Package 'MetMashR'

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Description A package to merge, filter sort, organise and otherwise mash together metabolite annotation tables. Metabolite annotations can be imported from multiple sources (software) and combined using workflow steps based on S4
class templates derived from the `struct` package. Other modular workflow steps such as filtering, merging, splitting, normalisation and rest-api queries are included.

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'compute_column_class.R' 'compute_record_class.R'
'database_lookup_class.R' 'dictionaries.R'
'eutils_lookup_class.R' 'excel_database_class.R'
'expand_records_class.R' 'filter_labels_class.R'
'filter_na_class.R' 'filter_range_class.R'
'filter_records_class.R' 'filter_venn_class.R'
'github_file_class.R' 'go_database_class.R'
'hmdb_lookup_class.R' 'id_count_class.R'
'import_source_class.R' 'kegg_lookup_class.R'
'lipidmaps_lookup_class.R' 'ls_source_class.R'
'model_apply_doc.R' 'mspurity_source_class.R'
'mwb_compound_lookup_class.R' 'mwb_refmet_database_class.R'
'mwb_structure_chart_class.R' 'mz_match_class.R'
'mzrt_match_class.R' 'normalise_lipids_class.R'
'normalise_strings_class.R' 'opsin_lookup_class.R'
'pivot_columns_class.R' 'prioritise_columns_class.R'
'pubchem_compound_lookup_class.R'
'pubchem_property_lookup_class.R'
'pubchem_structure_chart_class.R'
'pubchem_structure_lookup_class.R' 'pubchem_widget.R'
'rdata_database_class.R' 'rds_database_class.R'
'rds_cache_class.R' 'remove_columns_class.R'
'rename_columns_class.R' 'rt_match_class.R'
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`MetMashR-package` *MetMashR: Metabolite Mashing with R*

Description

A package to merge, filter sort, organise and otherwise mash together metabolite annotation tables. Metabolite annotations can be imported from multiple sources (software) and combined using workflow steps based on S4 class templates derived from the 'struct' package. Other modular workflow steps such as filtering, merging, splitting, normalisation and rest-api queries are included.

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See Also

Useful links:

- https://computational-metabolomics.github.io/MetMashR/
- Report bugs at https://github.com/computational-metabolomics/MetMashR/issues

---

`add_columns` *Add columns*

Description

A wrapper around `dplyr::left_join`. Adds columns to an annotation table by performing a left-join with an input data.frame (annotations on the left of the join).

Usage

```
add_columns(new_columns, by, ...)
```

Arguments

`new_columns`	(data.frame, annotation_database) A data.frame to be left-joined to the annotation table. Can also be an annotation_database.
`by`	(character) A (named) character vector of column names to join by e.g. `c("A" = "B")` (see `dplyr::left_join` for details).
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A add_columns object with the following output slots:

updated (annotation_source) The updated annotations as an annotation_source object.

Inheritance

A add_columns object inherits the following struct classes:

[add_columns] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

See Also

dplyr::left_join()

Examples

```
M <- add_columns(
        new_columns = data.frame(),
        by = "id")
```

---

add_labels *Add column of labels*

Description

Adds new columns with the specified labels for each record.

Usage

```
add_labels(labels, replace = FALSE, ...)
```

Arguments

labels	(list) A named list of columns and the label to use for all records in that column.
replace	(logical) Replace columns. Allowed values are limited to the following: • "TRUE": If present, the new columns will replace existing columns in the source data.frame. • "FALSE": An error will be thrown if the new columns are already in the source data.frame. The default is FALSE.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A add_labels object with the following output slots:

updated	(annotation_source) The updated annotations as an annotation_source object.

Inheritance

A add_labels object inherits the following struct classes:

[add_labels] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Examples

```
M <- add_labels(
        labels = list(),
        replace = FALSE)
```

AnnotationDb_database *AnnotationDb database*

Description

Retrieve a table from an AnnotationDb package.

Usage

```
AnnotationDb_database(source, table, ...)
```

Arguments

source	(character) The name of an AnnotationDb package to import the specified table from. Note the package should already be installed.
table	(character) The name of a table to import from the specified source AnnotationDb package.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- AnnotationDbi

Value

A AnnotationDb_database object. This object has no output slots.

Inheritance

A AnnotationDb_database object inherits the following struct classes:

[AnnotationDb_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Pagès H, Carlson M, Falcon S, Li N (2025). *AnnotationDbi: Manipulation of SQLite-based annotations in Bioconductor*. doi:10.18129/B9.bioc.AnnotationDbi https://doi.org/10.18129/B9.bioc.AnnotationDbi, R package version 1.72.0, https://bioconductor.org/packages/AnnotationDbi.

See Also

AnnotationDbi::AnnotationDb

Other annotation databases: GO_database, annotation_database, annotation_source, excel_database, rdata_database, rds_cache, rds_database

Examples

```
M <- AnnotationDb_database(
        table = character(0),
        tag = character(0),
        data = data.frame(),
        source = character(0))
```

`AnnotationDb_select` *Select columns from AnnotationDb database*

Description

A wrapper around `[annotationDbi::select()]` that can be used to import columns from the database where the keys are provided by a column in the annotation table.

Usage

```
AnnotationDb_select(
  database,
  key_column,
  key_type,
  database_columns,
  drop_na = TRUE,
  ...
)
```

Arguments

`database`	(character) The name of the AnnotationDbi package/object to import.
`key_column`	(character) The name of a column in the annotation table containing key values used to extract records from the AnnotationDbi database.
`key_type`	(character) The name of a column in the AnnoationDb database searched for matches to the key values.
`database_columns`	(character) The name of columns to import from the AnnoationDb database. Special case `.all` can be used to get all columns.
`drop_na`	(logical) Drop NA. Allowed values are limited to the following: • `"TRUE"`: Remove rows where all columns of the returned database are NA. • `"FALSE"`: Keep rows where all columns of the returned database are NA. The default is `TRUE`.
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- dplyr
- AnnotationDbi

Value

A AnnotationDb_select object with the following output slots:

updated (annotation_source) The updated annotations as an annotation_source object.

Inheritance

A AnnotationDb_select object inherits the following struct classes:

[AnnotationDb_select] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Pagès H, Carlson M, Falcon S, Li N (2025). *AnnotationDbi: Manipulation of SQLite-based annotations in Bioconductor*. doi:10.18129/B9.bioc.AnnotationDbi https://doi.org/10.18129/B9.bioc.AnnotationDbi, R package version 1.72.0, https://bioconductor.org/packages/AnnotationDbi.

See Also

dplyr::left_join()

AnnotationDbi::select()

Examples

```
M <- AnnotationDb_select(
        database = "",
        key_column = "",
        key_type = "",
        database_columns = ".all",
        drop_na = FALSE)
```

annotation_bar_chart *Annotation bar chart*

Description

Display a bar chart of labels in the specified column of an annotation_source.

Usage

```
annotation_bar_chart(
  factor_name,
  label_rotation = FALSE,
  label_location = "inside",
  label_type = "percent",
  legend = FALSE,
  ...
)
```

Arguments

factor_name	(character) The name of the column in the annotation_source to generate a chart from.
label_rotation	(logical) Rotate labels. Allowed values are limited to the following: • "TRUE": Rotate labels to match segments. • "FALSE": Do not rotate labels. The default is FALSE.
label_location	(character) Label location. Allowed values are limited to the following: • "inside": Labels are displayed inside the bars. • "outside": Labels are displayed outside the bars. The default is "inside".
label_type	(character) Label type. Allowed values are limited to the following: • "percent": Labels will include the percentage for the segment. • "count": Labels will include the count for the segment. • "none": Labels will not include extra information. The default is "percent".
legend	(logical) Display legend. Allowed values are limited to the following: • "TRUE": Groups are indicated using a legend. • "FALSE": Groups are indicated in the labels. The default is FALSE.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- ggplot2

Value

A annotation_bar_chart object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A annotation_bar_chart object inherits the following struct classes:

[annotation_bar_chart] -> [chart] -> [struct_class]

References

Wickham H (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.

Examples

```
M <- annotation_bar_chart(
        factor_name = "V1",
        label_location = "inside",
        label_rotation = FALSE,
        legend = FALSE,
        label_type = "percent")
```

---

annotation_database *An annotation database*

Description

An annotation_database is an annotation_source() where the imported data.frame contains meta data for annotations. For example it might be a table of molecular identifiers, associated pathways etc.

Usage

```
annotation_database(data = data.frame(), tag = "", ...)
```

Arguments

data	(data.frame, NULL) A data.frame of annotation data. The default is data.frame().
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "".
...	Additional slots and values passed to struct_class.

Value

A annotation_database object. This object has no output slots.

Inheritance

A annotation_database object inherits the following struct classes:

[annotation_database] -> [annotation_source] -> [struct_class]

See Also

Other annotation databases: AnnotationDb_database, GO_database, annotation_source, excel_database, rdata_database, rds_cache, rds_database

Other annotation sources: annotation_table, cd_source, ls_source, mspurity_source

Examples

```
M <- annotation_database(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

annotation_histogram *Annotation histogram*

Description

Display a histogram of value in the specified column of an annotation_source.

Usage

```
annotation_histogram(
  factor_name,
  bins = 30,
  bin_edge = "grey",
  bin_fill = "lightgrey",
  vline = NULL,
  vline_colour = "red",
  ...
)
```

Arguments

factor_name	(character) The name of the column in the annotation_source to generate a histogram from.
bins	(numeric, integer) The number of bins to use when computing the histogram. The default is 30.
bin_edge	(character) The colour to use when plotting the edges of bins. The default is "grey".
bin_fill	(character) The colour to use when plotting the bins. The default is "lightgrey".
vline	(numeric, NULL, list) The x-axis location of veritcal lines used to indicate e.g. upper and lower limits. Use NULL if not required. The default is NULL.
vline_colour	(character) The colour to use when plotting vertical lines. The default is "red".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- ggplot2

Value

A annotation_histogram object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A annotation_histogram object inherits the following struct classes:

[annotation_histogram] -> [chart] -> [struct_class]

References

Wickham H (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.

Examples

```
M <- annotation_histogram(
        factor_name = "V1",
        bins = 30,
        bin_edge = "grey",
        bin_fill = "lightgrey",
        vline = NULL,
        vline_colour = "red")
```

annotation_histogram2d

Annotation 2D histogram

Description

Display a histogram of value in the specified columns of an annotation_source.

Usage

```
annotation_histogram2d(
  factor_name,
  bins = 30,
  bin_edge = "grey",
  bin_fill = "lightgrey",
  vline = NULL,
  vline_colour = "red",
  ...
)
```

Arguments

factor_name	(character) The names of the two columns in the annotation_source to generate histograms from.
bins	(numeric, integer) The number of bins to use when computing the histograms. The default is 30.
bin_edge	(character) The colour to use when plotting the edges of bins. The default is "grey".
bin_fill	(character) The colour to use when plotting the bins. The default is "lightgrey".
vline	(numeric, NULL, list) The x-axis location of lines used to indicate e.g. upper and lower limits. Use NULL if not required. A 2 element list can be provided to set vlines for each factor_name. The default is NULL.
vline_colour	(character) The colour to use when plotting vertical lines. The default is "red".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- ggplot2
- patchwork

Value

A annotation_histogram2d object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A annotation_histogram2d object inherits the following struct classes:

[annotation_histogram2d] -> [annotation_histogram] -> [chart] -> [struct_class]

References

Wickham H (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.

Pedersen T (2025). *patchwork: The Composer of Plots*. doi:10.32614/CRAN.package.patchwork https://doi.org/10.32614/CRAN.package.patchwork, R package version 1.3.2, https://CRAN.R-project.org/package=patchwork.

Examples

```
M <- annotation_histogram2d(
        factor_name = "V1",
        bins = 30,
        bin_edge = "grey",
        bin_fill = "lightgrey",
        vline = NULL,
        vline_colour = "red")
```

---

annotation_pie_chart *Annotation pie chart*

Description

Display a pie chart of labels in the specified column of an annotation_source.

Usage

```
annotation_pie_chart(
  factor_name,
  label_rotation = FALSE,
  label_location = "inside",
  label_type = "percent",
  legend = FALSE,
  pie_rotation = 0,
  centre_radius = 0,
  centre_label = NULL,
  count_na = FALSE,
  ...
)
```

Arguments

factor_name	(character) The name of the column in the annotation_source to generate a pie chart from.
label_rotation	(logical) Rotate labels. Allowed values are limited to the following: • "TRUE": Rotate labels to match segments. • "FALSE": Do not rotate labels. The default is FALSE.
label_location	(character) Label location. Allowed values are limited to the following: • "inside": Labels are displayed inside the segments. • "outside": Labels are displayed outside the segments. The default is "inside".
label_type	(character) Label type. Allowed values are limited to the following: • "percent": Labels will include the percentage for the segment. • "count": Labels will include the count for the segment. • "none": Labels will not include extra information. The default is "percent".
legend	(logical) Display legend. Allowed values are limited to the following: • "TRUE": Groups are indicated using a legend. • "FALSE": Groups are indicated in the labels. The default is FALSE.
pie_rotation	(numeric) The number of degrees to rotate the pie chart by, clockwise. The default is 0.
centre_radius	(numeric, integer) The radius of the centre circle. Used to make a "donut" plot. Should be a value between 0 and 1. The default is 0.
centre_label	(NULL, character) The text to display in the centre of the pie chart. Mostly used with donut plots where centre_radius is greater than 0. The default is NULL.
count_na	(logical) Include the number of missing values in the pie chart. The default is FALSE.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- ggplot2

Value

A annotation_pie_chart object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A annotation_pie_chart object inherits the following struct classes:

[annotation_pie_chart] -> [chart] -> [struct_class]

References

Wickham H (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.

Examples

```
M <- annotation_pie_chart(
        factor_name = "V1",
        label_location = "inside",
        label_rotation = FALSE,
        legend = FALSE,
        pie_rotation = 0,
        label_type = "percent",
        centre_radius = 0,
        centre_label = NULL,
        count_na = FALSE)
```

---

annotation_source *An annotation source*

Description

A base class defining an annotation source. This object is extended by MetmashR to define other objects.

Usage

```
annotation_source(source = character(0), data = data.frame(), tag = "", ...)
```

Arguments

source	(ANY) The source of annotation data. The default is character(0).
data	(data.frame, NULL) A data.frame of annotation data. The default is data.frame().
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "".
...	Additional slots and values passed to struct_class.

Value

A annotation_source object. This object has no output slots.

Inheritance

A annotation_source object inherits the following struct classes:

[annotation_source] -> [struct_class]

See Also

Other annotation databases: AnnotationDb_database, GO_database, annotation_database, excel_database, rdata_database, rds_cache, rds_database

Examples

```
M <- annotation_source(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

annotation_table *An annotation table*

Description

An annotation_table is an annotation_source() where the imported data.frame contains measured experimental data. An id_column of values is required to uniquely indentify each record (row) in the table (NB these are NOT molecule identifiers, which may be be present in multiple records).

Usage

```
annotation_table(data = data.frame(), tag = "", id_column = NULL, ...)
```

Arguments

data	(data.frame, NULL) A data.frame of annotation data. The default is data.frame().
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "".
id_column	(character) The column name of the annotation data.frame containing row identifers. If NULL This will be generated automatically. The default is NULL.
...	Additional slots and values passed to struct_class.

Value

A annotation_table object. This object has no output slots.

Inheritance

A annotation_table object inherits the following struct classes:

[annotation_table] -> [annotation_source] -> [struct_class]

See Also

Other annotation tables: cd_source, ls_source

Other annotation sources: annotation_database, cd_source, ls_source, mspurity_source

Examples

```
M <- annotation_table(
        id_column = "id",
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

annotation_upset_chart

Annotation UpSet chart

Description

Display an UpSet chart of labels in the specified column of an annotation_source.

Usage

```
annotation_upset_chart(
  factor_name,
  group_column = NULL,
  order_intersect_by = "size",
  order_set_by = "name",
  nintersects = NULL,
  filter = NULL,
  relative_width = 0.3,
  relative_height = 3,
  top_bar_color = "grey30",
  top_bar_y_label = NULL,
  top_bar_show_numbers = TRUE,
  top_bar_numbers_size = 3,
  sets_bar_color = "grey30",
  sets_bar_show_numbers = FALSE,
  sets_bar_x_label = "Set Size",
  sets_bar_position = "left",
  intersection_matrix_color = "grey30",
```

```
  specific = TRUE,
  ...
)
```

Arguments

factor_name	(character) The name of the column(s) in the annotation_source(s) to generate an UpSet chart from.
group_column	(character, NULL) The name of the column in the annotation_source to create groups from in the Venn diagram. This parameter is ignored if there are multiple input tables, as each table is considered to be a group. This parameter is also ignored if more than one factor_name is provided, as each column is considered a group. The default is NULL.
order_intersect_by	(character) Order intersect by. Allowed values are limited to the following: • "size": Intersections are sorted by size (largest first). • "name": Intersections are sorted by name alphabetically. • "none": Intersections are not sorted. The default is "size".
order_set_by	(character) Order set by. Allowed values are limited to the following: • "size": Sets are sorted by size (largest first). • "name": Sets are sorted by name alphabetically. • "none": Sets are not sorted. The default is "name".
nintersects	(numeric, integer, NULL) The number of intersections to include in the plot. The default is NULL.
filter	(function, NULL) A function or list of functions to filter intersections based on their properties. The function(s) should take region_data as input and return a logical vector indicating which intersections to keep. Use upset_min_size(), upset_min_groups(), upset_max_groups(), upset_intersections(), or create custom filter functions. The default is NULL.
relative_width	(numeric) The relative width of the left panel in the upset plot. The default is 0.3.
relative_height	(numeric) The relative height of the top panel in the upset plot. The default is 3.
top_bar_color	(character) The color of the top bar chart showing intersection sizes. The default is "grey30".
top_bar_y_label	(character, NULL) The label for the Y-axis of the top bar chart. The default is NULL.
top_bar_show_numbers	(logical) Whether to show numbers on the top bar chart. The default is TRUE.

top_bar_numbers_size
: (numeric) The text size of numbers on the top bar chart. The default is 3.

sets_bar_color
: (character) The color of the sets bar chart. The default is "grey30".

sets_bar_show_numbers
: (logical) Whether to show numbers on the sets bar chart. The default is FALSE.

sets_bar_x_label
: (character) The label for the X-axis of the sets bar chart. The default is "Set Size".

sets_bar_position
: (character) Sets bar position. Allowed values are limited to the following:

  - "left": Position the sets bar chart on the left side.
  - "right": Position the sets bar chart on the right side.

  The default is "left".

intersection_matrix_color
: (character) The color of the intersection matrix dots and lines. The default is "grey30".

specific
: (logical) Whether to include only specific items in subsets (TRUE) or all overlapping items (FALSE). The default is TRUE.

...
: Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- ggVennDiagram

The plot object returned is of class 'aplot' which may not be compatible with all plot combination functions. To combine with other ggplot objects using cowplot or patchwork, use ggplotify::as.ggplot() to convert the plot object:

```
library(ggplotify)
g <- chart_plot(C, data)
g_ggplot <- as.ggplot(g)
cowplot::plot_grid(g1, g_ggplot, nrow = 1)
```

Value

A annotation_upset_chart object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A annotation_upset_chart object inherits the following struct classes:

[annotation_upset_chart] -> [chart] -> [struct_class]

Filtering

Use the `filter` parameter to filter intersections based on their properties:

```
# Filter by minimum size
C <- annotation_upset_chart(factor_name = "V1", filter = upset_min_size(5))

# Filter by minimum number of groups
C <- annotation_upset_chart(factor_name = "V1", filter = upset_min_groups(3))

# Filter to show only specific combinations
C <- annotation_upset_chart(factor_name = "V1",
                            filter = upset_intersections(c("A/B", "B/C")))

# Custom filter function
custom_filter <- function(region_data) {
  region_data$count >= 3 & grepl("A", region_data$name)
}
C <- annotation_upset_chart(factor_name = "V1", filter = custom_filter)
```

Note

The interface to this class has changed. Some parameters have been renamed:

- 'width_ratio' -> 'relative_width'
- 'xlabel' -> 'top_bar_y_label'
- 'sort_intersections' -> 'order_intersect_by'
- 'intersections' -> 'nintersects'
- 'n_intersections' -> 'nintersects'
- 'queries' -> (removed)
- 'keep_empty_group' -> (removed)
- 'sort_sets' -> 'order_set_by'

Old parameter names will trigger deprecation warnings.

References

Gao C, Dusa A (2025). *ggVennDiagram: A 'ggplot2' Implement of Venn Diagram*. doi:10.32614/CRAN.package.ggVennDiag
https://doi.org/10.32614/CRAN.package.ggVennDiagram, R package version 1.5.4, https:
//CRAN.R-project.org/package=ggVennDiagram.

Examples

```
M <- annotation_upset_chart(
        factor_name = "V1",
        group_column = NULL,
        order_intersect_by = "size",
        order_set_by = "name",
```

```
        nintersects = NULL,
        filter = NULL,
        relative_width = 0.3,
        relative_height = 3,
        top_bar_color = "grey30",
        top_bar_y_label = NULL,
        top_bar_show_numbers = FALSE,
        top_bar_numbers_size = 3,
        sets_bar_color = "grey30",
        sets_bar_show_numbers = FALSE,
        sets_bar_x_label = "Set Size",
        sets_bar_position = "left",
        intersection_matrix_color = "grey30",
        specific = FALSE)
```

`annotation_venn_chart` *Annotation venn chart*

Description

Display a venn diagram of labels present in two annotation_sources.

Usage

```
annotation_venn_chart(
  factor_name,
  group_column = NULL,
  fill_colour = "white",
  line_colour = "black",
  labels = TRUE,
  legend = FALSE,
  ...
)
```

Arguments

`factor_name`	(character) The name of the column(s) in the `annotation_source` to generate a chart from. Up to seven columns can be compared for a single `annotation_source`.
`group_column`	(character, NULL) The name of the column in the `annotation_source` to create groups from in the Venn diagram. This parameter is ignored if there are multiple input tables, as each table is considered to be a group. This parameter is also ignored if more than one `factor_name` is provided, as each column is considered a group. The default is `NULL`.
`fill_colour`	(character) The line colour of the groups in a format compatible with ggplot e.g. "black" or "#000000". Special case ".group" sets the colour based on the group label and "none" will not fill the groups. The default is `"white"`.

`line_colour` (character) The line colour of the groups in a format compatible with ggplot e.g. "black" or "#000000". Special case ".group" sets the colour based on the group label, and ".none" will not display lines. The default is `"black"`.

`labels` (logical) Group labels. Allowed values are limited to the following:

- `"TRUE"`: Include group labels on the plot.
- `"FALSE"`: Do not inlude group labels on the plot.

The default is `TRUE`.

`legend` (logical) Legend. Allowed values are limited to the following:

- `"TRUE"`: Include a legend in the plot.
- `"FALSE"`: Do not inlude a legend in the plot.

The default is `FALSE`.

`...` Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `ggVennDiagram`

Value

A `annotation_venn_chart` object. This object has no `output` slots. See `chart_plot` in the `struct` package to plot this chart object.

Inheritance

A `annotation_venn_chart` object inherits the following `struct` classes:

`[annotation_venn_chart]` -> `[chart]` -> `[struct_class]`

References

Gao C, Dusa A (2025). *ggVennDiagram: A 'ggplot2' Implement of Venn Diagram*. doi:10.32614/CRAN.package.ggVennDia
https://doi.org/10.32614/CRAN.package.ggVennDiagram, R package version 1.5.4, https:
//CRAN.R-project.org/package=ggVennDiagram.

Examples

```
M <- annotation_venn_chart(
        factor_name = "V1",
        line_colour = ".group",
        fill_colour = ".group",
        labels = FALSE,
        legend = FALSE,
        group_column = NULL)
```

BiocFileCache_database *Cached database*

Description

A cached resource using BiocFileCache.

Usage

```
BiocFileCache_database(
  source,
  bfc_path = NULL,
  resource_name,
  bfc_fun = cache_as_is,
  import_fun = read.csv,
  offline = FALSE,
  ...
)
```

Arguments

source	(ANY) The source of annotation data.
bfc_path	(character, NULL) BiocFileCache is used to cache the database locally and prevent unnecessary downloads. If a path is provided then BiocFileCache will use this location. If NULL it will use the default location (see BiocFileCache::BiocFileCache() for details). The default is NULL.
resource_name	(character) The name given to this resource in the cache. (see BiocFileCache::BiocFileCache() for details).
bfc_fun	(function) A function to process the object before storing it in the cache, e.g. to store an unzipped file in the cache instead of the zipped version. This would prevent needing to unzip the resource each time it is retrieved from the cache, but would mean using more space on disk. The default function does nothing to the resource. See BiocFileCache::bfcdownload() for details.
import_fun	(function) A function to process the object after retrieving it from the cache e.g. it might need to be unzipped before importingas a data.frame. This function should take the path to the cached object as the first input and return a data.frame.
offline	(logical) If offline = FALSE then checks to determine if the resource has expired will be skipped, and retrieved directly from the cache. The default is FALSE.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- BiocFileCache

Value

A BiocFileCache_database object. This object has no output slots.

Inheritance

A BiocFileCache_database object inherits the following struct classes:

[BiocFileCache_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Shepherd L, Morgan M (2025). *BiocFileCache: Manage Files Across Sessions*. doi:10.18129/B9.bioc.BiocFileCache https://doi.org/10.18129/B9.bioc.BiocFileCache, R package version 3.0.0, https://bioconductor.org/packages/BiocFileCache.

See Also

Other database: sqlite_database

Examples

```
M <- BiocFileCache_database(
        bfc_path = NULL,
        resource_name = "bfc",
        bfc_fun = function(){},
        import_fun = function(){},
        offline = FALSE,
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

cache_as_is *Cache file with no changes using BiocFileCache*

Description

This helper function is for use with BiocFileCache objects. Using it will copy the file directly to the cache without making any changes.

Usage

```
cache_as_is(from, to)
```

Arguments

from	incoming path
to	the outgoing path

Value

TRUE if successful

Examples

```
M <- BiocFileCache_database(
    source = tempfile(),
    resource_name = "example",
    bfc_fun = cache_as_is
)
```

---

calc_ppm_diff *Calculate ppm difference*

Description

Calculate ppm difference between two columns in an annotation_table. e.g. for comparing observed m/z to theortical ones.

Usage

```
calc_ppm_diff(
  obs_mz_column,
  ref_mz_column,
  out_column,
  check_names = "unique",
  ...
)
```

Arguments

obs_mz_column	(character) Column name in annotation_table containing the observed m/z values.
ref_mz_column	(character) Column name in annotation table containing the .
out_column	(character) Column name in annotation table to store the computed ppm differences.
check_names	(character) Check names. Allowed values are limited to the following: • "stop": If the output column already exists an error will be thrown. • "unique": If the output column already exists a unique column name will be generated.

- "replace": If the output column already exists it will be replaced.

The default is "unique".

... Additional slots and values passed to struct_class.

Value

A calc_ppm_diff object with the following output slots:

updated (annotation_table) The input annotation source with the computed ppm diffences in a new column.

Inheritance

A calc_ppm_diff object inherits the following struct classes:

[calc_ppm_diff] -> [model] -> [struct_class]

Examples

```
M <- calc_ppm_diff(
        obs_mz_column = character(0),
        ref_mz_column = "reference (theoretical) m/z values.",
        out_column = character(0),
        check_names = "unique")
```

---

calc_rt_diff *Calculate RT difference*

Description

Calculate RT difference between two RT values

Usage

```
calc_rt_diff(
  obs_rt_column,
  ref_rt_column,
  out_column,
  check_names = "unique",
  ...
)
```

Arguments

obs_rt_column	(character) Column name in annotation table containing the observed (measured) RT values.
ref_rt_column	(character) Column name in annotation table containing the reference (theoretical) RT values.
out_column	(character) Column name in annotation table to store the computed RT differences.
check_names	(character) Check names. Allowed values are limited to the following: • "stop": If the output column already exists an error will be thrown. • "unique": If the output column already exists a unique column name will be generated. • "replace": If the output column already exists it will be replaced. The default is "unique".
...	Additional slots and values passed to struct_class.

Value

A calc_rt_diff object with the following output slots:

updated	(annotation_table) The input annotation source with the newly generated column.

Inheritance

A calc_rt_diff object inherits the following struct classes:

[calc_rt_diff] -> [model] -> [struct_class]

Examples

```
M <- calc_rt_diff(
        obs_rt_column = character(0),
        ref_rt_column = character(0),
        out_column = character(0),
        check_names = "unique")
```

---

cd_source *LCMS table*

Description

An LCMS table extends annotation_table() to represent annotation data for an LCMS experiment. Columns representing m/z and retention time are required for an lcms_table.

Usage

```
cd_source(
  source,
  sheets = c(1, 1),
  tag = "CD",
  mz_column = "mz",
  rt_column = "rt",
  id_column = "id",
  data = NULL,
  ...
)
```

Arguments

source	(character) The path to the Compound Discoverer Excel files to import. Both the compounds and isomers file should be included, in that order.
sheets	(character, numeric, integer) The name or index of the sheets to read from the source file(s). A sheet should be provided for each input file. The default is c(1, 1).
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "CD".
mz_column	(character) The column name of the annotation data.frame containing m/z values. The default is "mz".
rt_column	(character) The column name of the annotation data.frame containing retention time values. The default is "rt".
id_column	(character) The column name of the annotation data.frame containing row identifers. If NULL This will be generated automatically. The default is "id".
data	(data.frame, NULL) A data.frame of annotation data. The default is NULL.
...	Additional slots and values passed to struct_class.

Value

A cd_source object. This object has no output slots.

Inheritance

A cd_source object inherits the following struct classes:

[cd_source] -> [lcms_table] -> [annotation_table] -> [annotation_source] -> [struct_class]

See Also

Other annotation sources: annotation_database, annotation_table, ls_source, mspurity_source

Other annotation tables: annotation_table, ls_source

Examples

```
M <- cd_source(
        sheets = c(1, 1),
        mz_column = "mz",
        rt_column = "rt",
        id_column = "id",
        tag = character(0),
        data = data.frame(),
        source = character(0))
```

---

chart_plot,annotation_bar_chart,annotation_source-method

chart_plot method

Description

Plots a chart object

Usage

```
## S4 method for signature 'annotation_bar_chart,annotation_source'
chart_plot(obj, dobj)

## S4 method for signature 'annotation_histogram,annotation_source'
chart_plot(obj, dobj)

## S4 method for signature 'annotation_histogram2d,annotation_source'
chart_plot(obj, dobj)

## S4 method for signature 'annotation_pie_chart,annotation_source'
chart_plot(obj, dobj)

## S4 method for signature 'annotation_venn_chart,annotation_source'
chart_plot(obj, dobj, ...)

## S4 method for signature 'annotation_venn_chart,list'
chart_plot(obj, dobj)

## S4 method for signature 'annotation_upset_chart,annotation_source'
chart_plot(obj, dobj, ...)

## S4 method for signature 'annotation_upset_chart,list'
chart_plot(obj, dobj)

## S4 method for signature 'mwb_structure,annotation_source'
chart_plot(obj, dobj)
```

```
## S4 method for signature 'pubchem_structure,annotation_source'
chart_plot(obj, dobj)

## S4 method for signature 'pubchem_widget,annotation_source'
chart_plot(obj, dobj)
```

Arguments

obj	a chart object
dobj	a struct object
...	additiional inputs to chart_plot

Value

a plot object

Examples

```
C <- example_chart()
chart_plot(C, example_model())
```

---

check_for_columns *Check for columns in an* annotation_source

---

Description

This method checks for the presence of columns by name in an annotation_source(). It returns TRUE if all are present, or a vector of messages indicating which columns are missing from the data.frame. It is used by MetMashR to ensure validity of certain objects.

Usage

```
check_for_columns(obj, ..., msg = FALSE)

## S4 method for signature 'annotation_source'
check_for_columns(obj, ..., msg = FALSE)
```

Arguments

obj	an annotation_source() object
...	the column names to check for
msg	TRUE/FALSE indicates whether to return a message if some columns are missing. If msg = FALSE then the function returns FALSE if all columns are not present.

Value

logical if all columns are present, or a vector of messages if requested.

Examples

```
# test if column present
AT <- annotation_source(data = data.frame(id = character(0)))
check_for_columns(AT, "id") # TRUE
check_for_columns(AT, "cake") # FALSE

# return a message if missing
check_for_columns(AT, "cake", msg = TRUE)
```

---

classyfire_lookup *Query ClassyFire database*

Description

Queries the ClassyFire database by inchikey to obtain chemical ontology information.

Usage

```
classyfire_lookup(
  query_column,
  output_items = "kingdom",
  output_fields = "name",
  suffix = "_cf",
  ...
)
```

Arguments

query_column	(character) The name of a column in the annotation table containing values to search in the api call.
output_items	(character) The names of the items to return from the results of the search. Can include any number of "kingdom", "superclass", "class", "subclass", "direct_parent", "intermediate_nodes", "substituents", "smiles", "molecular_framework", "description", "ancestors", "predicted_chebi_terms". Keyword ".all" may be used to return all items. The default is "kingdom".
output_fields	(character) The names of fields to return for each output_item. Can include any of "name", "description", "chemont_id" and "url". Keyword ".all" may be used to return all fields. Some items do not have fields, so output_category is ignored. The default is "name".
suffix	(character) A suffix appended to all column names in the returned result. The default is "_cf".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr
- httr

Value

A classyfire_lookup object with the following output slots:

updated (annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A classyfire_lookup object inherits the following struct classes:

[classyfire_lookup] -> [rest_api] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Wickham H (2023). *httr: Tools for Working with URLs and HTTP*. doi:10.32614/CRAN.package.httr https://doi.org/10.32614/CRAN.package.httr, R package version 1.4.7, https://CRAN.R-project.org/package=httr.

See Also

Other REST API's: kegg_lookup, lipidmaps_lookup, mwb_compound_lookup, rest_api

Examples

```
M <- classyfire_lookup(
        output_items = "kingdom",
        output_fields = "name",
        base_url = "http://classyfire.wishartlab.com/entities",
        url_template = "<base_url>/<query_column>.json",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

combine_columns *Combine columns*

Description

A wrapper for `paste()` and `interaction()`. Combines the values in multiple columns row-wise.

Usage

```
combine_columns(
  column_names,
  separator = "_",
  prefix = NULL,
  suffix = NULL,
  output_column = "combined",
  clean = TRUE,
  ...
)
```

Arguments

`column_names`	(character) The column name(s) in the annotation_source to combine.
`separator`	(character) A string placed in between the two being joined. The default is `"_"`.
`prefix`	(character, NULL) A string placed at the start of the combined strings. The default is `NULL`.
`suffix`	(character, NULL) A string placed at the end of the combined strings. The default is `NULL`.
`output_column`	(character) The name of a column to store the combined values in. The default is `"combined"`.
`clean`	(logical) Clean old columns. Allowed values are limited to the following: • `"TRUE"`: The named columns are removed after being combined. • `"FALSE"`: The named columns are retained after being combined. The default is `TRUE`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `combine_columns` object with the following `output` slots:

`updated`	(annotation_source) The annotation_source after combining the columns.

Inheritance

A combine_columns object inherits the following struct classes:

[combine_columns] -> [model] -> [struct_class]

Examples

```
M <- combine_columns(
        column_names = "V1",
        separator = "_",
        output_column = "combined",
        clean = FALSE,
        prefix = NULL,
        suffix = NULL)
```

---

combine_records *Combine annotation records (rows)*

Description

Combine annotation records (rows) based on a key. All records with the same key will be combined. A number of helper functions are provided for common approaches to merging records.

Usage

```
combine_records(
  group_by,
  default_fcn = fuse(separator = " || "),
  fcns = list(),
  ...
)
```

Arguments

group_by	(character) The column used as the key for grouping records.
default_fcn	(function) The default function to use for summarising columns when combining records and a specific function has not been provided in fcns. The default is fuse(separator = " || ").
fcns	(list) A named list of functions to use for summarising named columns when combining records. Names should correspond to the columns in the annotation table. The default is list().
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A `combine_records` object with the following `output` slots:

`updated` (annotation_source) The input annotation source with the newly generated column.

Inheritance

A `combine_records` object inherits the following `struct` classes:

`[combine_records]` -> `[model]` -> `[struct_class]`

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Lloyd GR, Jankevics A, Weber RJM (2020). "struct: an R/Bioconductor-based framework for standardized metabolomics data analysis and beyond." *Bioinformatics*, *36*(22-23), 5551-5552.

Examples

```
M <- combine_records(
        fcns = list(),
        group_by = character(0),
        default_fcn = function(){})
```

---

combine_records_helper_functions

Combine records helper functions

Description

This page documents helper functions for use with `combine_records()`.

Usage

```
compute_mode(ties = FALSE, na.rm = TRUE)

compute_mean(na.rm = TRUE)

compute_median(na.rm = TRUE)

fuse(separator, na_string = "NA")

select_max(max_col, use_abs = FALSE, keep_NA = FALSE)
```

```
select_min(min_col, use_abs = FALSE, keep_NA = FALSE)

select_match(match_col, search_col, separator, na_string = "NA")

select_exact(match_col, match, separator, na_string = "NA")

fuse_unique(
  separator,
  na_string = "NA",
  digits = 6,
  drop_na = FALSE,
  sort = FALSE
)

prioritise(match_col, priority, separator, no_match = NA, na_string = "NA")

nothing()

count_records()

select_grade(grade_col, keep_NA = FALSE, upper_case = TRUE)
```

Arguments

ties	(logical) If TRUE then all records matching the tied groups are returned. Otherwise the first record is returned.
na.rm	(logical) If TRUE then NA is ignored
separator	(character, NULL) if !NULL this string is used to collapse matches with the same priority
na_string	(character) NA values are replaced with this string
max_col	(character) the column name to search for the maximum value.
use_abs	(logical) If TRUE then the sign of the values is ignored.
keep_NA	(logical) If TRUE keeps records with NA values
min_col	(character) the column name to search for the minimum value.
match_col	(character) the column with labels to prioritise
search_col	(character) the name of a column to use as a reference for locating values in the matching column.
match	(character) a value to search for in the matching column.
digits	(numeric) the number of digits to use when converting numerical values to characters when determining if values are unique.
drop_na	(logical) exclude NA from the list of unique entires
sort	(logical) sort the values before collapsing.
priority	(character) a list of labels in priority order

no_match	(character, NULL) if !NULL then annotations not matching any of the priority labels are replaced with this value
grade_col	(character) the name of a column containing grades
upper_case	(logical) If TRUE then grades are compared to upper case letters to determine their ordering, otherwise lower case.

Value

A function for use with `combine_records()`

Functions

- `compute_mode()`: returns the most common value, excluding NA. If `ties == TRUE` then all tied values are returned, otherwise the first value in a sorted unique list is returned (equal to min if numeric). If `na.rm = FALSE` then NA are included when searching for the modal value and placed last if `ties = FALSE` (values are returned preferentially over NA).
- `compute_mean()`: calculates the mean value, excluding NA if `na.rm = TRUE`
- `compute_median()`: calculates the median value, excluding NA if `na.rm = TRUE`
- `fuse()`: collapses multiple matching records into a single string using the provided separator.
- `select_max()`: selects a record based on the index of the maximum value in a another column.
- `select_min()`: selects a record based on the index of the minimum in a second column.
- `select_match()`: returns all records based on the indices of identical matches in a second column and collapses them using the provided separator.
- `select_exact()`: returns records based on the index of identical value matching the `match` parameter within the current column, and collapses them using the provided separator if necessary.
- `fuse_unique()`: collapses a set of records to a set of unique values using the provided separator. `digits` can be provided for numeric columns to control the precision used when determining unique values.
- `prioritise()`: reduces a set of annotations by prioritising values according to the input. If there are multiple matches with the same priority then they are collapsed using a separator.
- `nothing()`: a pass-through function to allow some annotation table columns to remain unchanged.
- `count_records()`: adds a new column indicating the number of annotations that match the given grouping variable.
- `select_grade()`: returns records based on the index of the best grade in a second list. The best grade is defined as "A" for `upper_case = TRUE` or "a" for `upper_case = FALSE` and the worst grade is "Z" or "z". Any non-exact matches to a character in `LETTERS` or `letters` are replaced with NA.

Examples

```
# Select matching records
M <- combine_records(
    group_by = "example",
```

```
    default_fcn = select_exact(
        match_col = "match_column",
        match = "find_me",
        separator = ", ",
        na_string = "NA"
    )
)

# Collapse unique values
M <- combine_records(
    group_by = "example",
    default_fcn = fuse_unique(
        digits = 6,
        separator = ", ",
        na_string = "NA",
        sort = FALSE
    )
)

# Prioritise by source
M <- combine_records(
    group_by = "InChiKey",
    default_fcn = prioritise(
        match_col = "source",
        priority = c("CD", "LS"),
        separator = "  || "
    )
)

# Do nothing to all columns
M <- combine_records(
    group_by = "InChiKey",
    default_fcn = nothing()
)

# Add a column with the number of records with a matching inchikey
M <- combine_records(
    group_by = "InChiKey",
    fcns = list(
        count = count_records()
    )
)

# Select annotation with highest (best) grade
M <- combine_records(
    group_by = "InChiKey",
    default_fcn = select_grade(
        grade_col = "grade",
        keep_NA = FALSE,
        upper_case = TRUE
    )
)
```

combine_sources *Combine annotation sources (tables)*

Description

Annotation tables are joined and matching columns merged.

Usage

```
combine_sources(
  source_list,
  matching_columns = NULL,
  keep_cols = NULL,
  source_col = "annotation_source",
  exclude_cols = NULL,
  tag = "combined",
  as = annotation_source(name = "combined", description =
    paste0("A source created by combining two or ", "more sources")),
  ...
)
```

Arguments

source_list	(list) A list of annotation sources to be combined.
matching_columns	(character, NULL) A named vector of columns names to be created by merging columns from individual sources. e.g. `c('hello'='world')` will rename the 'hello' column to 'world' if found in any of the tables. The default is `NULL`.
keep_cols	(character, NULL) A list of column names to keep in the combined table (padded with NA) if detected in one of the input tables. Special case ".all" will keep all columns from all tables. The default is `NULL`.
source_col	(character) The column name that will be created to contain a tag to indicate which source the annotation originated from. The default is `"annotation_source"`.
exclude_cols	(NULL, character) Column names to be excluded from the merged annotation table. Note this is applied after `keep_cols`. The default is `NULL`.
tag	(character) The tag given to the newly combined table. The default is `"combined"`.
as	(annotation_source) An annotation_source object to use as the base class for the combined sources. The default is `annotation_source(name = "combined", description = paste0("A source created by combining two or ", "more sources"))`.
...	Additional slots and values passed to `struct_class`.

Value

A combine_sources object with the following output slots:

combined_table (annotation_source) The annotation tabel after combining the input tables.

Inheritance

A combine_sources object inherits the following struct classes:

[combine_sources] -> [model] -> [struct_class]

Examples

```
M <- combine_sources(
        source_list = list(),
        matching_columns = NULL,
        keep_cols = NULL,
        source_col = "annotation_source",
        exclude_cols = NULL,
        tag = "combined",
        as = annotation_source())
```

CompoundDb_source *Import CompDB source*

Description

Imports the compounds table of a CompDB source as an annotation_source.

Usage

```
CompoundDb_source(source, tag = "cdb", ...)
```

Arguments

source	(ANY) The source of annotation data.
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "cdb".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- CompoundDb

Value

A CompoundDb_source object. This object has no output slots.

Inheritance

A CompoundDb_source object inherits the following struct classes:

[CompoundDb_source] -> [annotation_source] -> [struct_class]

References

Rainer J, Vicini A, Salzer L, Stanstrup J, Badia J, Neumann S, Stravs M, Verri Hernandes V, Gatto L, Gibb S, Witting M (2022). "A Modular and Expandable Ecosystem for Metabolomics Data Annotation in R." *Metabolites*, *12*, 173. doi:10.3390/metabo12020173 https://doi.org/10.3390/metabo12020173, https://www.mdpi.com/2218-1989/12/2/173.

Examples

```
M <- CompoundDb_source(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

compute_column *Compute a column*

Description

Compute values for a new column based on an input column.

Usage

```
compute_column(input_columns, output_column, fcn, ...)
```

Arguments

input_columns	(character) The name of a column in the input table used to compute a new column.
output_column	(character) The name of the newply computed column.
fcn	(function) The function used to compute the values for the new column.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A compute_column object with the following output slots:

updated (annotation_source) The updated annotations as an annotation_source object.

Inheritance

A compute_column object inherits the following struct classes:

[compute_column] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Examples

```
M <- compute_column(
        input_columns = character(0),
        output_column = character(0),
        fcn = function(){})
```

---

compute_record *Compute a value for a record*

Description

Compute values for a record based on other values in a record

Usage

```
compute_record(fcn, ...)
```

Arguments

fcn	(function) The function used to compute the values for the record.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A compute_record object with the following output slots:

updated (annotation_source) The updated annotations as an annotation_source object.

Inheritance

A compute_record object inherits the following struct classes:

[compute_record] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Examples

```
M <- compute_record(
        fcn = function(){})
```

---

database_lookup *ID lookup by database*

Description

Search a database (data.frame) for annotation matches based on values in a specified column.

Usage

```
database_lookup(
  query_column,
  database_column,
  database,
  include = NULL,
  suffix = NULL,
  not_found = NA,
  ...
)
```

Arguments

query_column	(character) The annotation table column name to use as the reference for searching the database e.g. "HMBD_ID".
database_column	(character) The database column to search for matches to the values in annoation_column.
database	(data.frame, annotation_database) A database to be searched. Can be a data.frame or a annotation_database object.
include	(character, NULL) The name of the database columns to be added to the annotations. If NULL, all columns are retained. The default is NULL.
suffix	(character, NULL) A string appended to the column names from the database. Used to distinguish columns from different databases with identical column names.If suffix = NULL then the column names are not changed. The default is NULL.
not_found	(character, numeric, logical, NULL) The returned value when there are no matches. The default is NA.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A database_lookup object with the following output slots:

updated	(annotation_source) The input annotation_source is updated with matching columns from the database.

Inheritance

A database_lookup object inherits the following struct classes:

[database_lookup] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Examples

```
M <- database_lookup(
        query_column = "V1",
        database_column = "",
        database = data.frame(),
        include = NULL,
        suffix = NULL,
        not_found = NULL)
```

`eutils_lookup` *NCBI E-utils query*

Description

Submit a query to one of the NCBI E-utils databases. See https://www.ncbi.nlm.nih.gov/books/NBK25501/ for details.

Usage

```
eutils_lookup(query_column, database, term, result_fields = "idlist", ...)
```

Arguments

`query_column`	(character) The column name to use as the reference for searching the database e.g. "HMBD_ID".
`database`	(character) The name of the E-utils database to search. See https://www.ncbi.nlm.nih.gov/books/NBK255 for details.
`term`	(character) A correctly formated search term to use with E-utils. See https://www.ncbi.nlm.nih.gov/books/ for details. When used with the provided url template will automatically include the value from the `query_column` at the beginning of the term.
`result_fields`	(character) The name of the search result field to return. For E-utils this is often "idlist". The default is `"idlist"`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `eutils_lookup` object with the following `output` slots:

`updated` (annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A `eutils_lookup` object inherits the following `struct` classes:

`[eutils_lookup]` -> `[rest_api]` -> `[model]` -> `[struct_class]`

Examples

```
M <- eutils_lookup(
        database = "gene",
        term = "[pdat]",
        result_fields = "idlist",
        base_url = "https://eutils.ncbi.nlm.nih.gov/entrez/eutils",
     url_template = "<base_url>/esearch.fcgi?db=<database>&term=<query_column><term>&retmode=json",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

---

excel_database *Excel database*

Description

A data.frame imported from the sheet of an excel file

Usage

```
excel_database(
  source = character(0),
  sheet = 1,
  rowNames = FALSE,
  colNames = TRUE,
  startRow = 1,
  ...
)
```

Arguments

source	(ANY) The source of annotation data. The default is character(0).
sheet	(character) The name of the sheet to import. The default is 1.
rowNames	(logical) If TRUE, first column of data will be used as row names. The default is FALSE.
colNames	(logical) If TRUE, first row of data will be used as column names. The default is TRUE.
startRow	(numeric, integer) First row to begin looking for data. Empty rows at the top of a file are always skipped, regardless of the value of startRow. The default is 1.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- openxlsx

Value

A excel_database object. This object has no output slots.

Inheritance

A excel_database object inherits the following struct classes:

[excel_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Schauberger P, Walker A (2025). *openxlsx: Read, Write and Edit xlsx Files*. doi:10.32614/CRAN.package.openxlsx https://doi.org/10.32614/CRAN.package.openxlsx, R package version 4.2.8.1, https://CRAN.R-project.org/package=openxlsx.

See Also

Other annotation databases: AnnotationDb_database, GO_database, annotation_database, annotation_source, rdata_database, rds_cache, rds_database

Examples

```
M <- excel_database(
        sheet = character(0),
        rowNames = FALSE,
        colNames = FALSE,
        startRow = 1,
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

filter_labels *Filter by factor labels*

Description

Removes (or includes) annotations such that the named column excludes (or includes) the specified labels.

Usage

```
filter_labels(
  column_name,
  labels,
  mode = "exclude",
  perl = FALSE,
  fixed = FALSE,
  match_na = FALSE,
  ...
)
```

Arguments

column_name	(character) The column name to filter.
labels	(character) The labels to filter by. Uses [grepl()] so regex is accepted e.g. for partial matching or labels.
mode	(character) Filter mode. Allowed values are limited to the following: • "exclude": The specified labels are removed from the annotation table. • "include": Only the specified labels are retained in the annotation table. The default is "exclude".
perl	(logical) Use a Perl-compatible regex. The default is FALSE.
fixed	(logical) Use exact matching. The default is FALSE.
match_na	(logical) Match NA. Allowed values are limited to the following: • "TRUE": NA values will be treated as if they matched to one of the labels. • "FALSE": NA values will be treated as though they did not match to any of the labels. The default is FALSE.
...	Additional slots and values passed to struct_class.

Value

A filter_labels object with the following output slots:

filtered	(annotation_source) The annotation_source after filtering.
flags	(data.frame) A list of flags indicating which annotations had a matching label.

Inheritance

A filter_labels object inherits the following struct classes:

[filter_labels] -> [model] -> [struct_class]

Examples

```
M <- filter_labels(
        column_name = "V1",
        labels = "",
        mode = "exclude",
        perl = FALSE,
        fixed = FALSE,
        match_na = FALSE)
```

`filter_na` *Filter by missing values*

Description

Filters annotations where the named column is NA

Usage

```
filter_na(column_name, mode = "exclude", ...)
```

Arguments

`column_name`	(character) The column name to use for filtering.
`mode`	(character) Filter mode. Allowed values are limited to the following: • `"include"`: Rows with NA are kept and all others removed. • `"exclude"`: Rows with NA are excluded and all other kept. The default is `"exclude"`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `filter_na` object with the following `output` slots:

`filtered`	(annotation_source) Annotation_source after filtering.
`flags`	(data.frame) A list of flags indicating which annotations were removed.

Inheritance

A `filter_na` object inherits the following `struct` classes:

`[filter_na]` -> `[model]` -> `[struct_class]`

Examples

```
M <- filter_na(
        column_name = "V1",
        mode = "exclude")
```

`filter_range` *Filter by range*

Description

Removes annotations where the names column is greater than an upper limit or less than a lower limit.

Usage

```
filter_range(
  column_name,
  upper_limit = Inf,
  lower_limit = -Inf,
  equal_to = TRUE,
  ...
)
```

Arguments

`column_name`	(character) The column name to filter.
`upper_limit`	(numeric, integer, function) The upper limit used for filtering. Can be a value, or a function that computes a value (e.g. mean). The default is `Inf`.
`lower_limit`	(numeric, integer, function) The lower limit used for filtering. Can be a value, or a function that computes a value (e.g. mean). The default is `-Inf`.
`equal_to`	(logical) Equal to limits. Allowed values are limited to the following: • `"TRUE"`: Greater/less than or equal to the limits are excluded. • `"FALSE"`: Greater/less than the limits are excluded. The default is `TRUE`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `filter_range` object with the following `output` slots:

`filtered`	(annotation_source) Annotation_source after filtering.
`flags`	(data.frame) A list of flags indicating which annotations were removed.

Inheritance

A filter_range object inherits the following struct classes:

[filter_range] -> [model] -> [struct_class]

Examples

```
M <- filter_range(
        column_name = "V1",
        upper_limit = Inf,
        lower_limit = -Inf,
        equal_to = FALSE)
```

---

filter_records *Filter rows*

Description

A wrapper around dplyr::filter. Select rows from an annotation table using tidy grammar.

Usage

```
filter_records(where = wherever(A > 0), ...)
```

Arguments

where	(quosures) A list of rlang::quosure for evaluation e.g. A>10 willselect all rows where the values in column A are greater than10. A helper function wherever is provided to generatea suitable list of quosures. The default is wherever(A > 0).
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr
- rlang

Value

A `filter_records` object with the following `output` slots:

`updated` (annotation_source) The updated annotations as an `annotation_source` object.

Inheritance

A `filter_records` object inherits the following `struct` classes:

`[filter_records]` -> `[model]` -> `[struct_class]`

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Henry L, Wickham H (2025). *rlang: Functions for Base Types and Core R and 'Tidyverse' Features*. doi:10.32614/CRAN.package.rlang https://doi.org/10.32614/CRAN.package.rlang, R package version 1.1.6, https://CRAN.R-project.org/package=rlang.

See Also

`dplyr::filter()`

`wherever()`

Examples

```
M <- filter_records(
        where = wherever(A>10))
```

`filter_venn` *Filter by factor levels*

Description

Removes (or includes) annotations such that the named column excludes (or includes) the specified intersection levels. Supports any number of groups using intersection-based filtering. If no levels are specified, all available intersection levels will be returned for inspection. If invalid levels are specified, a warning will be shown with the list of valid levels.

Usage

```
filter_venn(
  factor_name,
  group_column = NULL,
  tables = NULL,
  filter = NULL,
  mode = "include",
  ...
)
```

Arguments

factor_name	(character) The name of the column(s) in the annotation_source to generate intersection groups from. Supports any number of columns for intersection-based filtering.
group_column	(character, NULL) The name of the column in the annotation_source to create groups from in the Venn diagram. This parameter is ignored if !is.null(tables), as each table is considered to be a group. This parameter is also ignored if more than one factor_name is provided, as each column is considered a group. The default is NULL.
tables	(list, NULL) A list of annotation_sources to generate the venn groups from. If the only table of interest is the table coming in from model_apply then set tables = NULL and use group_column. The default is NULL.
filter	(function, NULL) A function to filter intersections based on their properties. The function should take region_data as input and return a logical vector indicating which intersections to keep. Use upset_intersections(), upset_min_size(), upset_min_groups(), upset_max_groups(), or create custom filter functions. The default is NULL.
mode	(character) Filter mode. Allowed values are limited to the following: • "include": Only items that appear in the filtered intersections are kept in the output. • "exclude": Items that appear in the filtered intersections are removed from the output. The default is "include".
...	Additional slots and values passed to struct_class.

Value

A filter_venn object with the following output slots:

filtered	(annotation_source) Annotation_source after filtering.
flags	(data.frame) A list of flags indicating which annotations were removed.

Inheritance

A filter_venn object inherits the following struct classes:

[filter_venn] -> [model] -> [struct_class]

Examples

```
M <- filter_venn(
        factor_name = "V1",
        group_column = NULL,
        tables = NULL,
        filter = NULL,
        mode = "include")
```

---

github_file *GitHub file*

Description

Uses the GitHub REST API to retrieve a file from a specifiedGitHub repository.

Usage

```
github_file(
  username,
  repository_name,
  file_path,
  bfc_path = NULL,
  resource_name = paste(username, repository_name, file_path, sep = "_"),
  ...
)
```

Arguments

username	(character) The GitHub username to retireve the file from.
repository_name	(character) The name of a repository for the specified GitHub usernamethat contains the file to download.
file_path	(character) The path to the file to download within the specified GitHub repository.
bfc_path	(character, NULL) BiocFileCache is used to cache the database locally and prevent unnecessary downloads. If a path is provided then BiocFileCache will use this location. If NULL it will use the default location (see BiocFileCache::BiocFileCache() for details). The default is NULL.

resource_name	(character) The name given to this resource in the cache. (see BiocFileCache::BiocFileCache() for details). The default is paste(username, repository_name, file_path, sep = "_").
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- BiocFileCache
- httr

Value

A github_file object. This object has no output slots.

Inheritance

A github_file object inherits the following struct classes:

[github_file] -> [BiocFileCache_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Shepherd L, Morgan M (2025). *BiocFileCache: Manage Files Across Sessions*. doi:10.18129/B9.bioc.BiocFileCache https://doi.org/10.18129/B9.bioc.BiocFileCache, R package version 3.0.0, https://bioconductor.org/packages/BiocFileCache.

Wickham H (2023). *httr: Tools for Working with URLs and HTTP*. doi:10.32614/CRAN.package.httr https://doi.org/10.32614/CRAN.package.httr, R package version 1.4.7, https://CRAN.R-project.org/package=httr.

Examples

```
M <- github_file(
        username = character(0),
        repository_name = character(0),
        file_path = character(0),
        bfc_path = NULL,
        resource_name = "bfc",
        bfc_fun = function(){},
        import_fun = function(){},
        offline = FALSE,
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

GO_database *GO.db*

Description

Retrieve a table from the Gene Ontology using the GO.db package.

Usage

```
GO_database(source = "GO.db", table = "GOBPOFFSPRING", ...)
```

Arguments

source	(character) The name of an AnnotationDb package to import the specified table from. Note the package should already be installed. The default is "GO.db".
table	(character) The name of a table to import from the GO.db package. Allowed tables include: GOBPANCESTOR,GOBPPARENTS,GOBPCHILDREN,GOBPOFFSPRING (and their CC or MF equivalents), GOTERM, GOSYNONYM, GOOBSOLETE. The default is "GOBPOFFSPRING".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- GO.db

Value

A GO_database object. This object has no output slots.

Inheritance

A GO_database object inherits the following struct classes:

[GO_database] -> [AnnotationDb_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Carlson M (2025). *GO.db: A set of annotation maps describing the entire Gene Ontology*. R package version 3.22.0.

Pagès H, Carlson M, Falcon S, Li N (2025). *AnnotationDbi: Manipulation of SQLite-based annotations in Bioconductor*. doi:10.18129/B9.bioc.AnnotationDbi https://doi.org/10.18129/B9.bioc.AnnotationDbi, R package version 1.72.0, https://bioconductor.org/packages/AnnotationDbi.

See Also

GO.db

Other annotation databases: AnnotationDb_database, annotation_database, annotation_source, excel_database, rdata_database, rds_cache, rds_database

Examples

```
M <- GO_database(
        table = "GOBPCHILDREN",
        tag = character(0),
        data = data.frame(),
        source = character(0))
```

---

greek_dictionary *Greek dictionary*

Description

A dictionary for converting Greek characters to Romanised names. It is intended for use with the normalise_strings() object.

Usage

```
greek_dictionary
```

Format

An object of class list of length 48.

Value

A dictionary for use with normalise_strings()

Examples

```
M <- normalise_strings(
    search_column = "example",
    output_column = "result",
    dictionary = greek_dictionary
)
```

hmdb_lookup *Compound ID lookup via pubchem*

Description

Requests HMBD records based on HMDB identifiers.

Usage

```
hmdb_lookup(query_column, suffix = "_hmdb", output = "inchikey", ...)
```

Arguments

query_column	(character) The name of a column in the annotation table containing values to search in the api call.
suffix	(character) A suffix appended to all column names in the returned result. The default is "_hmdb".
output	(character) The value returned from the HMDB xml. The default is "inchikey".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- XML

Value

A hmdb_lookup object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A hmdb_lookup object inherits the following struct classes:

[hmdb_lookup] -> [rest_api] -> [model] -> [struct_class]

References

Temple Lang D (2025). *XML: Tools for Parsing and Generating XML Within R and S-Plus*. doi:10.32614/CRAN.package.XML https://doi.org/10.32614/CRAN.package.XML, R package version 3.99-0.20, https://CRAN.R-project.org/package=XML.

Examples

```
M <- hmdb_lookup(
        output = "inchikey",
        base_url = "http://www.hmdb.ca/metabolites",
        url_template = "<base_url>/<query_column>.xml",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

---

id_counts *id counts*

Description

Adds the number of times an identical identifier is present to each record.

Usage

```
id_counts(id_column, count_column = "id_counts", count_na = TRUE, ...)
```

Arguments

id_column	(character) Column name of the variable ids in variable_meta.
count_column	(character) The name of the new column to store the counts in. The default is "id_counts".
count_na	(logical) Count NA. Allowed values are limited to the following: • "TRUE": Report number of NA. • "FALSE": Do not report number of NA. The default is TRUE.
...	Additional slots and values passed to struct_class.

Value

A id_counts object with the following output slots:

updated	(annotation_source) The input annotation source with the newly generated column.

Inheritance

A id_counts object inherits the following struct classes:

[id_counts] -> [model] -> [struct_class]

Examples

```
M <- id_counts(
        id_column = character(0),
        count_column = character(0),
        count_na = FALSE)
```

`import_source` *Import_source*

Description

A wrapper for `read_source()` that can be used in an annotation workflow to import an annotation source.

Usage

```
import_source(...)
```

Arguments

`...`	Additional slots and values passed to `struct_class`.

Value

A `import_source` object with the following `output` slots:

`imported` (annotation_source) The `annotation_source` after importing the data.

Inheritance

A `import_source` object inherits the following `struct` classes:

`[import_source]` -> `[model]` -> `[struct_class]`

Examples

```
M <- import_source()
```

is_writable *Is database writable*

Description

A function that returns TRUE if the database has been designed for use in read and write mode.

Usage

```
is_writable(obj, ...)

## S4 method for signature 'annotation_database'
is_writable(obj)

## S4 method for signature 'rdata_database'
is_writable(obj)
```

Arguments

obj	A annotation_database object
...	additional database specific inputs

Value

TRUE if the database is writable; FALSE otherwise. This method does not check file properties, only the intended usage of the object.

Examples

```
M <- annotation_database()
is_writable(M)
```

kegg_lookup *Convert to or from kegg identifiers*

Description

Searches the Kegg database to obtain external identifiers. KEGG compound, drug and glycan databases can be queried for pubchem and chebi identifiers, and vice-versa.

Usage

```
kegg_lookup(
  get = "pubchem",
  from = "compound",
  query_column,
  suffix = "_kegg",
  ...
)
```

Arguments

get	(character) Get identifier. Allowed values are limited to the following: • "compound": KEGG small molecule database. • "glycan": KEGG glycan database. • "drug": KEGG drug database. • "chebi": Chemical Entities of Biological Interest (ChEBI) database. • "pubchem": PubChem Substance Identifier. The default is "pubchem".
from	(character) From identifier. Allowed values are limited to the following: • "compound": KEGG small molecule database. • "glycan": KEGG glycan database. • "drug": KEGG drug database. • "chebi": Chemical Entities of Biological Interest (ChEBI) database. • "pubchem": PubChem Substance Identifier. The default is "compound".
query_column	(character) The name of the column containing identifiers to search the database for. They should be identifiers of the type selected for the "from" slot.
suffix	(character) A suffix appended to all column names in the returned result. The default is "_kegg".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- KEGGREST
- dplyr

Value

A kegg_lookup object with the following output slots:

updated	(annotation_source) An annotation_source object with a new column of compound identifiers.

Inheritance

A kegg_lookup object inherits the following struct classes:

[kegg_lookup] -> [model] -> [struct_class]

References

Tenenbaum D, Maintainer B (2025). *KEGGREST: Client-side REST access to the Kyoto Encyclopedia of Genes and Genomes (KEGG)*. doi:10.18129/B9.bioc.KEGGREST https://doi.org/10.18129/B9.bioc.KEGGREST, R package version 1.50.0, https://bioconductor.org/packages/KEGGREST.

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

See Also

Other REST API's: classyfire_lookup, lipidmaps_lookup, mwb_compound_lookup, rest_api

Examples

```
M <- kegg_lookup(
        get = "pubchem",
        from = "compound",
        query_column = "V1",
        suffix = "_kegg")
```

---

lcms_table *LCMS table*

Description

An LCMS table extends annotation_table() to represent annotation data for an LCMS experiment. Columns representing m/z and retention time are required for an lcms_table.

Usage

```
lcms_table(
  data = NULL,
  tag = "",
  id_column = "id",
  mz_column = "mz",
  rt_column = "rt",
  ...
)
```

Arguments

data	(data.frame, NULL) A data.frame of annotation data. The default is NULL.
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is "".
id_column	(character) The column name of the annotation data.frame containing row identifers. If NULL This will be generated automatically. The default is "id".
mz_column	(character) The column name of the annotation data.frame containing m/z values. The default is "mz".
rt_column	(character) The column name of the annotation data.frame containing retention time values. The default is "rt".
...	Additional slots and values passed to struct_class.

Value

A lcms_table object. This object has no output slots.

Inheritance

A lcms_table object inherits the following struct classes:

[lcms_table] -> [annotation_table] -> [annotation_source] -> [struct_class]

Examples

```
M <- lcms_table(
        mz_column = "mz",
        rt_column = "rt",
        id_column = "id",
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

lipidmaps_lookup *LipidMaps api lookup*

Description

Search the LipidMaps database using the API

Usage

```
lipidmaps_lookup(
  query_column,
  context,
  context_item,
  output_item = "all",
  suffix = "_lipidmaps",
  ...
)
```

Arguments

query_column	(character) The name of a column in the annotation table containing values to search in the api call.
context	(character) The search API context. Must be one of "compound", "gene", or "protein".
context_item	(character) The context item being searched. See https://lipidmaps.org/resources/rest for details.
output_item	(character) The names of the columns to return from the results of the search. See https://lipidmaps.org/resources/rest for details. The default is "all".
suffix	(character) A suffix appended to all column names in the returned result. The default is "_lipidmaps".
...	Additional slots and values passed to struct_class.

Value

A lipidmaps_lookup object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A lipidmaps_lookup object inherits the following struct classes:

[lipidmaps_lookup] -> [rest_api] -> [model] -> [struct_class]

See Also

Other REST API's: classyfire_lookup, kegg_lookup, mwb_compound_lookup, rest_api

Examples

```
M <- lipidmaps_lookup(
        query_column = character(0),
        output_item = "input",
        context = "compound",
        context_item = character(0),
```

```
    base_url = "https://www.lipidmaps.org/rest",
url_template = "<base_url>/<context>/<context_item>/<query_column>/<output_item>/json",
    cache = NULL,
    status_codes = list(),
    delay = 0.5,
    suffix = "_rest_api")
```

`ls_source` *LCMS table*

Description

An LCMS table extends `annotation_table()` to represent annotation data for an LCMS experiment. Columns representing m/z and retention time are required for an `lcms_table`.

Usage

```
ls_source(
  source,
  tag = "LS",
  mz_column = "mz",
  rt_column = "rt",
  id_column = "id",
  data = NULL,
  ...
)
```

Arguments

`source`	(ANY) The source of annotation data.
`tag`	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is `"LS"`.
`mz_column`	(character) The column name of the annotation data.frame containing m/z values. The default is `"mz"`.
`rt_column`	(character) The column name of the annotation data.frame containing retention time values. The default is `"rt"`.
`id_column`	(character) The column name of the annotation data.frame containing row identifers. If NULL This will be generated automatically. The default is `"id"`.
`data`	(data.frame, NULL) A data.frame of annotation data. The default is `NULL`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `ls_source` object. This object has no `output` slots.

Inheritance

A `ls_source` object inherits the following `struct` classes:

`[ls_source]` -> `[lcms_table]` -> `[annotation_table]` -> `[annotation_source]` -> `[struct_class]`

See Also

Other annotation sources: `annotation_database`, `annotation_table`, `cd_source`, `mspurity_source`

Other annotation tables: `annotation_table`, `cd_source`

Examples

```
M <- ls_source(
        mz_column = "mz",
        rt_column = "rt",
        id_column = "id",
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

model_apply,model,annotation_source-method

Apply method

Description

Applies method to the input DatasetExperiment

Usage

```
## S4 method for signature 'model,annotation_source'
model_apply(M, D)

## S4 method for signature 'model,list'
model_apply(M, D)

## S4 method for signature 'model_seq,list'
model_apply(M, D)

## S4 method for signature 'model_seq,annotation_source'
model_apply(M, D)

## S4 method for signature 'AnnotationDb_select,annotation_source'
model_apply(M, D)

## S4 method for signature 'CompoundDb_source,annotation_source'
```

```
model_apply(M, D)

## S4 method for signature 'add_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'add_labels,annotation_source'
model_apply(M, D)

## S4 method for signature 'calc_ppm_diff,annotation_table'
model_apply(M, D)

## S4 method for signature 'calc_rt_diff,annotation_table'
model_apply(M, D)

## S4 method for signature 'rest_api,annotation_source'
model_apply(M, D)

## S4 method for signature 'combine_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'combine_records,annotation_source'
model_apply(M, D)

## S4 method for signature 'combine_sources,annotation_source'
model_apply(M, D)

## S4 method for signature 'combine_sources,list'
model_apply(M, D)

## S4 method for signature 'compute_column,annotation_source'
model_apply(M, D)

## S4 method for signature 'compute_record,annotation_source'
model_apply(M, D)

## S4 method for signature 'database_lookup,annotation_source'
model_apply(M, D)

## S4 method for signature 'split_records,annotation_source'
model_apply(M, D)

## S4 method for signature 'filter_labels,annotation_source'
model_apply(M, D)

## S4 method for signature 'filter_na,annotation_source'
model_apply(M, D)

## S4 method for signature 'filter_range,annotation_source'
```

```
model_apply(M, D)

## S4 method for signature 'filter_records,annotation_source'
model_apply(M, D)

## S4 method for signature 'filter_venn,annotation_source'
model_apply(M, D)

## S4 method for signature 'id_counts,annotation_source'
model_apply(M, D)

## S4 method for signature 'import_source,annotation_source'
model_apply(M, D)

## S4 method for signature 'kegg_lookup,annotation_source'
model_apply(M, D)

## S4 method for signature 'mspurity_source,lcms_table'
model_apply(M, D)

## S4 method for signature 'mz_match,annotation_source'
model_apply(M, D)

## S4 method for signature 'mzrt_match,lcms_table'
model_apply(M, D)

## S4 method for signature 'normalise_lipids,annotation_source'
model_apply(M, D)

## S4 method for signature 'normalise_strings,annotation_source'
model_apply(M, D)

## S4 method for signature 'pivot_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'prioritise_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'remove_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'rename_columns,annotation_source'
model_apply(M, D)

## S4 method for signature 'rt_match,annotation_table'
model_apply(M, D)

## S4 method for signature 'select_columns,annotation_source'
```

```
model_apply(M, D)

## S4 method for signature 'split_column,annotation_source'
model_apply(M, D)

## S4 method for signature 'trim_whitespace,annotation_source'
model_apply(M, D)

## S4 method for signature 'unique_records,annotation_source'
model_apply(M, D)
```

Arguments

M	a method object
D	another object used by the first

Value

Returns a modified method object

Examples

```
M <- example_model()
M <- model_apply(M, iris_DatasetExperiment())
```

`mspurity_source` *msPurity source*

Description

An annotation source for importing an annotation table from the format created by the `msPurity` package.

Usage

```
mspurity_source(source, tag = "msPurity", ...)
```

Arguments

source	(ANY) The source of annotation data.
tag	(character) A (short) character string that is used to represent this source e.g. in column names or source columns when used in a workflow. The default is `"msPurity"`.
...	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- msPurity

Value

A mspurity_source object. This object has no output slots.

Inheritance

A mspurity_source object inherits the following struct classes:

[mspurity_source] -> [annotation_source] -> [struct_class]

References

Lawson, Nigel T, Weber, M. RJ, Jones, R. M, Chetwynd, J. A, Blanco R, Alejandro G, Guida D, Riccardo, Viant, R. M, Dunn, B W (2017). "msPurity: Automated Evaluation of Precursor Ion Purity for Mass Spectrometry-Based Fragmentation in Metabolomics." *Analytical Chemistry*, *89*, 2432-2439. doi:10.1021/acs.analchem.6b04358 https://doi.org/10.1021/acs.analchem.6b04358.

See Also

Other annotation sources: annotation_database, annotation_table, cd_source, ls_source

Examples

```
M <- mspurity_source(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

MTox700plus_database *MTox700plus_database*

Description

Imports the MTox700+ database, which is made available under the ODC Attribution License. MTox700+ is a list of toxicologically relevant metabolites derived from publications, public databases and relevant toxicological assays.

Usage

```
MTox700plus_database(
  version = "latest",
  bfc_path = NULL,
  resource_name = "MetMashR_MTox700plus",
  ...
)
```

Arguments

version	(character) The version number of the MTox700+ database to import. Available versions are listed here. version should match the tag of the release e.g. "v1.0". For convenience version = "latest" will always retrieve the most recent release. To prevent unecessary downloads BiocFileCache is used to store a local copy. The default is "latest".
bfc_path	(character, NULL) BiocFileCache is used to cache the database locally and prevent unnecessary downloads. If a path is provided then BiocFileCache will use this location. If NULL it will use the default location (see BiocFileCache::BiocFileCache() for details). The default is NULL.
resource_name	(character) The name given to this resource in the cache. (see BiocFileCache::BiocFileCache() for details). The default is "MetMashR_MTox700plus".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- BiocFileCache
- httr

Value

A MTox700plus_database object. This object has no output slots.

Inheritance

A MTox700plus_database object inherits the following struct classes:

[MTox700plus_database] -> [BiocFileCache_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Shepherd L, Morgan M (2025). *BiocFileCache: Manage Files Across Sessions*. doi:10.18129/B9.bioc.BiocFileCache https://doi.org/10.18129/B9.bioc.BiocFileCache, R package version 3.0.0, https://bioconductor.org/packages/BiocFileCache.

Wickham H (2023). *httr: Tools for Working with URLs and HTTP*. doi:10.32614/CRAN.package.httr https://doi.org/10.32614/CRAN.package.httr, R package version 1.4.7, https://CRAN.R-project.org/package=httr.

Sostare E, Lawson TN, Saunders LR, Colbourne JK, Weber RJM, Sobanski T, Viant MR (2022). "Knowledge-Driven Approaches to Create the MTox700+ Metabolite Panel for Predicting Toxicity." *Toxicological Sciences*, *186*, 208-220. doi:10.1093/toxsci/kfac007 https://doi.org/10.1093/toxsci/kfac007.

Examples

```
M <- MTox700plus_database(
        version = "v1.0",
        bfc_path = NULL,
        resource_name = "bfc",
        bfc_fun = function(){},
        import_fun = function(){},
        offline = FALSE,
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

mwb_compound_lookup *Convert to/from kegg identifiers*

Description

Searches MetabolomicsWorkbench for compound identifiers.

Usage

```
mwb_compound_lookup(
  input_item = "inchi_key",
  query_column,
  output_item = "pubchem_id",
  suffix = "_mwb",
  ...
)
```

Arguments

input_item	(character) A valid input item for the compound context (see https://www.metabolomicsworkbench.org/to The values in the query_column should be of this type. The default is "inchi_key".
query_column	(character) The name of a column in the annotation table containing values to search in the api call.
output_item	(character) A comma separated list of Valid output items for the compound context (see https://www.metabolomicsworkbench.org/tools/mw_rest.php). The default is "pubchem_id".

suffix	(character) A suffix appended to all column names in the returned result. The default is "_mwb".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- metabolomicsWorkbenchR
- dplyr

Value

A mwb_compound_lookup object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A mwb_compound_lookup object inherits the following struct classes:

[mwb_compound_lookup] -> [rest_api] -> [model] -> [struct_class]

References

Lloyd GR, Weber RJM (2025). *metabolomicsWorkbenchR: Metabolomics Workbench in R*. doi:10.18129/B9.bioc.metabolom https://doi.org/10.18129/B9.bioc.metabolomicsWorkbenchR, R package version 1.19.0, https://bioconductor.org/packages/metabolomicsWorkbenchR.

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

See Also

Other REST API's: classyfire_lookup, kegg_lookup, lipidmaps_lookup, rest_api

Examples

```
M <- mwb_compound_lookup(
        input_item = "inchi_key",
        output_item = "inchi_key",
        base_url = "https://www.metabolomicsworkbench.org/rest",
        url_template = "<base_url>/compound/<input_item>/<query_column>/<output_item>",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

mwb_refmet_database *mwb_refmet_database*

Description

Imports the Metabolomics Workbench refmet database.

Usage

```
mwb_refmet_database(bfc = NULL, ...)
```

Arguments

bfc	(character) BiocFileCache is used to cache database locally and prevent unnecessary downloads. If a path is provided then BiocFileCache will use this location. If NULL it will use the default location (see BiocFileCache::BiocFileCache for details). The default is NULL.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- BiocFileCache
- httr
- plyr

Value

A mwb_refmet_database object. This object has no output slots.

Inheritance

A mwb_refmet_database object inherits the following struct classes:

[mwb_refmet_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Shepherd L, Morgan M (2025). *BiocFileCache: Manage Files Across Sessions*. doi:10.18129/B9.bioc.BiocFileCache https://doi.org/10.18129/B9.bioc.BiocFileCache, R package version 3.0.0, https://bioconductor.org/packages/BiocFileCache.

Wickham H (2023). *httr: Tools for Working with URLs and HTTP*. doi:10.32614/CRAN.package.httr https://doi.org/10.32614/CRAN.package.httr, R package version 1.4.7, https://CRAN.R-project.org/package=httr.

Wickham H (2011). "The Split-Apply-Combine Strategy for Data Analysis." *Journal of Statistical Software*, *40*(1), 1-29. https://www.jstatsoft.org/v40/i01/.

Examples

```
M <- mwb_refmet_database(
        bfc = character(0),
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

`mwb_structure` *MWB molecular structure*

Description

Query the Metabolomic Workbench API and retrieve a display an image of the matching molecular structure.

Usage

```
mwb_structure(query_column, row_index, ...)
```

Arguments

`query_column`	(character) The name of the `annotation_source` column with regno compound identifiers.
`row_index`	(integer, numeric) The row index of the `annotation_source` to request an image of the molecular structure of.
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `cowplot`
- `metabolomicsWorkbenchR`

This object queries the Metabolomics Workbench API for matches to your query without caching the results. It is therefore intended for limited use. If you wish to obtain images for a large number of molecules you should seek an alternative solution.

Value

A `mwb_structure` object. This object has no `output` slots. See `chart_plot` in the `struct` package to plot this chart object.

Inheritance

A `mwb_structure` object inherits the following `struct` classes:

`[mwb_structure]` -> `[chart]` -> `[struct_class]`

References

Wilke C (2025). *cowplot: Streamlined Plot Theme and Plot Annotations for 'ggplot2'*. doi:10.32614/CRAN.package.cowplot https://doi.org/10.32614/CRAN.package.cowplot, R package version 1.2.0, https://CRAN.R-project.org/package=cowplot.

Lloyd GR, Weber RJM (2025). *metabolomicsWorkbenchR: Metabolomics Workbench in R*. doi:10.18129/B9.bioc.metabolom https://doi.org/10.18129/B9.bioc.metabolomicsWorkbenchR, R package version 1.19.0, https://bioconductor.org/packages/metabolomicsWorkbenchR.

Examples

```
M <- mwb_structure(
        row_index = 1,
        query_column = "V1")
```

`mzrt_match` *mz matching*

Description

Annotations will be matched to the measured data variable meta data.frame by determining which annotations ppm AND rt windows overlap with the ppm AND rt windows of the measured mz.

Usage

```
mzrt_match(
  variable_meta,
  mz_column,
  rt_column,
  ppm_window,
  rt_window,
  id_column,
  ...
)
```

Arguments

`variable_meta`	(data.frame) A data.frame of variable IDs and their corresponding mz values.
`mz_column`	(character) Column name of the mz values in variable_meta.
`rt_column`	(character) Column name of the rt values in variable_meta.
`ppm_window`	(numeric, integer) Ppm window to use for matching. If a single value is provided then the same ppm is used for both variable meta and the annotations. A named vector can also be provided e.g. c("variable_meta"=5,"annotations"=2) to use different ", "windows for each data table.

rt_window	(numeric, integer) Rt window to use for matching. If a single value is provided then the same rt is used for both variable meta and the annotations. A named vector can also be provided e.g. c("variable_meta"=5,"annotations"=2) to use different ", "windows for each data table.
id_column	(character) Column name of the variable ids in variable_meta. ", "id_column="rownames" will use the rownames as ids.
...	Additional slots and values passed to struct_class.

Value

A mzrt_match object with the following output slots:

updated (annotation_source) The input annotation source with the newly generated column.

Inheritance

A mzrt_match object inherits the following struct classes:

[mzrt_match] -> [model] -> [struct_class]

Examples

```
M <- mzrt_match(
        variable_meta = data.frame(),
        mz_column = character(0),
        ppm_window = 5,
        id_column = character(0),
        rt_column = character(0),
        rt_window = 20)
```

---

mz_match *mz matching*

Description

Annotations will be matched to the measured data variable meta data.frame by determining which annotations ppm window overlaps with the ppm window from the measured mz.

Usage

```
mz_match(variable_meta, mz_column, ppm_window, id_column, ...)
```

Arguments

variable_meta	(data.frame) A data.frame of variable IDs and their corresponding mz values.
mz_column	(character) Column name of the mz values in variable_meta.
ppm_window	(numeric, integer) Ppm window to use for matching. If a single value is provided then the same ppm is used for both variable meta and the annotations. A named vector can also be provided e.g. c("variable_meta"=5,"annotations"=2) to use ", "different windows for each data table.
id_column	(character) Column name of the variable ids in variable_meta. id_column="rownames" will use the rownames as ids.
...	Additional slots and values passed to struct_class.

Value

A mz_match object with the following output slots:

updated (annotation_source) The input annotation source with the newly generated column.

Inheritance

A mz_match object inherits the following struct classes:

[mz_match] -> [model] -> [struct_class]

Examples

```
M <- mz_match(
        variable_meta = data.frame(),
        mz_column = character(0),
        ppm_window = 5,
        id_column = character(0))
```

---

normalise_lipids *Normalise Lipids nomenclature*

Description

Normalises differently formated lipid names to a consistent format.

Usage

```
normalise_lipids(
  column_name,
  grammar = ".all",
  columns = ".all",
  suffix = "_goslin",
  batch_size = 10000,
  ...
)
```

Arguments

column_name	(character) The name of the column containing Lipids names to normalise.
grammar	(character) The grammar to use for normalising lipid names. Allowed values are: Shorthand2020, Goslin, FattyAcids, LipidMaps, SwissLipids, HMDB or .all. The default is ".all".
columns	(character) Column names to include from the goslin output. Can be any of "Normalized.Name", "Original.Name", "Grammar", "Adduct", "Adduct.Charge", "Lipid.Maps.Category", "Lipid.Maps.Main.Class", "Species.Name", "Extended.Species.Name", "Molecular.Species.Name", "Sn.Position.Name", "Structure.Defined.Name", "Full.Structure.Name", "Functional.Class.Abbr", "Functional.Class.Synonyms", "Level", "Total.C", "Total.OH", "Total.O", "Total.DB", "Mass", "Sum.Formula"."all" will return all columns. ". The default is ".all".
suffix	(character) A suffic added to the column names of the goslin output. The default is "_goslin".
batch_size	(numeric, integer) The maximum number of annotations to be parsed by rgoslin at a time. If the batch size is less than the total number of records then the records will be split into multiple batches to help prevent crashes. The default is 10000.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- rgoslin

Value

A normalise_lipids object with the following output slots:

updated	(annotation_source) Annotation_source after normalising lipid names.

Inheritance

A normalise_lipids object inherits the following struct classes:

[normalise_lipids] -> [model] -> [struct_class]

References

Kopczynski D, Hoffmann N, Peng B, Ahrends R (2020). "Goslin: A Grammar of Succinct Lipid Nomenclature." *Analytical Chemistry*, *92*(16), 10957-10960. https://pubs.acs.org/doi/10.1021/acs.analchem.0c01690.

Examples

```
M <- normalise_lipids(
        column_name = "V1",
        grammar = ".all",
        columns = ".all",
        suffix = "_goslin",
        batch_size = 10000)
```

---

normalise_strings *Normalise string*

Description

Replace matching (sub)strings based on a provided dictionary of search terms and their replacements.

Usage

```
normalise_strings(
  search_column,
  output_column = NULL,
  dictionary = list(),
  ...
)
```

Arguments

search_column	(character) The column name of the input annotation_source that will be searched for matching (sub)strings.
output_column	(character, NULL) The name of a new column that the modified strings will be stored in. If NULL the search_column will be replaced. The default is NULL.
dictionary	(list, annotation_database) A list of patterns and functions that take the input pattern and return a replacement string. A annotation_database object containing a suitable list can also be used here. The default is list().
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Each item of the dictionary list should #' have at least two fields: "pattern" and "replace". "pattern" is used as inputs to the [grepl()] function to detect matches to the input pattern. Parameters such as perl = TRUE can also be included in the list and these will be passed to [grepl()], otherwise the defaults are used. When a match is detected the function in "replace" is called with the same inputs as [grepl()]. The "replace" function should return a new string. Alternatively replace = NA can be used to return NA for a matching pattern. If a character string is provided then [gsub()] will be used by default.

Value

A normalise_strings object with the following output slots:

updated	(annotation_source) The updated annotations as an annotation_source object.

Inheritance

A normalise_strings object inherits the following struct classes:

[normalise_strings] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

See Also

grepl(), gsub()

Examples

```
M <- normalise_strings(
        search_column = character(0),
        output_column = NULL,
        dictionary = list())
```

opsin_lookup *Compound ID lookup via OPSIN*

Description

Uses the OPSIN API to search for identifers based on the input annotation column.

Usage

```
opsin_lookup(query_column, suffix = "_opsin", output = "cids", ...)
```

Arguments

query_column	(character) The column name to use as the reference for searching the database e.g. "compound_name". OPSIN expect molecule names as input.
suffix	(character) A suffix appended to all column names in the returned result. The default is "_opsin".
output	(character) The value returned from the pubchem database. The default is "cids".
...	Additional slots and values passed to struct_class.

Value

A opsin_lookup object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A opsin_lookup object inherits the following struct classes:

[opsin_lookup] -> [rest_api] -> [model] -> [struct_class]

References

Lowe, M. D, Corbett, T. P, Murray-Rust, Peter, Glen, C. R (2011). "Chemical Name to Structure: OPSIN, an Open ", "Source Solution." *Journal of Chemical Information and Modeling*, *51*(3), 793-753. doi:10.1021/ci100384d https://doi.org/10.1021/ci100384d.

Examples

```
M <- opsin_lookup(
        output = "stdinchikey",
        base_url = "https://opsin.ch.cam.ac.uk/opsin",
        url_template = "<base_url>/<query_column>.<output>",
        query_column = character(0),
        cache = NULL,
```

```
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

`PathBank_metabolite_database` *PathBank_metabolite_database*

Description

Imports the PathBank database (https://pathbank.org/) of metabolites linked to pathways.

Usage

```
PathBank_metabolite_database(
  version = "primary",
  bfc_path = NULL,
  resource_name = "MetMashR_PathBank",
  ...
)
```

Arguments

`version`	(character) PathBank version. Allowed values are limited to the following: • `""`: The version of the PatchBank database to import. To prevent unecessary downloads `BiocFileCache` is used to store a local copy. • `"complete"`: The complete PathBank metabolite database. • `"primary"`: The PathBank metabolite database for primary pathways only. The default is `"primary"`.
`bfc_path`	(character, NULL) `BiocFileCache` is used to cache the database locally and prevent unnecessary downloads. If a path is provided then `BiocFileCache` will use this location. If NULL it will use the default location (see `BiocFileCache::BiocFileCache()` for details). The default is `NULL`.
`resource_name`	(character) The name given to this resource in the cache. (see `BiocFileCache::BiocFileCache()` for details). The default is `"MetMashR_PathBank"`.
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `BiocFileCache`
- `httr`

Value

A PathBank_metabolite_database object. This object has no output slots.

Inheritance

A PathBank_metabolite_database object inherits the following struct classes:

[PathBank_metabolite_database] -> [BiocFileCache_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

References

Shepherd L, Morgan M (2025). *BiocFileCache: Manage Files Across Sessions*. doi:10.18129/B9.bioc.BiocFileCache https://doi.org/10.18129/B9.bioc.BiocFileCache, R package version 3.0.0, https://bioconductor.org/packages/BiocFileCache.

Wickham H (2023). *httr: Tools for Working with URLs and HTTP*. doi:10.32614/CRAN.package.httr https://doi.org/10.32614/CRAN.package.httr, R package version 1.4.7, https://CRAN.R-project.org/package=httr.

Wishart, S D, Li, Carin, Marcu, Ana, Badran, Hasan, Pon, Allison, Budinski, Zachary, Patron, Jonas, Lipton, Debra, Cao, Xuan, Oler, Eponine, Li, Krissa, Paccoud, Maïlys, Hong, Chelsea, Guo, C A, Chan, Christopher, Wei, William, Ramirez-Gaona, Miguel (2019). "PathBank: a comprehensive pathway database for model organisms." *Nucleic Acids Research*, *48*, D470-D478. doi:10.1093/nar/gkz861 https://doi.org/10.1093/nar/gkz861.

Examples

```
M <- PathBank_metabolite_database(
        version = "primary",
        bfc_path = NULL,
        resource_name = "bfc",
        bfc_fun = function(){},
        import_fun = function(){},
        offline = FALSE,
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

pivot_columns *Pivot longer*

Description

Combine multiple groups of columns into a single group of columns with group labels.

Usage

```
pivot_columns(column_groups, group_labels, ...)
```

Arguments

column_groups	(list) A named list of columns to group together into a single group of columns. There should be the same number of columns in each group.
group_labels	(list) A named list of columns and the label to use for all records in that column.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- dplyr

Value

A pivot_columns object with the following output slots:

updated	(annotation_source) The updated annotations as an annotation_source object.

Inheritance

A pivot_columns object inherits the following struct classes:

[pivot_columns] -> [model] -> [struct_class]

References

Wickham H, François R, Henry L, Müller K, Vaughan D (2023). *dplyr: A Grammar of Data Manipulation*. doi:10.32614/CRAN.package.dplyr https://doi.org/10.32614/CRAN.package.dplyr, R package version 1.1.4, https://CRAN.R-project.org/package=dplyr.

Examples

```
M <- pivot_columns(
        group_labels = list(),
        column_groups = list())
```

---

prioritise_columns *Combine several columns into a single column.*

Description

Several columns are merged into a single column. If multiple columns contain overlapping values then priority can be given columns earlier in the list.

Usage

```
prioritise_columns(
  column_names,
  output_name,
  source_name,
  source_tags = column_names,
  clean = TRUE,
  ...
)
```

Arguments

column_names	(character) The name(s) of column(s) to be combined.
output_name	(character) The name of the new column.
source_name	(character) The column name used to indicate the where the merged values originated.
source_tags	(character) The tags used to identify the source of each item in the new column. A tag should be provided for each column_name. By default the column name is used.
clean	(logical) Clean old columns. Allowed values are limited to the following: • "TRUE": The named columns are removed after being combined. • "FALSE": The named columns are retained after being combined. The default is TRUE.
...	Additional slots and values passed to struct_class.

Value

A prioritise_columns object with the following output slots:

updated (annotation_source) The input annotation source with the newly generated column.

Inheritance

A prioritise_columns object inherits the following struct classes:

[prioritise_columns] -> [model] -> [struct_class]

Examples

```
M <- prioritise_columns(
        column_names = "V1",
        output_name = "",
        clean = FALSE,
        source_name = "source_name",
        source_tags = "x")
```

pubchem_compound_lookup

Compound ID lookup via PubChem

Description

Uses the PubChem API to search for CID based on the input annotation column.

Usage

```
pubchem_compound_lookup(
  query_column,
  search_by,
  suffix = "_pubchem",
  output = "cids",
  records = "best",
  ...
)
```

Arguments

query_column	(character) The column name to use as the reference for searching the database e.g. "HMBD_ID".
search_by	(character) The PubChem domain to search for matches to the annotation_column.
suffix	(character) A suffix appended to all column names in the returned result. The default is "_pubchem".
output	(character) The value returned from the pubchem database. The default is "cids".
records	(character) Returned record(s). Allowed values are limited to the following: • "": Sometimes there are multiple matches to the PubChem, database especially when searhcing by name. • "best": Return only the best matching record. • "all": Return all matching records. The default is "best".
...	Additional slots and values passed to struct_class.

Value

A pubchem_compound_lookup object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A pubchem_compound_lookup object inherits the following struct classes:

[pubchem_compound_lookup] -> [rest_api] -> [model] -> [struct_class]

Examples

```
M <- pubchem_compound_lookup(
        search_by = "cid",
        output = "cids",
        records = "best",
        base_url = "https://pubchem.ncbi.nlm.nih.gov/rest/pug/compound",
        url_template = "<base_url>/<search_by>/<query_column>/<output>/JSON",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

---

pubchem_property_lookup

Compound property lookup via pubchem

Description

Uses the PubChem API to search for CID based onthe input annotation column and returns property information.

Usage

```
pubchem_property_lookup(
  query_column,
  search_by,
  suffix = "_pubchem",
  property = "InChIKey",
  ...
)
```

Arguments

query_column	(character) The column name to use as the reference for searching the database e.g. "HMBD_ID".
search_by	(character) The PubChem domain to search for matches to the annotation_column.
suffix	(character) A suffix appended to all column names in the returned result. The default is "_pubchem".
property	(character) A comma separated list of properties to return from the pubchem database. (see https://pubchem.ncbi.nlm.nih.gov/docs/pug-rest#section=Compound-Property-Tables for details). Keyword ".all" will return all properties. The default is "InChIKey".
...	Additional slots and values passed to struct_class.

Value

A pubchem_property_lookup object with the following output slots:

updated (annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A pubchem_property_lookup object inherits the following struct classes:

[pubchem_property_lookup] -> [pubchem_compound_lookup] -> [rest_api] -> [model] -> [struct_class]

Examples

```
M <- pubchem_property_lookup(
        search_by = "cid",
        property = "InChIKey",
        output = "cids",
        records = "best",
        base_url = "https://pubchem.ncbi.nlm.nih.gov/rest/pug/compound",
        url_template = "<base_url>/<search_by>/<query_column>/property/<property>/JSON",
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

---

pubchem_structure *PubChem molecular structure*

Description

Query the PubChem api and retrieve a display an image of the matching molecular structure.

Usage

```
pubchem_structure(
  query_column,
  search_by,
  row_index,
  record_type = "2d",
  image_size = "large",
  ...
)
```

Arguments

query_column	(character) The name of the annotation_source column with compound identifiers of the type specified in the search_by param.
search_by	(character) The PubChem domain to search for matches to the annotation_column.
row_index	(integer, numeric) The row index of the annotation_source to request an image of the molecular structure of.
record_type	(character) The record type to return from the PubChem query. Can be one of "2d" or "3d". The default is "2d".
image_size	(character) The size of the image to return from the PubChem query. Can be one of "large" or "small". For record_type = "2d" an arbitrary image size can be specified e.g. 123x123. The default is "large".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- cowplot

This object queries the PubChem API for matches to your query without caching the results. It is therefore intended for limited use. If you wish to obtain images for a large number of moelucules you should seek an alternative solution.

Value

A pubchem_structure object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A pubchem_structure object inherits the following struct classes:

[pubchem_structure] -> [chart] -> [struct_class]

References

Wilke C (2025). *cowplot: Streamlined Plot Theme and Plot Annotations for 'ggplot2'*. doi:10.32614/CRAN.package.cowplot https://doi.org/10.32614/CRAN.package.cowplot, R package version 1.2.0, https://CRAN.R-project.org/package=cowplot.

Examples

```
M <- pubchem_structure(
        query_column = "V1",
        search_by = "cid",
        row_index = 1,
        record_type = "2d",
        image_size = "large")
```

pubchem_widget *PubChem widget*

Description

Display a PubChem HTML widget for a compound.

Usage

```
pubchem_widget(
  query_column,
  row_index,
  record_type = "2D-Structure",
  hide_title = FALSE,
  width = "600px",
  height = "650px",
  display = TRUE,
  ...
)
```

Arguments

query_column	(character) The name of the annotation_source column with compound identifiers of the type specified in the search_by param.
row_index	(integer, numeric) The row index of the annotation_source to request an image of the molecular structure of.
record_type	(character) The record type for the widget. The default is "2D-Structure".
hide_title	(logical) Hide widget title. Allowed values are limited to the following: • "TRUE": The title is displayed. • "FALSE": The title is not displayed. The default is FALSE.
width	(integer, numeric, character) The width of the widget in a CSS style compatible format. Numerical values will be converted to character. The default is "600px".
height	(integer, numeric, character) The height of the widget in a CSS style compatible format.Numerical values will be converted to character. The default is "650px".
display	(logical) Display widget. Allowed values are limited to the following: • "TRUE": Display the widget. • "FALSE": Do not display the widget and only return the HTML. The default is TRUE.
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- htmltools

Value

A pubchem_widget object. This object has no output slots. See chart_plot in the struct package to plot this chart object.

Inheritance

A pubchem_widget object inherits the following struct classes:

[pubchem_widget] -> [chart] -> [struct_class]

References

Cheng J, Sievert C, Schloerke B, Chang W, Xie Y, Allen J (2025). *htmltools: Tools for HTML*. doi:10.32614/CRAN.package.htmltools https://doi.org/10.32614/CRAN.package.htmltools, R package version 0.5.9, https://CRAN.R-project.org/package=htmltools.

Examples

```
M <- pubchem_widget(
        query_column = "V1",
        row_index = 1,
        record_type = "2D-Structure",
        hide_title = FALSE,
        width = 600,
        height = 400,
        display = FALSE)
```

---

racemic_dictionary *Racemic dictionary*

Description

This dictionary removes racemic properties from molecule names. It is intended for use with the normalise_strings() object.

Usage

```
racemic_dictionary
```

Format

An object of class list of length 5.

Value

A dictionary for use with normalise_strings()

Examples

```
M <- normalise_strings(
    search_column = "example",
    output_column = "result",
    dictionary = racemic_dictionary
)
```

---

rdata_database *rdata database*

Description

A data.frame stored as an RData file.

Usage

```
rdata_database(source = character(0), variable_name, ...)
```

Arguments

source	(ANY) The source of annotation data. The default is character(0).
variable_name	(character, function) The name of the data.frame in the imported workspace to use as the data.frame for this source. A function can be provided to e.g. extract a data.frame from a list in the imported environment.
...	Additional slots and values passed to struct_class.

Value

A rdata_database object. This object has no output slots.

Inheritance

A rdata_database object inherits the following struct classes:

[rdata_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

See Also

Other annotation databases: AnnotationDb_database, GO_database, annotation_database, annotation_source, excel_database, rds_cache, rds_database

Examples

```
M <- rdata_database(
        variable_name = "a data frame",
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

---

rds_cache *rds cache*

Description

A data.frame stored as an RDS file. Intended to be used with rest_api objects as mechanism for caching search results. The data.frame for an rds_cache object must have a column named ".search".

Usage

```
rds_cache(
  source = character(0),
  data = data.frame(.search = character(0)),
  ...
)
```

Arguments

source	(ANY) The source of annotation data. The default is character(0).
data	(data.frame, NULL) A data.frame of annotation data. The default is data.frame(.search = character(0)).
...	Additional slots and values passed to struct_class.

Value

A rds_cache object. This object has no output slots.

Inheritance

A rds_cache object inherits the following struct classes:

[rds_cache] -> [rds_database] -> [annotation_database] -> [annotation_source] -> [struct_class]

See Also

Other annotation databases: AnnotationDb_database, GO_database, annotation_database, annotation_source, excel_database, rdata_database, rds_database

Examples

```
M <- rds_cache(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

`rds_database` *rds database*

Description

A data.frame stored as an RDS file.

Usage

```
rds_database(source = character(0), ...)
```

Arguments

`source`	(ANY) The source of annotation data. The default is `character(0)`.
`...`	Additional slots and values passed to `struct_class`.

Value

A `rds_database` object. This object has no `output` slots.

Inheritance

A `rds_database` object inherits the following `struct` classes:

`[rds_database]` -> `[annotation_database]` -> `[annotation_source]` -> `[struct_class]`

See Also

Other annotation databases: `AnnotationDb_database`, `GO_database`, `annotation_database`, `annotation_source`, `excel_database`, `rdata_database`, `rds_cache`

Examples

```
M <- rds_database(
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

read_database *Read a database*

Description

Reads an annotation_database and returns the data.frame.

Usage

```
read_database(obj, ...)

## S4 method for signature 'annotation_database'
read_database(obj)

## S4 method for signature 'AnnotationDb_database'
read_database(obj)

## S4 method for signature 'BiocFileCache_database'
read_database(obj)

## S4 method for signature 'MTox700plus_database'
read_database(obj)

## S4 method for signature 'PathBank_metabolite_database'
read_database(obj)

## S4 method for signature 'excel_database'
read_database(obj)

## S4 method for signature 'github_file'
read_database(obj)

## S4 method for signature 'mwb_refmet_database'
read_database(obj)

## S4 method for signature 'rdata_database'
read_database(obj)

## S4 method for signature 'rds_database'
read_database(obj)

## S4 method for signature 'sqlite_database'
read_database(obj)
```

Arguments

obj	An annotation_database object

...	additional database specific inputs

Value

A data.frame

Examples

```
M <- rds_database(tempfile())
df <- read_database(M)
```

`read_source` *Import annotation source*

Description

Import an data from e.g. a raw file and parse it into an `annotation_source()` object.

Usage

```
read_source(obj, ...)

## S4 method for signature 'annotation_source'
read_source(obj)

## S4 method for signature 'annotation_database'
read_source(obj)

## S4 method for signature 'cd_source'
read_source(obj)

## S4 method for signature 'ls_source'
read_source(obj)
```

Arguments

obj	an `annotation_source()` object
...	not currently used

Value

an `annotation_table()` or `annotation_database()` object

Examples

```
# prepare source
CD <- cd_source(
    source = system.file(
        paste0("extdata/MTox/CD/HILIC_POS.xlsx"),
        package = "MetMashR"
    )
)
```

`remove_columns` *Select columns*

Description

A wrapper around `tidyselect::eval_select`. Remove columns from an annotation table using tidy grammar.

Usage

```
remove_columns(expression = everything(), ...)
```

Arguments

`expression`	(call) A valid rlang::expr for tidy evaluation via eval_select. e.g. `expression = all_of(c("foo","bar"))` will select columns named "foo" and "bar" from the annotation data.frame. . The default is `everything()`.
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `tidyselect`
- `rlang`

Value

A `remove_columns` object with the following `output` slots:

`updated`	(annotation_source) The updated annotations as an `annotation_source` object.

Inheritance

A `remove_columns` object inherits the following `struct` classes:

`[remove_columns]` -> `[model]` -> `[struct_class]`

References

Henry L, Wickham H (2024). *tidyselect: Select from a Set of Strings*. doi:10.32614/CRAN.package.tidyselect https://doi.org/10.32614/CRAN.package.tidyselect, R package version 1.2.1, https://CRAN.R-project.org/package=tidyselect.

Henry L, Wickham H (2025). *rlang: Functions for Base Types and Core R and 'Tidyverse' Features*. doi:10.32614/CRAN.package.rlang https://doi.org/10.32614/CRAN.package.rlang, R package version 1.1.6, https://CRAN.R-project.org/package=rlang.

See Also

dplyr::select()

tidyselect::eval_select()

Examples

```
M <- remove_columns(
        expression = call("example"))
```

`rename_columns` *Select columns*

Description

A wrapper around dplyr::rename. Rename columns from an annotation table using tidy grammar.

Usage

```
rename_columns(expression, ...)
```

Arguments

`expression`	(call) A valid rlang::expr for tidy evaluation e.g. `expression = all_of(c("foo"="bar"))` will rename the column named "bar" and "foo". .
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `tidyselect`
- `rlang`

Value

A rename_columns object with the following output slots:

updated (annotation_source) The updated annotations as an annotation_source object.

Inheritance

A rename_columns object inherits the following struct classes:

[rename_columns] -> [model] -> [struct_class]

References

Henry L, Wickham H (2024). *tidyselect: Select from a Set of Strings*. doi:10.32614/CRAN.package.tidyselect https://doi.org/10.32614/CRAN.package.tidyselect, R package version 1.2.1, https://CRAN.R-project.org/package=tidyselect.

Henry L, Wickham H (2025). *rlang: Functions for Base Types and Core R and 'Tidyverse' Features*. doi:10.32614/CRAN.package.rlang https://doi.org/10.32614/CRAN.package.rlang, R package version 1.1.6, https://CRAN.R-project.org/package=rlang.

Examples

```
M <- rename_columns(
        expression = call("example"))
```

---

required_cols *Required columns in an annotation source*

Description

Some annotation_sources, such as LCMS tables (lcms_table), require that certain columns are present in the data.frame. These are defined by slots in the source definition. The name of slots containing the required column names for a source can be retrieved using the required_cols function, which will collect and return the names of slots containing required column names for the object and all of its parent objects.

Usage

```
required_cols(obj, ...)

## S4 method for signature 'annotation_source'
required_cols(obj)
```

Arguments

obj	an annotation_source object
...	additional source specific inputs

Value

a character vector of slot names

Examples

```
# prepare object
M <- lcms_table(id_column = "id", mz_column = "mz", rt_column = "rt")

#' # get values for required slots
r <- required_cols(M)

# get slot names for required columns
names(r)
```

---

rest_api *rest_api*

Description

A base class providing common methods for making REST API calls.

Usage

```
rest_api(
  base_url,
  url_template,
  suffix,
  status_codes,
  delay,
  cache = NULL,
  query_column,
  ...
)
```

Arguments

base_url	(character) The base URL of the API.
url_template	(character) A template describing how the URL should be constructed from the base URL and input parameters. e.g. <base_url>//<input_item>/<search_term>/json.The url will be constructed by replacing the values enclosed in <> with the value from corresponding input parameter of the rest_api object.
suffix	(character) A suffix appended to all column names in the returned result.

status_codes	(list) Named list of status codes and function indicating how to respond. Should minimally contain a function to parse a successful response for status code 200. Any codes not provided will be passed to httr::stop_for_status().
delay	(numeric, integer) Delay in seconds between API calls.
cache	(annotation_database, NULL) A struct cache object that contains parsed responses to previous api queries. If not using a cache then set to NULL. The default is NULL.
query_column	(character) The name of a column in the annotation table containing values to search in the api call.
...	Additional slots and values passed to struct_class.

Value

A rest_api object with the following output slots:

updated	(annotation_source) The annotation_source after adding data returned by the API.

Inheritance

A rest_api object inherits the following struct classes:

[rest_api] -> [model] -> [struct_class]

See Also

Other REST API's: classyfire_lookup, kegg_lookup, lipidmaps_lookup, mwb_compound_lookup

Examples

```
M <- rest_api(
        base_url = "V1",
        url_template = character(0),
        query_column = character(0),
        cache = NULL,
        status_codes = list(),
        delay = 0.5,
        suffix = "_rest_api")
```

---

rt_match *rt matching*

Description

Annotations will be matched to the measured variable meta data.frame by determining which annotations rt window overlaps with the rt window from the measured rt.

Usage

```
rt_match(variable_meta, rt_column, rt_window, id_column, ...)
```

Arguments

variable_meta	(data.frame) A data.frame of variable IDs and their corresponding rt values.
rt_column	(character) Column name of the rt values in variable_meta.
rt_window	(numeric, integer) Rt window to use for matching. If a single value is provided then the same rt is used for both variable meta and the annotations. A named vector can also be provided e.g. c("variable_meta"=5,"annotations"=2) to use different ", "windows for each data table.
id_column	(character) Column name of the variable ids in variable_meta. ", "id_column="rownames" will use the rownames as ids.
...	Additional slots and values passed to struct_class.

Value

A rt_match object with the following output slots:

updated	(annotation_table) The input annotation source with the newly generated column.

Inheritance

A rt_match object inherits the following struct classes:

[rt_match] -> [model] -> [struct_class]

Examples

```
M <- rt_match(
        variable_meta = data.frame(),
        rt_column = character(0),
        rt_window = 20,
        id_column = character(0))
```

---

select_columns *Select columns*

Description

A wrapper around tidyselect::eval_select. Select columns from an annotation table using tidy grammar. This imitates dplyr::select().

Usage

```
select_columns(expression = everything(), ...)
```

Arguments

expression	(call) A valid rlang::expr for tidy evaluation via eval_select. e.g. `expression = all_of(c("foo","bar"))` will select columns named "foo" and "bar" from the annotation data.frame. . The default is `everything()`.
...	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `tidyselect`
- `rlang`

Value

A `select_columns` object with the following `output` slots:

`updated`	(annotation_source) The updated annotations as an `annotation_source` object.

Inheritance

A `select_columns` object inherits the following `struct` classes:

`[select_columns]` -> `[model]` -> `[struct_class]`

References

Henry L, Wickham H (2024). *tidyselect: Select from a Set of Strings*. doi:10.32614/CRAN.package.tidyselect https://doi.org/10.32614/CRAN.package.tidyselect, R package version 1.2.1, https://CRAN.R-project.org/package=tidyselect.

Henry L, Wickham H (2025). *rlang: Functions for Base Types and Core R and 'Tidyverse' Features*. doi:10.32614/CRAN.package.rlang https://doi.org/10.32614/CRAN.package.rlang, R package version 1.1.6, https://CRAN.R-project.org/package=rlang.

See Also

`dplyr::select()`

`tidyselect::eval_select()`

Examples

```
M <- select_columns(
        expression = call("example"))
```

split_column *Split a column*

Description

A wrapper for strsplit. Divides a column into multiple columns by dividing the contents

Usage

```
split_column(
  column_name,
  separator = "_",
  padding = NA,
  keep_indices = NULL,
  clean = TRUE,
  ...
)
```

Arguments

column_name	(character) The column name in the annotation_source split.
separator	(character) A substring to split the column by. The default is "_".
padding	(character, logical) A character string used to represent missing and zero length strings after splitting. The default is NA.
keep_indices	(numeric, integer) The indices of columns to keep after splitting. If NULL then all columns are retained. The default is NULL.
clean	(logical) Clean old columns. Allowed values are limited to the following: • "TRUE": The named columns are removed after being split. • "FALSE": The named columns are retained after being split. The default is TRUE.
...	Additional slots and values passed to struct_class.

Value

A split_column object with the following output slots:

updated	(annotation_source) The annotation_source after splitting the column.

Inheritance

A split_column object inherits the following struct classes:

[split_column] -> [model] -> [struct_class]

Examples

```
M <- split_column(
        column_name = "V1",
        separator = "_",
        clean = FALSE,
        padding = FALSE,
        keep_indices = numeric(0))
```

---

split_records *Expand records*

Description

Expand single records into multiple records by splitting strings in a named column at the chosen separator. For example, if a for a record the column `synonyms = c("glucose,dextrose")` then by splitting at the comma results in two records, one for glucose and one for dextrose with identical values (apart from the column being split). The original record is removed.

Usage

```
split_records(column_name, separator, clean = TRUE, ...)
```

Arguments

`column_name`	(character) The column name of the `annotation_source` to split intomultiple records.
`separator`	(character) The substring used to split the values in column_name into multiple records.
`clean`	(logical) Remove the original column. If FALSE the original column will be retained in the final output with .original appended to the column name. The default is `TRUE`.
`...`	Additional slots and values passed to `struct_class`.

Details

This object makes use of functionality from the following packages:

- `tidytext`

Value

A `split_records` object with the following `output` slots:

`updated`	(annotation_source) The updated annotations as an `annotation_source` object.

Inheritance

A split_records object inherits the following struct classes:

[split_records] -> [model] -> [struct_class]

References

Silge J, Robinson D (2016). "tidytext: Text Mining and Analysis Using Tidy Data Principles in R." *JOSS*, *1*(3). doi:10.21105/joss.00037 https://doi.org/10.21105/joss.00037, http://dx.doi.org/10.21105/joss.00037.

Examples

```
M <- split_records(
        column_name = character(0),
        separator = ",",
        clean = FALSE)
```

---

sqlite_database *SQLite database*

Description

A data.frame stored in an SQLite database.

Usage

```
sqlite_database(source, table = "annotation_database", ...)
```

Arguments

source	(ANY) The source of annotation data.
table	(character) The name of a table in the SQLite database. The default is "annotation_database".
...	Additional slots and values passed to struct_class.

Details

This object makes use of functionality from the following packages:

- RSQLite

Value

A sqlite_database object. This object has no output slots.

Inheritance

A `sqlite_database` object inherits the following `struct` classes:

`[sqlite_database]` -> `[annotation_database]` -> `[annotation_source]` -> `[struct_class]`

References

Müller K, Wickham H, James DA, Falcon S (2025). *RSQLite: SQLite Interface for R*. doi:10.32614/CRAN.package.RSQLite https://doi.org/10.32614/CRAN.package.RSQLite, R package version 2.4.5, https://CRAN.R-project.org/package=RSQLite.

See Also

Other database: BiocFileCache_database

Examples

```
M <- sqlite_database(
        table = character(0),
        tag = character(0),
        data = data.frame(),
        source = "ANY")
```

`trim_whitespace` *Trim whitespace*

Description

A wrapper for `trimws()`. Removes leading and/or trailing whitespace from character strings.

Usage

```
trim_whitespace(column_names, which = "both", whitespace = "[ \t\r\n]", ...)
```

Arguments

`column_names`	(character) The column name(s) in the annotation_source to trim white space from. Special case ".all" will apply to all columns.
`which`	(character) Trailing and/or leading whitespace. Allowed values are limited to the following: • `""`: A character string specifying the location of whitespace to remove. • `"left"`: Remove leading whitespace. • `"right"`: Remove trailing whitespace. • `"both"`: Remove both leading and trailing whitespace. The default is `"both"`.

whitespace	(character) A string specifying a regular expression to match (one character of) "white space". See trimws() for details. The default is "[ ]".
...	Additional slots and values passed to struct_class.

Value

A trim_whitespace object with the following output slots:

updated	(annotation_source) The annotation_source after trimming whitespace.

Inheritance

A trim_whitespace object inherits the following struct classes:

[trim_whitespace] -> [model] -> [struct_class]

Examples

```
M <- trim_whitespace(
        column_names = "V1",
        which = "both",
        whitespace = "[
]")
```

---

tripeptide_dictionary *Tripeptide dictionary*

Description

A dictionary for converting tripeptides encoded using single letter IUPAC codes to use three letter codes for amino acids separated by hyphens. e.g. INK becomes Ile-Asn-Lys

Usage

```
tripeptide_dictionary
```

Format

An object of class list of length 1.

Value

A dictionary for use with normalise_strings()

Examples

```
M <- normalise_strings(
    search_column = "example",
    output_column = "result",
    dictionary = tripeptide_dictionary
)
```

`unique_records` *Keep unique_records*

Description

reduces an annotation source to unique records only; all duplicates are removed.

Usage

```
unique_records(...)
```

Arguments

`...`	Additional slots and values passed to `struct_class`.

Value

A `unique_records` object with the following `output` slots:

`updated` (annotation_source) The updated annotations as an `annotation_source` object.

Inheritance

A `unique_records` object inherits the following `struct` classes:

`[unique_records]` -> `[model]` -> `[struct_class]`

Examples

```
M <- unique_records()
```

unzip_before_cache *Unzip file before caching with BiocFileCache_database*

Description

This helper function is for use with `BiocFileCache_database()` objects. Using it as the `bfc_fun` input for this object will unzip a downloaded resource into a temporary folder before storing it in the cache.

Usage

```
unzip_before_cache(from, to)
```

Arguments

`from`	incoming path
`to`	the outgoing path

Value

TRUE if successful

Examples

```
M <- BiocFileCache_database(
    source = tempfile(),
    resource_name = "example",
    bfc_fun = unzip_before_cache
)
```

upset_min_size *UpSet chart filter helper functions*

Description

These functions create filters for the `annotation_upset_chart` class to control which intersections are displayed in UpSet plots. Each function returns a filter function that can be used with the `filter` parameter.

Usage

```
upset_min_size(min_size)

upset_min_groups(min_groups)

upset_max_groups(max_groups)

upset_intersections(combinations)
```

Arguments

min_size	numeric The minimum number of items in an intersection
min_groups	numeric The minimum number of groups in an intersection
max_groups	numeric The maximum number of groups in an intersection
combinations	character Vector of specific intersection combinations to include (e.g., c("A/B", "B/C"))

Details

These filter functions work by analyzing the region data from the Venn diagram to determine which intersections meet the specified criteria:

- upset_min_size(): Filters intersections based on the number of items
- upset_min_groups(): Filters intersections based on the minimum number of groups involved
- upset_max_groups(): Filters intersections based on the maximum number of groups involved
- upset_intersections(): Filters to show only specific intersection combinations (e.g., "A/B", "B/C", "A/B/C")

For complex filtering logic, create custom filter functions:

```
# Single filter
filter = upset_min_size(5)

# Specific combinations only
filter = upset_intersections(c("A/B", "B/C"))

# Custom filter function with AND logic
custom_filter <- function(region_data) {
  region_data$count >= 3 & region_data$count <= 10 & grepl("A", region_data$name)
}

# Custom filter function with OR logic
or_filter <- function(region_data) {
  region_data$count >= 5 | grepl("B/C", region_data$name)
}
```

Value

A function that takes `region_data` as input and returns a logical vector indicating which intersections to keep.

Examples

```
## Not run:
# Filter to show only intersections with 5+ items
C <- annotation_upset_chart(factor_name = "V1", filter = upset_min_size(5))

# Filter to show only intersections involving 3+ groups
C <- annotation_upset_chart(factor_name = "V1", filter = upset_min_groups(3))

# Filter to show only intersections involving 2-4 groups (custom function)
group_range_filter <- function(region_data) {
  group_counts <- sapply(region_data$name, function(x) {
    if (x == "") return(0)
    groups <- strsplit(x, "/")[[1]]
    length(groups)
  })
  group_counts >= 2 & group_counts <= 4
}
C <- annotation_upset_chart(factor_name = "V1", filter = group_range_filter)

# Filter to show only specific combinations
C <- annotation_upset_chart(factor_name = "V1",
                            filter = upset_intersections(c("A/B", "B/C")))

# Custom filter combining size and group criteria
size_and_group_filter <- function(region_data) {
  region_data$count >= 3 & sapply(region_data$name, function(x) {
    if (x == "") return(FALSE)
    groups <- strsplit(x, "/")[[1]]
    length(groups) >= 2
  })
}
C <- annotation_upset_chart(factor_name = "V1", filter = size_and_group_filter)

## End(Not run)
```

---

vertical_join *Join sources vertically*

Description

A function to join sources vertically. A vertical join involves matching common columns across source data.frames and padding missing columns to create a single new data.frame with data and records from multiple sources.

Usage

```
vertical_join(x, y, ...)

## S4 method for signature 'annotation_source,annotation_source'
vertical_join(
  x,
  y,
  matching_columns = NULL,
  keep_cols = NULL,
  source_col = "annotation_source",
  exclude_cols = NULL,
  as = annotation_source()
)

## S4 method for signature 'list,missing'
vertical_join(
  x,
  y,
  matching_columns = NULL,
  keep_cols = NULL,
  source_col = "annotation_source",
  exclude_cols = NULL,
  as = annotation_source()
)
```

Arguments

x	an annotation_source object
y	an second annotation_source object to join with the first
...	additional inputs (not currently used)
matching_columns	(list) a named list of column names that all contain the same information. All columns named in the same list element will be merged into a single column with the same name as the list element.
keep_cols	(character) a list of column names to keep in the final joined table. All other columns will be dropped.
source_col	(character) the name of a new column that will contain the tags of the original source object for each row in the joined table.
exclude_cols	(character) the names of columns to exclude from the joined table.
as	(character) the type of object the joined table should be returned as e.g. "lcms_table".

Value

an annotation_source object

Examples

```
M <- annotation_source(data = data.frame(id = 1, value = "A"))
N <- annotation_source(data = data.frame(id = 2, value = "B"))
O <- vertical_join(M, N, keep_cols = ".all")
```

---

wherever *Filter helper function to select records*

Description

Returns a list of quosures for use with `filter_records` to allow the use of dplyr-style expressions. See examples.

Usage

```
wherever(...)
```

Arguments

`...`	Expressions that return a logical value and are defined in terms of the columns in the annotation_source. If multiple conditions are included then they are combined with the `&` operator. Only records for which all conditions evaluate to `TRUE` are kept.

Value

a list of quosures for use with `filter_records`

See Also

`filter_records()`

Examples

```
# some annotation data
AN <- annotation_source(data = iris)

# filter to setosa where Sepal length is less than 5
M <- filter_records(
    wherever(
        Species == "setosa",
        Sepal.Length < 5
    )
)
M <- model_apply(M, AN)
predicted(M) # 20 rows
```

write_database *Write to a database*

Description

Writes a data.frame to a annotation_database.

Usage

```
write_database(obj, ...)

## S4 method for signature 'annotation_database'
write_database(obj, df)

## S4 method for signature 'rds_database'
write_database(obj, df)

## S4 method for signature 'sqlite_database'
write_database(obj, df)
```

Arguments

obj	A annotation_database object
...	additional database specific inputs
df	(data.frame) the data.frame to store in the database.

Value

Silently returns TRUE if successful, FALSE otherwise

Examples

```
M <- rds_database(tempfile())
write_database(M, data.frame())
```

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