Package ‘gCMAPWeb’

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Type Package

Title A web interface for gene-set enrichment analyses

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Description The gCMAPWeb R package provides a graphical user interface for the gMAP 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.

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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, hgfocus.db, hgu133a.db, mgug4104a.db, org.Hs.eg.db, org.Mm.eg.db, RUnit
Enhances  bigmemory, bigmemoryExtras
bioViews  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'
RoxygenNote  5.0.1
NeedsCompilation  no

R topics documented:

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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 of deployed through an Apache2 webserver, gCMAPWeb allows users to search reference datasets stored in NChannelSet or 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.
Author(s)

Thomas Sandmann

References


Examples

example( gCMAPWeb )

addLinks

Adding links to columns of a data.frame

Description

This function identifies column pairs from a data.frame that differ only in a string suffix (default: .url). The column with the suffix is used to add http href tags to the other column and is then removed.

Usage

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("\"\")

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
cmap-data  

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
- row.order: integer vector with the row.order obtained after hierarchical clustering or NULL if no clustering was performed

Author(s)

Thomas Sandmann

cmapRun

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
**conversion_html**  
*Identifier conversion html output*

**Description**

This function formats a data.frame with the results of the gene identifier conversion to html code, including an interactive dataTable. The html page is saved to disk and the path to the output file is returned as a character string.

**Usage**

```r
conversion_html(df, result.dir, file.name, tmp_filename, url.base = NULL, message = NULL)
```

**Arguments**

- `df`: data.frame with old/new gene identifiers
- `result.dir`: character, path to result directory
- `file.name`: character, output filename
- `tmp_filename`: character, name of the session-specific subdirectory
- `url.base`: character, path to htdocs directory (optional)
- `message`: character, optional message to display above the result table

**Value**

character, name of the output html file

**Author(s)**

Thomas Sandmann

---

**convert_gene_identifiers**  
*Entrez mapper*

**Description**

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

**Usage**

```r
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
Value
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

Author(s)
Thomas Sandmann

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**

```r
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**

```r
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

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_legend

Arguments

res CMAPResults object
reference.name character, name of the reference database used
keep character, a vector with column names that are always included in the legend
swap.colnames list, containing alternative names for CMAPResults columns.

Value

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

Author(s)

Thomas Sandmann
create_overview_plot  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 intermediat 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
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
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
```r
eexamplePost(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, explicitly 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.
Usage

```r
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.
Author(s)
Thomas Sandmann

gene_density_profile_legend

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>text</td>
<td>Character, text for the legend of the density plot on gene-level reports for profile queries. Can be set as the global variable &quot;gene.profile.legend&quot;.</td>
</tr>
</tbody>
</table>

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
### html_body_last

**Description**
Closing html code, including references to jQuery, Bootstrap and DataTables JavaScript libraries

**Usage**

```r
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

### html_header

**Description**
Html header including link to the Bootstrap cerulean CSS stylesheet

**Usage**

```r
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**

```r
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**

```r
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

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

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

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

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**

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**

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**

*Loading reference datasets*

**Description**

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

**Usage**

```r
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**

```r
temporary <- read_config_file()
ref.cmaps <- load_cmaps( conf_data )
```

---

**parse_file_input**

*Uploaded file parser*

**Description**

This functions parses the user-uploaded files

**Usage**

```r
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

**Description**

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

**Usage**

```r
code
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**

```r
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**

```r
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**
```r
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**
```r
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**

```r
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**

```r
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
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

Description

This function generates the html code required to display radio buttons for all species specified in the gCMAPWeb 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

Strip prefix from gene identifier names

Description
This function strips a prefix from gene identifier strings

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

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

Usage
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 will 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

validate_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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