purposes. Complete formula libraries are available in the 'ume.formulas' data package.

Usage

```
lib_demo
```

Format

A data.table having ~115,111 rows and 12 variables:

vkey First two digits represent the formula library version; last digits are unique identifiers for each formula

mf Neutral molecular formula (no differentiation of isotopes)

mass Calculated exact neutral mass of a formula (based on ume::masses)

See Also

Other ume data: known_mf, masses, mf_data_demo, nice_labels_dt, peaklist_demo, tab_ume_labels

Examples

```
data(peaklist_demo)
```

masses *Masses: Elements and isotopes*

Description

Contains masses, valences, isotopes and isotope ratios of elements based on data by NIST Physical Measurement Laboratory (https://www.nist.gov/pml).

Usage

```
masses
```

Format

A data.table having 288 rows and 23 variables:

element Element symbol in lower case

symbol Element symbol in upper case

isotope Isotope symbol in lower case

label Isotope symbol in upper case

nm Nominal mass of the isotope

exact_mass Exact mass of the isotope

mole_fraction Mole fraction compared to all isotopes of an element

relative_abundance Relative abundance compared to the main (most abundant) isotope

valence Valence at standard conditions

valence2 Alternative valence at standard conditions

hill_order Rank in Hill Order for molecular formulas (cf. https://en.wikipedia.org/wiki/Chemical_formula)

Source

https://www.nist.gov/pml/atomic-weights-and-isotopic-compositions-relative-atomic-masses

See Also

Other ume data: `known_mf`, `lib_demo`, `mf_data_demo`, `nice_labels_dt`, `peaklist_demo`, `tab_ume_labels`

Examples

```
data(masses)
```

`mf_data_demo` *mf_data_demo*

Description

Contains molecular formula data and metainformation on formulas. The metainformation

Usage

```
mf_data_demo
```

Format

A data.table with ~9245 rows (formulas) and 65 variables:

file_id Unique ID (integer) for each analysis

peak_id Unique ID (integer) for each mass peak in the peak list 'pl'

mz Mass to charge ratio of the singly charged molecular ion (numeric)

i_magnitude Measured mass peak magnitude of the singly charged molecular ion (numeric)

norm_int Normalized intensity as calculated by calc_norm_int()

m Neutral measured mass of the molecular ion

m_cal Neutral calculated mass of the assigned formula

ppm Realtive mass accuracy of measured mass compared to m_cal (in ppm)

nm Nominal mass of the neutral molecule

mf molecular formula (no differentiation of isotopes)

dbe Double bond equivalent

`12C` Number of carbon atoms (12C)

`1H` Number of hydrogen atoms

hc hydrogen / carbon ratio in a molecular formula

oc oxygen / carbon ratio in a molecular formula

nc nitrogen / carbon ratio in a molecular formula

sc sulfur / carbon ratio in a molecular formula

ai Aromaticity index according to Koch and Dittmar (2008, 2016)

z z score according to Stenson et al. (2003)

kmd Kendrick mass defect (based on CH2-units) according to Kendrick (1963)

ppm_filt Calculated threshold value for relative mass accuracy (in ppm) that can be used for formular filtering

mf_id Identifier for each unique molecular formula identified in the unfiltered dataset

CRAM Molecular formula that was identified (CRAM == 1) as carboxylic rich alicyclic molecule according to Hertkorn et al. (2006). See ume::known_mf for details.

int13c Measured relative peak magnitude of the 13C1 isotope compared to the parent ion (0 if isotope was not existing)

int15n Measured relative peak magnitude of the 15N1 isotope compared to the parent ion (0 if isotope was not existing)

int34s Measured relative peak magnitude of the 34S1 isotope compared to the parent ion (0 if isotope was not existing)

dev_n_c Deviation of the 12C/13C isotope ratio represented in carbon numbers according to Koch et al. (2007)

dbe_o DBE minus O

nosc Nominal oxidation state of carbon according to LaRowe & Van Cappellen (2011)

delg0_cox Standard molal Gibbs energies of the oxidation half reactions of organic compounds according to LaRowe & Van Cappellen (2011)

co_tot Total number of carbon and oxygen atoms in a molecular formula

nsp_tot Total number of nitrogen, sulfur, and phosphorus atoms in a molecular formula

n_occurrence_orig Number of occurrences of a molecular formula in the entire unfiltered set of formulas

n_assignments_orig Number of molecular formula assignments per molecular mass in the unfiltered set of formulas

n_assignments Number of molecular formula assignments per molecular mass after filter process

int_bp Magnitude of the base peak in a mass spectrum

int_bp Total magnitude of the reference that was used for normalization (cf. calc_norm_int())

Source

taken from www.awi.de

See Also

Other ume data: known_mf, lib_demo, masses, nice_labels_dt, peaklist_demo, tab_ume_labels

Examples

```
data(mf_data_demo)
```

`nice_labels_dt` *nice_labels_dt*

Description

nice_labels_dt

Usage

```
nice_labels_dt
```

Format

A data.table with labels that can be used for plots

name_substitute Name that will be displayed instead of the standard column name

name_pattern Name of the standard column in ume tables

Source

taken from www.awi.de

See Also

Other ume data: known_mf, lib_demo, masses, mf_data_demo, peaklist_demo, tab_ume_labels

Examples

```
data(nice_labels_dt)
```

`order_columns` *Order columns*

Description

Take most prominent columns required for data evaluation first - followed by all other columns.

Usage

```
order_columns(mfd, col_order = NULL, ...)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`col_order`	A list of column names that defines the order of columns of mfd. Default is: cols = c("sample_tag", "sample_id", "file", "file_id", "peak_id", "i_magnitude", "norm_int", "m", "m_cal", "ppm", "nm", "mf", "dbe", "c", "h", "n", "o", "p", "s", "hc", "oc", "nc", "sc", "ai", "z", "kmd") If "cols" is NULL the default order is applied.
`...`	Additional arguments passed to methods.

Value

A data.table containing isotope data for those isotopes present in mfd.

See Also

Other tools: `add_missing_element_columns()`

Examples

```
order_columns(mfd = mf_data_demo)
```

peaklist_demo *Demo peak list*

Description

Contains parts of the peaklist (200 - 300 m/z) from mass spectra to use as demonstration and validation dataset. The sample mass spectra contain one blank, three replicates of North Sea water, and three Arctic fjord samples as triplicates.

Usage

```
peaklist_demo
```

Format

A data.table having 31,091 rows and 7 variables:

file_id A unique identifier for a mass spectrum (integer)

file A unique label for a mass spectrum or sample (character)

peak_id A unique identifier for a peak in the entire peak list (integer)

mz Mass to charge ratio of the singly charged molecular ion (numeric)

i_magnitude Peak magnitude of the molecular ion (numeric)

s_n Signal to noise ratio of the molecular ion (numeric)

res Mass resolution of the peak / ion (numeric)

Source

taken from www.awi.de

See Also

Other ume data: known_mf, lib_demo, masses, mf_data_demo, nice_labels_dt, tab_ume_labels

Examples

```
data(peaklist_demo)
```

`remove_blanks` *Remove molecular formulas detected in blanks*

Description

Remove all molecular formulas that were detected in one or more blank analyses (identified via `blank_file_ids`). Matching is always on `mf`. If a retention-time column is present (or provided using `ret_time_col`), removal is restricted to the corresponding LC segment.

Usage

```
remove_blanks(
  mfd,
  blank_file_ids = NULL,
  blank_prevalence = 0.5,
  ret_time_col = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

`mfd`	data.table with molecular formula data as derived from `ume::assign_formulas`. Column names of elements/isotopes must match names in the `isotope` column of `ume::masses`; values are integers representing counts per formula.
`blank_file_ids`	Integer vector of `file_id` values that represent blank analyses.
`blank_prevalence`	Numeric between 0 and 1. Threshold for blank filtering: the proportion of blanks in which a molecular formula must occur before it is excluded from the sample data. For example, `blank_prevalence = 0` (default) removes any formula detected in at least one blank, while `blank_prevalence = 0.5` removes formulas detected in 50% or more of the blanks.
`ret_time_col`	Character scalar. Name of the retention-time column that contains the beginning of the retention time segment that corresponds to the mass spectrum. If `NULL` (default), the function will auto-detect the first column in `c("ret_time_min","retention_time","rt",` that exists in `mfd`. If none is found, blanks are removed ignoring retention time.
`verbose`	logical; if `TRUE`, show progress messages.
`...`	Additional arguments passed to methods.

Details

- Requires a unique integer `file_id` per analysis in `mfd`.
- Minimal required columns in `mfd`: `mf`, `file_id`.
- Optional column: a retention-time column (e.g. `"ret_time_min"`).

- If a retention-time column is used, formulas present in blanks are only removed for rows whose `mf` **and** retention time match
- The input `mfd` is **not** modified by reference; a subset is returned.

Value

`data.table`; subset of the original molecular formula table (`mfd`) with blank formulas removed (globally or LC-segment-wise).

Backward compatibility

The argument `LCMS` is deprecated and no longer used. Retention-time-aware removal is now enabled automatically when a retention-time column is present or explicitly provided via `ret_time_col`.

Author(s)

Boris P. Koch

See Also

Other Formula subsetting: `filter_int()`, `filter_mass_accuracy()`, `filter_mf_data()`, `subset_known_mf()`, `ume_assign_formulas()`, `ume_filter_formulas()`

Examples

```
# Presence/absence removal, no retention time:
remove_blanks(mfd = mf_data_demo,
              remove_blank_list = "Blank",
              verbose = TRUE)
```

---

remove_empty_columns *Remove empty columns*

Description

Removes columns that contain only `NA` values from a `data.table`. Columns listed in `excl_cols` are retained even if they are empty.

Usage

```
remove_empty_columns(df, excl_cols = NULL, ...)
```

Arguments

`df`	A `data.table` from which empty columns should be removed.
`excl_cols`	Optional character vector of column names that must be preserved, even if all values in those columns are missing.
`...`	Additional arguments passed to methods.

Value

A `data.table` containing all original non-empty columns, plus any columns listed in `excl_cols`, regardless of whether they are empty. Columns that contain only `NA` values and are *not* explicitly preserved are removed from the output.

Examples

```
dt <- data.table::data.table(
  c = c(2, 2, 2),
  x = c(NA, NA, NA),
  y = c(NA, NA, NA)
)
remove_empty_columns(dt, excl_cols = "y")
```

`remove_id_columns` *Remove columns that contain ID's*

Description

This functions removes columns ID columns ('_id') and hierarchical search columns ('_lft', '_rgt') from a table. Only exceptions are "sample_id" and "bottle_id that are always kept in the output table.

Usage

```
remove_id_columns(df, ...)
```

Arguments

`df`	data.table that contains ID columns
`...`	Additional arguments passed to methods.

See Also

Other Clean data output: `remove_unknown_columns()`

remove_unknown_columns

Remove columns that only have one specific value

Description

This function removes columns that exclusively contain the value defined in 'search_term' (such as " unknown" (default)).

Usage

```
remove_unknown_columns(df, excl_cols = NULL, search_term = " unknown", ...)
```

Arguments

df	data.table that contains empty columns
excl_cols	List of column names that should not be removed, even if all values contain search_term
search_term	String that uniquely occurs in one column
...	Additional arguments passed to methods.

See Also

Other Clean data output: remove_id_columns()

subset_known_mf

Subsetting known molecular formula categories

Description

Subset all molecular formulas that are present in one or more categories of ume::known_mf. Based on presence / absence.

Usage

```
subset_known_mf(
  mfd,
  select_category = NULL,
  exclude_category = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
select_category	List of category names that should be selected
exclude_category	List of category names that should be ignored
verbose	logical; if TRUE, show progress messages.
...	Additional arguments passed to methods.

Value

data.table; subset of original molecular formula data.table (mfd)

See Also

Other Formula subsetting: filter_int(), filter_mass_accuracy(), filter_mf_data(), remove_blanks(), ume_assign_formulas(), ume_filter_formulas()

Examples

```
subset_known_mf(category_list = c("marine_dom"), mfd = mf_data_demo, verbose = TRUE)
```

---

tab_ume_labels *Labels of UME columns.*

Description

Labels of UME columns.

Usage

```
tab_ume_labels
```

Format

A data.table that is derived from the MarChem database:

label Identifier for each label

nice_label Label that can be used e.g. in figures

use_in_ume Shows if label is used in the UME shiny app

Source

taken from www.awi.de

See Also

Other ume data: known_mf, lib_demo, masses, mf_data_demo, nice_labels_dt, peaklist_demo

Examples

```
data(tab_ume_labels)
```

`theme_uplots` *theme_uplots*

Description

Applies a clean UME-style theme used across all uplot_* visualisations. Matches the styling of `uplot_vk()`: white background, no grid, black axis lines, black ticks, and consistent font sizing.

Usage

```
theme_uplots(base_size = 12, base_family = "")
```

Arguments

`base_size`	Numeric base font size (default = 12).
`base_family`	Base font family.

Details

Unified UME Theme for All uplot_* Functions

Value

A ggplot2 theme object.

`ume_assign_formulas` *Complete formula assignment (wrapper function)*

Description

Assigns molecular formulas to neutral molecular masses and calculates all parameters required for data evaluation, such as a posteriori filtering of molecular formulas, plotting, and statistics. The function uses a pre-build molecular formula library.

Usage

```
ume_assign_formulas(pl, formula_library, verbose = FALSE, ...)
```

Arguments

pl	data.table containing peak data. Mandatory columns include neutral molecular mass (mass), peak magnitude (i_magnitude), and a peak identifier (peak_id).
formula_library	Molecular formula library: a predefined data.table used for assigning molecular formulas to a peak list and for mass calibration. The library requires a fixed format, including mass values for matching. Predefined libraries are available in the R package *ume.formulas* and further described in Leefmann et al. (2019). A standard library for marine dissolved organic matter is ume.formulas::lib_02. New libraries can be built using ume::create_ume_formula_library().
verbose	logical; if TRUE, show progress messages.
...	Arguments passed on to calc_ma_abs, calc_neutral_mass, assign_formulas, eval_isotopes, calc_eval_params, add_known_mf, calc_norm_int m Measured mass ma_dev Mass accuracy in +/- parts per million (ppm) mz Numeric vector of m/z values (> 0). pol Character: "neg", "pos", or "neutral". remove_isotopes If set to TRUE (default), all entries for isotopologues are removed from mfd. The main isotope information for each parent ion is still maintained in the "intxy"-columns. mfd data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula. mf_col Name of the column in mfd that has the molecular formula information (default: "mf"). Formulas have upper case element symbols and elements in the formula are ordered according to the Hill system. known_mf data.table with known molecular formulas (ume::known_mf). ms_id Character; name of the column identifying individual spectra (default: "file_id"). peak_id Character; name of the column identifying unique peaks (default: "peak_id"). peak_magnitude Character; name of the column containing peak intensity values (default: "i_magnitude"). normalization Character; normalization method to apply. One of "bp", "sum", "sum_ubiq", "sum_rank", "none". Default is "bp". n_rank Integer; number of top-ranked peaks to use for "sum_rank" normalization (default: 200).

Details

All function arguments: args(filter_mf_data) args(filter_int)

Value

A data.table having molecular formula assignments for each mass.

See Also

Other Formula assignment: add_known_mf(), calc_eval_params(), check_formula_library(), eval_isotopes()

Other Formula subsetting: filter_int(), filter_mass_accuracy(), filter_mf_data(), remove_blanks(), subset_known_mf(), ume_filter_formulas()

Other ume wrapper: ume_filter_formulas()

Examples

```
ume_assign_formulas(pl = peaklist_demo, formula_library = lib_demo, pol = "neg", ma_dev = 0.2)
```

---

ume_filter_formulas *Complete Formula subsetting / filtering (wrapper)*

Description

A wrapper function to filter molecular formulas according to a evaluation parameters.

Usage

```
ume_filter_formulas(mfd, verbose = FALSE, ...)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
verbose	logical; if TRUE, show progress messages.
...	Arguments passed on to filter_mf_data, subset_known_mf, calc_norm_int, filter_int, remove_blanks
	c_iso_check (TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope
	n_iso_check (TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope
	s_iso_check (TRUE / FALSE); check if formulas are verified by the presence of the main daughter isotope
	ma_dev Deviation range of mass accuracy in +/- ppm (default: 3 ppm)
	dbe_max Maximum number for DBE
	dbe_o_min Minimum number for DBE minus O atoms
	dbe_o_max Maximum number for DBE minus O atoms
	mz_min Minimum of mass to charge value
	mz_max Maximum of mass to charge value
	n_min Minimum number of nitrogen atoms
	n_max Maximum number of nitrogen atoms

`s_min` Minimum number of nitrogen atoms

`s_max` Maximum number of nitrogen atoms

`p_min` Minimum number of nitrogen atoms

`p_max` Maximum number of nitrogen atoms

`oc_min` Minimum atomic ratio of oxygen / carbon

`oc_max` Maximum atomic ratio of oxygen / carbon

`hc_min` Minimum atomic ratio of hydrogen / carbon

`hc_max` Maximum atomic ratio of hydrogen / carbon

`nc_min` Minimum atomic ratio of nitrogen / carbon

`nc_max` Maximum atomic ratio of nitrogen / carbon

`select_category` List of category names that should be selected

`exclude_category` List of category names that should be ignored

`ms_id` Character; name of the column identifying individual spectra (default: `"file_id"`).

`peak_id` Character; name of the column identifying unique peaks (default: `"peak_id"`).

`peak_magnitude` Character; name of the column containing peak intensity values (default: `"i_magnitude"`).

`normalization` Character; normalization method to apply. One of `"bp"`, `"sum"`, `"sum_ubiq"`, `"sum_rank"`, `"none"`. Default is `"bp"`.

`n_rank` Integer; number of top-ranked peaks to use for `"sum_rank"` normalization (default: 200).

`norm_int_min` Lower threshold (>=) of (normalized) peak magnitude

`norm_int_max` Upper threshold (<=) of (normalized) peak magnitude

`blank_file_ids` Integer vector of `file_id` values that represent blank analyses.

`blank_prevalence` Numeric between 0 and 1. Threshold for blank filtering: the proportion of blanks in which a molecular formula must occur before it is excluded from the sample data. For example, `blank_prevalence = 0` (default) removes any formula detected in at least one blank, while `blank_prevalence = 0.5` removes formulas detected in 50% or more of the blanks.

`ret_time_col` Character scalar. Name of the retention-time column that contains the beginning of the retention time segment that corresponds to the mass spectrum. If `NULL` (default), the function will auto-detect the first column in `c("ret_time_min","retention_time","rt","RT")` that exists in `mfd`. If none is found, blanks are removed ignoring retention time.

Value

A data.table having molecular formula assignments for each mass. ume_filter_formulas(mfd = mf_data_demo, dbe_o_max = 15, norm_int_min = 2)

See Also

Other Formula subsetting: `filter_int()`, `filter_mass_accuracy()`, `filter_mf_data()`, `remove_blanks()`, `subset_known_mf()`, `ume_assign_formulas()`

Other ume wrapper: `ume_assign_formulas()`

uplot_cluster *uplot_cluster*

Description

This function plots the results of a cluster analysis and a multi-dimensional scaling (MDS) plot based on the input data. It first creates a hierarchical cluster dendrogram using the Bray-Curtis dissimilarity index, followed by an MDS plot for dimensionality reduction. The function outputs both plots side by side.

Usage

```
uplot_cluster(mfd, grp = "file_id", int_col = "norm_int", ...)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
grp	Character vector. Names of columns (e.g., sample or file identifiers) used to aggregate results.
int_col	Character. The name of the column that contains the intensity values to be used (e.g. for clustering or color coding). Default usually is "norm_int" for normalized intensity values.
...	Additional arguments passed to methods.

Details

Plot Cluster Analysis and Multi-Dimensional Scaling

Value

A named list with two elements:

dendrogram A recordedplot object containing the hierarchical clustering dendrogram generated from the Bray–Curtis dissimilarity matrix.

mds A plotly object representing the two-dimensional Multi-Dimensional Scaling (MDS) scatter plot. This can be rendered interactively in HTML or converted to a static ggplot object if needed.

The function always returns a list with these two components.

Note

This function requires the vegan package for the Bray-Curtis dissimilarity and MDS calculations.

See Also

Other plots: uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
# Example with demo data
  out <- uplot_cluster(mfd = mf_data_demo, grp = "file", int_col = "norm_int")
  out$dendrogram
  out$mds
```

---

uplot_cvm *Plot of Molecular Mass (M) vs. Number of Carbon Atoms (C)*

Description

Generates a scatter plot of *molecular mass (M)* versus *carbon atom count (C)*, color-coded by a selected variable (z_var).

This visualization follows the concept of the Carbon-vs-Mass (CvM) diagram introduced by **Reemtsma (2010)**.

Usage

```
uplot_cvm(
  df,
  z_var = "co_tot",
  palname = "redblue",
  tf = FALSE,
  col_bar = TRUE,
  gg_size = 12,
  logo = TRUE,
  plotly = FALSE,
  ...
)
```

Arguments

df	A data.table containing columns: nm Molecular mass (Da) 12C Number of carbon atoms z_var Variable used for color projection
z_var	Character. Column used for color mapping.
palname	Character. Palette name passed to f_colorz().

tf	Logical. If TRUE, applies a transformation to the color scale (default is FALSE).
col_bar	Logical. If TRUE, adds a color legend (default is TRUE).
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages.

Details

Plot of Molecular Mass (M) vs. Number of Carbon Atoms (C)

Value

A ggplot2 or Plotly object.

References

Reemtsma, T. (2010). *The carbon versus mass diagram to visualize and exploit FTICR-MS data of natural organic matter.* J. Mass Spectrom., **45**, 382–390. doi:10.1002/jms.1722

See Also

Other plots: uplot_cluster(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_cvm(mf_data_demo, z_var = "co_tot", logo = FALSE)
```

---

uplot_dbe_minus_o_freq

Frequency Plot of DBE - O

Description

Creates a bar plot showing the frequency distribution of dbe_o (DBE minus oxygen). The plot uses the unified UME plotting theme and optionally adds a small UME caption. A Plotly version can be returned.

Usage

```
uplot_dbe_minus_o_freq(df, gg_size = 12, logo = TRUE, plotly = FALSE, ...)
```

Arguments

df	A data.table containing at least the column dbe_o.
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.
...	Additional arguments passed to methods.

Value

A ggplot2 object or, if requested, a Plotly object.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_dbe_minus_o_freq(mf_data_demo)
```

---

uplot_dbe_vs_c *Plot DBE vs Carbon Atoms*

Description

Creates a scatter plot of DBE (double bond equivalents) vs. number of carbon atoms. Points are color-coded by a selected variable (z_var). The plot follows the same stylistic conventions as the other uplot_* functions, including the unified theme and optional UME caption.

Usage

```
uplot_dbe_vs_c(
  df,
  z_var = "norm_int",
  palname = "redblue",
  col_bar = TRUE,
  tf = FALSE,
  logo = TRUE,
  gg_size = 12,
```

```
  plotly = FALSE,
  ...
)
```

Arguments

df	A data.table containing columns: 12C, dbe, and the variable given in z_var.
z_var	Variable used for color coding (default "norm_int").
palname	Color palette name for f_colorz() (viridis, magma, plasma, etc.).
col_bar	Logical. If TRUE, adds a color legend (default is TRUE).
tf	Logical. If TRUE, applies a transformation to the color scale (default is FALSE).
logo	Logical. If TRUE, adds a UME caption.
gg_size	Base text size for theme_uplots(). Default = 12.
plotly	If TRUE, returns a plotly interactive plot.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages.

Value

A ggplot2 object or a plotly object (if plotly = TRUE).

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_dbe_vs_c(mf_data_demo, z_var = "norm_int")
```

---

uplot_dbe_vs_o *Plot DBE vs Oxygen Atoms (cf. Herzsprung et al. 2014) with Option for Interactive Plot*

Description

This function generates a scatter plot of Double Bond Equivalent (DBE) versus the number of oxygen atoms (o). It allows for optional customization of colors based on a specified variable (z_var) and offers the option to convert the plot to an interactive plotly object.

Usage

```
uplot_dbe_vs_o(
  df,
  z_var = "norm_int",
  palname = "redblue",
  col_bar = TRUE,
  tf = FALSE,
  logo = TRUE,
  cex.axis = 12,
  cex.lab = 15,
  plotly = FALSE,
  ...
)
```

Arguments

df	A data frame containing the data. The columns 160 (number of oxygen atoms), dbe (DBE values), and the column specified in z_var should be present in the data.
z_var	Character. Column name for variable used for color-coding. Content of column should be numeric.
palname	Color palette name for f_colorz() (viridis, magma, plasma, etc.).
col_bar	Logical. If TRUE, adds a color legend (default is TRUE).
tf	Logical. If TRUE, applies a transformation to the color scale (default is FALSE).
logo	Logical. If TRUE, adds a UME caption.
cex.axis	Numeric. Size of axis text (default is 1).
cex.lab	Numeric. Size of axis labels (default is 1.4).
plotly	Logical. If TRUE, return interactive plotly object.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages.

Value

A ggplot object or a plotly object depending on the plotly argument.

uplot_dbe_vs_ppm *Plot DBE vs ppm with Option for Interactive Plot*

Description

This function generates a scatter plot of DBE (Double Bond Equivalent) versus parts per million (ppm) from the provided data. It also provides the option to customize the appearance and to return an interactive `plotly` plot.

Usage

```
uplot_dbe_vs_ppm(
  df,
  size_dots = 0.5,
  cex.axis = 1,
  cex.lab = 1.4,
  plotly = FALSE,
  ...
)
```

Arguments

`df`	A data frame containing the data. The columns `ppm` (ppm values), `dbe` (DBE values), and `file_id` (for coloring the points) should be present in the data.
`size_dots`	Numeric. Size of the dots in the plot (default = 0.5).
`cex.axis`	Numeric. Size of axis text (default is `1`).
`cex.lab`	Numeric. Size of axis labels (default is `1.4`).
`plotly`	Logical. If TRUE, return interactive plotly object.
`...`	Additional arguments passed to methods.

Value

A `ggplot` object or a `plotly` object depending on the `plotly` argument.

uplot_freq *Frequency Plot of a Selected Variable*

Description

Creates a frequency plot (bar plot) for a selected variable in a molecular formula dataset. Values are grouped and counted, then visualized as bars. A unified UME plot theme is applied for consistent styling across all uplot_* functions.

Usage

```
uplot_freq(
  mfd,
  var = "14N",
  col = "grey",
  space = 0.5,
  width = 0.3,
  logo = TRUE,
  gg_size = 12,
  plotly = FALSE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
var	Character. Name of the variable for which the frequency distribution should be plotted (e.g. "14N").
col	Bar fill color.
space	Not used (kept for backward compatibility).
width	Bar width.
logo	Logical. If TRUE, adds a UME caption.
gg_size	Base text size for theme_uplots(). Default = 12.
plotly	Logical. If TRUE, return interactive plotly object.
...	Additional arguments passed to methods.

Value

A ggplot object, or a plotly object when plotly = TRUE.

---

uplot_freq_ma *Histogram of Mass Accuracy*

Description

Creates a histogram of mass accuracy values (ppm). Includes summary statistics (median, 2.5% and 97.5% quantiles). Follows general uplot behavior:

- returns a ggplot2 object by default
- converts to plotly *only if* plotly = TRUE
- uses caption-style UME logo

Usage

```
uplot_freq_ma(
  mfd,
  ma_col = "ppm",
  col = "grey",
  gg_size = 12,
  logo = TRUE,
  plotly = FALSE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
ma_col	Character string. Column name containing mass accuracy values.
col	Histogram fill color.
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.
...	Additional arguments passed to methods.

Value

ggplot2 object, or plotly object if plotly = TRUE.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

---

uplot_freq_vs_ppm *Mass Accuracy Frequency Histogram*

Description

Creates a histogram showing the frequency distribution of mass accuracy values (ppm). Displays median and quantile statistics in the title and optionally adds a UME caption (logo). The plot uses the unified UME theme (theme_uplots()), ensuring visual consistency across all uplot_* functions.

Usage

```
uplot_freq_vs_ppm(
  df,
  col = "grey",
  width = 0.01,
  gg_size = 12,
  logo = TRUE,
  plotly = FALSE
)
```

Arguments

df	A data.table or data.frame containing columns: • ppm — mass accuracy in ppm • 14N, 32S, 31P, dbe_o — required for consistency with UME QC tools
col	Character. Histogram bar color. Default "grey".
width	Numeric. Histogram bin width (not used when bins = 100).
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.

Details

This plot is useful for visual inspection of mass accuracy performance. The required additional columns (14N, 32S, 31P, dbe_o) ensure that the dataset is a complete UME molecular formula table and can be compared to other quality-control plots.

Value

A **ggplot2 histogram**, or a **plotly object** if plotly = TRUE.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_freq_vs_ppm(mf_data_demo)
```

uplot_hc_vs_m *H/C vs Molecular Mass Plot*

Description

Creates a scatter plot of the hydrogen-to-carbon ratio (H/C) versus molecular mass (nm). Points are color-coded according to a selected intensity or property column (int_col). This visualization follows the conceptual design in Schmitt-Kopplin et al. (2010).

The function can optionally add a branding label ("UltraMassExplorer") and can optionally return an interactive Plotly version of the plot.

Usage

```
uplot_hc_vs_m(
  df,
  int_col = "norm_int",
  palname = "redblue",
  size_dots = 1.2,
  gg_size = 12,
  logo = TRUE,
  plotly = FALSE,
  ...
)
```

Arguments

df	A data.table containing columns: • nm: molecular mass • hc: hydrogen-to-carbon ratio • int_col: the column used for color-coding
int_col	Character, column used for color-coding. Default "norm_int".
palname	Character, palette name passed to f_colorz().
size_dots	Numeric. Size of the dots in the plot (default = 0.5).
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages. tf Logical. If TRUE, applies a transformation to the color scale (default is FALSE).

Value

A ggplot2 scatter plot, or a plotly object if plotly = TRUE.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_hc_vs_m(mf_data_demo, int_col = "norm_int")
```

---

uplot_heteroatoms *Heteroatom Combination vs Mass Accuracy*

Description

Produces a boxplot visualizing the distribution of mass accuracy (ppm) for different heteroatom combinations (nsp_type) defined by the number of nitrogen (N), sulfur (S), and phosphorus (P) atoms in each formula.

The plot can be returned as either a ggplot object or as an interactive plotly object (plotly = TRUE). An optional "UltraMassExplorer" watermark can be added.

Usage

```
uplot_heteroatoms(df, col = "grey", gg_size = 12, logo = TRUE, plotly = FALSE)
```

Arguments

df	A data.table containing at least: • nsp_type: character or factor indicating heteroatom combinations • ppm: numeric mass accuracy values
col	Character. Box color. Default "grey".
gg_size	Base text size for theme_uplots(). Default = 12.
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.

Value

A ggplot or plotly interactive boxplot.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_heteroatoms(mf_data_demo)
```

`uplot_isotope_precision`

Precision of Isotope Abundance

Description

Visualizes the deviation between measured and theoretical 13C isotope ratios. Supports optional data reduction (binning) to greatly enhance interactive rendering speed in Plotly.

Usage

```
uplot_isotope_precision(
  mfd,
  z_var = "nsp_tot",
  int_col = "norm_int",
  size_dots = 1.5,
  bins = 100,
  data_reduction = FALSE,
  tf = FALSE,
  logo = TRUE,
  plotly = FALSE,
  cex.axis = 1,
  cex.lab = 1.4
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
z_var	Column used for color mapping (default: "nsp_tot")
int_col	Intensity column (default: "norm_int")
size_dots	Numeric. Size of the dots in the plot (default = 0.5).
bins	Number of bins used when data_reduction = TRUE

data_reduction	Logical. If TRUE, bins the data and uses bin medians (recommended for very large datasets; speeds up rendering massively).
tf	Logical. If TRUE, applies a transformation to the color scale (default is FALSE).
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. Return a plotly object instead of ggplot.
cex.axis	Numeric. Size of axis text (default is 1).
cex.lab	Numeric. Size of axis labels (default is 1.4).

Value

A ggplot or plotly object.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

---

uplot_kmd *Kendrick Mass Defect (KMD) vs. Nominal Mass Plot*

Description

This function generates a scatter plot of Kendrick Mass Defect (KMD) versus nominal mass (nm), with color-coding based on a specified variable (z_var). Optionally, the plot can be returned as an interactive Plotly object.

Usage

```
uplot_kmd(
  df,
  z_var = "norm_int",
  palname = "redblue",
  size_dots = 0.5,
  col_bar = TRUE,
  tf = FALSE,
  logo = TRUE,
  cex.axis = 12,
  cex.lab = 15,
  plotly = FALSE,
  ...
)
```

Arguments

df	A data.table or data.frame containing columns: • nm (nominal mass) • kmd (Kendrick mass defect) • the color variable given in z_var.
z_var	Character. Name of the column used for color mapping.
palname	Character. Palette name passed to f_colorz().
size_dots	Numeric. Point size.
col_bar	Logical. (Reserved for future use; currently ignored.)
tf	Logical. (Reserved for future use; currently passed to f_colorz() via ... if desired.)
logo	Logical. If TRUE, adds a UME caption.
cex.axis	Numeric. Axis text size.
cex.lab	Numeric. Axis label size.
plotly	Logical. If TRUE, return interactive plotly object.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages.

Details

Kendrick Mass Defect (KMD) vs. Nominal Mass Plot

Value

A ggplot object (or a plotly object if plotly = TRUE) showing KMD vs nominal mass.

References

Kendrick E. (1963). A mass scale based on CH_2 = 14.0000 for high resolution mass spectrometry of organic compounds. *Analytical Chemistry*, **35**, 2146–2154.

Hughey C.A., Hendrickson C.L., Rodgers R.P., Marshall A.G., Qian K.N. (2001). Kendrick mass defect spectrum: A compact visual analysis for ultrahigh-resolution broadband mass spectra. *Analytical Chemistry*, **73**, 4676–4681. doi:10.1021/ac010560w

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_kmd(mf_data_demo, z_var = "norm_int", plotly = TRUE)
```

`uplot_lcms` *Plot LC-MS Spectrum (or fallback MS if no RT available)*

Description

Creates a 3D LC–MS plot (RT x m/z x intensity) **when retention time is available**. If no retention-time column exists (e.g., with DI-FTMS demo data), the function gracefully falls back to `uplot_ms()` and issues an informative message.

Usage

```
uplot_lcms(
  pl,
  mass = "mz",
  peak_magnitude = "i_magnitude",
  retention_time = "ret_time_min",
  label = "file_id",
  logo = FALSE,
  ...
)
```

Arguments

`pl`	data.table containing peak data. Mandatory columns include neutral molecular mass (`mass`), peak magnitude (`i_magnitude`), and a peak identifier (`peak_id`).
`mass`	Column containing m/z values (default `"mz"`).
`peak_magnitude`	Column containing intensity (default `"i_magnitude"`).
`retention_time`	Column with retention time (default `"ret_time_min"`).
`label`	Sample/group labeling column (default `"file_id"`).
`logo`	Logical. If TRUE, adds a UME caption.
`...`	Additional arguments passed to methods.

Value

A plotly 3D visualization (LC-MS) or a 2D MS spectrum fallback.

See Also

Other plots: `uplot_cluster()`, `uplot_cvm()`, `uplot_dbe_minus_o_freq()`, `uplot_dbe_vs_c()`, `uplot_freq_ma()`, `uplot_freq_vs_ppm()`, `uplot_hc_vs_m()`, `uplot_heteroatoms()`, `uplot_isotope_precision()`, `uplot_kmd()`, `uplot_ma_vs_mz()`, `uplot_ms()`, `uplot_n_mf_per_sample()`, `uplot_pca()`, `uplot_ratios()`, `uplot_reproducibility()`, `uplot_ri_vs_sample()`, `uplot_vk()`

uplot_ma_vs_mz *Plot Mass Accuracy vs m/z*

Description

Generates a UME-style scatter plot showing mass accuracy (ppm) versus mass-to-charge ratio (m/z).

Summary statistics (median, 2.5% and 97.5% quantiles) are displayed as horizontal reference lines and an annotation panel.

The plot is returned as a **ggplot2 object** by default, with optional **plotly** conversion for interactivity.

Usage

```
uplot_ma_vs_mz(mfd, ma_col = "ppm", logo = FALSE, plotly = FALSE, ...)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
ma_col	Character. Column containing mass accuracy (ppm).
logo	Logical. If TRUE, adds a UME caption.
plotly	Logical. If TRUE, return interactive plotly object.
...	Additional arguments passed to methods.

Value

A ggplot or plotly object.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_ma_vs_mz(mf_data_demo, ma_col = "ppm")
```

uplot_ms *Plot Mass Spectrum*

Description

Plots the mass spectrum, showing magnitude versus mass-to-charge ratio (m/z). Optionally reduces the data by selecting the top `data_reduction` most abundant peaks per spectrum.

Usage

```
uplot_ms(
  pl,
  mass = "mz",
  peak_magnitude = "i_magnitude",
  label = "file_id",
  logo = FALSE,
  plotly = TRUE,
  data_reduction = 1,
  ...
)
```

Arguments

`pl`	A data table that must contain columns for mass-to-charge ratio and peak magnitude (could be peak list or molecular formula data).
`mass`	Character. Name of the column containing mass-to-charge or mass information (default = "mz").
`peak_magnitude`	Character. Name of the column containing (relative) peak magnitude information (default = "i_magnitude").
`label`	Character. Name of the column containing the names of the mass spectra to be displayed (default = "file_id").
`logo`	Logical. If TRUE, adds a UME caption.
`plotly`	Logical. If TRUE, return interactive plotly object.
`data_reduction`	Numeric. The percentage of the most abundant peaks to select per spectrum. This value should be between 0 and 1 (default = 1, which means all data will be displayed). If set to 0, no data reduction will occur, but a minimum value of 0.01 will be used to ensure some data is displayed.
`...`	Additional arguments passed to methods.

Value

A ggplot (class "ggplot") or plotly (class "htmlwidget") object representing the mass spectrum.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_ms(pl = peaklist_demo, data_reduction = 0.1, plotly = TRUE)
uplot_ms(pl = peaklist_demo, data_reduction = 1, plotly = FALSE)
```

---

uplot_n_mf_per_sample *Number of Molecular Formulas per Sample Plot*

Description

Creates a bar plot showing how many molecular formulas were assigned per sample (file_id). The plot title contains the mean and standard deviation of assigned molecular formulas across samples. Optionally, the plot can be converted to an interactive Plotly plot or display the UltraMassExplorer logo.

Usage

```
uplot_n_mf_per_sample(
  df,
  col = "grey",
  logo = TRUE,
  width = 0.3,
  gg_size = 12,
  plotly = FALSE
)
```

Arguments

df	A data.table containing at least a file_id column.
col	Character. Fill color for the bars (default "grey").
logo	Logical. If TRUE, adds a UME caption.
width	Numeric. Width of bars (default 0.3).
gg_size	Base text size for theme_uplots(). Default = 12.
plotly	Logical. If TRUE, return interactive plotly object.

Details

Number of Molecular Formulas per Sample / File

Value

A ggplot object, or a plotly object if plotly = TRUE.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
uplot_n_mf_per_sample(mf_data_demo)
```

---

uplot_pca *uplot_pca*

Description

This function performs Principal Component Analysis (PCA) on a dataset, and visualizes the results in various ways, including a scatter plot of the first two principal components (PC1 vs PC2) and a Van Krevelen plot projected using PC1 values. The PCA is performed on the molecular formula data, aggregated by a grouping variable, and handles cases where columns exhibit zero variance (which cannot be included in PCA).

Usage

```
uplot_pca(
  mfd,
  grp,
  int_col = "norm_int",
  palname = "viridis",
  col_bar = TRUE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
grp	Character vector. Names of columns (e.g., sample or file identifiers) used to aggregate results.
int_col	Character. The name of the column that contains the intensity values to be used (e.g. for clustering or color coding). Default usually is "norm_int" for normalized intensity values.

palname	Color palette name for f_colorz() (viridis, magma, plasma, etc.).
col_bar	Logical. If TRUE, adds a color legend (default is TRUE).
...	Additional arguments passed to methods.

Details

Principal Component Analysis (PCA) Plotting

Value

A list containing:

pca	The PCA model object (class prcomp).
t_score	A data table of PCA scores (principal component values for each sample).
fig_vk	A Van Krevelen plot projected with PC1 values.
fig_pca	A scatter plot of the first two principal components (PC1 vs PC2).
mfd	The input data table, augmented with principal component values.

Note

The function uses prcomp for PCA and uplot_vk for the Van Krevelen plot.

See Also

uplot_vk for the Van Krevelen plot function.

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

---

uplot_ppm_avg *Plot Median of Mass Accuracy per Sample (ppm)*

Description

This function generates a bar plot showing the median of mass accuracy (ppm) for each sample. It also provides the option to convert the plot into an interactive plotly object.

Usage

```
uplot_ppm_avg(df, cex.axis = 12, cex.lab = 15, plotly = FALSE, ...)
```

Arguments

df	A data frame containing the data. The columns ppm (ppm values) and file_id (sample identifiers) should be present in the data.
cex.axis	Numeric. Size of axis text (default is 1).
cex.lab	Numeric. Size of axis labels (default is 1.4).
plotly	Logical. If TRUE, return interactive plotly object.
...	Additional arguments passed to methods.

Value

A ggplot object or a plotly object depending on the plotly argument.

---

uplot_ratios *Molecular Formula Ratio Plot (Sample vs Control)*

Description

Computes the intensity ratio between a sample and a control group and visualizes it in a Van Krevelen diagram. Optionally highlights unique molecular formulas and plots the ratio distribution.

Usage

```
uplot_ratios(
  df,
  upper = 90,
  lower = -90,
  grp = "file_id",
  int_col = "norm_int",
  control,
  sample,
  uniques = FALSE,
  conservative = FALSE,
  palname = "ratios",
  distrib = TRUE,
  main = NA,
  plotly = FALSE,
  ...
)
```

Arguments

df	A data.table containing at least columns: mf, oc, hc, grouping variable grp, and intensity column int_col.
upper, lower	Ratio filtering limits (default 90 / -90)
grp	Column defining sample/control grouping

int_col	Intensity column to use
control	Character: control group name
sample	Character: sample group name
uniques	Logical: highlight uniquely present formulas
conservative	Logical: stricter uniqueness definition
palname	Color palette for projection
distrib	Logical: include ratio distribution plot
main	Optional main title
plotly	Logical: convert output plots to plotly
...	Additional arguments passed to methods.

Details

Ratio Plot in Van Krevelen Space

Value

A list with:

- ratio_table
- plot_ratio_vk
- plot_ratio_distr

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_reproducibility(), uplot_ri_vs_sample(), uplot_vk()

Examples

```
out <- uplot_ratios(
  df = mf_data_demo,
  grp = "file",
  control = "Nsea_a",
  sample  = "Fjord 01a"
)
```

`uplot_reproducibility` *Check Reproducibility of Sample Analyses*

Description

Computes reproducibility of sample analyses based on the relative intensity column (`norm_int`). For each molecular formula (`mf`), the function calculates:

- number of occurrences (`N`)
- median relative intensity (`ri`)
- relative standard deviation (RSD = sd/median × 100)

It also bins `ri` into integer bins and calculates the median RSD per bin.

The function returns:

- processed tables
- two **ggplot2** objects:
  - intensity vs RSD scatter plot
  - binned median RSD plot

Usage

```
uplot_reproducibility(df, ri = "norm_int")
```

Arguments

`df`	A data.table or data.frame containing at least columns `mf` and the intensity column defined in `ri`.
`ri`	Character string: name of the intensity column. Default: `"norm_int"`.

Value

A list containing:

`tmp` Summary table by molecular formula

`tmp2` Binned median RSD table

`plot_rsd` Scatter plot of RI vs RSD (ggplot2)

`plot_bins` Median RSD per bin (ggplot2)

See Also

Other plots: `uplot_cluster()`, `uplot_cvm()`, `uplot_dbe_minus_o_freq()`, `uplot_dbe_vs_c()`, `uplot_freq_ma()`, `uplot_freq_vs_ppm()`, `uplot_hc_vs_m()`, `uplot_heteroatoms()`, `uplot_isotope_precision()`, `uplot_kmd()`, `uplot_lcms()`, `uplot_ma_vs_mz()`, `uplot_ms()`, `uplot_n_mf_per_sample()`, `uplot_pca()`, `uplot_ratios()`, `uplot_ri_vs_sample()`, `uplot_vk()`

Examples

```
out <- uplot_reproducibility(mf_data_demo, ri = "norm_int")
out$plot_rsd
out$plot_bins
```

`uplot_ri_vs_sample` *Average Relative Intensity per Sample*

Description

Creates a bar plot showing the **median relative intensity** (default: `norm_int`) for each sample (grouped by `file_id`). The overall dataset-wide median and standard deviation are shown in the title.

Usage

```
uplot_ri_vs_sample(
  df,
  int_col = "norm_int",
  grp = "file_id",
  col = "grey",
  logo = TRUE,
  width = 0.3,
  gg_size = 12
)
```

Arguments

`df`	A data.table containing at least: • a column with relative intensity values (`int_col`) • a sample or file identifier (`grp`)
`int_col`	Character. Column name containing relative intensity values.
`grp`	Character. Column name specifying sample / file grouping.
`col`	Character. Fill color for bars.
`logo`	Logical. If TRUE, adds a UME caption.
`width`	Numeric. Width of bars (default `0.3`).
`gg_size`	Base text size for `theme_uplots()`. Default = 12.

Details

Plot Average Relative Intensity per Sample

Value

A **ggplot2 object** containing a bar plot of per-sample median relative intensity.

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_vk()

Examples

```
uplot_ri_vs_sample(mf_data_demo, int_col = "norm_int", grp = "file")
```

---

uplot_vk *uplot_vk*

Description

Creates a Van Krevelen diagram (H/C vs O/C).

Usage

```
uplot_vk(
  mfd,
  z_var = "norm_int",
  nice_labels = TRUE,
  projection = TRUE,
  palname = "viridis",
  median_vK = TRUE,
  col_median = "white",
  ai = TRUE,
  logo = TRUE,
  size_dots = 3,
  col_bar = TRUE,
  tf = FALSE,
  cex.axis = 12,
  cex.lab = 15,
  plotly = FALSE,
  ...
)
```

Arguments

mfd	data.table with molecular formula data as derived from ume::assign_formulas. Column names of elements/isotopes must match names in the isotope column of ume::masses; values are integers representing counts per formula.
z_var	Character. Column name for variable used for color-coding. Content of column should be numeric.

nice_labels	Logical. If true (default) axis/legend labels are generated from ume::nice_labels_dt.
projection	If TRUE, median z-values per (oc,hc) are used.
palname	Color palette name for f_colorz() (viridis, magma, plasma, etc.).
median_vK	Add median VK point.
col_median	Color of the marker for the median O/C and H/C value (Default = "white")
ai	Add aromaticity index threshold lines.
logo	Logical. If TRUE, adds a UME caption.
size_dots	Numeric. Size of the dots in the plot (default = 0.5).
col_bar	Logical. If TRUE, adds a color legend (default is TRUE).
tf	Logical. If TRUE, applies a transformation to the color scale (default is FALSE).
cex.axis	Numeric. Size of axis text (default is 1).
cex.lab	Numeric. Size of axis labels (default is 1.4).
plotly	Logical. If TRUE, return interactive plotly object.
...	Arguments passed on to f_colorz z Numeric vector. Values whose colors should be computed. col_num Integer. Number of colors in the palette (default: 100). verbose logical; if TRUE, show progress messages.

Details

Plot Van Krevelen Diagram

Value

ggplot or plotly object

References

Van Krevelen D. (1950). Graphical-statistical method for the study of structure and reaction processes of coal. *Fuel*, **29**, 269-284.

Kim S., Kramer R.W., Hatcher P.G. (2003). Graphical method for analysis of ultrahigh-resolution broadband mass spectra of natural organic matter, the Van Krevelen Diagram. *Analytical Chemistry*, **75**, 5336-5344. doi:10.1021/ac034415p

See Also

Other plots: uplot_cluster(), uplot_cvm(), uplot_dbe_minus_o_freq(), uplot_dbe_vs_c(), uplot_freq_ma(), uplot_freq_vs_ppm(), uplot_hc_vs_m(), uplot_heteroatoms(), uplot_isotope_precision(), uplot_kmd(), uplot_lcms(), uplot_ma_vs_mz(), uplot_ms(), uplot_n_mf_per_sample(), uplot_pca(), uplot_ratios(), uplot_reproducibility(), uplot_ri_vs_sample()

ustats_outlier *Outlier detection using multiple statistical tests*

Description

This function computes an out_score for each value in a selected column. The score increases when a value is flagged as an outlier by one or more tests: IQR test, quantile cutoffs, and Hampel filter.

Usage

```
ustats_outlier(dt, check_col = "ppm", verbose = FALSE, ...)
```

Arguments

dt	A data.table or data.frame.
check_col	A character string naming the column to test for outliers.
verbose	Logical; print summary statistics when TRUE.
...	Additional arguments passed to methods.

Value

A data.table containing new columns: out_score, out_box, out_quantile, and out_hampel.

Examples

```
ustats_outlier(mf_data_demo, check_col = "ppm")
```

Index

∗ **Clean data output**
remove_id_columns, 48
remove_unknown_columns, 49
∗ **Formula assignment**
add_known_mf, 3
calc_eval_params, 11
eval_isotopes, 33
ume_assign_formulas, 51
∗ **Formula subsetting**
filter_int, 34
filter_mass_accuracy, 35
filter_mf_data, 36
remove_blanks, 46
subset_known_mf, 49
ume_assign_formulas, 51
ume_filter_formulas, 53
∗ **ID**
remove_id_columns, 48
∗ **Remove**
remove_id_columns, 48
remove_unknown_columns, 49
∗ **calculations**
calc_data_summary, 8
calc_dbe, 10
calc_eval_params, 11
calc_exact_mass, 12
calc_ideg, 13
calc_ma, 16
calc_neutral_mass, 18
calc_nm, 19
calc_norm_int, 20
calc_number_assignment, 21
∗ **check ume objects**
as_peaklist, 7
∗ **chemistry**
convert_data_table_to_molecular_formulas, 27
convert_molecular_formula_to_data_table, 29
∗ **columns.**
remove_id_columns, 48
∗ **columns**
remove_unknown_columns, 49
∗ **contain**
remove_unknown_columns, 49
∗ **datasets**
known_mf, 39
lib_demo, 40
masses, 40
mf_data_demo, 41
nice_labels_dt, 43
peaklist_demo, 45
tab_ume_labels, 50
∗ **exclusively**
remove_unknown_columns, 49
∗ **filter_int**
ume_filter_formulas, 53
∗ **helper**
classify_files, 25
∗ **index calculations**
calc_iterr, 15
∗ **misc**
add_known_mf, 3
calc_iterr, 15
calc_ma, 16
calc_ma_abs, 17
calc_number_assignment, 21
filter_int, 34
filter_mass_accuracy, 35
filter_mf_data, 36
get_isotope_info, 38
order_columns, 44
remove_blanks, 46
subset_known_mf, 49
ume_assign_formulas, 51
ustats_outlier, 82
∗ **missing**
remove_unknown_columns, 49

∗ **molecular formula functions**
convert_data_table_to_molecular_formulas, 27
convert_molecular_formula_to_data_table, 29
∗ **molecular-formula**
convert_data_table_to_molecular_formulas, 27
convert_molecular_formula_to_data_table, 29
∗ **plots**
uplot_cluster, 55
uplot_cvm, 56
uplot_dbe_minus_o_freq, 57
uplot_dbe_vs_c, 58
uplot_freq_ma, 62
uplot_freq_vs_ppm, 63
uplot_hc_vs_m, 65
uplot_heteroatoms, 66
uplot_isotope_precision, 67
uplot_kmd, 68
uplot_lcms, 70
uplot_ma_vs_mz, 71
uplot_ms, 72
uplot_n_mf_per_sample, 73
uplot_pca, 74
uplot_ratios, 76
uplot_reproducibility, 78
uplot_ri_vs_sample, 79
uplot_vk, 80
∗ **that**
remove_unknown_columns, 49
∗ **tools**
add_missing_element_columns, 4
order_columns, 44
∗ **ume data**
known_mf, 39
lib_demo, 40
masses, 40
mf_data_demo, 41
nice_labels_dt, 43
peaklist_demo, 45
tab_ume_labels, 50
∗ **ume wrapper**
ume_assign_formulas, 51
ume_filter_formulas, 53
∗ **utils**
calc_number_assignment, 21
∗ **values.**
remove_unknown_columns, 49

add_known_mf, 3, *12*, *33*, *52, 53*
add_missing_element_columns, 4, *44*
as_peaklist, 7
as_peaklist(), *6*
assign_formulas, 5, *52*

calc_data_summary, 8, *10*, *12–14*, *17–19*, *21*, *22*
calc_dbe, *9*, 10, *12–14*, *17–19*, *21, 22*
calc_eval_params, *4*, *9, 10*, 11, *13, 14*, *17–19*, *21, 22*, *33*, *52, 53*
calc_exact_mass, *9, 10*, *12*, 12, *14*, *17–19*, *21, 22*
calc_ideg, *9, 10*, *12, 13*, 13, *17–19*, *21, 22*
calc_iterr, 15
calc_ma, *9, 10*, *12–14*, 16, *18, 19*, *21, 22*
calc_ma_abs, *6*, 17, *52*
calc_ma_abs(), *6*
calc_neutral_mass, *6*, *9, 10*, *12–14*, *17*, 18, *19*, *21, 22*, *52*
calc_neutral_mass(), *6*
calc_nm, *9, 10*, *12–14*, *17, 18*, 19, *21, 22*
calc_norm_int, *9, 10*, *12–14*, *17–19*, 20, *22*, *34*, *52, 53*
calc_number_assignment, *9, 10*, *12–14*, *17–19*, *21*, 21
calc_number_occurrence, *9, 10*, *12–14*, *17–19*, *21, 22*
calc_pielou_evenness, 22
calc_recalibrate_ms, *9, 10*, *12–14*, *17–19*, *21, 22*
calc_shannon_index, 23
calc_simpson_index, 24
check_formula_library, *4*, *8*, *12*, *33*, *53*
check_mfd, *8*
classify_files, 25
color.palette, 26
convert_data_table_to_molecular_formulas, 27, *30*
convert_molecular_formula_to_data_table, *28*, 29
create_ume_formula_library, 30

download_library, 32

eval_isotopes, *4*, *12*, 33, *52, 53*

f_colorz, *57*, *59, 60*, *65*, *69*, *81*
filter_int, 34, *35*, *37*, *47*, *50*, *53, 54*
filter_mass_accuracy, *34*, 35, *37*, *47*, *50*, *53, 54*
filter_mf_data, *34, 35*, 36, *47*, *50*, *53, 54*

get_isotope_info, 38

is_ume_peaklist, 38

known_mf, 39, *40, 41*, *43*, *45*, *51*

lib_demo, *39*, 40, *41*, *43*, *45*, *51*

masses, *38–40*, 40, *43*, *45*, *51*
mf_data_demo, *39–41*, 41, *43*, *45*, *51*

nice_labels_dt, *39–41*, *43*, 43, *45*, *51*

order_columns, *5*, 44

peaklist_demo, *39–41*, *43*, 45, *51*

remove_blanks, *34, 35*, *37*, 46, *50*, *53, 54*
remove_empty_columns, 47
remove_id_columns, 48, *49*
remove_unknown_columns, *48*, 49

subset_known_mf, *34, 35*, *37*, *47*, 49, *53, 54*

tab_ume_labels, *39–41*, *43*, *45*, 50
theme_uplots, 51

ume_assign_formulas, *4*, *12*, *33–35*, *37*, *47*, *50*, 51, *54*
ume_filter_formulas, *34, 35*, *37*, *47*, *50*, *53*, 53
uplot_cluster, 55, *57–59*, *63, 64*, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_cvm, *56*, 56, *58, 59*, *63, 64*, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_dbe_minus_o_freq, *56, 57*, 57, *59*, *63, 64*, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_dbe_vs_c, *56–58*, 58, *63, 64*, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_dbe_vs_o, 59
uplot_dbe_vs_ppm, 61
uplot_freq, 61
uplot_freq_ma, *56–59*, 62, *64*, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_freq_vs_ppm, *56–59*, *63*, 63, *66–71*, *73–75*, *77, 78*, *80, 81*
uplot_hc_vs_m, *56–59*, *63, 64*, 65, *67–71*, *73–75*, *77, 78*, *80, 81*
uplot_heteroatoms, *56–59*, *63, 64*, *66*, 66, *68–71*, *73–75*, *77, 78*, *80, 81*
uplot_isotope_precision, *56–59*, *63, 64*, *66, 67*, 67, *69–71*, *73–75*, *77, 78*, *80, 81*
uplot_kmd, *56–59*, *63, 64*, *66–68*, 68, *70, 71*, *73–75*, *77, 78*, *80, 81*
uplot_lcms, *56–59*, *63, 64*, *66–69*, 70, *71*, *73–75*, *77, 78*, *80, 81*
uplot_ma_vs_mz, *56–59*, *63, 64*, *66–70*, 71, *73–75*, *77, 78*, *80, 81*
uplot_ms, *56–59*, *63, 64*, *66–71*, 72, *74, 75*, *77, 78*, *80, 81*
uplot_n_mf_per_sample, *56–59*, *63, 64*, *66–71*, *73*, 73, *75*, *77, 78*, *80, 81*
uplot_pca, *56–59*, *63, 64*, *66–71*, *73, 74*, 74, *77, 78*, *80, 81*
uplot_ppm_avg, 75
uplot_ratios, *56–59*, *63, 64*, *66–71*, *73–75*, 76, *78*, *80, 81*
uplot_reproducibility, *56–59*, *63, 64*, *66–71*, *73–75*, *77*, 78, *80, 81*
uplot_ri_vs_sample, *56–59*, *63, 64*, *66–71*, *73–75*, *77, 78*, 79, *81*
uplot_vk, *56–59*, *63, 64*, *66–71*, *73–75*, *77, 78*, *80*, 80
ustats_outlier, 82