Package 'simplifyEnrichment'

October 25, 2025

Type Package

Title Simplify Functional Enrichment Results

Version 2.3.0

Date 2024-09-13

Depends R (>= 4.0.0)

Imports simona, ComplexHeatmap (>= 2.7.4), grid, circlize, GetoptLong, digest, tm, GO.db, AnnotationDbi, slam, methods, clue, grDevices, stats, utils, cluster (>= 1.14.2), colorspace, GlobalOptions (>= 0.1.0)

Suggests knitr, ggplot2, cowplot, mclust, apcluster, MCL, dbscan, igraph, gridExtra, dynamicTreeCut, testthat, gridGraphics, flexclust, BiocManager, InteractiveComplexHeatmap (>= 0.99.11), shiny, shinydashboard, cola, hu6800.db, rmarkdown, genefilter, gridtext, fpc

Description
A new clustering algorithm, ``binary cut'', for clustering similarity matrices of functional terms is implemeted in this package. It also provides functions for visualizing, summarizing and comparing the clusterings.

biocViews Software, Visualization, GO, Clustering, GeneSetEnrichment

URL https://github.com/jokergoo/simplifyEnrichment, https://simplifyEnrichment.github.io

VignetteBuilder knitr

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

git_url https://git.bioconductor.org/packages/simplifyEnrichment

git_branch devel

git_last_commit 2471b28

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-10-24

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Contents

`anno_word_cloud` *Word cloud annotations*

Description

Word cloud annotations

Usage

```
anno_word_cloud(
  align_to,
  term,
  exclude_words = NULL,
  max_words = 10,
  word_cloud_grob_param = list(),
  fontsize_range = c(4, 16),
  value_range = NULL,
  bg_gp = gpar(fill = "#DDDDDD", col = "#AAAAAA"),
  side = c("right", "left"),
  add_new_line = FALSE,
  count_words_param = list(),
  ...,
  return_gbl = FALSE
)
```

Arguments

align_to	How to align the annotations to the heatmap. Similar as in ComplexHeatmap::anno_link, the value of align_to can be a list of row indices or a categorical vector where each vector in the list corresponds to a word cloud. If it is a categorical vector, rows with the same level correspond to a same word cloud. If align_to is a categorical vector and term is a list, names of term should have overlap to the levels in align_to. When align_to is set as a categorical vector, normally the same value is set to row_split in the main heatmap so that each row slice can correspond to a word cloud.
term	The description text used for constructing the word clouds. The value should have the same format as align_to. If align_to is a list, term should also be a list. In this case, the length of vectors in term is not necessarily the same as in align_to. E.g. length(term[[1]]) is not necessarily equal to length(align_to[[1]]. If align_to is a categorical vector, term should also be a character vector with the same length as align_to. To make it more genrall, when align_to is a list, term can also be a list of data frames where the first column contains keywords and the second column contains numeric values that will be mapped to font sizes in the word clouds.
exclude_words	The words excluced for construcing word cloud.
max_words	Maximal number of words visualized in the word cloud.
word_cloud_grob_param	A list of graphics parameters passed to word_cloud_grob.
fontsize_range	The range of the font size. The value should be a numeric vector with length two. The font size interpolation is linear.
value_range	The range of values to map to font sizes.
bg_gp	Graphics parameters for controlling the background.
side	Side of the annotation relative to the heatmap.
add_new_line	Whether to add new line after every word? If TRUE, each word will be in a separated line.
count_words_param	A list of parameters passed to count_words.
...	Other parameters.
return_gbl	Internally used.

Details

The word cloud annotation is constructed by ComplexHeatmap::anno_link.

If the annotation is failed to construct or no keyword is found, the function returns a ComplexHeatmap::anno_empty with 1px width.

English stop words, punctuation and numbers are removed by default when counting words. As specific stop words might coincide with gene or pathway names, and numbers in genes names might be meaningful it is recommended to adjust this behaviour by passing appropriate arguments to the count_words function using count_words_param.

Examples

```
gm = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds", package = "simplifyEnrichment"))
go_id = rownames(gm)
go_term = AnnotationDbi::select(GO.db::GO.db, keys = go_id, columns = "TERM")$TERM
```

```
split = sample(letters[1:4], 100, replace = TRUE)
align_to = split(1:100, split)
term = lapply(letters[1:4], function(x) sample(go_term, sample(100:400, 1)))
names(term) = letters[1:4]

require(ComplexHeatmap)
mat = matrix(rnorm(100*10), nrow = 100)
Heatmap(mat, cluster_rows = FALSE, row_split = split,
 right_annotation = rowAnnotation(foo = anno_word_cloud(align_to, term)))
```

`anno_word_cloud_from_GO` *Word cloud annotations from GO*

Description

Word cloud annotations from GO

Usage

```
anno_word_cloud_from_GO(
  align_to,
  go_id,
  stat = c("pvalue", "count"),
  min_stat = ifelse(stat == "count", 5, 0.05),
  term = NULL,
  exclude_words = NULL,
  ...
)
```

Arguments

`align_to`	The same format as in `anno_word_cloud`.
`go_id`	The value should be in the same format as `align_to`. If `go_id` is a vector, it should have the same length as `align_to`, and if `go_id` is a list, note, e.g. `length(go_id[[1]])` is not necessarily equal to `length(align_to[[1]]`. If `align_to` is a categorical vector and `go_id` is a list, names of `go_id` should have overlap to the levels in `align_to`.
`stat`	What type of value to map to font sizes of the keywords. There are two possible values. "pvalue": enrichment is applied to keywords and -log10(p-value) is used to map to font size; "count": simply word frequency of keywords.
`min_stat`	Minimal value for `stat` for selecting keywords.
`term`	Alternatively the GO description can be set via the `term` argument. The same format as in `anno_word_cloud`.
`exclude_words`	The words excluced for construcing word cloud. Some words are internally exclucded: `c("via", "protein", "factor", "side", "type", "specific")`.
`...`	All other arguments passed to `anno_word_cloud`.

area_above_ecdf *Area above the eCDF curve*

Description

Area above the eCDF curve

Usage

```
area_above_ecdf(x)
```

Arguments

x	A vector of similarity values.

Details

Denote `F(x)` as the eCDF (empirical Cumulative Distribution Function) of the similarity vector `x`, this function calculates the area above the eCDF curve, which is `1 - \int_0^1 F(x)dx`.

Value

A numeric value.

cluster_terms *Cluster terms based on their similarity matrix*

Description

Cluster terms based on their similarity matrix

Usage

```
cluster_terms(
  mat,
  method = "binary_cut",
  control = list(),
  verbose = se_opt$verbose
)

cluster_by_kmeans(mat, max_k = max(2, min(round(nrow(mat)/5), 100)), ...)

cluster_by_pam(mat, max_k = max(2, min(round(nrow(mat)/10), 100)), ...)

cluster_by_dynamicTreeCut(mat, minClusterSize = 5, ...)

cluster_by_fast_greedy(mat, ...)

cluster_by_leading_eigen(mat, ...)
```

```
cluster_by_louvain(mat, ...)

cluster_by_walktrap(mat, ...)

cluster_by_mclust(mat, G = seq_len(max(2, min(round(nrow(mat)/5), 100))), ...)

cluster_by_apcluster(mat, s = apcluster::negDistMat(r = 2), ...)

cluster_by_hdbscan(mat, minPts = 5, ...)

cluster_by_MCL(mat, addLoops = TRUE, ...)
```

Arguments

mat	A similarity matrix.
method	The clustering methods. Value should be in all_clustering_methods().
control	A list of parameters passed to the corresponding clustering function.
verbose	Whether to print messages.
max_k	Maximal k for k-means/PAM clustering. K-means/PAM clustering is applied from k = 2 to k = max_k.
...	Other arguments.
minClusterSize	Minimal number of objects in a cluster. Pass to dynamicTreeCut::cutreeDynamic().
G	Passed to the G argument in mclust::Mclust() which is the number of clusters.
s	Passed to the s argument in apcluster::apcluster().
minPts	Passed to the minPts argument in dbscan::hdbscan().
addLoops	Passed to the addLoops argument in MCL::mcl().

Details

New clustering methods can be registered by register_clustering_methods().

Please note it is better to directly use cluster_terms() for clustering while not the individual cluster_by_* functions because cluster_terms() does additional cluster label adjustment.

By default, there are the following clustering methods and corresponding clustering functions:

- kmeans see cluster_by_kmeans().
- dynamicTreeCut see cluster_by_dynamicTreeCut().
- mclust see cluster_by_mclust().
- apcluster see cluster_by_apcluster().
- hdbscan see cluster_by_hdbscan().
- fast_greedy see cluster_by_fast_greedy().
- louvain see cluster_by_louvain().
- walktrap see cluster_by_walktrap().
- MCL see cluster_by_MCL().
- binary_cut see binary_cut().

The additional argument in individual clustering functions can be set with the `control` argument in `cluster_terms()`.

`cluster_by_kmeans()`: The best k for k-means clustering is determined according to the "elbow" or "knee" method on the distribution of within-cluster sum of squares (WSS) on each k. All other arguments are passed from ... to `stats::kmeans()`.

`cluster_by_pam()`: PAM is applied by `fpc::pamk()` which can automatically select the best k. All other arguments are passed from ... to `fpc::pamk()`.

`cluster_by_dynamicTreeCut()`: All other arguments are passed from ... to `dynamicTreeCut::cutreeDynamic()`.

`cluster_by_fast_greedy()`: All other arguments are passed from ... to `igraph::cluster_fast_greedy()`.

`cluster_by_leading_eigen()`: All other arguments are passed from ... to `igraph::cluster_leading_eigen()`.

`cluster_by_louvain()`: All other arguments are passed from ... to `igraph::cluster_louvain()`.

`cluster_by_walktrap()`: All other arguments are passed from ... to `igraph::cluster_walktrap()`.

`cluster_by_mclust()`: All other arguments are passed from ... to `mclust::Mclust()`.

`cluster_by_apcluster()`: All other arguments are passed from ... to `apcluster::apcluster()`.

`cluster_by_hdbscan()`: All other arguments are passed from ... to `dbscan::hdbscan()`.

`cluster_by_MCL()`: All other arguments are passed from ... to `MCL::mcl()`.

Value

A vector of numeric cluster labels.

`cmp_make_clusters` *Compare clustering methods*

Description

Compare clustering methods

Usage

```
cmp_make_clusters(
  mat,
  method = setdiff(all_clustering_methods(), "mclust"),
  verbose = TRUE
)

cmp_make_plot(mat, clt, plot_type = c("mixed", "heatmap"), nrow = 3)

compare_clustering_methods(
  mat,
  method = setdiff(all_clustering_methods(), "mclust"),
  plot_type = c("mixed", "heatmap"),
  nrow = 3,
  verbose = TRUE
)
```

Arguments

mat	The similarity matrix.
method	Which methods to compare. All available methods are in all_clustering_methods(). A value of "all" takes all available methods. By default "mclust" is excluded because its long runtime.
verbose	Whether to print messages.
	Ddetails The function compares following default clustering methods by default:
	-kmeans see cluster_by_kmeans. -pam see cluster_by_pam. -dynamicTreeCut see cluster_by_dynamicTreeCut. -mclust see cluster_by_mclust. By default it is not included. -apcluster see cluster_by_apcluster. -hdbscan see cluster_by_hdbscan. -fast_greedy see cluster_by_fast_greedy. -louvain see cluster_by_louvain. -walktrap see cluster_by_walktrap. -MCL see cluster_by_MCL. -binary_cut see binary_cut.
	Also the user-defined methods in all_clustering_methods are also compared.
clt	A list of clusterings from cmp_make_clusters().
plot_type	What type of plots to make. See **Details**.
nrow	Number of rows of the layout when plot_type is set to "heatmap".

Details

For cmp_make_plot(), if plot_type is the default value "mixed", a figure with three panels will be generated:

- A heatmap of the similarity matrix with different classifications as row annotations.
- A heatmap of the pair-wise concordance of the classifications of every two clustering methods.
- Barplots of the difference scores for each method (calculated by difference_score), the number of clusters (total clusters and the clusters with size >= 5) and the mean similarity of the terms that are in the same clusters.

If plot_type is "heatmap". There are heatmaps for the similarity matrix under clusterings from different methods. The last panel is a table with the number of clusters under different clusterings.

compare_clustering_methods() is basically a wrapper function of cmp_make_clusters() and cmp_make_plot().

Value

cmp_make_clusters() returns a list of cluster label vectors from different clustering methods.

cmp_make_plot() returns no value.

compare_clustering_methods() returns no value.

Examples

```
mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
compare_clustering_methods(mat)
compare_clustering_methods(mat, plot_type = "heatmap")
```

count_words *Calculate word frequency*

Description

Calculate word frequency

Usage

```
count_words(
  term,
  exclude_words = NULL,
  stop_words = stopwords(),
  min_word_length = 1,
  tokenizer = "words",
  transform_case = tolower,
  remove_numbers = TRUE,
  remove_punctuation = TRUE,
  custom_transformer = NULL,
  stemming = FALSE,
  dictionary = NULL
)
```

Arguments

term	A vector of description texts.
exclude_words	The words that should be excluded.
stop_words	The stop words that should be be removed.
min_word_length	Minimum length of the word to be counted.
tokenizer	The tokenizer function, one of the values accepted by tm::termFreq.
transform_case	The function normalizing lettercase of the words.
remove_numbers	Whether to remove numbers.
remove_punctuation	Whether to remove punctuation.
custom_transformer	Custom function that transforms words.
stemming	Whether to only keep the roots of inflected words.
dictionary	A vector of words to be counted (if given all other words will be excluded).

Details

The text preprocessing followings the instruction from http://www.sthda.com/english/wiki/word-cloud-generator-in-r-one-killer-function-to-do-everything-you-need.

Value

A data frame with words and frequencies.

Examples

```
gm = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds", package = "simplifyEnrichment"))
go_id = rownames(gm)
go_term = AnnotationDbi::select(GO.db::GO.db, keys = go_id, columns = "TERM")$TERM
count_words(go_term) |> head()
```

---

dend_node_apply *Apply functions on every node in a dendrogram*

Description

Apply functions on every node in a dendrogram

Usage

```
dend_node_apply(dend, fun)

edit_node(dend, fun = function(d, index) d)
```

Arguments

dend	A dendrogram object.
fun	A self-defined function.

Details

dend_node_apply() returns a vector or a list as the same length as the number of nodes in the dendrogram.

The self-defined function can have one single argument which is the sub-dendrogram at a certain node. E.g. to get the number of members at every node:

```
dend_node_apply(dend, function(d) attr(d, "members"))
```

The self-defined function can have a second argument, which is the index of current sub-dendrogram in the complete dendrogram. E.g. dend[[1]] is the first child node of the complete dendrogram and dend[[c(1, 2)]] is the second child node of dend[[1]], et al. This makes that at a certain node, it is possible to get information of its child nodes and parent nodes.

```
dend_node_apply(dend, function(d, index) {
    dend[[c(index, 1)]] # is the first child node of d, or simply d[[1]]
    dend[[index[-length(index)]]] # is the parent node of d
    ...
})
```

Note for the top node, the value of index is NULL.

In edit_node(), if fun only has one argument, it is basically the same as stats::dendrapply(), but it can have a second argument which is the index of the node in the dendrogram, which makes it possible to get information of child nodes and parent nodes for a specific node.

As an example, we first assign random values to every node in the dendrogram:

```
mat = matrix(rnorm(100), 10)
dend = as.dendrogram(hclust(dist(mat)))
dend = edit_node(dend, function(d) {attr(d, 'score') = runif(1); d})
```

Then for every node, we take the maximal absolute difference to all its child nodes and parent node as the attribute `abs_diff`.

```
dend = edit_node(dend, function(d, index) {
    n = length(index)
    s = attr(d, "score")
    if(is.null(index)) {  # d is the top node
        s_children = sapply(d, function(x) attr(x, "score"))
        s_parent = NULL
    } else if(is.leaf(d)) { # d is the leaf
        s_children = NULL
        s_parent = attr(dend[[index[-n]]], "score")
    } else {
        s_children = sapply(d, function(x) attr(x, "score"))
        s_parent = attr(dend[[index[-n]]], "score")
    }
    abs_diff = max(abs(s - c(s_children, s_parent)))
    attr(d, "abs_diff") = abs_diff
    return(d)
})
```

Value

`dend_node_apply()` returns a vector or a list, depends on whether `fun` returns a scalar or more complex values.

`edit_node()` returns a `dendrogram` object.

Examples

```
mat = matrix(rnorm(100), 10)
dend = as.dendrogram(hclust(dist(mat)))
# number of members on every node
dend_node_apply(dend, function(d) attr(d, "members"))
# the depth on every node
dend_node_apply(dend, function(d, index) length(index))
```

`difference_score` *Difference score*

Description

Difference score

Usage

```
difference_score(mat, cl)
```

Arguments

mat	The similarity matrix.
cl	Cluster labels.

Details

This function measures the different between the similarity values for the terms that belong to the same clusters and in different clusters. The difference score is the Kolmogorov-Smirnov statistic between the two distributions.

Value

A numeric scalar.

Examples

```
mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
cl = binary_cut(mat)
difference_score(mat, cl)
```

---

export_to_shiny_app *Interactively visualize the similarity heatmap*

Description

Interactively visualize the similarity heatmap

Usage

```
export_to_shiny_app(mat, cl = binary_cut(mat))
```

Arguments

mat	A similarity matrix.
cl	Cluster labels inferred from the similarity matrix, e.g. from cluster_terms() or binary_cut().

Value

A shiny application.

Examples

```
if(interactive()) {
    mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
        package = "simplifyEnrichment"))
    cl = binary_cut(mat)
    export_to_shiny_app(mat, cl)
}
```

GO_similarity *Calculate Gene Ontology (GO) semantic similarity matrix*

Description

Calculate Gene Ontology (GO) semantic similarity matrix

Usage

```
GO_similarity(
  go_id,
  ont = NULL,
  db = "org.Hs.eg.db",
  measure = "Sim_XGraSM_2013"
)

guess_ont(go_id, db = "org.Hs.eg.db")

random_GO(n, ont = c("BP", "CC", "MF"), db = "org.Hs.eg.db")
```

Arguments

go_id	A vector of GO IDs.
ont	Sub-ontology of GO. Value should be one of "BP", "CC" or "MF". If it is not specified, the function automatically identifies it by random sampling 10 IDs from go_id (see guess_ont()).
db	Annotation database. It should be an OrgDb package name from https://bioconductor.org/packages/release/BiocViews.html#___OrgDb. The value can also directly be an OrgDb object.
measure	Semantic measure for the GO similarity, pass to simona::term_sim(). All valid values are in simona::all_term_sim_methods().
n	Number of GO IDs.

Details

The default similarity method is "Sim_XGraSM_2013". Since the semantic similarities are calculated based on gene annotations to GO terms, I suggest users also try the following methods:

- "Sim_Lin_1998"
- "Sim_Resnik_1999"
- "Sim_Relevance_2006"
- "Sim_SimIC_2010"
- "Sim_XGraSM_2013"
- "Sim_EISI_2015"
- "Sim_AIC_2014"
- "Sim_Wang_2007"
- "Sim_GOGO_2018"

In guess_ont(), only 10 random GO IDs are checked.

In random_GO(), only GO terms with gene annotations are sampled.

Value

`GO_similarity()` returns a symmetric matrix.

`guess_ont()` returns a single character scalar of "BP", "CC" or "MF". If there are more than one ontologies detected. It returns `NULL`.

`random_GO()` returns a vector of GO IDs.

Examples

```
go_id = random_GO(100)
mat = GO_similarity(go_id)


go_id = random_GO(100)
guess_ont(go_id)
```

`ht_clusters` *Visualize the similarity matrix and the clustering*

Description

Visualize the similarity matrix and the clustering

Usage

```
ht_clusters(
  mat,
  cl,
  dend = NULL,
  col = c("white", "red"),
  draw_word_cloud = TRUE,
  min_term = round(nrow(mat) * 0.01),
  order_by_size = FALSE,
  stat = "pvalue",
  min_stat = ifelse(stat == "count", 5, 0.05),
  exclude_words = character(0),
  max_words = 10,
  word_cloud_grob_param = list(),
  fontsize_range = c(4, 16),
  bg_gp = gpar(fill = "#DDDDDD", col = "#AAAAAA"),
  column_title = NULL,
  ht_list = NULL,
  use_raster = TRUE,
  run_draw = TRUE,
  ...
)
```

Arguments

mat	A similarity matrix.
cl	Cluster labels inferred from the similarity matrix, e.g. from cluster_terms() or binary_cut().
dend	Used internally.
col	A vector of colors that map from 0 to the 97.5^th percentile of the similarity values. The value can also be a color mapping function generated by circlize::colorRamp2().
draw_word_cloud	Whether to draw the word clouds.
min_term	Minimal number of functional terms in a cluster. All the clusters with size less than min_term are all merged into one separated cluster in the heatmap.
order_by_size	Whether to reorder clusters by their sizes. The cluster that is merged from small clusters (size < min_term) is always put to the bottom of the heatmap.
stat	Type of value for mapping to the font size of keywords in the word clouds. There are two options: "count": simply number of keywords; "pvalue": enrichment on keywords is performed (by fisher's exact test) and -log10(pvalue) is used to map to font sizes.
min_stat	Minimal value for stat for selecting keywords.
exclude_words	Words that are excluded in the word cloud.
max_words	Maximal number of words visualized in the word cloud.
word_cloud_grob_param	A list of graphic parameters passed to word_cloud_grob().
fontsize_range	The range of the font size. The value should be a numeric vector with length two. The font size interpolation is linear.
bg_gp	Graphics parameters for controlling word cloud annotation background.
column_title	Column title for the heatmap.
ht_list	A list of additional heatmaps added to the left of the similarity heatmap.
use_raster	Whether to write the heatmap as a raster image.
run_draw	Internally used.
...	Other arguments passed to ComplexHeatmap::draw,HeatmapList-method.

Value

A ComplexHeatmap::HeatmapList object.

Examples

```
mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
cl = binary_cut(mat)
ht_clusters(mat, cl, word_cloud_grob_param = list(max_width = 80))
ht_clusters(mat, cl, word_cloud_grob_param = list(max_width = 80),
    order_by_size = TRUE)
```

keyword_enrichment_from_GO *Keyword enrichment for GO terms*

Description

Keyword enrichment for GO terms

Usage

```
keyword_enrichment_from_GO(go_id, min_bg = 5, min_term = 2)
```

Arguments

go_id	A vector of GO IDs.
min_bg	Minimal number of GO terms (in the background, i.e. all GO temrs in the GO database) that contain a specific keyword.
min_term	Minimal number of GO terms (GO terms in go_id) that contain a specific keyword.

Details

The enrichment is applied by Fisher's exact test. For a keyword, there is the following 2x2 contigency table:

```
                  | contains the keyword | does not contain the keyword
In the GO set     |          s11         |          s12
Not in the GO set |          s21         |          s22
```

where s11, s12, s21 and s22 are the counts of GO terms in the four categories.

Value

A data frame with keyword enrichment results.

Examples

```
go_id = random_GO(100)
keyword_enrichment_from_GO(go_id)
```

partition_by_kmeans *Partition the matrix*

Description

Partition the matrix

Usage

```
partition_by_kmeans(mat, n_repeats = 10)

partition_by_pam(mat)

partition_by_hclust(mat)

partition_by_kmeanspp(mat)
```

Arguments

mat	The submatrix in the binary cut clustering process.
n_repeats	Number of repeated runs of k-means clustering.

Details

These functions can be set to the partition_fun argument in binary_cut().

partition_by_kmeans(): Since k-means clustering brings randomness, this function performs k-means clustering several times (controlled by n_repeats) and uses the final consensus partitioning results.

partition_by_pam(): The clustering is performed by cluster::pam() with the pamonce argument set to 5.

partition_by_hclust(): The "ward.D2" clusering method was used.

partition_by_kmeanspp(): It uses the kmeanspp method from the **flexclust** package.

Value

All partitioning functions split the matrix into two groups and return a categorical vector of labels of 1 and 2.

plot_binary_cut *Cluster functional terms by recursively binary cutting the similarity matrix*

Description

Cluster functional terms by recursively binary cutting the similarity matrix

Usage

```
plot_binary_cut(
  mat,
  value_fun = area_above_ecdf,
  cutoff = 0.85,
  partition_fun = partition_by_pam,
  dend = NULL,
  dend_width = unit(3, "cm"),
  depth = NULL,
  show_heatmap_legend = TRUE,
  ...
)

binary_cut(
  mat,
  value_fun = area_above_ecdf,
  partition_fun = partition_by_hclust,
  cutoff = 0.85,
  try_all_partition_fun = TRUE,
  partial = nrow(mat) > 1500
)
```

Arguments

mat	A similarity matrix.
value_fun	A function that calculates the scores for the four submatrices on a node.
cutoff	The cutoff for splitting the dendrogram.
partition_fun	A function to split each node into two groups. Pre-defined functions in this package are partition_by_kmeanspp(), partition_by_pam() and partition_by_hclust().
dend	A dendrogram object, used internally.
dend_width	Width of the dendrogram on the plot.
depth	Depth of the recursive binary cut process.
show_heatmap_legend	Whether to show the heatmap legend.
...	Other arguments.
try_all_partition_fun	Different partition_fun may give different clusterings. If the vaule of try_all_partition_fun is set to TRUE, the similarity matrix is clustered by three partitioning method: partition_by_pam(), partition_by_kmeanspp() and partition_by_hclust(). The clustering with the highest difference score is finally selected as the final clustering.
partial	Whether to generate the complete clustering or the clustering stops when submatrices cannot be split anymore.

Details

After the functions which perform clustering are executed, such as simplifyGO() or binary_cut(), the dendrogram is temporarily saved and plot_binary_cut() directly uses this dendrogram.

Value

`binary_cut()` returns a vector of numeric cluster labels.

Examples

```
mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
plot_binary_cut(mat, depth = 1)
plot_binary_cut(mat, depth = 2)
plot_binary_cut(mat)

mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
binary_cut(mat)
```

---

register_clustering_methods

Configure clustering methods

Description

Configure clustering methods

Usage

```
register_clustering_methods(...)

all_clustering_methods()

remove_clustering_methods(method)

reset_clustering_methods()
```

Arguments

`...`	A named list of clustering functions, see in **Details**.
`method`	A vector of method names.

Details

The user-defined functions should accept at least one argument which is the input matrix. The second optional argument should always be `...` so that parameters for the clustering function can be passed by the `control` argument from `cluster_terms()`, `simplifyGO()` or `simplifyEnrichment()`. If users forget to add `...`, it is added internally.

Please note, the user-defined function should automatically identify the optimized number of clusters.

The function should return a vector of cluster labels. Internally it is converted to numeric labels.

The default clustering methods are:

- `kmeans` see `cluster_by_kmeans()`.

- dynamicTreeCut see cluster_by_dynamicTreeCut().
- mclust see cluster_by_mclust().
- apcluster see cluster_by_apcluster().
- hdbscan see cluster_by_hdbscan().
- fast_greedy see cluster_by_fast_greedy().
- louvain see cluster_by_louvain().
- walktrap see cluster_by_walktrap().
- MCL see cluster_by_MCL().
- binary_cut see binary_cut().

Value

all_clustering_methods() returns a vector of clustering method names.

Examples

```
register_clustering_methods(
    # assume there are 5 groups
    random = function(mat, ...) sample(5, nrow(mat), replace = TRUE)
)
all_clustering_methods()
remove_clustering_methods("random")
all_clustering_methods()
remove_clustering_methods(c("kmeans", "mclust"))
all_clustering_methods()
reset_clustering_methods()
all_clustering_methods()
```

---

scale_fontsize *Scale font size*

Description

Scale font size

Usage

```
scale_fontsize(x, rg = c(1, 30), fs = c(4, 16))
```

Arguments

x	A numeric vector.
rg	The range.
fs	Range of the font size.

Details

It is a linear interpolation.

Value

A numeric vector.

Examples

```
x = runif(10, min = 1, max = 20)
# scale x to fontsize 4 to 16.
scale_fontsize(x)
```

`select_cutoff` *Select the cutoff for binary cut*

Description

Select the cutoff for binary cut

Usage

```
select_cutoff(
  mat,
  cutoff = seq(0.6, 0.98, by = 0.01),
  verbose = se_opt$verbose,
  ...
)
```

Arguments

`mat`	A similarity matrix.
`cutoff`	A list of cutoffs to test. Note the range of the cutoff values should be inside `[0.5, 1]`.
`verbose`	Whether to print messages.
`...`	Pass to `binary_cut()`.

Details

Binary cut is applied to each cutoff and the clustering results are evaluated by following metrics:

- difference score, calculated by `difference_score()`.
- number of clusters.
- block mean, which is the mean similarity in the blocks in the diagonal of the heatmap.

Examples

```
mat = readRDS(system.file("extdata", "random_GO_BP_sim_mat.rds",
    package = "simplifyEnrichment"))
select_cutoff(mat)
```

se_opt *Global parameters*

Description

Global parameters

Usage

```
se_opt(..., RESET = FALSE, READ.ONLY = NULL, LOCAL = FALSE, ADD = FALSE)
```

Arguments

...	Arguments for the parameters, see "details" section.
RESET	Whether to reset to default values.
READ.ONLY	Please ignore.
LOCAL	Please ignore.
ADD	Please ignore.

Details

There are the following global options:

- verobse: Whether to print messages.

Value

A GlobalOptionsFun object.

simplifyGO *Simplify Gene Ontology (GO) enrichment results*

Description

Simplify Gene Ontology (GO) enrichment results

Usage

```
simplifyGO(
  mat,
  method = "binary_cut",
  control = list(),
  plot = TRUE,
  verbose = TRUE,
  column_title = qq("@{nrow(mat)} GO terms clustered by '@{method}'"),
  ht_list = NULL,
  ...
)

simplifyEnrichment(...)
```

Arguments

mat	A GO similarity matrix. You can also provide a vector of GO IDs to this argument.
method	Method for clustering the matrix. See cluster_terms().
control	A list of parameters for controlling the clustering method, passed to cluster_terms().
plot	Whether to make the heatmap.
verbose	Whether to print messages.
column_title	Column title for the heatmap.
ht_list	A list of additional heatmaps added to the left of the similarity heatmap.
...	Arguments passed to ht_clusters().

Details

This is basically a wrapper function that it first runs cluster_terms() to cluster GO terms and then runs ht_clusters() to visualize the clustering.

The arguments in simplifyGO() passed to ht_clusters() are:

- draw_word_cloud: Whether to draw the word clouds.
- min_term: Minimal number of GO terms in a cluster. All the clusters with size less than min_term are all merged into one single cluster in the heatmap.
- order_by_size: Whether to reorder GO clusters by their sizes. The cluster that is merged from small clusters (size < min_term) is always put to the bottom of the heatmap.
- stat: What values of keywords are used to map to font sizes in the word clouds.
- exclude_words: Words that are excluded in the word cloud.
- max_words: Maximal number of words visualized in the word cloud.
- word_cloud_grob_param: A list of graphic parameters passed to word_cloud_grob().
- fontsize_range The range of the font size. The value should be a numeric vector with length two. The minimal font size is mapped to word frequency value of 1 and the maximal font size is mapped to the maximal word frequency. The font size interlopation is linear.
- bg_gp: Graphic parameters for controlling the background of word cloud annotations.

Value

A data frame with two columns: GO IDs and cluster labels.

Examples

```
set.seed(123)
go_id = random_GO(500)
mat = GO_similarity(go_id)
df = simplifyGO(mat, word_cloud_grob_param = list(max_width = 80))
head(df)
```

`simplifyGOFromMultipleLists` *Perform simplifyGO analysis with multiple lists of GO IDs*

Description

Perform simplifyGO analysis with multiple lists of GO IDs

Usage

```
simplifyGOFromMultipleLists(
  lt,
  go_id_column = NULL,
  padj_column = NULL,
  padj_cutoff = 0.01,
  filter = function(x) any(x < padj_cutoff),
  default = 1,
  ont = NULL,
  db = "org.Hs.eg.db",
  measure = "Sim_XGraSM_2013",
  heatmap_param = list(NULL),
  show_barplot = TRUE,
  method = "binary_cut",
  control = list(),
  min_term = NULL,
  verbose = TRUE,
  column_title = NULL,
  ...
)
```

Arguments

`lt`	A data frame, a list of numeric vectors (e.g. adjusted p-values) where each numeric vector has GO IDs as names, or a list of GO IDs.
`go_id_column`	Column index of GO ID if `lt` contains a list of data frames.
`padj_column`	Column index of adjusted p-values if `lt` contains a list of data frames.
`padj_cutoff`	Cut off for adjusted p-values.
`filter`	A self-defined function for filtering GO IDs. By default it requires GO IDs should be significant in at least one list.
`default`	The default value for the adjusted p-values. See **Details**.
`ont`	Pass to `GO_similarity()`.
`db`	Pass to `GO_similarity()`.
`measure`	Pass to `GO_similarity()`.
`heatmap_param`	Parameters for controlling the heatmap, see **Details**.
`show_barplot`	Whether draw barplots which shows numbers of significant GO terms in clusters.
`method`	Pass to `simplifyGO()`.

control	Pass to simplifyGO().
min_term	Pass to simplifyGO().
verbose	Pass to simplifyGO().
column_title	Pass to simplifyGO().
...	Pass to simplifyGO().

Details

The input data can have three types of formats:

- A list of numeric vectors of adjusted p-values where each vector has the GO IDs as names.
- A data frame. The column of the GO IDs can be specified with go_id_column argument and the column of the adjusted p-values can be specified with padj_column argument. If these columns are not specified, they are automatically identified. The GO ID column is found by checking whether a column contains all GO IDs. The adjusted p-value column is found by comparing the column names of the data frame to see whether it might be a column for adjusted p-values. These two columns are used to construct a numeric vector with GO IDs as names.
- A list of character vectors of GO IDs. In this case, each character vector is changed to a numeric vector where all values take 1 and the original GO IDs are used as names of the vector.

Now let's assume there are n GO lists, we first construct a global matrix where columns correspond to the n GO lists and rows correspond to the "union" of all GO IDs in the lists. The value for the ith GO ID and in the jth list are taken from the corresponding numeric vector in lt. If the jth vector in lt does not contain the ith GO ID, the value defined by default argument is taken there (e.g. in most cases the numeric values are adjusted p-values, default is set to 1). Let's call this matrix as M0.

Next step is to filter M0 so that we only take a subset of GO IDs of interest. We define a proper function via argument filter to remove GO IDs that are not important for the analysis. Functions for filter is applied to every row in M0 and filter function needs to return a logical value to decide whether to remove the current GO ID. For example, if the values in lt are adjusted p-values, the filter function can be set as function(x) any(x < padj_cutoff) so that the GO ID is kept as long as it is signfiicant in at least one list. After the filter, let's call the filtered matrix M1.

GO IDs in M1 (row names of M1) are used for clustering. A heatmap of M1 is attached to the left of the GO similarity heatmap so that the group-specific (or list-specific) patterns can be easily observed and to corresponded to GO functions.

Argument heatmap_param controls several parameters for heatmap M1:

- transform: A self-defined function to transform the data for heatmap visualization. The most typical case is to transform adjusted p-values by -log10(x).
- breaks: break values for color interpolation.
- col: The corresponding values for breaks.
- labels: The corresponding labels.
- name: Legend title.

Examples

```
# perform functional enrichment on the signatures genes from cola anlaysis
require(cola)
data(golub_cola)
res = golub_cola["ATC:skmeans"]
require(hu6800.db)
x = hu6800ENTREZID
mapped_probes = mappedkeys(x)
id_mapping = unlist(as.list(x[mapped_probes]))
lt = functional_enrichment(res, k = 3, id_mapping = id_mapping) # you can check the value of `lt`

# a list of data frames
simplifyGOFromMultipleLists(lt, padj_cutoff = 0.001)

# a list of numeric values
lt2 = lapply(lt, function(x) structure(x$p.adjust, names = x$ID))
simplifyGOFromMultipleLists(lt2, padj_cutoff = 0.001)

# a list of GO IDS
lt3 = lapply(lt, function(x) x$ID[x$p.adjust < 0.001])
simplifyGOFromMultipleLists(lt3)
```

---

summarizeGO *A simplified way to visualize enrichment in GO clusters*

Description

A simplified way to visualize enrichment in GO clusters

Usage

```
summarizeGO(
  go_id,
  value = NULL,
  aggregate = mean,
  method = "binary_cut",
  control = list(),
  verbose = TRUE,
  axis_label = "Value",
  title = "",
  legend_title = axis_label,
  min_term = round(nrow(mat) * 0.01),
  stat = "pvalue",
  min_stat = ifelse(stat == "count", 5, 0.05),
  exclude_words = character(0),
  max_words = 6,
  word_cloud_grob_param = list(),
  fontsize_range = c(4, 16),
  bg_gp = gpar(fill = "#DDDDDD", col = "#AAAAAA")
)
```

Arguments

go_id	A vector of GO IDs.
value	A list of numeric value associate with go_id. We suggest to use -log10(p.adjust) or -log2(fold enrichment) as the values.
aggregate	Function to aggregate values in each GO cluster.
method	Method for clustering the matrix. See cluster_terms().
control	A list of parameters for controlling the clustering method, passed to cluster_terms().
verbose	Whether to print messages.
axis_label	X-axis label.
title	Title for the whole plot.
legend_title	Title for the legend.
min_term	Minimal number of functional terms in a cluster. All the clusters with size less than min_term are all merged into one separated cluster in the heatmap.
stat	Type of value for mapping to the font size of keywords in the word clouds. There are two options: "count": simply number of keywords; "pvalue": enrichment on keywords is performed (by fisher's exact test) and -log10(pvalue) is used to map to font sizes.
min_stat	Minimal value for stat for selecting keywords.
exclude_words	Words that are excluded in the word cloud.
max_words	Maximal number of words visualized in the word cloud.
word_cloud_grob_param	A list of graphic parameters passed to word_cloud_grob.
fontsize_range	The range of the font size. The value should be a numeric vector with length two. The font size interpolation is linear.
bg_gp	Graphics parameters for controlling word cloud annotation background.

Details

There are several other ways to specify GO IDs and the associated values.

1. specify value as a named vector where GO IDs are the names.
2. specify value as a list of numeric named vectors. In this case, value contains multiple enrichment results.

Please refer to https://jokergoo.github.io/2023/10/02/simplified-simplifyenrichment-plot/ for more examples of this function.

---

word_cloud_grob *A simple grob for the word cloud*

Description

A simple grob for the word cloud

Usage

```
word_cloud_grob(
  text,
  fontsize,
  line_space = unit(4, "pt"),
  word_space = unit(4, "pt"),
  max_width = unit(80, "mm"),
  col = function(fs) circlize::rand_color(length(fs), luminosity = "dark"),
  add_new_line = FALSE,
  test = FALSE
)

## S3 method for class 'word_cloud'
widthDetails(x)

## S3 method for class 'word_cloud'
heightDetails(x)
```

Arguments

`text`	A vector of words.
`fontsize`	The corresponding font size. With the frequency of the words known, `scale_fontsize` can be used to linearly interpolate frequencies to font sizes.
`line_space`	Space between lines. The value can be a `grid::unit` object or a numeric scalar which is measured in mm.
`word_space`	Space between words. The value can be a `grid::unit` object or a numeric scalar which is measured in mm.
`max_width`	The maximal width of the viewport to put the word cloud. The value can be a `grid::unit` object or a numeric scalar which is measured in mm. Note this might be larger than the final width of the returned grob object.
`col`	Colors for the words. The value can be a vector, in numeric or character, which should have the same length as `text`. Or it is a self-defined function that takes the font size vector as the only argument. The function should return a color vector. See Examples.
`add_new_line`	Whether to add new line after every word? If `TRUE`, each word will be in a separated line.
`test`	Internally used. It basically adds borders to the words and the viewport.
`x`	The `word_cloud` grob returned by `word_cloud_grob`.

Value

A `grid::grob` object. The width and height of the grob can be get by `grid::grobWidth` and `grid::grobHeight`.

Examples

```
# very old R versions do not have strrep() function
if(!exists("strrep")) {
    strrep = function(x, i) paste(rep(x, i), collapse = "")
}
words = sapply(1:30, function(x) strrep(sample(letters, 1), sample(3:10, 1)))
```

```
require(grid)
gb = word_cloud_grob(words, fontsize = runif(30, min = 5, max = 30),
    max_width = 100)
grid.newpage(); grid.draw(gb)

# color as a single scalar
gb = word_cloud_grob(words, fontsize = runif(30, min = 5, max = 30),
    max_width = 100, col = 1)
grid.newpage(); grid.draw(gb)

# color as a vector
gb = word_cloud_grob(words, fontsize = runif(30, min = 5, max = 30),
    max_width = 100, col = 1:30)
grid.newpage(); grid.draw(gb)

# color as a function
require(circlize)
col_fun = colorRamp2(c(5, 17, 30), c("blue", "black", "red"))
gb = word_cloud_grob(words, fontsize = runif(30, min = 5, max = 30),
    max_width = 100, col = function(fs) col_fun(fs))
grid.newpage(); grid.draw(gb)
```

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