Package ‘gCMAPWeb’

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Type   Package
Title   A web interface for gene-set enrichment analyses
Version 1.14.0
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Description The gCMAPWeb R package provides a graphical user interface for the gCMAP package. gCMAPWeb uses the Rook package and can be used either on a local machine, leveraging R’s internal web server, or run on a dedicated rApache web server installation.

gCMAPWeb allows users to search their own data sources and instructions to generate reference datasets from public repositories are included with the package. The package supports three common types of analyses, specifically queries with 1. one or two sets of query gene identifiers, whose members are expected to show changes in gene expression in a consistent direction. For example, an up-regulated gene set might contain genes activated by a transcription factor, a down-regulated geneset targets repressed by the same factor. 2. a single set of query gene identifiers, whose members are expected to show divergent differential expression (non-directional query). For example, members of a particular signaling pathway, some of which may be up- some down-regulated in response to a stimulus. 3. a query with the complete results of a differential expression profiling experiment. For example, gene identifiers and z-scores from a previous perturbation experiment. gCMAPWeb accepts three types of identifiers: EntrezIds, gene Symbols and microarray probe ids and can be configured to work with any species supported by Bioconductor. For each query submission, significantly similar reference datasets will be identified and reported in graphical and tabular form.

Note gCMAPWeb is not compatible with the RStudio IDE, but can be used from the command line or via R’s standard GUI.

License Artistic-2.0
Depends Biobase, gCMAP (>= 1.3.0), methods, R (>= 3.3.0), Rook
Imports brew, BiocGenerics, annotate, AnnotationDbi, grDevices, GSEABase, hwriter, parallel, yaml
Suggests  affy, ArrayExpress, hgfocuss.db, hgu133a.db, mgug4104a.db, org.Hs.eg.db, org.Mm.eg.db, RUnit
Enhances  bigmemory, bigmemoryExtras
biocViews  GUI, GeneSetEnrichment, Visualization
LazyLoad  yes
Collate  'gCMAPWeb-package.R' 'AllGenerics.R' 'cmapRun-methods.R'
         'cmap.R' 'cmapAnalysis.R' 'cmapHeatmap.R' 'createObject.R'
         'example_objects.R' 'file_io.R' 'html_elements.R'
         'plotting_functions.R' 'reporting.R'
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NeedsCompilation no

R topics documented:

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gCMAPWeb-package

A web-interface for gene-set enrichment analysis

Description

A web-interface for gene-set enrichment analysis

Details

This package provides a stand-alone web interface for gene-set enrichment analysis. Run either through R’s internal Rhttpd server or deployed through an Apache2 server, gCMAPWeb allows users to search reference datasets stored in \texttt{NChannelSet} or \texttt{CMAPCollection} objects via three different methods:

- Directional queries performed by calculating the parametric JG score from the reference datasets
- Non-directional queries performed via Fisher’s exact test
- Profile queries performed by calculating the parametric JG score from the query data

A web interface is populated based on a configuration file in YAML format and additional information from the reference dataset objects (if available). For each query, a report is generated in HTML format, including graphs and tabular output. Extensive customization of the graphical user interface can easily be performed through global options.
addLinks

Author(s)
Thomas Sandmann

References

Examples

example( gCMAPWeb )

addLinks df, pattern = ".url$", swap.colnames =getOption("swap.colnames", default = list(padj = "FDR", nFound = "Genes")))

Arguments
df data.frame, must contain both target and url columns
pattern character, the suffix linking target and url columns. Default=c(., "url")
swap.colnames list, containing alternative names for CMAPResults columns.

Details
To annotate columns with links to other urls, the urls must be included in the data.frame in a separate column matching the target column name but carrying the additional suffix in the column name. For example, to add links to the `id` column, an additional id.url column can be used. Multiple columns can be processed simultaneously, if each of them has a matching url column.

Value
Data frame with href html tags in the target column(s)

Author(s)
Thomas Sandmann
add_geneScores_to_df  

CMAPResults data.frame with gene-level scores

Description
This function converts a CMAPResults object into a data.frame and adds the gene-level scores as an additional column.

Usage
add_geneScores_to_df(cmap.result)

Arguments
cmap.result  
CMAPResults object

Value
A data.frame with gene-level scores in column `Scores`

Author(s)
Thomas Sandmann

body_first  

Definition of html navigation bar elements

Description
Shared html code, constituting the first part of the body section

Usage
body_first(url.base = NULL)

Arguments
url.base  
character, path to htdocs directory (optional)

Value
Html code as a character string

Author(s)
Thomas Sandmann
Example reference datasets

Description

Five example reference datasets containing simulated data to demonstrate the functionality of the gCMAPWeb package. These objects were generated with the `exampleCMAP` function using different seeds.

Format

cmap1 to 4 are `NChannelSet` objects each with 1000 simulated z-scores for 10 samples. cmap5 is a `CMAPCollection` with membership information about 1000 genes and 10 gene sets.

Details

cmap1, cmap2, cmap3 and cmap5 contain data for 1000 human Entrez identifiers. cmap1, cmap2 and cmap3 are `NChannelSet` objects with one channel, the 'z' AssayDataElement. cmap4 is an `NChannelSet` with data for 1000 mouse Entrez identifiers in the 'z' and 'log_fc' channels. cmap5 is a codeCMAPCollection.

cmapAnalysis  Function controlling the gCMAP analysis workflow

Description

This function controls the gCMAPWeb analysis workflow

Usage

cmapAnalysis(req, conf_data, reference.cmaps, element = getOption("element", default = "z"), save.intermediates = getOption("save.intermediates", default = FALSE))

Arguments

- `req` a Rook Request object
- `conf_data` list, the configuration data as returned by the read_config_file function
- `reference.cmaps` list, containing the reference database eSet objects
- `element` character, identifying the elementName of the channel extracted from NChannelSet objects
- `save.intermediates` logical, if TRUE rdata files of intermediate results will be stored in the temporary directory for debugging

Value

a list with three elements: conversion, reports and tmp_filename
**cmapHeatmap**

**Function to create an annotated heatmap of gene scores**

**Description**

This function takes a numerical matrix (with samples in columns and genes in rows), preprocesses the data (if desired), determines the optimal height for the heatmap and calls the .ImagePlot function to create the final heatmap figure.

**Usage**

```r
cmapHeatmap(x, reference.name, col.anno = NULL, row.anno = NULL,
file.name = "heatmap", url.base = NULL, main = "Query gene scores",
ColorRamp = colorRampPalette(c("#044381FF", "grey95", "grey95", "firebrick"))(100),
col.col = c(down = "black", up = "grey"),
row.col = c(correlated = "#1B9E77", anticorrelated = "#044381FF", over = 
"#1B9E77", under = "#044381FF"), order.by.score = TRUE,
cluster.rows = TRUE, score.cap = c(-5, 5),
ylab = "Significant datasets")
```

**Arguments**

- **x**: numerical matrix with samples in rows and genes in columns.
- **reference.name**: character, names of the reference cmap, used to construct the html image reference.
- **col.anno**: character vector with column annotations to be displayed as (horizontal) annotation bar above the heatmap. If not NULL, must contain one element for each column of 'x'.
- **row.anno**: character vector with row annotations to be displayed as (vertical) annotation to the right of the heatmap. If not NULL, must contain one element for each row of 'x'.
- **file.name**: character, the path and filename (without suffix) to save the png file to.
- **url.base**: character, prefix for the html image reference.
- **main**: Character, main title of the plot.
- **ColorRamp**: vector of colors used for the heatmap, e.g. generated by a call to colorRampPalette.
- **col.col**: named vector with a color for each level of col.anno (e.g. `c(up="firebrick", down="blue")`)
- **row.col**: named vector with a color for each level of row.anno (e.g. `c(correlated="firebrick",anticorrelated="#044381FF")`)
- **order.by.score**: logical, should gene scores be reordered independently for each sample ?
- **cluster.rows**: logical, perform hierarchical clustering on significant gene sets ?
- **score.cap**: numerical vector of length two, specifying the limits of the color scale. Scores > max(score.cap) or < min(score.cap) will be set to score.cap. Default: c(-5,5)
- **ylab**: character, y-axis label.
**Value**

list with two elements, 1. image.html: a character string with html code with the image tag referring to the output png 2. row.order: integer vector with the row.order obtained after hierarchical clustering or NULL if no clustering was performed

**Author(s)**

Thomas Sandmann

---

**Description**

This S4 method dispatches a gCMap analysis and selects a suitable gene-set-enrichment analysis method based on the class of its arguments.

**Usage**

cmapRun(user.input, cmap, ...)

## S4 method for signature 'CMAPCollection,CMAPCollection'
cmapRun(user.input, cmap)

## S4 method for signature 'GeneSet,CMAPCollection'
cmapRun(user.input, cmap, ...)

## S4 method for signature 'GeneSet,eSet'
cmapRun(user.input, cmap, ...)

## S4 method for signature 'CMAPCollection,eSet'
cmapRun(user.input, cmap, lower = getOption("lower.threshold", default = -3), higher = getOption("higher.threshold", default = 3), element = getOption("element", default = "z"), min.set.size = getOption("min.set.size", default = 5), keep.scores = TRUE)

## S4 method for signature 'SignedGeneSet,eSet'
cmapRun(user.input, cmap, element = getOption("element", default = "z"))

## S4 method for signature 'eSet,CMAPCollection'
cmapRun(user.input, cmap, element = getOption("element", default = "z"))

## S4 method for signature 'eSet,eSet'
cmapRun(user.input, cmap, lower = getOption("lower.threshold", default = -3), higher = getOption("higher.threshold", default = 3), element = getOption("element", default = "z"))
Arguments

user.input An object of class GeneSet, SignedGeneSet, eSet or CMAPCollection with the user-provided query.
cmap The reference database, a CMAPCollection or eSet object.
... Arguments specific to individual methods
lower Numeric, when reference databases are thresholded, genes with scores less than 'lower' are considered down-regulated. Default: getOption( "lower.threshold", default="-3")
higher Numeric, when reference databases are thresholded, genes with scores larger than 'higher' are considered up-regulated. Default: getOption( "higher.threshold", default="3")
element Character, specifying which channel / assayDataElement of the reference database to query. Default: getOption( "element", default="z")
min.set.size integer, gene sets with less than min.set.size members will be dropped from CMAPCollections. Default: getOption( "min.set.size", default=5)
keep.scores Scalar boolean, include scores in the result object?

Details

The cmapRun methods choose one of three approaches for gene-set-enrichment analyses, depending on the nature of the user-provided query and the data available in the reference databases.

1. for non-directional gene set queries (e.g. a list of gene identifiers) a Fisher exact test is performed (with a call to the fisher_score method from the gCMAP package) to evaluate the overlap with significantly up- or down-regulated gene sets from the reference database. If the reference object is an NChannelSet, it is thresholded on the fly to obtain a set of up- or down-regulated genes. If the reference database is a CMAPCollection, the gene sets are used directly. Please note that the Fisher exact test does not take into account information about the directionality of gene regulation (potentially) available in the reference database.

2. for directional gene set queries (e.g. two separate lists of up- and down-regulated genes of interest) the gene expression scores available in the reference database are summarized as the JG score by running the gsealm_jg_score method from the gCMAP package.

3. for queries with complete differential gene expression profiles, directional gene sets are induced from the reference database. As above, the JG score is used to summarize the expression changes for each gene set, but this time the sets are derived from the database, while the scores are provided by the user.

This method is called by the cmapAnalysis function of the gCMAPWeb package.

Please note: Most of the parameters of the cmapRun methods can be set as global options.

Value

A CMAPResults object

See Also

gsealm_jg_score and fisher_score
convert_gene_identifiers

Description
This function maps the submitted gene identifiers to Entrez identifiers and returns a translation table with the original and mapped ids.

Usage
convert_gene_identifiers(gene.ids, query.IdType, species)

Arguments
- gene.ids Character vector with gene ids
- query.IdType A GeneIdentifierType object
- species String identifying the species, will be inserted into a new EntrezIdentifier object and returned with the translated results

Author(s)
Thomas Sandmann
A list with the following elements
- gene.ids, a character vector of unique EntrezIds
- query.IdType, an EntrezIdentifier object with the species
- conversion, a list containing the full translation table and a summary message
- original.ids, a character vector of the submitted ids corresponding to the returned EntrezIds

create_figure_legend

This function generates the figure legend, with a separate dom identifier for each output panel

description

This function generates the figure legend, with a separate dom identifier for each output panel

Usage
create_figure_legend(reference.name)

Arguments
- reference.name, character, name of the reference database used

Value
character string with the html code element required to insert the figure legend into the html report

Author(s)
Thomas Sandmann

create_GeneIdentifierType
GeneIdentifierType creator

Description
This function extracts the species or platform information from the POST request and constructs GeneIdentifierType objects

Usage
create_GeneIdentifierType(post, conf_data)
create_gene_report

Arguments

post list, POST component of the Rook request
conf_data list, the configuration data as returned by the read_config_file function

Value

GeneIdentifierType object

Author(s)

Thomas Sandmann

create_GeneSet GeneSet creator

Description

This function creates a GeneSet object from user-specified identifiers

Usage

create_GeneSet(post, conf_data)

Arguments

post list, POST component of the Rook request
conf_data list, the configuration data as returned by the read_config_file function

Value

GeneSet object

Author(s)

Thomas Sandmann

create_gene_report This function compiles a gene-level report from a CMAPResults object.

Description

Usually called by the generate_report function

Usage

create_gene_report(cmap.result, query, result.dir, url.base, reference.cmap, figure.dir, element = getOption("element", default = "z"), annotation.db = "org.Hs.eg.db", gene.level.plot = getOption("gene.level.plot", default = TRUE))
create_gene_table_legend

Arguments

- cmap.result: a CMAPResults object
- query: a GeneSet, SignedGeneSet or ExpressionSet object used as query for the gene-set-enrichment analysis giving rise to `cmap.result`
- result.dir: character, path to gene_results folder in the per-session output directory
- url.base: character, the name of the reference database
- reference.cmap: eSet, the reference database used for the gCMAP analysis
- figure.dir: character, path to figure folder in the per-session output directory
- element: character, the assayDataElementName to extract from NChannelSet objects
- annotation.db: character, the name of the annotation package used to lookup gene identifiers
- gene.level.plot: logical: should gene-level plots be included in the report?

Value

character string with the relative url to the report html, which is directly written to disk.

Author(s)

Thomas Sandmann

create_gene_table_legend

This function reads an eSet object and returns the html code to display a legend for all columns that have more descriptive annotations in the varMetadata slot.

Description

This function reads an eSet object and returns the html code to display a legend for all columns that have more descriptive annotations in the varMetadata slot.

Usage

create_gene_table_legend(col.names, eset)

Arguments

- col.names: character, a vector with column names that are always included in the legend
- eset: eSet object

Value

character string with the html code element required to insert the legend into the html report

Author(s)

Thomas Sandmann
create_heatmap_legend  Legend for overview heatmap

Description
Content for the legend of the overview heatmap plot displayed on the main results page for directional and non-directional queries

Usage
create_heatmap_legend(text)

Arguments
text Character, text for the legend of the density plot the main report page. Can be set as the global variable "gene.set.legend".

Value
Character

Author(s)
Thomas Sandmann

create_legend This function reads a CMAPResults object and returns the html code to display a legend for all columns that have more descriptive annotations in the varMetadata slot. A standard set of columns is selected for display in the legend through the 'keep' parameter. In addition, all columns with annotations in the labelDescription field of the varMetadata slot are included if the field content differs from the column name.

Description
This function reads a CMAPResults object and returns the html code to display a legend for all columns that have more descriptive annotations in the varMetadata slot. A standard set of columns is selected for display in the legend through the 'keep' parameter. In addition, all columns with annotations in the labelDescription field of the varMetadata slot are included if the field content differs from the column name.

Usage
create_legend(res, reference.name, keep = c("set", "trend", "FDR", "effect", "nSet", "Genes"), swap.colnames = getOption("swap.colnames", default = list(padj = "FDR", nFound = "Genes")))
create_overview_legend

Legend for overview density plot

Description

Content for the legend of the overview density plot displayed on every main results page

Usage

create_overview_legend(text)

Arguments

text Character, text for the legend of the density plot the main report page. Can be set as the global variable "gene.set.legend".

Value

Character

Author(s)

Thomas Sandmann
create_overview_plot

Description

This function creates an overview density plot summarizing the similarity scores obtained for all instances in the reference database.

Usage

create_overview_plot(effect.sample, effect.population, file.name, reference.name, main = "Distribution of similarity scores", xlab = "Effect size", col.set = "black", col.up = "#1B9E77", col.down = "blue", strip.cutoffs = c(-3, 3), strip.bounds = c(-6, 6), strip.col = c("#1B9E77", "white", "blue"), url.base = NULL, up.label = "Correlated", down.label = "Anti-correlated")

Arguments

effect.sample numeric, the scores for all gene sets in the reference database deemed significantly similar
effect.population numeric, the scores for all gene sites in the reference database
file.name character, path and name of the output file
reference.name name of the reference database
main main title of the plot
xlab x-axis label
col.set color used for the significant samples in the density plot
col.up color used to indicate significantly correlated/enriched gene sets in the rug plot
col.down color used to indicate significantly anti-correlated/depleted gene sets in the rug plot
strip.cutoffs numeric vector, indicating the area of the heat-strip set to the intermediate strip.col. Default=c(-3,3)
strip.bounds numeric vector, indicating the cutoffs above/below which the color of the heat-strip is set to maximum. Default=c(-6,6)
strip.col character vector with three elements, indicating high, neutral and low scores, respectively. Default=c("#1B9E77", "white", "blue")
url.base path the location of the output files relative to the gCMAPWeb home directory
up.label character, legend label for positive scores
down.label character, legend label for negative scores

Value

None. Pdf and png versions of the overview file are written to file.

Author(s)

Thomas Sandmann
**create_profile_ExpressionSet**  
*ExpressionSet creator*

### Description
This function creates an ExpressionSet object from user-specified identifiers and scores.

### Usage
```r
create_profile_ExpressionSet(post, conf_data)
```

### Arguments
- **post**: list, POST component of the Rook request
- **conf_data**: list, the configuration data as returned by the read_config_file function

### Value
ExpressionSet object

### Author(s)
Thomas Sandmann

---

**create_query_objects**  
*Query object creator*

### Description
This function generates an appropriate R data object from the user query

### Usage
```r
create_query_objects(post, conf_data)
```

### Arguments
- **post**: list, POST component of the Rook request
- **conf_data**: list, the configuration data as returned by the read_config_file function

### Value
one of GeneSet, SignedGeneSet or ExpressionSet

### Author(s)
Thomas Sandmann
create_SignedGeneSet  SignedGeneSet creator

Description

This function creates a SignedGeneSet object from user-specified identifiers.

Usage

create_SignedGeneSet(post, conf_data)

Arguments

post list, POST component of the Rook request
conf_data list, the configuration data as returned by the read_config_file function

Value

SignedGeneSet object

Author(s)

Thomas Sandmann

create_tab  Create tab-delimited output

Description

This function exports results in tab-delimited format

Usage

create_tab(df, result.dir, url.base = NULL, file.name)

Arguments

df data.frame
result.dir character, path to the output directory
url.base character, the name of the reference database
file.name character, name of the report file

Value

character string with the html code pointing to the download URL

Author(s)

Thomas Sandmann
create_zip

Export gCMAPWeb report as zip archive

Description
This function exports the complete report in a zip file.

Usage
create_zip(tmp_filename, out.dir)

Arguments
- tmp_filename: character, name of the per-session result directory to be archived.
- out.dir: character, output directory to save zip archive into.

Value
Nothing, the zip archive is written to disk.

Author(s)
Thomas Sandmann

entrez_GeneSets
GeneSet Entrez mapper

Description
This function maps the gene identifiers of a GeneSet object to Entrez identifiers and returns an error if none of them could be found.

Usage
entrez_GeneSets(gs)

Arguments
- gs: GeneSet or SignedGeneSet

Details
gCMAPWeb uses this function to ensure that all submitted / retrieved Entrez Ids are valid.

Value
GeneSet or SignedGeneSet

Author(s)
Thomas Sandmann
exampleCMAP

Generate example NChannelSets

Description

This function generates NChannelSets from randomly selected gene identifiers and scores. Scores of the first (simulated) sample will be shifted up by the amount specified by the 'add' parameter for the first 50 genes and down by the same amount for genes 51-100.

Usage

exampleCMAP(universe = "org.Hs.eg.db", idType = "ENTREZID", rows = 1000, cols = 20, seed = 123, add = 3)

Arguments

universe character, the name of an available annotation package. Default=org.Hs.eg.db
idType character, a valid identifier type supported by the selected annotation package. Default=ENTREZID
rows integer, the number of genes to sample. Default=1000
cols integer, the number of samples to generate. Default=20
seed numeric, seed for the random number generator. Default=123
add numeric, score shift for scores in the first sample column. Scores for genes 1-50 will be shifted up, those for genes 51-100 down.

Details

This function is mainly intended for testing purposes.

Value

NChannelSet with simulated scores.

Author(s)

Thomas Sandmann

Examples

```r
## generate example NChannelSet with 100 features and 10 columns
## for human EntrezIds
if( require( "org.Hs.eg.db", character.only=TRUE)){
  e <- exampleCMAP( universe="org.Hs.eg.db", rows=100, cols=10)
  dim( e )
  head( featureNames( e ))
  assayDataElementNames( e )
  ## or gene symbols
  s <- exampleCMAP( universe="org.Hs.eg.db", idType="SYMBOL")
  head( featureNames( s ))
}
```
examplePost

Simulate POST request

Description
This function returns a simulated POST request, similar to those generated from user-input into the web interface.

Usage
examplePost(cmap, inputType = "non-directional", species = "human", array.platform = NULL, idType = "entrez", rows = 1000, add = 3, seed = 123)

Arguments
- cmap: NChannelSet object, e.g. generated by the exampleCMAP function
- inputType: character, one of directional, non-directional, profile
- species: character, should match a species supported by the loaded gCMAPWeb configuration file
- array.platform: character, should match an array platform supported by the loaded gCMAPWeb configuration file
- idType: character, one of entrez, symbol or probe
- rows: integer, number of genes to include in a 'profile' query.
- add: numeric, score shift for scores in the first sample column. Scores for genes 1-50 will be shifted up, those for genes 51-100 down. Only used to simulate 'profile' queries.
- seed: numeric, seed for the random number generator. Default=123

Details
This function is mainly intended for testing purposes.

Value
list, containing the same elements as a gCMAPWeb POST request

Author(s)
Thomas Sandmann

Examples
```r
if( require("org.Hs.eg.db", character.only=TRUE)){
  ## generate an example NChannelSet for human EntrezIds
  e <- exampleCMAP( universe="org.Hs.eg", rows=1000, cols=10)
  ## generate a matching example Post, simulating a non-directional query
  examplePost( cmap=e )
  ## or a directional query
  examplePost( cmap=e, inputType="directional")
}
```
gCMAPWeb

Start local gCMAPWeb instance

Description
This function starts a gCMAPWeb instance on the local machine using R's internal web server.

Usage

```r
gCMAPWeb(config.file.path = system.file("config", "config.yml", package = "gCMAPWeb"), url.root = system.file("htdocs", package = "gCMAPWeb"))
```

Arguments

- `config.file.path` character, path to a gCMAPWeb configuration file in yaml format
- `url.root` character, path to the htdocs folder

Value
an Rhttpd class object

Author(s)
Thomas Sandmann

Examples

```r
if (interactive()) {
  ## start a gCMAPWeb instance with the example data and
  ## configuration provided in the package
  gCMAPWeb()
  ## same as above, explicitely specifying the location
  ## of the configuration file
  gCMAPWeb(
    config.file.path = system.file("config", "config.yml",
                              package = "gCMAPWeb")
  )
}
```

---

generate_report

gCMAPWeb reporting function

Description
This function receives the results of a gene-set enrichment analysis and the original reference databases to generate plots and html code elements for the final report.
generate_report

Usage

generate_report(cmap.result, reference, reference.name, annotation.db, element, query, tmp_filename, title = "", max.results = getOption("max.results", default = 50), min.found = getOption("min.found", default = 1), max.padj = getOption("max.padj", default = 0.1), gene.level.report = getOption("gene.level.report", default = TRUE), gene.level.plot = getOption("gene.level.plot", default = TRUE), reportDirectory = tempdir(), excluded.cols = getOption("excluded.cols", default = c("geneScores", "signed", "pval", "UID", "z.shift", "log_fc.shift", "mod_fc.shift")), swap.colnames = getOption("swap.colnames", default = list(padj = "FDR", nFound = "Genes"))

Arguments

cmap.result CMAPResults object
reference eSet object, the full reference database, typically an NChannelSet or CMAPCollection object
reference.name character, the name of the reference database
annotation.db character, the name of the annotation package used to lookup gene identifiers
element character, the assayDataElementName to extract from NChannelSet objects
query a GeneSet, SignedGeneSet or ExpressionSet object used as query for the gene-set-enrichment analysis giving rise to 'cmap.result'
tmp_filename character, the name of the temporary output folder
title character, title of the report
max.results integer, maximum number of results to return
min.found integer, minimum number of gene set members that need to overlap with the user query. Gene sets with matching members less than min.found will not be returned as results.
max.padj numeric, maximum adjusted p-value for a gene set to be considered significantly similar. Results with adjusted p-values larger than max.padj will not be returned.
gene.level.report logical, create gene-level reports?
gene.level.plot logical, create gene-level plots?
reportDirectory character, path to temporary output directory for this session. Default=tempdir()
excluded.cols character vector listing columns in the CMAPResults objects that should NOT be included in the report
swap.colnames list, containing alternative names for CMAPResults columns.

Details

This function is called by the cmapAnalysis function

Value

a list of character strings, either containing html code snippets or paths to result files. These elements are used to brew the final result html page.
**gene_density_profile_legend**

*Html code for the legend of the density charts of the gene-level reports from Profile queries*

**Description**

Html code for the legend of the density charts of the gene-level reports from Profile queries

**Usage**

gene_density_profile_legend(text)

**Arguments**

text Character, text for the legend of the density plot on gene-level reports for profile queries. Can be set as the global variable "gene.profile.legend".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

**gene_density_chart_legend**

*Html code for the legend of the pie chart of the gene-level report*

**Description**

Html code for the legend of the pie chart of the gene-level report

**Usage**

gene_density_chart_legend(text)

**Arguments**

text Character, text for the legend of the density plot on gene-level reports for non-directional and directional queries. Can be set as the global variable "gene.density.legend".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann
gene_pie_chart_legend  *Html code for the legend of the pie chart of the gene-level report*

---

**Description**

Html code for the legend of the pie chart of the gene-level report

**Usage**

`gene_pie_chart_legend(text)`

**Arguments**

- **text**
  
  Character, text for the legend of the pie chart on gene-level reports for non-directional queries. Can be set as the global variable "gene.pie.legend".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

hide_species_js  *Javascript code to hide html elements*

---

**Description**

Javascript code to hide html elements for all but the first species listed in the configuration file

**Usage**

`hide_species_js(conf_data)`

**Arguments**

- **conf_data**
  
  list, the configuration data as returned by the `read_config_file` function

**Value**

javascript call as character string

**Author(s)**

Thomas Sandmann
Description
Closing html code, including references to jQuery, Bootstrap and DataTables JavaScript libraries.

Usage
html_body_last(url.base = NULL)

Arguments
url.base character, path to htdocs directory (optional)

Value
Html code as character string

Author(s)
Thomas Sandmann

Description
Html header including link to the Bootstrap Cerulean CSS stylesheet.

Usage
html_header(url.base = NULL)

Arguments
url.base character, path to htdocs directory (optional)

Value
Html code as character string

Author(s)
Thomas Sandmann
html_table

Format data.frame as html table

Description
Function to format a data.frame as an html table

Usage
html_table(df, table_id)

Arguments
df A data frame
table_id Character, specifying the id tag for the html table

Details
This function uses the thead and tbody tags required for the dataTables javascript to create interactive html tables.

Value
Html code as a character string.

Author(s)
Thomas Sandmann

identifier_radio_html
Html code for identifier type radio button selectors

Description
This function generates the html code required to display radio buttons for the supported identifier types specified in the gCMAPWeb configuration file

Usage
identifier_radio_html(conf_data, single = FALSE)

Arguments
conf_data list, the configuration data as returned by the read_config_file function
single, logical, use singular nouns for radiobutton labels?

Value
Html code as character string.
index_message

Html code for text of the additional message on the index page (warning box)

Description

Html code for text of the additional message on the index page (warning box)

Usage

index_message(text)

Arguments

text Character, text for the additional message on the index page (warning box)

Value

text Character string with html code

Author(s)

Thomas Sandmann

index_quote

Html code for quote on the index page

Description

Html code for quote on the index page

Usage

index_quote(text)

Arguments

text Character, the content of the blockquote field on the index.rhtml page. Can be set as the global variable "index.quote".

Value

Character string with html code

Author(s)

Thomas Sandmann
index_subtitle

**Description**

Html code for subtitle of the hero unit of the index.rhtml page

**Usage**

`index_subtitle(text)`

**Arguments**

- **text**: Character, subtitle of the hero unit on the index.rhtml page. Can be set as the global variable "index.sub".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

index_text

**Description**

Html code for text of the hero unit of the index.rhtml page

**Usage**

`index_text(text)`

**Arguments**

- **text**: Character, text of the hero unit on the index.rhtml page. Can be set as the global variable "index.text".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann
**index_title**

*Html code for title of the hero unit of the index.rhtml page*

**Description**

Html code for title of the hero unit of the index.rhtml page

**Usage**

```r
index_title(text = getOption("index.main", default = "gConnectivity Map"))
```

**Arguments**

- `text`: Character, main title of the hero unit on the index.rhtml page. Can be set as the global variable "index.main".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

**inputType_buttons**

*Html code for query type selection buttons on the gCMAPWeb index page*

**Description**

This function generates the html code required to generate the query type selection buttons on the main index.rhtml page

**Usage**

```r
inputType_buttons(conf_data)
```

**Arguments**

- `conf_data`: list, the configuration data as returned by the read_config_file function

**Value**

Html code as character string.

**Author(s)**

Thomas Sandmann
load_cmaps

Description

This function connects to / loads all reference datasets and returns them in a list

Usage

load_cmaps(conf_data, min.set.size = getOption("min.set.size", default = 5))

Arguments

conf_data list, the configuration data as returned by the read_config_file function
min.set.size integer, gene sets with less than min.set.size members will be dropped from CMAPCollections

Value

list of eSet objects

Author(s)

Thomas Sandmann

Examples

library(yaml)
## read the example configuration file
conf_data <- yaml.load_file( system.file("config", "config.yml", package="gCMAPWeb") )
## load the example reference NChannelSet objects specified in
## the configuration file
ref.cmaps <- load_cmaps( conf_data )
class( ref.cmaps )
names( ref.cmaps )
ref.cmaps[[1]]

parse_file_input

Description

This functions parses the user-uploaded files

Usage

parse_file_input(temp.file, regexp = "[+;\t ]+", n.score.col = 1)
parse_request

Arguments

temp.file character, path to temporary file (usually part of the POST request)
regexp character, a regular expression matching all separators used to separate gene identifiers
n.score.col integer, for profile uploads n.score.col specifies the number of data columns (usually 1)

Value

list of character vectors, one element for each row of temp.file

Author(s)

Thomas Sandmann

parse_request POST request parser

Description

This function parses the a POST request and decodes the user-provided information

Usage

parse_request(request, conf_data,
cmaps.concatenated.by = getOption("cmaps.concatenated.by", default = ",")("))

Arguments

request Request object as defined by the Rook package
conf_data list, the configuration data as returned by the read_config_file function
cmaps.concatenated.by character, specifying the separator (e.g. semicolon, comma) used to concatenate multiple requested reference databases

Value

list, all elements from POST request, decoded if necessary

Author(s)

Thomas Sandmann
**parse_textarea_input**

**Textarea parser**

**Description**

This function parses user-specified data pasted into the textarea fields of the input form.

**Usage**

```
parse_textarea_input(textarea.input, regexp = "[+,;\t ]+"
```

**Arguments**

- `textarea.input`: character, the user-input extracted from the POST request.
- `regexp`: character, a regular expression matching all separators used to separate gene identifiers.

**Value**

List of character vectors, one element for each original row of textarea.input.

**Author(s)**

Thomas Sandmann

---

**platform_radio_html**

**Html code for platform radio button selectors**

**Description**

This function generates the html code required to display radio buttons for all array platforms specified in the gCMAPWeb configuration file.

**Usage**

```
platform_radio_html(conf_data)
```

**Arguments**

- `conf_data`: list, the configuration data as returned by the read_config_file function.

**Value**

Html code as character string.

**Author(s)**

Thomas Sandmann
process_score_input  Score parser

Description
This function reformats score input uploaded or pasted by the user

Usage
process_score_input(query_data, n.score.col = 1)

Arguments
query_data  list of row-vectors, as generated by parse_file_input function
n.score.col  integer, specifies the number of data columns (usually 1)

Value
matrix of expression scores

Author(s)
Thomas Sandmann

profile_input_example  Html code for generating an example query button on the profile submission page

Description
Content can be provided / modified through the global parameters profile.input.example.popover (text for popover help) profile.input.example (gene identifiers and scores)

Usage
profile_input_example()

Value
Character string with html code

Author(s)
Thomas Sandmann
read_config_file

Parser for gCMAPWeb configuration file

Description
This function parses the gCMAPWeb configuration file (in yaml format) and returns the information as a list.

Usage
read_config_file(config.file.path = system.file("config", "config.yml", package = "gCMAPWeb"))

Arguments
config.file.path
character, full path to gCMAPWeb configuration file

Value
a nested list

Author(s)
Thomas Sandmann

reference_radio_html
Html code for reference cmap radio button selectors

Description
This function generates the html code required to display radio buttons for the reference datasets specified in the gCMAPWeb configuration file.

Usage
reference_radio_html(conf_data, reference.cmaps)

Arguments
conf_data
list, the configuration data as returned by the read_config_file function
reference.cmaps
list containing all reference cmaps as eSet-like objects (e.g. NChannelSet, CMAP-Collection)

Value
Html code as character string.

Author(s)
Thomas Sandmann
## retrieve_annotation

*Gene symbol and name lookup*

**Description**

This function retrieves the official gene symbol and name for Entrez identifiers.

**Usage**

`retrieve_annotation(entrez, annotation.db)`

**Arguments**

- `entrez` character, Entrez identifier to look up
- `annotation.db` character, name of the annotation package to use for lookup

**Value**

data.frame with entrez, symbol and name columns

**Author(s)**

Thomas Sandmann

## signed_input_example

*Html code for generating and example query button on the signed gene set submission page*

**Description**

Content can be provided / modified through the global parameters `signed.input.example.popover` (text for popover help), `signed.input.example.up` (up-regulated gene identifiers), `signed.input.example.down` (down-regulated gene identifiers).

**Usage**

`signed_input_example()`

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann
single_input_example

**Description**

Content can be provided / modified through the global parameters single.gene.example.popover (text for popover help) single.gene.example (gene identifiers)

**Usage**

single_input_example()

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

species_radio_html

**Description**

This function generates the html code required to display radio buttons for all species specified in the gCMAWEB configuration file.

**Usage**

species_radio_html(conf_data)

**Arguments**

- conf_data : list, the configuration data as returned by the read_config_file function

**Value**

Html code as character string.

**Author(s)**

Thomas Sandmann
### stripPrefix

**Description**

This function strips a prefix from gene identifier strings.

**Usage**

```r
stripPrefix(ids, prefix = c("^GeneID:", "^GeneID"))
```

**Arguments**

- `ids` character, vector of gene identifiers
- `prefix` character, one or more strings to be removed

**Value**

character, gene identifiers without prefix

**Author(s)**

Thomas Sandmann

---

### unsigned_input_example

**Description**

Html code for generating and example query button on the unsigned gene set submission page.

**Usage**

```r
unsigned_input_example()
```

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann
validate_config_file

Validation of gCMAPWeb configuration file

Description

This function validates the content of the gCMAPWeb configuration file.

Usage

validate_config_file(config.file.path)

Arguments

config.file.path
  full path to gCMAPWeb configuration file (in yaml format)

Details

Verifies that 1. all required fields are present 2. at least one species has been defined 3. all supported annotation packages are available 4. all cmaps have unique labels 5. each supported species has at least one associated reference dataset

Value

Information from a valid configuration file is returned as a nested list. Invalid entries in the config file with cause an error.

Author(s)

Thomas Sandmann

Examples

```r
## read the example configuration yaml file without validation
library(yaml)
conf1 <- yaml.load_file( system.file("config", "config.yml", package="gCMAPWeb") )
## read the example configuration file and validate that
## all required information is provided and valid
conf2 <- validate_config_file( system.file("config", "config.yml", package="gCMAPWeb") )
identical( conf1, conf2)
```
validate_request

**Description**

This function extracts the content from a POST request and validates its content.

**Usage**

```r
cbind_request(req, conf_data,
cmaps.concatenated.by = getOption("cmaps.concatenated.by", default = ",",))
```

**Arguments**

- `req`: Request object as defined by the Rook package.
- `conf_data`: list, the configuration data as returned by the `read_config_file` function.
- `cmaps.concatenated.by`: character, specifying the separator (e.g. semicolon, comma) used to concatenate multiple requested reference databases.

**Value**

Logical, TRUE if all required fields could be validated, FALSE otherwise.

**Author(s)**

Thomas Sandmann
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