

# Package ‘gCMAPWeb’

October 17, 2017

**Type** Package

**Title** A web interface for gene-set enrichment analyses

**Version** 1.16.0

**Date** 2017-01-19

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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 (>= 3.4), Rook

**Imports** brew, BiocGenerics, annotate, AnnotationDbi, graphics, grDevices, GSEABase, hwriter, parallel, stats, utils, yaml

**Suggests** affy, ArrayExpress, hgfocus.db, hgu133a.db, mgug4104a.db, org.Hs.eg.db, org.Mm.eg.db, RUnit

**Enhances** bigmemory, bigmemoryExtras

**biocViews** GUI, GeneSetEnrichment, Visualization, GeneExpression, Transcription, Microarray, DifferentialExpression

**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

**OS\_type** unix

**NeedsCompilation** no

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gCMAPWeb-package	<i>A web-interface for gene-set enrichment analysis</i>
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## 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 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**

Jiang Z, Gentleman R., Extensions to gene set enrichment. *Bioinformatics*. 2007 Feb 1;23(3):306-13 <http://www.ncbi.nlm.nih.gov/pubmed/17127676>

**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('.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

---

cmap-data	<i>Example reference datasets</i>
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---

### 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	<i>Function controlling the gCMAP analysis workflow</i>
--------------	---

---

### 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

<code>req</code>	a Rook Request object
<code>conf_data</code>	list, the configuration data as returned by the <code>read_config_file</code> function
<code>reference.cmaps</code>	list, containing the reference database <code>eSet</code> objects
<code>element</code>	character, identifying the <code>elementName</code> of the channel extracted from <code>NChannelSet</code> objects
<code>save.intermediates</code>	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`

**Author(s)**

Thomas Sandmann

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**

```
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",over="firebrick",under="grey95"))
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 thw row.order obtained after hierarchical clustering or NULL if no clustering was performed

**Author(s)**

Thomas Sandmann

---

cmapRun

*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: <code>getOption("lower.threshold", default="-3")</code>
higher	Numeric, when reference databases are thresholded, genes with scores larger than 'higher' are considered up-regulated. Default: <code>getOption("higher.threshold", default="3")</code>
element	Character, specifying which channel / assayDataElement of the reference database to query. Default: <code>getOption("element", default="z")</code>
min.set.size	integer, gene sets with less than min.set.size members will be dropped from CMAPCollections. Default: <code>getOption("min.set.size", default=5)</code>
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

```
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

```
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)
```

**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))
```

**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 variabel "gene.set.legend".

### Value

Character

### Author(s)

Thomas Sandmann

---

create_legend	<i>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.</i>
---------------	---

---

### 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")))
```

**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\_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 variabel "gene.set.legend".

**Value**

Character

**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 dabatase
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	<i>Export gCMAPWeb report as zip archive</i>
------------	--

---

**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	<i>GeneSet Entrez mapper</i>
-----------------	------------------------------

---

**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**

```
## 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	<i>Simulate POST request</i>
-------------	------------------------------

---

### 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

```
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**

```
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**

```
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**

```
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\_chart\_legend

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

---

**Description**

Html code for the legend of pie 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 variabel "gene.density.legend".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

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 variabel "gene.profile.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 variabel "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	<i>Html footer</i>
----------------	--------------------

---

**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

---

html_header	<i>Html header and bootstrap css stylesheet</i>
-------------	---

---

**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 a character string

**Author(s)**

Thomas Sandmann

---

html_table	<i>Format data.frame as html table</i>
------------	--

---

**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	<i>Html code for identifier type radio button selectors</i>
-----------------------	---

---

**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.

**Author(s)**

Thomas Sandmann

---

index_message	<i>Html code for text of the additional message on the index page (warning box)</i>
---------------	---

---

**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	<i>Html code for quote on the index page</i>
-------------	--

---

**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 variabel "index.quote".

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

index_subtitle	<i>Html code for subtitle of the hero unit of the index.rhtml page</i>
----------------	--

---

**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 variabel "index.sub".
------	--

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

index_text	<i>Html code for text of the hero unit of the index.rhtml page</i>
------------	--

---

**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 variabel "index.text".
------	---

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

index_title	<i>Html code for title of the hero unit of the index.rhtml page</i>
-------------	---

---

**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 variabel "index.main".
------	---

**Value**

Character string with html code

**Author(s)**

Thomas Sandmann

---

inputType_buttons	<i>Html code for the query type selection buttons on the gCMAPWeb index page</i>
-------------------	--

---

**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	<i>Loading reference datasets</i>
------------	-----------------------------------

---

**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	<i>Uploaded file parser</i>
------------------	-----------------------------

---

**Description**

This functions parses the user-uploaded files

**Usage**

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

**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	<i>POST request parser</i>
---------------	----------------------------

---

**Description**

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

**Usage**

```
parse_request(request, conf_data,
  cmap.concatenated.by = getOption("cmap.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
cmap.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 *Html code for generating and example query button on the single gene query submission page*

---

**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 *Html code for species radio button selectors*

---

**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	<i>Strip prefix from gene identifier names</i>
-------------	--

---

**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	<i>Html code for generating and example query button on the unsigned gene set submission page</i>
------------------------	---

---

**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 with cause an error.

### **Author(s)**

Thomas Sandmann

### **Examples**

```
## read the example configuration yaml file without validation
library(yaml)
conf1 <- yaml.load_file( system.file("config", "config.yaml",
                                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.yaml",
                                package="gCMAPWeb") )
identical( conf1, conf2)
```

---

validate\_request      *Html request validation*

---

**Description**

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

**Usage**

```
validate_request(req, conf_data,  
  cmap.concatenated.by = getOption("cmap.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  
cmap.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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