Package ‘ReactomeGSA’

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Type Package

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

Version 1.16.1

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 web application. 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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### Description

Adds a dataset to the analysis request

### Usage

```r
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)
...

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, 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

## 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
comparison_factor
class: 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
class: character. Name of the first group within comparison_factor to use for the comparison.

comparison_group_2
class: 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,DGEList-method,add_dataset,ReactomeAnalysisRequest,EList-method,add_dataset,ReactomeAnalysisRequest,ExpressionSet-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",
                           overwrite = TRUE)
```

Comparison_group_2 = "MCM",
additional_factors = c("cell.type", "patient.id")

Description

Adds a dataset to the analysis request

Usage

## 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

...  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,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"))

add_dataset,ReactomeAnalysisRequest,EList-method

Description

Adds a dataset to the analysis request
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

```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

`add_dataset,ReactomeAnalysisRequest,ExpressionSet-method`

**add_dataset - ExpressionSet**

**Description**

Adds a dataset to the analysis request

**Usage**

```r
## 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

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, matrix-method

#### 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`, `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",
                           overwrite = TRUE)
```

...
analysiscclusters

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
analyse_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

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

A ReactomeAnalysisResult object.

# 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)

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

break_names(the_names, long_name_limit = 46)

A vector of names

The limit to define a long name (default 46 chars.)

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

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

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
get_fc_for_dataset

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  data.frame created by the pathways function

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

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

get_reactome_analysis_status

Retrieves the status of the submitted analysis using start_reactome_analysis

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**

```r
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

```r
# 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()
```

Description

Returns all available analysis methods from the Reactome analysis service.

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>print_methods</code></td>
<td>If set to TRUE (default) a (relatively) nice formatted version of the result is printed.</td>
</tr>
<tr>
<td><code>print_details</code></td>
<td>If set to TRUE detailed information about every method, including available parameters and description are displayed. This does not affect the data returned if <code>return_result</code> is TRUE.</td>
</tr>
<tr>
<td><code>return_result</code></td>
<td>If set to TRUE, the result is returned as a data.frame (see below)</td>
</tr>
<tr>
<td><code>method</code></td>
<td>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 <code>return_result</code> is TRUE.</td>
</tr>
<tr>
<td><code>reactome_url</code></td>
<td>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 <a href="http://your.service:1234">http://your.service:1234</a>)</td>
</tr>
</tbody>
</table>
get_result

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

# 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[, "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.

name 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)

get_result,ReactomeAnalysisResult-method

get_result,ReactomeAnalysisResult-method

get_result(x, type, name)
is_gsva_result

Arguments

x ReactomeAnalysisResult.

Arguments

type the type of result. Use result_types to retrieve all available types.

Arguments

name the name of the result. Use names to retrieve all available results.

Arguments

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)
Value

Boolean indicating whether the object is a GSVA result.

Description

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

Usage

```r
## 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

```r
# 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**

`open_reactome(x, ...)`

**Arguments**

- `x` ReactomeAnalysisResult.
- `...` 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**

# 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)
open_reactome, ReactomeAnalysisResult-method

`open_reactome` - `ReactomeAnalysisResult`

**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)

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
call(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

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

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

head(pathway_result)
```
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

```r
# 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

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,
    verbose = TRUE,
    compress = TRUE,
    reactome_url = NULL
)

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

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]])`
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

```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]])`
```
**plot_gsva_heatmap**

---

**Description**

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

**Usage**

```r
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 specific implementations.

**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**

```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
                  lwid=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,
                   ...)    # remove the white space on the left
```

### 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

plot_gsva_pathway

Description

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

Usage

plot_gsva_pathway(object, pathway_id, ...)

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, 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")

Description

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

Usage

## 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.

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")

**Description**

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

**Usage**

```r
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 `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 `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 `prcomp`

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)

plot_heatmap <- plot_gsva_pca(gsva_result)
```

Description

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

Usage

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

# 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

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

```r
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

```
## 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`, `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)`

print(ReactomeAnalysisRequest)

Description

Shows a ReactomeAnalysisRequest object summary.

Usage

## S4 method for signature ’ReactomeAnalysisRequest’
print(x, ...)

Arguments

x  ReactomeAnalysisRequest
...

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
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, ReactomeAnalysisRequest-method

Examples

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

```r
# 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

## 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

# 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`
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

```r
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

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.
## set_method

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)
```

---

## set_method

### Description

Set the analysis method used by the `ReactomeAnalysisRequest`.

### Usage

```r
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

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

print(my_request)

---

### set_parameters

**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")
```
set_parameters, ReactomeAnalysisRequest-method

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

## 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

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")
show,ReactomeAnalysisRequest-method

Description

Shows a ReactomeAnalysisRequest object summary.

Usage

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

Arguments

object ReactomeAnalysisRequest

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)

show,ReactomeAnalysisResult-method

Description

Displays basic information about the ReactomeAnalysisResult object.

Usage

## S4 method for signature 'ReactomeAnalysisResult'
show(object)
**start_reactome_analysis**

### Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>ReactomeAnalysisResult.</td>
</tr>
</tbody>
</table>

### Value

character classname of the object

### Examples

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

### Description

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

### Usage

```r
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.
Value

class('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)
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