

Package ‘CEMiTool’

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Title Finds Gene Co-expression Modules

Version 0.0.0.9000

Description

CEMiTool improves WGCNA gene co-expression module discovery by optimizing network parameter selection. This package also performs enrichment analysis with the discovered modules.

Depends R (>= 3.3.1)

Imports methods,

data.table (>= 1.9.4),

WGCNA,

ggplot2,

clusterProfiler,

fgsea,

stringr,

rmarkdown,

igraph,

ggnetwork,

DT,

htmltools,

pracma

Suggests testthat

Remotes ctfab/fgsea

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 5.0.1

R topics documented:

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cem	<i>CEMiTool Object</i>
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Description

This object, can be used as input for CEMiTool functions

cemitoool	<i>Full gene co-expression analysis</i>
-----------	---

Description

Defines co-expression modules and functionally characterizes each one of them.

Usage

```
cemitoool(expr, annot, gmt, interactions, filter = TRUE, filter_pval = 0.1,
n_genes, cor_method = c("pearson", "spearman"),
sample_name_column = "SampleName", class_column = "Class",
merge_similar = TRUE, split_modules = FALSE, ora_pval = 0.05,
min_nngen = 30, diss_thresh = 0.8, plot = FALSE, directed = FALSE,
verbose = FALSE)
```

Arguments

<code>expr</code>	Gene expression data.frame.
<code>annot</code>	Sample annotation data.frame.
<code>gmt</code>	a list from function <code>prepare_gmt</code> containing the gene sets.
<code>interactions</code>	a data.frame containing two columns with gene names.
<code>filter</code>	logical. If TRUE, will filter expression data.
<code>filter_pval</code>	P-value threshold for filtering.
<code>n_genes</code>	Number of genes left after filtering.
<code>cor_method</code>	A character string indicating which correlation coefficient is to be computed. One of "pearson" or "spearman". Default "pearson".
<code>sample_name_column</code>	A character string indicating the sample column name of the annotation table.
<code>class_column</code>	A character string indicating the class column name of the annotation table.
<code>merge_similar</code>	Logical. If TRUE, merge similar modules.
<code>split_modules</code>	Logical. If TRUE, splits modules by correlation sign.
<code>ora_pval</code>	P-value for overrepresentation analysis. Default 0.05.
<code>min_nngen</code>	Minimal number of genes per submodule. Default 30.
<code>diss_thresh</code>	Module merging correlation threshold for eigengene similarity. Default 0.8.
<code>plot</code>	Logical. If TRUE, plots all figures.
<code>directed</code>	Logical. If TRUE, the igraph objects in interactions slot will be directed.
<code>verbose</code>	Logical. If TRUE, reports analysis steps.

Value

a cemitool object

Examples

```
cemitool(expr=expr)
```

CEMiTool-class

An S4 class to represent the CEMiTool analysis.

Description

An S4 class to represent the CEMiTool analysis.

Slots

- expression Gene expression data.frame.
- sample_annotation Sample annotation data.frame.
- module Genes in modules information data.frame.
- enrichment list with modules enrichment results for sample classes.
- ora Over-representation analysis results data.frame.
- profile_plot list of ggplot graphs with gene expression profile per module.
- enrichment_plot ggplot graph for enrichment analysis results
- barplot_ora list of ggplot graphs with over-representation analysis resultsper module

cemoverlap	<i>Integrates CEMiTool analyses</i>
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Description

Returns the occurence of edges between different analyses

Usage

cemoverlap(analyses)

Arguments

analyses List of objects of class CEMiTool

Examples

```
studies <- list('GSE12345'=cem1, 'GSE54321'=cem2)
overlaps <- cemoverlap(studies)
```

expr	<i>Gene Expression Dataset</i>
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Description

This dataset, together with sample_annotation_data can be used as input for CEMiTool functions

expr_data	<i>Retrieve and set expression attribute</i>
-----------	--

Description

Retrieve and set expression attribute

Usage

```
expr_data(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
expr_data(cem, filtered = T)  
  
expr_data(cem) <- value  
  
## S4 replacement method for signature 'CEMiTool'  
expr_data(cem) <- value
```

Arguments

cem	Object of class CEMiTool
filtered	logical. If TRUE retrieves filtered expression data
value	Object of class data.frame with gene expression data

Value

Object of class data.frame with gene expression data

filter_expr	<i>Filter gene expression table</i>
-------------	-------------------------------------

Description

Filter gene expression table

Usage

```
filter_expr(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
filter_expr(cem, pval = 0.05, n_genes)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
pval	P-value cutoff for gene selection.
n_genes	Number of genes to be selected.

Value

Object of class CEMiTool with selected genes

find_modules	<i>Co-expression modules definition</i>
--------------	---

Description

Defines co-expression modules

Usage

```
find_modules(cem, ...)

## S4 method for signature 'CEMiTool'
find_modules(cem, cor_method = c("pearson", "spearman"),
  min_nngen = 30, merge_similar = T, diss_thresh = 0.8, verbose = F)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
cor_method	A character string indicating which correlation coefficient is to be computed.
min_nngen	Minimal number of genes per submodule. Default 30.
merge_similar	Logical. If TRUE, merge similar modules.
diss_thresh	Module merging correlation threshold for eigengene similarity. Default 0.8.
verbose	Logical. If TRUE, reports analysis steps.

Value

Object of class CEMiTool

Examples

```
cem <- new('CEMiTool', expression=expr)
cem <- find_modules(cem)
```

generate_report	<i>CEMiTool report</i>
-----------------	------------------------

Description

Creates report for CEMiTool results

Usage

```
generate_report(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
generate_report(cem, max_rows_ora = 50,  
  title = "Report", directory = "./reports", ...)
```

Arguments

cem	Object of class CEMiTool.
...	parameters to rmarkdown::render
max_rows_ora	maximum number of rows in Over Representation Analysis table results
title	Character string with the title of the report.
directory	Directory name for results.

get_hubs	<i>Get Hubs</i>
----------	-----------------

Description

Returns n genes in each module with high connectivity.

Usage

```
get_hubs(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
get_hubs(cem, n = 5)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
n	Number of genes to return in each module (default: 5).

Value

A list containing hub genes.

include_interactions	<i>Includes interaction information to CEMiTool object</i>
----------------------	--

Description

Includes interaction information to CEMiTool object

Usage

```
include_interactions(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
include_interactions(cem, int_df, directed = FALSE, ...)
```

Arguments

cem	Object of class CEMiTool.
...	parameters for <code>igraph::graph_from_data_frame</code>
int_df	a data.frame or matrix containing two columns
directed	Is the graph directed ? Default is FALSE

Value

Object of class CEMiTool

mod_colors	<i>Retrieve and set mod_colors attribute</i>
------------	--

Description

Retrieve and set mod_colors attribute

Usage

```
mod_colors(cem)  
  
## S4 method for signature 'CEMiTool'  
mod_colors(cem)  
  
mod_colors(cem) <- value  
  
## S4 replacement method for signature 'CEMiTool'  
mod_colors(cem) <- value
```


Arguments

cem	Object of class CEMiTool
value	a character vector containing colors for each module the names should match with module names

`mod_gsea`*Module Gene Set Enrichment Analysis*

Description

Performs gene set enrichment analysis for each co-expression module found.

Usage

```
mod_gsea(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
mod_gsea(cem, verbose = F)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
verbose	logical. Report analysis steps.

Value

GSEA results.

Examples

```
mod_gsea(cem)
```

mod_ora	<i>Module Overrepresentation Analysis</i>
---------	---

Description

Performs overrepresentation analysis for each co-expression module found.

Usage

```
mod_ora(cem, ...)
```

```
## S4 method for signature 'CEMiTool'
```

```
mod_ora(cem, gmt_in, verbose = FALSE)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
gmt_in	Output of CEMiTool::read_gmt function.
verbose	logical. Report analysis steps.

Value

Object of class CEMiTool

Examples

```
gmt <- read_gmt(system.file('extdata', 'pathways.gmt',
                           package='CEMiTool'))
```

```
mod_ora(cem, gmt)
```

mod_summary	<i>Co-expression module summarization</i>
-------------	---

Description

Summarizes modules using some statistics.

Usage

```
mod_summary(cem, ...)
```

```
## S4 method for signature 'CEMiTool'
```

```
mod_summary(cem, method = c("mean", "eigengene"),
  verbose = F)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
method	A character string indicating which summarization method is to be used. Default 'mean'.
verbose	Logical. If TRUE, reports analysis steps.

Value

A data.frame with summarized values.

Examples

```
mod_summary <- mod_summary(cem)
```

nmodules	<i>Get the number of modules on a cemitoool object</i>
----------	--

Description

Get the number of modules on a cemitoool object

Usage

```
nmodules(cem)

## S4 method for signature 'CEMiTool'
nmodules(cem)
```

Arguments

cem	Object of class CEMiTool
-----	--------------------------

Value

number of modules

plot_gsea	<i>GSEA visualization</i>
-----------	---------------------------

Description

Creates a heatmap with the results of gene set enrichment analysis (GSEA) of co-expression modules

Usage

```
plot_gsea(cem, ...)

## S4 method for signature 'CEMiTool'
plot_gsea(cem, pv_cut = 0.05)
```

Arguments

- cem Object of class CEMiTool.
- ... Optional parameters.
- pv_cut P-value cut-off. Default 0.05

Value

Object of class CEMiTool with GSEA plots

Examples

```
plot_gsea(enrichment)
```

plot_interactions	<i>Network visualization</i>
-------------------	------------------------------

Description

Creates a graph based on interactions provided

Usage

```
plot_interactions(cem, ...)

## S4 method for signature 'CEMiTool'
plot_interactions(cem, n = 10, ...)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
n	number of nodes to label

Value

Object of class CEMiTool with profile plots

Examples

```
plot_interactions(cem)
```

plot_ora	<i>ORA visualization</i>
----------	--------------------------

Description

Creates a bar plot with the results of overenrichment analysis of co-expression modules

Usage

```
plot_ora(cem, ...)  
  
## S4 method for signature 'CEMiTool'  
plot_ora(cem, n = 10, ...)
```

Arguments

cem	Object of class CEMiTool.
...	paramaters to plot_ora_single
n	number of modules to show

Value

Object of class CEMiTool with ORA plots

Examples

```
plot_ora(test)
```

plot_ora_single	<i>ORA visualization for one module</i>
-----------------	---

Description

ORA visualization for one module

Usage

```
plot_ora_single(es, ordr_by = "p.adjust", max_length = 50, pv_cut = 0.01,
  graph_color = "#4169E1", title = "Over Representation Analysis")
```

Arguments

es	a data.frame from ora function containing only one module
ordr_by	column to order the data.frame
max_length	max length of a gene set name
pv_cut	p-value cutoff
graph_color	color of bars
title	title of the graph

Value

a list with ggplot2 object and the number of significant gene sets

Examples

```
plot_ora_single(test)
```

plot_profile	<i>Expression profile visualization</i>
--------------	---

Description

Creates a line plot of each gene inside the module through the samples

Usage

```
plot_profile(cem, ...)

## S4 method for signature 'CEMiTool'
plot_profile(cem, order = TRUE)
```

Arguments

cem	Object of class CEMiTool.
...	Optional parameters.
order	Logical. If TRUE, sorts samples by class.

Value

Object of class CEMiTool with profile plots

Examples

```
plot_profile(cem)
```

read_gmt	<i>Reads a GMT file</i>
----------	-------------------------

Description

Reads a GMT file

Usage

```
read_gmt(fname)
```

Arguments

fname	GMT file name.
-------	----------------

Value

a list containing genes and description of each pathway

sample_annotation	<i>Retrive or set the sample_annotation attribute</i>
-------------------	---

Description

Retrive or set the sample_annotation attribute

Usage

```
sample_annotation(cem)

## S4 method for signature 'CEMiTool'
sample_annotation(cem)

sample_annotation(cem) <- value

## S4 replacement method for signature 'CEMiTool'
sample_annotation(cem) <- value
```

Arguments

cem	Object of class CEMiTool
value	a data.frame containing the sample annotation, should have at least two columns containing the Class and the Sample Name that should match with samples in expression

sample_annotation_data	<i>Sample Annotation Dataset</i>
------------------------	----------------------------------

Description

This dataset, together with expr can be used as input for CEMiTool functions

show,CEMiTool-method	<i>Print a cemitool object</i>
----------------------	--------------------------------

Description

Print a cemitool object

Usage

```
## S4 method for signature 'CEMiTool'
show(object)
```

Arguments

object Object of class CEMiTool

split_modules	<i>Co-expression module refinement</i>
---------------	--

Description

Refines modules by splitting them into submodules based on correlation sign.

Usage

```
split_modules(cem, ...)
```

```
## S4 method for signature 'CEMiTool'
split_modules(cem, min_ngen = 30, verbose = F)
```

Arguments

cem Object of class CEMiTool.
... Optional parameters.
min_ngen Minimal number of genes per submodule. Default 30.
verbose Logical. If TRUE, reports analysis steps.

Value

An object of class CEMiTool.

Examples

```
splitted_mods <- split_modules(cem)
```

write_files	<i>Save the CEMiTool object in files</i>
-------------	--

Description

Save the CEMiTool object in files

Usage

```
write_files(cem, directory)

## S4 method for signature 'CEMiTool'
write_files(cem, directory)
```

Arguments

cem	Object of class CEMiTool
directory	a directory

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