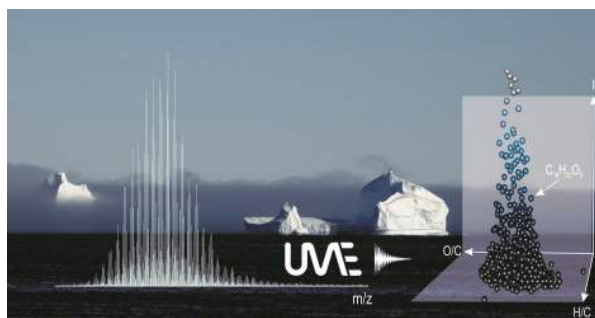


ume

Getting Started with UltraMassExplorer

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UltraMassExplorer (ume) provides a comprehensive workflow for ultrahigh-resolution mass spectrometry data analysis of complex organic matter. The package has been under active development since 2019 and comprises about 70 documented functions and supports workflows to calibrate, normalize, evaluate and visualize molecular formula results (details described in Leefmann et al. 2019). UME is also available as a graphical user interface via a UME R Shiny App.

Getting started

The peaklist (pl) is the main UME entry point.

Your peak list can be a data.frame / data.table or text-files (txt, csv, tsv). `as_peaklist()` checks and imports your source file.

```
pl <- as_peaklist("your_path_to.csv")
```

For quick-starting the UME demo peak list (`ume::peaklist_demo`) can be used.

Molecular formula assignment is based on the molecular formula library (`formula_library`). Two ready-to-use libraries can be downloaded from Zenodo:

```
lib <- download_library("lib_02.rds", dest = paste0(dirname(getwd()), "/lib_02.rds"))  
# lib <- download_library("lib_05.rds", dest = paste0(dirname(getwd()), "/lib_05.rds"))
```

If you provide a local path with the argument `dest =`, the download will be performed only once. After the first download, the local copy will be used.

For quick-starting, the demo library (`ume::lib_demo`) can be used.

1. Overview UME data workflow

1. Analyse the input format of the peak list.
2. Calculate neutral masses.
3. Assign molecular formulas (based on a pre-defined formula library).
4. Evaluate stable isotope information.
5. Add information on existing knowledge of molecular formulas.
6. Calculate evaluation parameters (e.g. DBE, nominal mass, KMD, etc.).
7. A posteriori formula filtering.
8. Normalize peak magnitudes.
9. Set the order of columns in the results.

All of these tasks can be executed in just two steps:

```
mfd <- ume_assign_formulas(pl = peaklist_demo,
                           formula_library = lib,
                           pol = "neg",
                           ma_dev = 0.5,
                           remove_isotopes = TRUE)
```

Formula assignment and calculation of evaluation parameters

```
mfd_filt <- ume_filter_formulas(
  mfd = mfd,
  remove_isotopes = TRUE,
  normalization = "bp",
  norm_int_min = 0.5,
  blank_file_ids = 1,
  blank_prevalence = 0.5,
  dbe_o_max = 10,
  oc_min = 0.2, oc_max = 1.2,
  c_iso_check = TRUE,
  dbe_max = 30,
  p_min = 0, p_max = 0,
  mz_min = 150, mz_max = 650
)
```

Formula filtering (subsetting) and normalization

Alternatively, the workflow can be performed in single steps:

```
# Step 1: Assign formulas (checks the peaklist format and calculates neutral masses and mass accuracy)
# calc_neutral_mass() and calc_ma_abs()
mfd <- assign_formulas(pl = ume::peaklist_demo, formula_library = ume::lib_demo,
                      pol = "neg", ma_dev = 0.5, verbose = TRUE)
```

```

# Step 2: Verify the existence of the major isotope signals and their magnitudes
mfd <- eval_isotopes(mfd = mfd, remove_isotopes = TRUE, verbose = TRUE)

# Step 3: Calculate evaluation parameters
mfd <- calc_eval_params(mfd = mfd, verbose = TRUE)

# Step 4: Add known classification for formulas
# to do: the categories should be listed in one column containing the category assignment
mfd <- add_known_mf(mfd = mfd)

# Step 5: Remove all formulas that occur in one or more blank analyses
# The demo peaklist contains one blank spectrum named "Blank" (file_id = 1)
# This removes all molecular formulas recorded in the blank from the entire dataset
mfd <- remove_blanks(mfd = mfd, blank_file_ids = 1, blank_prevalence = 0)

# Step 6: Filter formula table according to evaluation parameters (generated in step 3)
mfd_filt <- filter_mf_data(mfd = mfd,
                          select_file_ids = 2:5,
                          db_e_o_max = 10,
                          oc_min = 0.2,
                          oc_max = 1.2,
                          verbose = TRUE)

# Step 7: Normalize intensities
mfd_filt <- calc_norm_int(mfd = mfd_filt, normalization = "bp", verbose = TRUE)

# Step 8: Filter by (relative) peak magnitude (in this case: >= 5 percent base peak intensity)
mfd_filt <- filter_int(mfd = mfd_filt, norm_int_min = 0.5, verbose = TRUE)

# Step 9: Normalize intensities
mfd_filt <- calc_norm_int(mfd = mfd_filt, normalization = "bp", verbose = TRUE)

# Step 10: Order the columns of the results table
mfd_filt <- order_columns(mfd = mfd_filt)

# Alternative using pipe operator:
mf_data_demo |>
  eval_isotopes(remove_isotopes = TRUE) |>
  calc_eval_params() |>
  add_known_mf() |>
  order_columns()

```

2. Visualization and statistics

Selected plot functions:

```

# Mass spectrum
uplot_ms(pl = ume::peaklist_demo, label = "file",
         plotly = TRUE,
         logo = FALSE)

# Multivariate statistics
# Multi-dimensional scaling:

```

```

uplot_cluster(mf_data_demo[file != "Blank"], grp = "file", int_col = "i_magnitude")$mds

# Cluster dendrogram
uplot_cluster(mf_data_demo[file != "Blank"], grp = "file", int_col = "i_magnitude")$dendrogram

# Summary statistics
calc_data_summary(mfd = ume::mf_data_demo)

# Mass accuracy
uplot_freq_ma(mfd = ume::mf_data_demo)

# Element frequency
uplot_freq(mfd = ume::mf_data_demo, var = "14N")

# van Krevelen
uplot_vk(mfd = ume::mf_data_demo, size_dots = 3)

# Precision isotope abundance
uplot_isotope_precision(mfd = ume::mf_data_demo,
                        z_var = "nsp_tot",
                        tf = FALSE,
                        interactive = TRUE, logo = TRUE)

# Carbon versus mass
uplot_cvm(mfd = mf_data_demo, z_var = "co_tot", interactive = TRUE)

```

3. Re-calibration of peaklists

Automated calibration can be performed with existing calibration lists stored in `ume::known_mf`. The function `ume::calc_recalibrate_ms` assigns calibrants to the peak list and analyses the mass accuracy. Three outlier tests are performed and only those assigned calibrants that pass all three tests are used for recalibration. The recalibration is based on a linear model. The function output is a list object that contains a summary on calibrants and figures that compare the calibration status before and after recalibration. For example:

```

output_recal <- calc_recalibrate_ms(
  pl = peaklist_demo[file != "Blank"],
  calibr_list = "marine_dom",
  pol = "neg",
  min_no_calibrants = 3,
  ma_dev = 1,
  formula_library = lib_demo
)

summary(output_recal)
output_recal$cal_stats # summary statistics for each file_id in peaklist

# Result plots
output_recal$fig_box_before
output_recal$fig_box_after
output_recal$fig_hist_before
output_recal$fig_hist_after

```

```

# The re-calibrated peaklist is available via
output_recal$pl

# It can directly be used to start a new formula assignment process (see above):
mfd_recal <- ume::ume_assign_formulas(
  pl = output_recal$pl,
  formula_library = ume::lib_demo,
  pol = "neg",
  ma_dev = 1
)

# Automated mass accuracy sub-setting can be obtained using the column "ppm_filt".
# It is based on the quantiles 97.5% and 2.5% of all CHO formulas assigned.

mfd_recal <- mfd_recal[abs(ppm) <= ppm_filt]

uplot_freq_ma(mfd_recal)

```

4. UME core data objects

Mass Peak List

The mass calibrated *peak list* is the core of the **ume** work flow. The peak list (`pl`) is a table (as R `data.table`) that contains information from one or several mass spectrometric analyses:

- Analytical data:
 - Mass over charge value (`mz`)
 - Mass peak magnitude (`i_magnitude`)
 - Mass resolution (`res`)
 - Signal to noise ration (`s_n`)
- Metadata:
 - Unique identifier for each mass spectrum (`file`; data type: character)
 - An optional unique identifier for each mass spectrum (`file_id`; data type: integer). If `file_id` is not present, the first call of the peaklist will add a `file_id` column based on the unique entries in `file`.
 - Unique identifier for each mass peak (`peak_id`; data type: integer). If `peak_id` is not present, the first call of the peaklist table will add a unique identifier for each row (= `mz`) in the peaklist.

The package contains an example peak list:

```
ume::peaklist_demo[1:3]
```

Column names are explained here:

```
?ume::peaklist_demo
```

file_id	file	peak_id	mz	i_magnitude	s_n	res
1	Blank	23503862	200.09535	1711009	5.4	761606
1	Blank	23503863	200.11243	1533741	4.6	678315
1	Blank	23503864	200.11646	1735087	5.5	953755

file_id	file	peak_id	mz	i_magnitude	s_n	res
---------	------	---------	----	-------------	-----	-----

Isotopic masses

All calculated molecular masses in `ume` are based on the NIST data and available as a data resource in the package (`ume::masses`).

Isotope information of all elements:

`ume::masses`

Table 1: Table continues below

label	symbol	nm	exact_mass	mole_fraction	relative_abundance
12C	C	12	12	0.9893	1
13C	C	13	13.003355	0.0107	0.010816
1H	H	1	1.007825	0.999885	1

valence	hill_order
4	1
4	2
1	3

Column names are explained here:

`?ume::masses`

Molecular formula library

Molecular formula assignment in UME is based on a pre-defined molecular formula library (data.table format) containing:

- A version key (*vkey*) that uniquely identifies the version and each row of the library.
- A string of the molecular formula (*mf*; according to the hill nomenclature)
- The atom number of each isotope contained in a given molecular formula
- The exact mass of each formula (*mass*; as taken from *masses*; s. above)

Demo formula library:

`ume::lib_demo`

vkey	mf	mass	12C	13C	1H	14N	15N	16O	31P	32S	34S
9.9e+13	C9H2N4S	200.000407	8	1	2	3	1	0	0	1	0
9.9e+13	C5H4N4O3S	200.0004112	5	0	4	4	0	3	0	1	0
9.9e+13	C4H9NO4S2	200.000655	3	1	9	1	0	4	0	2	0

Column names are explained here:

`?ume::lib_demo`

Using Pre-defined UME Formula Libraries The UME package provides high-resolution molecular formula libraries that are too large to ship with the CRAN package itself (20–130 MB). These libraries are openly available through Zenodo at:

Zenodo DOI: <https://doi.org/10.5281/zenodo.17606457>

UME includes a convenience function, `download_library()`, that automatically:

1. Downloads the selected library (if only) once
2. Verifies its integrity via a SHA256 checksum
3. Loads it into the R session as a `data.table`
4. Caches it in memory for repeated use
5. Avoids repeated downloads unless `overwrite = TRUE`

```
# formula_library <- download_library("lib_02.rds")
```

Downloaded libraries are stored by default in: `~/ume/`

Create your own molecular formula library It is important to consider that the formula assignment process fundamentally depends on the content of the formula library.

Therefore, custom libraries can also be constructed:

```
ume_custom_library <- create_ume_formula_library(max_mass = 50, max_formula = "C5H12O10")
```

Molecular formula data

Molecular formula assignment and the calculation of evaluation parameters results in a molecular formula data object (`data.table`)

The package contains an molecular formula data table:

```
ume::mf_data_demo[1:3]
```

Column names are explained here:

```
?ume::mf_data_demo
```

5. What else can you do with ume?

Calculate standard parameters

Standard parameters can be calculated for a standard molecular formula data (mfd) table or for a molecular formula character vector.

```
# Calculate double bond equivalent (DBE) for a molecular formula
# Uses isotope masses and element valences defined in ume::masses
# Calculation based on a molecular formula character vector
calc_dbe("C2H4")
```

```

# Based on a UME standard table:
data("mf_data_demo")
mf_data_demo[, dbe_new:= calc_dbe(mf_data_demo)]

# Nominal mass
calc_nm(mfd = c("C2[13C]H4", "C2H4", "C2H5OH", "C2H5OH"))

# Exact mass
calc_exact_mass(mfd = "C2[13C]H4")

# Neutral mass for (de-) protonated ions
calc_neutral_mass(123.1241, pol = "neg")

# Calculate mass accuracy
calc_ma(m = 228.0269, m_cal = 228.0270026)
calc_ma(m = 228.0269, m_cal = calc_exact_mass("C9H8O7"))

# Extract the molecular formula from an InChI code:
inchi_to_mf("InChI=1S/C2H6O/c1-2-3/h3H,2H2,1H3")

```

Converting molecular formulas to a table and vice versa.

```

# Formula to table
convert_molecular_formula_to_data_table(mf = c("C2[13C]H4", "C2H5OH", "C2H6O"))

# In some specific cases the lightest isotope may not be the most abundant isotope.
# For these cases the function allows to choose between two interpretations of the
# element symbol:
convert_molecular_formula_to_data_table("FeC10H10", isotope_default = "most_abundant")
convert_molecular_formula_to_data_table("FeC10H10", isotope_default = "lightest")

# Table to formula
dt <- convert_molecular_formula_to_data_table(mf = c("C2[13C]H4", "C2H5OH", "C2H6O"))

convert_data_table_to_molecular_formulas(mfd = dt, isotope_formulas = TRUE)

```

Isotopes

Create isotope formulas for a parent formula For a given parent formula, the main daughter isotopes are added.

```
create_isotope_expanded_table("C2H6O", elements = c("C", "O"))
```

```

##      isotope_group_id iso_role iso_element iso_from iso_to vkey      mf      mf_iso      nm
##              <int>   <char>   <char>   <char> <char> <int> <char>      <char> <num>
## 1:                1   parent      <NA>   <NA>  <NA>    1  C2H6O  [12C2] [1H6] [160]    46
## 2:                1 daughter        C    12C   13C    1  C2H6O  [12C] [13C] [1H6] [160]    47
## 3:                1 daughter        O    16O   18O    1  C2H6O  [12C2] [1H6] [180]    48
##      mass  12C   1H   16O   13C   18O
##      <num> <int> <int> <int> <int> <int>

```

```
## 1: 46.04186      2      6      1      0      0
## 2: 47.04522      1      6      1      1      0
## 3: 48.04611      2      6      0      0      1
```

Create isotope pattern for a molecular formula Isotope calculator to determine the isotopic pattern for any given formula.

```
calc_isotope_pattern("C2H6O", rel_threshold = 0.01)
```

```
##      mf_old      mf      mf_iso isotope_peak      mass nominal_mass      prob relative_abundanc
##      <char> <char>      <char>      <int>      <num>      <num>      <num>      <num>
## 1:  C2H6O  C2H6O      [12C2] [1H6] [16O]          1 46.04186          46 0.97566274      1.000000
## 2:  C2H6O  C2H6O  [12C] [13C] [1H6] [16O]          2 47.04522          47 0.02110501      0.021631
```

6. Package content and documentation

Github for public releases of R code

-> <https://github.com/boriskoch/ume>

All package versions on Zenodo

Zenodo DOI: <https://doi.org/10.5281/zenodo.20108477>

Which version is installed and loaded?

```
packageVersion("ume") 1.7.1
```

What is new?

```
news(package = "ume")
```

Complete manual

```
vignette("ume")
```

-> The UME Vignette as pdf

7. UME installation

```
# Local installation from tarball
# This in case that you have previously installed the UME package:
detach("package:ume", unload = TRUE)
.rs.restartR()

# Install from tarball (adjust your path accordingly)
```

```
utils::install.packages(  
  "your_path_to/ume.tar.gz",  
  repos = NULL,  
  type = "source"  
)
```

8. UME shiny app

-> <https://www.awi.de/en/ume>