Package `ReactomeGSA`

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Type Package

Title Client for the Reactome Analysis Service for comparative multi-omics gene set analysis

Version 1.18.0

Description The ReactomeGSA packages uses Reactome's online analysis service to perform a multi-omics gene set analysis. The main advantage of this package is, that the retrieved results can be visualized using REACTOME's powerful webapplication. Since Reactome's analysis service also uses R to perform the actual gene set analysis you will get similar results when using the same packages (such as limma and edgeR) locally. Therefore, if you only require a gene set analysis, different packages are more suited.

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Encoding UTF-8

LazyData false

Imports jsonlite, httr, progress, ggplot2, methods, gplots, RColorBrewer, dplyr, tidyr, Biobase

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Suggests testthat, knitr, markdown, ReactomeGSA.data, devtools

Enhances limma, edgeR, Seurat (>= 3.0), scater

VignetteBuilder knitr

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add_dataset

Description

Adds a dataset to the analysis request

Usage

add_dataset(
    request,
    expression_values,
    name,
    type,
    comparison_factor,
    comparison_group_1,
    comparison_group_2,
    sample_data = NULL,
    additional_factors = NULL,
    overwrite = FALSE,
    ...
)
Arguments

request
The request to add the dataset to. Commonly a ReactomeAnalysisRequest object.

expression_values
Object containing the expression values of the dataset to add (multiple types supported).

name
character. Name of the dataset. This must be unique within one request.

type
character. The type of the dataset. Get available types using get_reactome_data_types

comparison_factor
character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from expression_values or from sample_data.

comparison_group_1
character. Name of the first group within comparison_factor to use for the comparison.

comparison_group_2
character. Name of the second group within comparison_factor to use for the comparison.

sample_data
data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there.

additional_factors
vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.

overwrite
boolean. If set to TRUE, datasets with the same name will be overwritten

Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.

Value

The ReactomeAnalysisRequest object with the added dataset

See Also

Other add_dataset methods: add_dataset, ReactomeAnalysisRequest, DGEList-method, add_dataset, ReactomeAnalysisRequest, add_dataset, ReactomeAnalysisRequest, ExpressionSet-method, add_dataset, ReactomeAnalysisRequest, data.frame-method, add_dataset, ReactomeAnalysisRequest, matrix-method

Examples

# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")
# since the expression_values object is a limma EList object, the sample_data is
# retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
expression_values = griss_melanoma_proteomics,
name = "Proteomics",
type = "proteomics_int",
comparison_factor = "condition",
comparison_group_1 = "MOCK",
comparison_group_2 = "MCM",
additional_factors = c("cell.type", "patient.id"))

---

### Description

Adds a dataset to the analysis request

### Usage

```r
## S4 method for signature 'ReactomeAnalysisRequest,data.frame'
add_dataset(
    request,
    expression_values,
    name,
    type,
    comparison_factor,
    comparison_group_1,
    comparison_group_2,
    sample_data = NULL,
    additional_factors = NULL,
    overwrite = FALSE,
    ...
)
```

### Arguments

- `request` : `ReactomeAnalysisRequest`
- `expression_values` : `data.frame`. In this case, the `sample_data` must be set.
- `name` : `character`. Name of the dataset. This must be unique within one request.
- `type` : `character`. The type of the dataset. Get available types using `get_reactome_data_types`
add_dataset, ReactomeAnalysisRequest, data.frame-method

- **comparison_factor**: character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from expression_values or from sample_data.

- **comparison_group_1**: character. Name of the first group within comparison_factor to use for the comparison.

- **comparison_group_2**: character. Name of the second group within comparison_factor to use for the comparison.

- **sample_data**: data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there.

- **additional_factors**: vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.

- **overwrite**: boolean. If set to TRUE, datasets with the same name will be overwritten.

- **...**: Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.

**Value**

The ReactomeAnalysisRequest object with the added dataset

**See Also**

Other add_dataset methods: add_dataset, ReactomeAnalysisRequest, DGEList-method, add_dataset, ReactomeAnalysisRequest, ExpressionSet-method, add_dataset, ReactomeAnalysisRequest, matrix-method.

**Examples**

```r
# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
                           expression_values = griss_melanoma_proteomics,
                           name = "Proteomics",
                           type = "proteomics_int",
                           comparison_factor = "condition",
                           comparison_group_1 = "MOCK","
```

---

The ReactomeAnalysisRequest object with the added dataset

**See Also**

Other add_dataset methods: add_dataset, ReactomeAnalysisRequest, DGEList-method, add_dataset, ReactomeAnalysisRequest, ExpressionSet-method, add_dataset, ReactomeAnalysisRequest, matrix-method.

**Examples**

```r
# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
                           expression_values = griss_melanoma_proteomics,
                           name = "Proteomics",
                           type = "proteomics_int",
                           comparison_factor = "condition",
                           comparison_group_1 = "MOCK",
```
```r
comparison_group_2 = "MCM",
additional_factors = c("cell.type", "patient.id")
```

**Description**

Adds a dataset to the analysis request

**Usage**

```r
## S4 method for signature 'ReactomeAnalysisRequest,DGEList'
add_dataset(
  request,
  expression_values,
  name,
  type,
  comparison_factor,
  comparison_group_1,
  comparison_group_2,
  sample_data = NULL,
  additional_factors = NULL,
  overwrite = FALSE,
  ...
)
```

**Arguments**

- `request`  
  ReactomeAnalysisRequest.
- `expression_values`  
  DGEList Here, the sample_data is automatically extracted from the expression_values object unless sample_data is specified as well.
- `name`  
  character. Name of the dataset. This must be unique within one request.
- `type`  
  character. The type of the dataset. Get available types using `get_reactome_data_types`
- `comparison_factor`  
  character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from expression_values or from sample_data.
- `comparison_group_1`  
  character. Name of the first group within comparison_factor to use for the comparison.
- `comparison_group_2`  
  character. Name of the second group within comparison_factor to use for the comparison.
sample_data  data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there.

additional_factors  vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.

overwrite  boolean. If set to TRUE, datasets with the same name will be overwritten.

Value

The ReactomeAnalysisRequest object with the added dataset.

See Also

Other add_dataset methods: add_dataset, ReactomeAnalysisRequest, EList-method, add_dataset, ReactomeAnalysisRequest, ExpressionSet-method, add_dataset, ReactomeAnalysisRequest, data.frame-method, add_dataset, ReactomeAnalysisRequest, matrix-method, add_dataset()

Examples

# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
expression_values = griss_melanoma_proteomics,
name = "Proteomics",
type = "proteomics_int",
comparison_factor = "condition",
comparison_group_1 = "MOCK",
comparison_group_2 = "MCM",
additional_factors = c("cell.type", "patient.id"))
Usage

```r
## S4 method for signature 'ReactomeAnalysisRequest,EList'
add_dataset(
  request,  
  expression_values,  
  name,  
  type,  
  comparison_factor,  
  comparison_group_1,  
  comparison_group_2,  
  sample_data = NULL,  
  additional_factors = NULL,  
  overwrite = FALSE,  
  ...
)
```

Arguments

- `request` ReactomeAnalysisRequest.  
- `expression_values` EList. Here, the sample_data is automatically extracted from the expression_values object unless sample_data is specified as well.  
- `name` character. Name of the dataset. This must be unique within one request.  
- `type` character. The type of the dataset. Get available types using `get_reactome_data_types`.  
- `comparison_factor` character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from expression_values or from sample_data.  
- `comparison_group_1` character. Name of the first group within comparison_factor to use for the comparison.  
- `comparison_group_2` character. Name of the second group within comparison_factor to use for the comparison.  
- `sample_data` data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there.  
- `additional_factors` vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.  
- `overwrite` boolean. If set to TRUE, datasets with the same name will be overwritten  
- `...` Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.

Value

The ReactomeAnalysisRequest object with the added dataset
See Also

Other add_dataset methods: add_dataset, ReactomeAnalysisRequest, DGEList-method, add_dataset, ReactomeAnalysisRequest, ExpressionSet-method, add_dataset, ReactomeAnalysisRequest, data.frame-method, add_dataset, ReactomeAnalysisRequest, matrix-method, add_dataset()

Examples

# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is
# retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
  expression_values = griss_melanoma_proteomics,
  name = "Proteomics",
  type = "proteomics_int",
  comparison_factor = "condition",
  comparison_group_1 = "MOCK",
  comparison_group_2 = "MCM",
  additional_factors = c("cell.type", "patient.id"))

add_dataset, ReactomeAnalysisRequest, ExpressionSet-method

Description

Adds a dataset to the analysis request

Usage

## S4 method for signature 'ReactomeAnalysisRequest,ExpressionSet'
add_dataset(
  request,
  expression_values,
  name,
  type,
  comparison_factor,
  comparison_group_1,
  comparison_group_2,
  sample_data = NULL,
  additional_factors = NULL,
overwrite = FALSE,
...
}

**Arguments**

- `request` : ReactomeAnalysisRequest.
- `expression_values` : ExpressionSet. Here, the sample_data is automatically extracted from the expression_values object unless sample_data is specified as well.
- `name` : character. Name of the dataset. This must be unique within one request.
- `type` : character. The type of the dataset. Get available types using `get_reactome_data_types`.
- `comparison_factor` : character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from expression_values or from sample_data.
- `comparison_group_1` : character. Name of the first group within comparison_factor to use for the comparison.
- `comparison_group_2` : character. Name of the second group within comparison_factor to use for the comparison.
- `sample_data` : data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there.
- `additional_factors` : vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.
- `overwrite` : boolean. If set to TRUE, datasets with the same name will be overwritten.
- `...` : Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.

**Value**

The `ReactomeAnalysisRequest` object with the added dataset.

**See Also**

Other `add_dataset` methods: `add_dataset, ReactomeAnalysisRequest,DGEList-method`, `add_dataset, ReactomeAnalysisRequest,EList-method`, `add_dataset, ReactomeAnalysisRequest, data.frame-method`, `add_dataset, ReactomeAnalysisRequest, matrix-method`, `add_dataset()`

**Examples**

```r
# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
```
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is
# retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
                          expression_values = griss_melanoma_proteomics,
                          name = "Proteomics",
                          type = "proteomics_int",
                          comparison_factor = "condition",
                          comparison_group_1 = "MOCK",
                          comparison_group_2 = "MCM",
                          additional_factors = c("cell.type", "patient.id"))

---

**Description**

Adds a dataset to the analysis request

**Usage**

```r
## S4 method for signature 'ReactomeAnalysisRequest,matrix'
add_dataset(
  request,
  expression_values,
  name,
  type,
  comparison_factor,
  comparison_group_1,
  comparison_group_2,
  sample_data = NULL,
  additional_factors = NULL,
  overwrite = FALSE,
  ...
)
```

**Arguments**

- `request` : ReactomeAnalysisRequest.
- `expression_values` : matrix. In this case, the `sample_data` must be set.
- `name` : character. Name of the dataset. This must be unique within one request.
add_dataset, ReactomeAnalysisRequest, matrix-method

type character. The type of the dataset. Get available types using `get_reactome_data_types`

comparison_factor character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from `expression_values` or from `sample_data`.

comparison_group_1 character. Name of the first group within `comparison_factor` to use for the comparison.

comparison_group_2 character. Name of the second group within `comparison_factor` to use for the comparison.

sample_data data.frame (optional) data.frame containing the sample metadata of the `expression_values`. Depending on the object type of `expression_values`, this information can also be extracted from there.

additional_factors vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.

overwrite boolean. If set to `TRUE`, datasets with the same name will be overwritten.

... Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.

Value

The `ReactomeAnalysisRequest` object with the added dataset

See Also

Other add_dataset methods: `add_dataset, ReactomeAnalysisRequest, DGEList-method`, `add_dataset, ReactomeAnalysisRequest, EList-method`, `add_dataset, ReactomeAnalysisRequest, ExpressionSet-method`, `add_dataset, ReactomeAnalysisRequest, data.frame-method`.

Examples

```r
# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# since the expression_values object is a limma EList object, the sample_data is retrieved from there

# add the dataset
my_request <- add_dataset(request = my_request,
                          expression_values = griss_melanoma_proteomics,
                          name = "Proteomics",
                          type = "proteomics_int",
                          comparison_factor = "condition")
```
analysse_sc_clusters

```r
comparison_group_1 = "MOCK",
comparison_group_2 = "MCM",
additional_factors = c("cell.type", "patient.id")
```

---

**Description**

Analyses cell clusters of a single-cell RNA-sequencing experiment to get pathway-level expressions for every cluster of cells.

**Usage**

```r
analysse_sc_clusters(
  object,
  use_interactors = TRUE,
  include_disease_pathways = FALSE,
  create_reactome_visualization = FALSE,
  create_reports = FALSE,
  report_email = NULL,
  verbose = FALSE,
  ...
)
```

**Arguments**

- **object** The object containing the single-cell RNA-sequencing data.
- **use_interactors** If set (default), protein-protein interactors from IntAct are used to extend Reactome pathways.
- **include_disease_pathways** If set, disease pathways are included as well. Disease pathways in Reactome follow a different annotation approach and can therefore lead to inaccurate results.
- **create_reactome_visualization** If set, the interactive visualization in Reactome’s PathwayBrowser is created.
- **create_reports** If set, PDF and Microsoft Excel reports are created. Links to these report files are send to the supplied e-mail address.
- **report_email** The e-mail address to which reports should be sent to.
- **verbose** If set, additional status messages are printed.
- **...** Parameters passed to the specific implementation. Detailed documentations can be found there.
Details

There are currently two specific implementations of this function, one to support Seurat objects and one to support Bioconductor's SingleCellExperiment class.

Value

A `ReactomeAnalysisResult` object.

Examples

```r
# This example shows how a Seurat object can be analysed
# the approach is identical for SingleCellExperiment objects
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
```

Description

Analyzes cell clusters of a single-cell RNA-sequencing experiment to get pathway-level expressions for every cluster of cells.

Usage

```r
## S4 method for signature 'Seurat'
analyse_sc_clusters(
  object,
  use_interactors = TRUE,
  include_disease_pathways = FALSE,
  create_reactome_visualization = FALSE,
  create_reports = FALSE,
  report_email = NULL,
  verbose = FALSE,
  assay = "RNA",
  slot = "counts",
  ...
)
```
Arguments

object The Seurat object containing the single cell RNA-sequencing data.

use_interactors If set (default), protein-protein interactors from IntAct are used to extend Reactome pathways.

include_disease_pathways If set, disease pathways are included as well. Disease pathways in Reactome follow a different annotation approach and can therefore lead to inaccurate results.

create.reactome.visualization If set, the interactive visualization in Reactome’s PathwayBrowser is created.

create.reports If set, PDF and Microsoft Excel reports are created. Links to these report files are sent to the supplied e-mail address.

report_email The e-mail address to which reports should be sent to.

verbose If set, additional status messages are printed.

assay By default, the "RNA" assay is used, which contains the original read counts.

slot The slot in the Seurat object to use. Default and recommended approach is to use the raw counts.

... Parameters passed to the specific implementation. Detailed documentations can be found there.

Details

There are currently two specific implementations of this function, one to support Seurat objects and one to support Bioconductor’s SingleCellExperiment class.

Value

A ReactomeAnalysisResult object.

Examples

# This example shows how a Seurat object can be analysed
# the approach is identical for SingleCellExperiment objects
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
Description

Analyses cell clusters of a single-cell RNA-sequencing experiment to get pathway-level expressions for every cluster of cells.

Usage

```r
## S4 method for signature 'SingleCellExperiment'
analyse_sc_clusters(
  object,
  use_interactors = TRUE,
  include_disease_pathways = FALSE,
  create.reactome_visualization = FALSE,
  create_reports = FALSE,
  report_email = NULL,
  verbose = FALSE,
  cell_ids,
  ...
)
```

Arguments

- `object`: The `SingleCellExperiment` object containing the single cell RNA-sequencing data.
- `use_interactors`: If set (default), protein-protein interactors from IntAct are used to extend Reactome pathways.
- `include_disease_pathways`: If set, disease pathways are included as well. Disease pathways in Reactome follow a different annotation approach and can therefore lead to inaccurate results.
- `create.reactome_visualization`: If set, the interactive visualization in Reactome’s PathwayBrowser is created.
- `create_reports`: If set, PDF and Microsoft Excel reports are created. Links to these report files are send to the supplied e-mail address.
- `report_email`: The e-mail address to which reports should be sent to.
- `verbose`: If set, additional status messages are printed.
- `cell_ids`: A factor specifying the group to which each cell belongs. For example, `object$cluster`. Alternatively, a string specifying the metadata field's name may be passed.
- `...`: Parameters passed to scater's `aggregateAcrossCells` function.
Details

There are currently two specific implementations of this function, one to support Seurat objects and one to support Bioconductor’s SingleCellExperiment class.

Value

A `ReactomeAnalysisResult` object.

Examples

```r
# This example shows how a Seurat object can be analysed
# the approach is identical for SingleCellExperiment objects
library(ReactomeGSA.data)
data(jerby_b_cells)

gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
```

Description

Introduce a line break in the middle of a long name.

Usage

```r
break_names(the_names, long_name_limit = 46)
```

Arguments

- `the_names`: A vector of names
- `long_name_limit`: The limit to define a long name (default 46 chars.)

Value

The list of adapted names
checkRequestValidity  
Check's if a ReactomeAnalysisRequest object is valid

Description
Check's if a ReactomeAnalysisRequest object is valid

Usage
checkRequestValidity(object)

Arguments
object         The request object to check.

Value
TRUE if the object is valid or a string with the reason why it is not

check_reactome_url  
check_reactome_url

Description
Makes sure the passed URL is valid. If not URL is passed, the one stored in the options is retrieved

Usage
check_reactome_url(reactome_url)

Arguments
reactome_url   character The URL to test. If NULL the URL is retrieved from the options.

Value
character The potentially cleaned / retrieved URL with a trailing "/"
**convert_reactome_result**

*Convert the Reactome JSON result to a ReactomeAnalysisResult object*

**Description**

Convert the Reactome JSON result to a ReactomeAnalysisResult object

**Usage**

`convert_reactome_result(reactome_result)`

**Arguments**

- `reactome_result`  
The JSON result already converted to R objects (name list)

**Value**

A `ReactomeAnalysisResult` object

---

**data_frame_as_string**  *Converts a data.frame to a string representation*

**Description**

A data.frame is converted into a single string using `\t` (the characters, not tab) as field delimiter and `\n` (the characters, not newline) as line delimiter

**Usage**

`data_frame_as_string(data)`

**Arguments**

- `data`  
The data.frame to convert

**Value**

A string representing the passed data.frame
_fetch_public_data_

**Description**

Loads an already available public dataset from ReactomeGSA and returns it as a Biobase::ExpressionSet object.

**Usage**

```r
fetch_public_data(dataset_entry, reactome_url)
```

**Arguments**

- `dataset_entry` The entry of the respective dataset as returned by the `find_public_datasets` function.
- `reactome_url` URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

**Value**

The loaded data as an ExpressionSet object.

---

**find_public_datasets**

**Description**

Search for a public dataset in the resources supported by ReactomeGSA as external data sources.

**Usage**

```r
find_public_datasets(
  search_term,
  species = "Homo sapiens",
  reactome_url = NULL
)
```
get_dataset_loading_status

Retrieves the status of the submitted dataset loading request

Description

Retrieves the status of the submitted dataset loading request

Usage

get_dataset_loading_status(loading_id, reactome_url = NULL)

Arguments

loading_id The dataset loading process’ id
reactome_url URL of the Reactome API Server. Overwrites the URL set in the ’reactome_gsa.url’ option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Arguments

search_term The search terms as a single string. Multiple words (seperated by a space) are combined by an "AND".

species Limit the search to selected species. The complete list of available species can be retrieved through get_public_species. By default, entries as limited to human datasets.

reactome_url URL of the Reactome API Server. Overwrites the URL set in the ’reactome_gsa.url’ option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

A data.frame containing a list of datasets found through the search.

Examples

# search for any public dataset relating to BRAF in melanoma
melanoma_datasets <- find_public_datasets("melanoma braf")

# it is also possible to limit this to another species than human
melanoma_mouse <- find_public_datasets("melanoma", species = "Mus musculus")

# the list of available species can be retrieved using get_public_species
all_species <- get_public_species()

# datasets can then be loaded using the load_public_dataset function
**get_fc_for_dataset**

**Value**
A list containing the id, status (can be "running", "complete", "failed"), description, and completed (numeric between 0 - 1)

**Description**
Retrieve the fold-changes for all pathways of the defined dataset

**Usage**
`get_fc_for_dataset(dataset, pathway_result)`

**Arguments**
- **dataset** Name of the dataset to retrieve the fold changes for.
- **pathway_result** The data.frame created by the `pathways` function.

**Value**
A vector of fold-changes

---

**get_is_sig_dataset**

**Description**
Determines how significant a pathway is across the datasets. Returns the lowest significance.

**Usage**
`get_is_sig_dataset(dataset, pathway_result)`

**Arguments**
- **dataset** Name of the dataset.
- **pathway_result** The data.frame created by the `pathways` function.

**Value**
A vector with 3=non-significant, 2=p<=0.05, 1=p<0.01
Description

Return the list of found species labels in the supported public data resources

Usage

get_public_species(reactome_url = NULL)

Arguments

reactome_url URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

A vector of species strings.

Examples

# get the available species
available_species <- get_public_species()

# inspect the first 1 - 3 entries
available_species[1:3]

get_reactome_analysis_result

Retrieves the result of the submitted analysis using perform_reactome_analysis

Description

The result is only available if get_reactome_analysis_status indicates that the analysis is complete.

Usage

get_reactome_analysis_result(analysis_id, reactome_url = NULL)
get_reactome_analysis_status

Retrieves the status of the submitted analysis using start_reactome_analysis

Arguments

- `analysis_id` The running analysis’ id
- `reactome_url` URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

- The result object

Description

Retrieves the status of the submitted analysis using start_reactome_analysis

Usage

get_reactome_analysis_status(analysis_id, reactome_url = NULL)

Arguments

- `analysis_id` The running analysis’ id
- `reactome_url` URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

- A list containing the id, status (can be "running", "complete", "failed"), description, and completed (numeric between 0 - 1)
get_reactome_data_types

ReactomeGSA supported data types

Description

ReactomeGSA supported data types

Usage

get_reactome_data_types(
  print_types = TRUE,
  return_result = FALSE,
  reactome_url = NULL
)

Arguments

print_types If set to TRUE (default) a (relatively) nice formatted version of the result is printed.
return_result If set to TRUE, the result is returned as a data.frame (see below)
reactome_url URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

A data.frame containing one row per data type with its id and description.

Author(s)

Johannes Griss

See Also

Other Reactome Service functions: get_reactome_methods()

Examples

# retrieve the available data types
available_types <- get_reactome_data_types(print_types = FALSE, return_result = TRUE)

# print all data type ids
available_types$id

# simply print the available methods
get_reactome_data_types()
get_reactome_methods

Description

Returns all available analysis methods from the Reactome analysis service.

Usage

get_reactome_methods(
  print_methods = TRUE,
  print_details = FALSE,
  return_result = FALSE,
  method = NULL,
  reactome_url = NULL
)

Arguments

print_methods  If set to TRUE (default) a (relatively) nice formatted version of the result is printed.

print_details  If set to TRUE detailed information about every method, including available parameters and description are displayed. This does not affect the data returned if return_result is TRUE.

return_result  If set to TRUE, the result is returned as a data.frame (see below)

method  If set to a method’s id, only information for this method will be shown. This is especially useful if detailed information about a single method should be retrieved. This does not affect the data returned if return_result is TRUE.

reactome_url  URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Details

Every method has a type, a scope, and sometimes a list of allowed values. The type (string, int = integer, float) define the expected data type. The scope defines at what level the parameter can be set. dataset level parameters can be set at the dataset level (using the add_dataset function) or at the analysis request level (using set_parameters). If these parameters are set at the analysis request level, this overwrites the default value for all datasets. analysis and global level parameters must only be set at the analysis request level using set_parameters. The difference between these two types of parameters is that while analysis parameters influence the results, global parameters only influence the behaviour of the analysis system (for example whether a Reactome visualization is created).
Value

If `return_result` is set to TRUE, a data.frame with one row per method. Each method has a name, description, and (optional) a list of parameters. Parameters again have a name, type, and description.

Author(s)

Johannes Griss

See Also

Other Reactome Service functions: `get.reactome.data_types()`

Examples

```r
# retrieve the available methods only in an object
available_methods <- get.reactome.methods(print.methods = FALSE, return_result = TRUE)

# print all method names
available_methods$name

# list all parameters for the first method
first_method_parameters <- available_methods[1, "parameters"]
first_method.parameters

# simply print the available methods
get.reactome.methods()

# get the details for PADOG
get.reactome.methods(print_details = TRUE, method = "PADOG")
```

Description

Retrieves a result from a `ReactomeAnalysisResult` object.

Usage

```
get_result(x, type, name)
```

Arguments

- `x`: ReactomeAnalysisResult.
- `type`: the type of result. Use `result_types` to retrieve all available types.
- `name`: the name of the result. Use `names` to retrieve all available results.
Value

A data.frame containing the respective result.

See Also

Other ReactomeAnalysisResult functions: names, ReactomeAnalysisResult-method, open_reactome(), pathways(), plot_correlations(), plot_gsva_heatmap(), plot_gsva_pathway(), plot_heatmap(), plot_volcano(), reactome_links(), result_types()

Examples

# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the available result types
result_types(griss_melanoma_result)

# get the dataset names
names(griss_melanoma_result)

# get the fold_changes for the first dataset
prot_fc <- get_result(griss_melanoma_result, type = "fold_changes", name = "proteomics")

head(prot_fc)
is_gsva_result

See Also

Other ReactomeAnalysisResult functions: names, ReactomeAnalysisResult-method, open_reactome(), pathways(), plot_correlations(), plot_gsva_heatmap(), plot_gsva_pathway(), plot_heatmap(), plot_volcano(), reactome_links(), result_types()

Examples

# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the available result types
result_types(griss_melanoma_result)

# get the dataset names
names(griss_melanoma_result)

# get the fold_changes for the first dataset
prot_fc <- get_result(griss_melanoma_result, type = "fold_changes", name = "proteomics")

head(prot_fc)

----------------------------------

is_gsva_result  is_gsva_result

----------------------------------

Description

is_gsva_result

Usage

is_gsva_result(object)

Arguments

object A ReactomeAnalysisResult object

Value

Boolean indicating whether the object is a GsvA result.
Description

Loads a public dataset that was found through the `find_public_datasets` function. The dataset is returned as a Biobase ExpressionSet object.

Usage

`load_public_dataset(dataset_entry, verbose = FALSE, reactome_url = NULL)`

Arguments

- `dataset_entry`: The entry of the respective dataset as returned by the `find_public_datasets` function.
- `verbose`: If set to `TRUE`, status messages and a status bar are displayed.
- `reactome_url`: URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

The loaded data as an ExpressionSet object.

Examples

```r
# As a first step, you need to find available datasets
available_datasets <- find_public_datasets("psoriasis tnf")

# have a quick look at the found datasets
available_datasets[, c("id", "title")]

# load the first one, use the whole row of the found datasets
# data.frame as the parameter
dataset_1 <- load_public_dataset(available_datasets[1,], verbose = TRUE)
```
names, ReactomeAnalysisResult - method

Description
Retrieves the names of the contained datasets within an ReactomeAnalysisResult object.

Usage
## S4 method for signature 'ReactomeAnalysisResult'

names(x)

Arguments
x
ReactomeAnalysisResult.

Value
character vector with the names of the contained datasets

See Also
Other ReactomeAnalysisResult functions: get_result(), open_reactome(), pathways(), plot_correlations(), plot_gsva_heatmap(), plot_gsva_pathway(), plot_heatmap(), plot_volcano(), reactome_links(), result_types()

Examples
# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the names of the available datasets
names(griss_melanoma_result)

open_reactome

Description
Opens the specified Reactome visualization in the system’s default browser.

Usage
doep_reactome(x, ...)

open_reactome
Arguments

x  ReactomeAnalysisResult.
...

Value

The opened link

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# Note: This function only works with a newly created result
# since the visualization links only stay active for 7 days

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the reactome link - this does only work
# with new results
# open_reactome(griss_melanoma_result)
```

Description

Opens the specified Reactome visualization in the system’s default browser.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
open_reactome(x, n_visualization = 1, ...)
```

Arguments

x  ReactomeAnalysisResult.
n_visualization  numeric The index of the visualization to display (default 1). Use `reactome_links` to retrieve all available visualizations and their index. By default, the first visualization is opened.
...

Additional parameters passed to downstream functions.
Value

The opened link

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# Note: This function only works with a newly created result
# since the visualization links only stay active for 7 days

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the reactome link - this does only work
# with new results
# open_reactome(griss_melanoma_result)
```

Description

Combines and returns the pathways of all analysed datasets.

Usage

```r
pathways(x, ...)
```

Arguments

- `x` ReactomeAnalysisResult.
- `...` Additional parameters for specific implementations.

Value

A `data.frame` containing all merged pathways.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `open_reactome()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`
Examples

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the combined pathway result
pathway_result <- pathways(griss_melanoma_result)

head(pathway_result)

---

Description

Combines and returns the pathways of all analysed datasets.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
pathways(x, p = 0.01, order_by = NULL, ...)
```

Arguments

- `x` : ReactomeAnalysisResult.
- `p` : Minimum p-value to accept a pathway as significantly regulated. Default is 0.01.
- `order_by` : Name of the dataset to sort the result list by. By default, the results are sorted based on the first dataset.
- `...` : Additional parameters for specific implementations.

Value

A data.frame containing all merged pathways.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names(ReactomeAnalysisResult-method)`, `open_reactome()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`
Examples

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the combined pathway result
pathway_result <- pathways(griss_melanoma_result)

head(pathway_result)

perform_reactome_analysis

Perform a Reactome Analysis

Description

This function wraps all steps required to perform an Analysis using the Reactome Analysis Service. It submits the passed ReactomeAnalysisRequest object to the Reactome Analysis Service API, checks the submitted analysis’ status and returns the result once the analysis is complete.

Usage

perform_reactome_analysis(
  request,  # ReactomeAnalysisRequest to submit.
  verbose = TRUE,  # logical. If FALSE status messages are not printed to the console.
  compress = TRUE,  # logical. If TRUE (default) the request data is compressed before submitting it to the ReactomeGSA API. This is the generally recommended way and should only be disabled for debugging purposes.
  reactome_url = NULL  # URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)
)

Arguments

request ReactomeAnalysisRequest to submit.
verbose logical. If FALSE status messages are not printed to the console.
compress logical. If TRUE (default) the request data is compressed before submitting it to the ReactomeGSA API. This is the generally recommended way and should only be disabled for debugging purposes.
reactome_url URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Value

The analysis’ result
Examples

```r
# create a request using Camera as an analysis
library(ReactomeGSA.data)
data(griss_melanoma_proteomics)

my_request <- ReactomeAnalysisRequest(method = "Camera")

# set maximum missing values to 0.5 and do not create any reactome visualizations
my_request <- set_parameters(request = my_request,
                             max_missing_values = 0.5,
                             create.reactome.visualization = FALSE)

# add the dataset
my_request <- add_dataset(request = my_request,
                           expression_values = griss_melanoma_proteomics,
                           name = "Proteomics",
                           type = "proteomics_int",
                           comparison_factor = "condition",
                           comparison_group_1 = "MOCK",
                           comparison_group_2 = "MCM",
                           additional_factors = c("cell.type", "patient.id"))

# perform the analysis
my_result <- perform_reactome_analysis(request = my_request, verbose = FALSE)
```

Description

Plots correlations of the average fold-changes of all pathways between the different datasets. This function is only available to GSA based results (not GSVA ones).

Usage

```r
plot_correlations(x, hide_non_sig = FALSE)
```

Arguments

- `x` ReactomeAnalysisResult. The result object to use as input
- `hide_non_sig` If set, non-significant pathways are not shown.

Value

A list of ggplot2 plot objects representing one plot per combination
See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names,ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the correlation plots
plot_objs <- plot_correlations(griss_melanoma_result)

# only one plot created for this result as it contains two datasets
length(plot_objs)

# show the plot using `print(plot_objs[[1]])`
```

Description

Plots correlations of the average fold-changes of all pathways between the different datasets. This function is only available to GSA based results (not GSVA ones).

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_correlations(x, hide_non_sig = FALSE)
```

Arguments

- `x` : ReactomeAnalysisResult. The result object to use as input
- `hide_non_sig` : If set, non-significant pathways are not shown.

Value

A list of ggplot2 plot objects representing one plot per combination

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names,ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`
Examples

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the correlation plots
plot_objs <- plot_correlations(griss_melanoma_result)

# only one plot created for this result as it contains two datasets
length(plot_objs)

# show the plot using `print(plot_objs[[1]])`


plot_gsva_heatmap

Description

Plots pathway expression values / sample as a heatmap. Ranks pathways based on their expression difference.

Usage

plot_gsva_heatmap(
  object,
  pathway_ids = NULL,
  max_pathways = 20,
  truncate_names = TRUE,
  ...
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>The ReactomeAnalysisResult object.</td>
</tr>
<tr>
<td>pathway_ids</td>
<td>A vector of pathway ids. If set, only these pathways are included in the plot.</td>
</tr>
<tr>
<td>max_pathways</td>
<td>The maximum number of pathways to include. Only takes effect if pathway_ids is not set.</td>
</tr>
<tr>
<td>truncate_names</td>
<td>If set, long pathway names are truncated.</td>
</tr>
</tbody>
</table>

Value

None
See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names()`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)

# plot the heatmap
relevant_pathways <- c("R-HSA-983170", "R-HSA-388841", "R-HSA-2132295",
"R-HSA-983705", "R-HSA-5690714")
plot_gsva_heatmap(gsva_result,
   pathway_ids = relevant_pathways, # limit to these pathways
   margins = c(6,30), # adapt the figure margins in heatmap.2
   dendrogram = "col", # only plot column dendrogram
   scale = "row", # scale for each pathway
   key = FALSE, # don't display the color key
   lwd=c(0.1,4)) # remove the white space on the left
```

Description

Plots pathway expression values / sample as a heatmap. Ranks pathways based on their expression difference.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_gsva_heatmap(
   object,
   pathway_ids = NULL,
   max_pathways = 20,
   truncate_names = TRUE,
   ...
)
```
Arguments

object The ReactomeAnalysisResult object.
pathway_ids A vector of pathway ids. If set, only these pathways are included in the plot.
max_pathways The maximum number of pathways to include. Only takes effect if pathway_ids is not set.
truncate_names If set, long pathway names are truncated.
... Additional parameters passed to the heatmap.2 function.

Value

None

See Also

Other ReactomeAnalysisResult functions: get_result(), names, ReactomeAnalysisResult-method, open_reactome(), pathways(), plot_correlations(), plot_gsva_pathway(), plot_heatmap(), plot_volcano(), reactome_links(), result_types()

Examples

# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)

# plot the heatmap
relevant_pathways <- c("R-HSA-983170", "R-HSA-388841", "R-HSA-2132295", "R-HSA-983705", "R-HSA-5690714")
plot_gsva_heatmap(gsva_result,
    pathway_ids = relevant_pathways, # limit to these pathways
    margins = c(6,30), # adapt the figure margins in heatmap.2
    dendrogram = "col", # only plot column dendrogram
    scale = "row", # scale for each pathway
    key = FALSE, # don't display the color key
    lwid=c(0.1,4)) # remove the white space on the left

Description

Plots the expression of a specific pathway from a ssGSEA result.

Usage

plot_gsva_pathway(object, pathway_id, ...)

plot_gsva_pathway  plot_gsva_pathway
Arguments

- **object**: The `ReactomeAnalysisResult` object.
- **pathway_id**: The pathway's id
- **...**: Additional parameters for specific implementations.

Value

A ggplot2 plot object

See Also

Other `ReactomeAnalysisResult` functions: `get_result()`, `names`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)

# create the plot
plot_obj <- plot_gsva_pathway(gsva_result, "R-HSA-389542")
```

Description

Plots the expression of a specific pathway from a ssGSEA result.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_gsva_pathway(object, pathway_id, ...)
```

Arguments

- **object**: The `ReactomeAnalysisResult` object.
- **pathway_id**: The pathway's id
- **...**: Additional parameters for specific implementations.
plot_gsva_pca

Value
A ggplot2 plot object

See Also
Other ReactomeAnalysisResult functions: get_result(), names, ReactomeAnalysisResult-method, open_reactome(), pathways(), plot_correlations(), plot_gsva_heatmap(), plot_heatmap(), plot_volcano(), reactome_links(), result_types()

Examples

# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)

# create the plot
plot_obj <- plot_gsva_pathway(gsva_result, "R-HSA-389542")

plot_gsva_pca

plot_gsva_pca

plot_gsva_pca

Description
Runs a Principal Component analysis (using prcomp) on the samples based on the pathway analysis results.

Usage
plot_gsva_pca(object, pathway_ids = NULL, ...)

Arguments

object A ReactomeAnalysisResult object containing a ssGSEA result
pathway_ids A character vector of pathway ids. If set, only these pathways will be used for the PCA analysis.
... Additional parameters passed to specific implementations.

Value
A ggplot2 object representing the plot.
Examples

```r
# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
```

Description

Runs a Principal Component analysis (using \texttt{prcomp}) on the samples based on the pathway analysis results.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_gsva_pca(object, pathway_ids = NULL, ...)
```

Arguments

- **object**: A \texttt{ReactomeAnalysisResult} object containing a ssGSEA result
- **pathway_ids**: A character vector of pathway ids. If set, only these pathways will be used for the PCA analysis.
- **...**: Additional parameters are passed to \texttt{prcomp}

Value

A \texttt{ggplot2} object representing the plot.

Examples

```r
# load the scRNA-seq example data
library(ReactomeGSA.data)
data(jerby_b_cells)

# perform the GSVA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
```
Description

Creates a heatmap to show which pathways are up- and down-regulated in different datasets

Usage

```r
plot_heatmap(
  x,
  fdr = 0.01,
  max_pathways = 30,
  break_long_names = TRUE,
  return_data = FALSE
)
```

Arguments

- **x**: ReactomeAnalysisResult. The result object to use as input
- **fdr**: numeric. The minimum FDR to consider a pathways as significantly regulated. (Default 0.01)
- **max_pathways**: numeric. The maximum number of pathways to plot. Pathways are sorted based on in how many datasets they are significantly regulated. This has no effect if `return_data` is set to `TRUE`.
- **break_long_names**: logical. If set, long pathway names are broken into two lines.
- **return_data**: logical. If set, only the plotting data, but not the plot object itself is returned. This can be used to create customized plots that use the same data structure.

Value

A ggplot2 plot object representing the heatmap of pathways

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_volcano()`, `reactome_links()`, `result_types()`

Examples

```r
# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the heatmap plot
```
plot_obj <- plot_heatmap(griss_melanoma_result)

# show the plot
print(plot_obj)

---

**plot_heatmap, ReactomeAnalysisResult-method**

*plot_heatmap - ReactomeAnalysisResult*

**Description**

Creates a heatmap to show which pathways are up- and down-regulated in different datasets

**Usage**

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_heatmap(
  x,
  fdr = 0.01,
  max_pathways = 30,
  break_long_names = TRUE,
  return_data = FALSE
)
```

**Arguments**

- `x` : ReactomeAnalysisResult. The result object to use as input
- `fdr` : numeric. The minimum FDR to consider a pathways as significantly regulated. (Default 0.01)
- `max_pathways` : numeric. The maximum number of pathways to plot. Pathways are sorted based on in how many datasets they are significantly regulated. This has no effect if `return_data` is set to TRUE.
- `break_long_names` : logical. If set, long pathway names are broken into two lines.
- `return_data` : logical. If set, only the plotting data, but not the plot object itself is returned. This can be used to create customized plots that use the same data structure.

**Value**

A ggplot2 plot object representing the heatmap of pathways

**See Also**

Other ReactomeAnalysisResult functions: `get_result()`, `names, ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_volcano()`, `reactome_links()`, `result_types()`
**Examples**

```r
# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the heatmap plot
plot_obj <- plot_heatmap(griss_melanoma_result)

# show the plot
print(plot_obj)
```

**Description**

Creates a volcano plot for the pathway analysis result. Every point represents one pathway, the x-axis the log fold-change and the y-axis the adjusted p-value (-log10).

**Usage**

```
plot_volcano(x, ...)
```

**Arguments**

- `x` ReactomeAnalysisResult. The analysis result to plot the volcano plot for.
- `...` Additional parameters for specific implementations.

**Details**

This function is only available for GSA-based analysis results.

**Value**

A ggplot2 plot object representing the volcano plot.

**See Also**

Other ReactomeAnalysisResult functions: `get_result()`, `names,ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `reactome_links()`., `result_types()`
Examples

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the volcano plot for the first dataset
plot_obj <- plot_volcano(griss_melanoma_result)

# display the plot using `print(plot_obj)`

Description

Creates a volcano plot for the pathway analysis result. Every point represents one pathway, the x-axis the log fold-change and the y-axis the adjusted p-value (-log10).

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
plot_volcano(x, dataset = 1, ...)
```

Arguments

- `x` : ReactomeAnalysisResult. The analysis result to plot the volcano plot for.
- `dataset` : The name or index of the dataset to plot (first one by default).
- `...` : Additional parameters for specific implementations.

Details

This function is only available for GSA-based analysis results.

Value

A ggplot2 plot object representing the volcano plot.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names(ReactomeAnalysisResult-method)`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `reactome_links()`, `result_types()`
Examples

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# create the volcano plot for the first dataset
plot_obj <- plot_volcano(griss_melanoma_result)

# display the plot using `print(plot_obj)`

Description

Shows a ReactomeAnalysisRequest object summary.

Usage

## S4 method for signature 'ReactomeAnalysisRequest'

print(x, ...)

Arguments

x ReactomeAnalysisRequest

... Not used

Value

The classname of the object

Examples

library(methods)

request <- ReactomeAnalysisRequest(method = "Camera")
print(request)

# add additional parameters
request <- set_parameters(request, "max_missing_values" = 0.5)
show(request)
**Description**

Displays basic information about the `ReactomeAnalysisResult` object.

**Usage**

```r
## S4 method for signature 'ReactomeAnalysisResult'
print(x, ...)
```

**Arguments**

- `x` : `ReactomeAnalysisResult`
- `...` : Not used

**Value**

character classname of the object

**Examples**

```r
calligraphy <- library(ReactomeGSA.data)
data(griss_melanoma_result)
print(griss_melanoma_result)
```

---

**ReactomeAnalysisRequest**

`ReactomeAnalysisRequest` class

**Description**

This class is used to collect all information required to submit an analysis request to the Reactome Analysis System.

**Usage**

```r
ReactomeAnalysisRequest(method)
```

**Arguments**

- `method` : character. Name of the method to use.
Value

A ReactomeAnalysisRequest object.

Slots

- `method` character. Name of the method to use
- `request_object` list. This slot should not be set manually. It stores the internal request representation and should be modified using the classes’ functions. To add parameters, use `set_parameters`.

Examples

```r
library(ReactomeGSA.data)
library(methods)

# create the request method and specify its method
request <- ReactomeAnalysisRequest(method = "Camera")

# add a dataset to the request
data(griss_melanoma_proteomics)

request <- add_dataset(request = request,
                        expression_values = griss_melanoma_proteomics,
                        name = "Proteomics",
                        type = "proteomics_int",
                        comparison_factor = "condition",
                        comparison_group_1 = "MOCK",
                        comparison_group_2 = "MCM",
                        additional_factors = c("cell.type", "patient.id"))

# to launch the actual analysis use the perform_reactome_analysis function
```

**ReactomeAnalysisResult-class**

**ReactomeAnalysisResult class**

**Description**

A ReactomeAnalysisResult object contains the pathway analysis results of all submitted datasets at once.

**Details**

This class represents a result retrieved from the Reactome Analysis Service. It is returned by `get_reactome_analysis_result` and its wrapper `perform_reactome_analysis`. Generally, object of this class should not be created manually.
Value

A ReactomeAnalysisResult object.

Slots

reactome_release  The Reactome version used to create this result.
mappings  Stores the mapping results that were generated for this analysis.
results A named list containing the actual analysis results for every dataset and possibly combined results as well.
reactome_links  Links pointing to reactome results as a list.

Methods

names: Retrieves the names of all datasets in the result object
result_types: Retrieves the available result types
pathways: Merges the pathway results of all analysed datasets.
get_result: Retrieve a specific result as data.frame
reactome_links: Displays / retrieves the URLs to the available visualizations in Reactome’s pathway browser.
open_reactome: Opens the specified Reactome visualization in the system’s default browser.

Examples

# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# retrieve the names of all datasets in the result
names(griss_melanoma_result)

# get the combined pathway result
pathway_result <- pathways(griss_melanoma_result)

# check which result types are available
result_types(griss_melanoma_result)

# get the fold changes for the first dataset
first_dataset_name <- names(griss_melanoma_result)[1]

first_fc <- get_result(griss_melanoma_result, "fold_changes", first_dataset_name)
Description

Displays detailed information about the result visualizations in Reactome.

Usage

```r
reactome_links(x, ...)
```

Arguments

- `x`: ReactomeAnalysisResult.
- `...`: Additional parameters for specific implementations.

Value

If `return_result` is set to `TRUE`, a vector of the available visualizations.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `result_types()`

Examples

```r
# Note: This function only works with a newly created result
# since the visualization links only stay active for 7 days

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the reactome link - this does only work
# with new results
reactome_links(griss_melanoma_result)
```
Description

Displays detailed information about the result visualizations in Reactome.

Usage

```r
# S4 method for signature 'ReactomeAnalysisResult'
reactome_links(x, print_result = TRUE, return_result = FALSE)
```

Arguments

- `x`: ReactomeAnalysisResult.
- `print_result`: If set to FALSE the links are not printed to the console.
- `return_result`: If TRUE the available visualizations are returned as a list containing named vectors for every visualization. These vectors' have a `url`, `name`, and optionally a `description` slot.

Value

If `return_result` is set to TRUE, a vector of the available visualizations.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names(ReactomeAnalysisResult-method)`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `result_types()`

Examples

```r
# Note: This function only works with a newly created result
# since the visualization links only stay active for 7 days

# load an example result
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the reactome link - this does only work
# with new results
reactome_links(griss_melanoma_result)
```
Description

Remove the dataset from the `ReactomeAnalysisRequest` object.

Usage

```r
remove_dataset(x, dataset_name)
```

Arguments

- `x`: The `ReactomeAnalysisRequest` to remove the dataset from
- `dataset_name`: character The dataset's name

Value

The updated `ReactomeAnalysisRequest`
result_types,ReactomeAnalysisResult-method

result_types

Description

Retrieves the available result types for the ReactomeAnalysisResult object. Currently, the Reactome Analysis System supports pathways and gene level fold_changes as result types. Not all analysis methods return both data types though. Use the names function to find out which datasets are available in the result object.

Usage

result_types(x)

Arguments

x

ReactomeAnalysisResult.

Value

A character vector of result types.

See Also

Other ReactomeAnalysisResult functions: get_result(), names, ReactomeAnalysisResult-method, open_reactome(), pathways(), plot_correlations(), plot_gsva_heatmap(), plot_gsva_pathway(), plot_heatmap(), plot_volcano(), reactome_links()

Examples

# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the available result types
result_types(griss_melanoma_result)
Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
result_types(x)
```

Arguments

- `x` : ReactomeAnalysisResult.

Value

A character vector of result types.

See Also

Other ReactomeAnalysisResult functions: `get_result()`, `names`, `ReactomeAnalysisResult-method`, `open_reactome()`, `pathways()`, `plot_correlations()`, `plot_gsva_heatmap()`, `plot_gsva_pathway()`, `plot_heatmap()`, `plot_volcano()`, `reactome_links()`

Examples

```r
# load an example result object
library(ReactomeGSA.data)
data(griss_melanoma_result)

# get the available result types
result_types(griss_melanoma_result)
```

Description

Set the analysis method used by the `ReactomeAnalysisRequest`

Usage

`set_method(request, method, ...)`

Arguments

- `request` : The `ReactomeAnalysisRequest` to adjust
- `method` : The name of the method to use. Use `get_reactome_methods` to retrieve all available methods
- `...` : Additional parameters passed to specific implementations

Value

The `ReactomeAnalysisRequest` with the adapted method
Examples

# create a request using Camera as an analysis
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")
print(my_request)

# change the method to ssGSEA
my_request <- set_method(my_request, "ssGSEA")
print(my_request)

---

Description

Set the analysis method used by the `ReactomeAnalysisRequest`

Usage

```r
## S4 method for signature 'ReactomeAnalysisRequest'
set_method(request, method, ...)
```

Arguments

- **request**: The `ReactomeAnalysisRequest` to adjust
- **method**: The name of the method to use. Use `get_reactome_methods` to retrieve all available methods
- **...**: Additional parameters passed to specific implementations

Value

The `ReactomeAnalysisRequest` with the adapted method

Examples

# create a request using Camera as an analysis
data(griss_melanoma_proteomics)
library(methods)

my_request <- ReactomeAnalysisRequest(method = "Camera")
print(my_request)
## Description

Sets the analysis parameters for the given `ReactomeAnalysisRequest`. If the parameter is already set, it is overwritten. Use `get_reactome_methods` to get a list of all available parameters for each available method.

## Usage

```r
set_parameters(request, ...)```

## Arguments

- `request` The `ReactomeAnalysisRequest` to set the parameters for.
- `...` Any name / value pair to set a parameter (see example). For a complete list of available parameters use `get_reactome_methods`.

## Details

Both, parameters with the scope "dataset" as well as "analysis" can be set on the analysis level. In this case, these parameters overwrite the system’s default values. If a parameter with the scope "dataset" is defined again at the dataset level, this value will overwrite the analysis’ scope value for the given dataset.

## Value

The modified `ReactomeAnalysisRequest` object

## Examples

```r
library(methods)

# create a request object
request <- ReactomeAnalysisRequest(method = "Camera")

# add a parameter
request <- set_parameters(request, max_missing_values = 0.5, discrete_norm_function = "TMM")```
Description

Sets the analysis parameters for the given ReactomeAnalysisRequest. If the parameter is already set, it is overwritten. Use get_reactome_methods to get a list of all available parameters for each available method.

Usage

```r
## S4 method for signature 'ReactomeAnalysisRequest'
set_parameters(request, ...)
```

Arguments

- `request` The ReactomeAnalysisRequest to set the parameters for.
- `...` Any name / value pair to set a parameter (see example). For a complete list of available parameters use get_reactome_methods

Details

Both, parameters with the scope "dataset" as well as "analysis" can be set on the analysis level. In this case, these parameters overwrite the system’s default values. If a parameter with the scope "dataset" is defined again at the dataset level, this value will overwrite the analysis’ scope value for the given dataset.

Value

The modified ReactomeAnalysisRequest object

Examples

```r
library(methods)

# create a request object
request <- ReactomeAnalysisRequest(method = "Camera")

# add a parameter
request <- set_parameters(request, max_missing_values = 0.5, discrete_norm_function = "TMM")
```
Description

Shows a ReactomeAnalysisRequest object summary.

Usage

```r
## S4 method for signature 'ReactomeAnalysisRequest'
show(object)
```

Arguments

- `object` 
  ReactomeAnalysisRequest

Value

The classname of the object

Examples

```r
library(methods)

request <- ReactomeAnalysisRequest(method = "Camera")
print(request)

# add additional parameters
request <- set_parameters(request, "max_missing_values" = 0.5)
show(request)
```

Description

Displays basic information about the ReactomeAnalysisResult object.

Usage

```r
## S4 method for signature 'ReactomeAnalysisResult'
show(object)
```
Arguments

object ReactomeAnalysisResult.

Value

character classname of the object

Examples

library(ReactomeGSA.data)
data(griss_melanoma_result)
show(griss_melanoma_result)

start_reactome_analysis

Description

Submits a ReactomeAnalysisRequest to the Reactome Analysis Service API and returns the analysis id of the submitted job.

Usage

start_reactome_analysis(request, compress = TRUE, reactome_url = NULL)

Arguments

request ReactomeAnalysisRequest object to submit.
compress If set (default) the JSON request data is compressed using gzip.
reactome_url URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url' option. Specific ports can be set using the standard URL specification (for example http://your.service:1234)

Details

This function should only be used for very large requests that likely take a long time to complete. By default, users should use the perform_reactome_analysis function to run an analysis.
wait_for_loading_dataset

Value

character The analysis job’s id.

#' @examples # create a request using Camera as an analysis library(ReactomeGSA.data) data(griss_melanoma_proteomics)
my_request <- ReactomeAnalysisRequest(method = "Camera")
# set maximum missing values to 0.5 and do not create any reactome visualizations my_request <-
set_parameters(request = my_request, max_missing_values = 0.5, create.reactome_visualization = FALSE)
# add the dataset my_request <- add_dataset(request = my_request, expression_values = griss_melanoma_proteomics,
name = "Proteomics", type = "proteomics.int", comparison_factor = "condition", comparison_group_1
= "MOCK", comparison_group_2 = "MCM", additional_factors = c("cell.type", "patient.id"))
# start the analysis analysis_id <- start.reactome_analysis(my_request)

wait_for_loading_dataset

Description

This function loops until the dataset is available. If verbose is set to TRUE, the progress is displayed
in a status bar.

Usage

wait_for_loading_dataset(request, verbose, reactome_url)

Arguments

request The httr request object of the dataset loading request.
verbose If set to TRUE, the progress is displayed as a status bar.
reactome_url URL of the Reactome API Server. Overwrites the URL set in the 'reactome_gsa.url'
option. Specific ports can be set using the standard URL specification (for ex-
ample http://your.service:1234)
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