

# Package ‘ReactomeGSA’

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**Type** Package

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

**Version** 1.21.2

**Author** Johannes Griss [aut, cre]  
(<https://orcid.org/0000-0003-2206-9511>)

**Maintainer** Johannes Griss <johannes.griss@meduniwien.ac.at>

**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.

**License** MIT + file LICENSE

**URL** <https://github.com/reactome/ReactomeGSA>

**BugReports** <https://github.com/reactome/ReactomeGSA/issues>

**Imports** Biobase, BiocSingular, dplyr, ggplot2, gplots, httr, igraph, jsonlite, methods, progress, RColorBrewer, SummarizedExperiment, tidy

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## Contents

|  |    |
|--|----|
| add_dataset . . . . .  | 4  |
| add_dataset,ReactomeAnalysisRequest,data.frame-method . . . . .    | 5  |
| add_dataset,ReactomeAnalysisRequest,DGEList-method . . . . .       | 7  |
| add_dataset,ReactomeAnalysisRequest,EList-method . . . . .         | 9  |
| add_dataset,ReactomeAnalysisRequest,ExpressionSet-method . . . . . | 11 |
| add_dataset,ReactomeAnalysisRequest,matrix-method . . . . .        | 13 |
| analyse_sc_clusters . . . . .                                      | 14 |
| analyse_sc_clusters,Seurat-method . . . . .                        | 16 |
| analyse_sc_clusters,SingleCellExperiment-method . . . . .          | 17 |
| break_names . . . . .  | 18 |
| checkRequestValidity . . . . .                                     | 19 |
| check_reactome_url . . . . .                                       | 19 |
| convert_reactome_result . . . . .                                  | 20 |
| data_frame_as_string . . . . .                                     | 20 |
| fetch_public_data . . . . .  | 21 |
| find_public_datasets . . . . .                                     | 21 |
| generate_metadata . . . . .  | 22 |
| generate_metadata,data.frame-method . . . . .                      | 23 |
| generate_pseudo_bulk_data . . . . .                                | 24 |
| generate_pseudo_bulk_data,Seurat-method . . . . .                  | 25 |
| generate_pseudo_bulk_data,SingleCellExperiment-method . . . . .    | 26 |
| get_dataset_loading_status . . . . .                               | 26 |
| get_fc_for_dataset . . . . .                                       | 27 |
| get_is_sig_dataset . . . . .                                       | 27 |
| get_public_species . . . . .                                       | 28 |
| get_reactome_analysis_result . . . . .                             | 28 |
| get_reactome_analysis_status . . . . .                             | 29 |
| get_reactome_data_types . . . . .                                  | 30 |
| get_reactome_methods . . . . .                                     | 31 |
| get_result . . . . .   | 32 |
| get_result,ReactomeAnalysisResult-method . . . . .                 | 33 |
| is_gsva_result . . . . .   | 34 |
| load_public_dataset . . . . .                                      | 35 |
| names,ReactomeAnalysisResult-method . . . . .                      | 36 |
| open_reactome . . . . .  | 36 |
| open_reactome,ReactomeAnalysisResult-method . . . . .              | 37 |
| pathways . . . . .   | 38 |

|   |    |
|---|----|
| pathways,ReactomeAnalysisResult-method . . . . .          | 39 |
| perform_reactome_analysis . . . . .                       | 40 |
| plot_correlations . . . . .                               | 41 |
| plot_correlations,ReactomeAnalysisResult-method . . . . . | 42 |
| plot_gsva_heatmap . . . . .                               | 43 |
| plot_gsva_heatmap,ReactomeAnalysisResult-method . . . . . | 44 |
| plot_gsva_pathway . . . . .                               | 45 |
| plot_gsva_pathway,ReactomeAnalysisResult-method . . . . . | 46 |
| plot_gsva_pca . . . . .                                   | 47 |
| plot_gsva_pca,ReactomeAnalysisResult-method . . . . .     | 48 |
| plot_heatmap . . . . .                                    | 49 |
| plot_heatmap,ReactomeAnalysisResult-method . . . . .      | 50 |
| plot_volcano . . . . .                                    | 51 |
| plot_volcano,ReactomeAnalysisResult-method . . . . .      | 52 |
| print,ReactomeAnalysisRequest-method . . . . .            | 53 |
| print,ReactomeAnalysisResult-method . . . . .             | 54 |
| ReactomeAnalysisRequest . . . . .                         | 54 |
| ReactomeAnalysisResult-class . . . . .                    | 55 |
| reactome_links . . . . .                                  | 57 |
| reactome_links,ReactomeAnalysisResult-method . . . . .    | 58 |
| remove_dataset . . . . .                                  | 59 |
| remove_dataset,ReactomeAnalysisRequest-method . . . . .   | 59 |
| result_types . . . . .                                    | 60 |
| result_types,ReactomeAnalysisResult-method . . . . .      | 60 |
| set_method . . . . .                                      | 61 |
| set_method,ReactomeAnalysisRequest-method . . . . .       | 62 |
| set_parameters . . . . .                                  | 63 |
| set_parameters,ReactomeAnalysisRequest-method . . . . .   | 64 |
| show,ReactomeAnalysisRequest-method . . . . .             | 65 |
| show,ReactomeAnalysisResult-method . . . . .              | 65 |
| split_clustering . . . . .                                | 66 |
| split_random_sce . . . . .                                | 67 |
| split_subclustering_sce . . . . .                         | 67 |
| split_variable . . . . .                                  | 68 |
| split_variable_random . . . . .                           | 69 |
| split_variable_sce . . . . .                              | 69 |
| start_reactome_analysis . . . . .                         | 70 |
| wait_for_loading_dataset . . . . .                        | 71 |

---

|             |                    |
|-------------|--------------------|
| add_dataset | <i>add_dataset</i> |
|-------------|--------------------|

---

## 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 <a href="#">ReactomeAnalysisRequest</a> 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 <a href="#">get_reactome_data_types</a>   |
| comparison_factor  | character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from <code>expression_values</code> or from <code>sample_data</code> .                                |
| comparison_group_1 | character. Name of the first group within <code>comparison_factor</code> to use for the comparison.   |
| comparison_group_2 | character. Name of the second group within <code>comparison_factor</code> to use for the comparison.  |
| sample_data        | data.frame (optional) data.frame containing the sample metadata of the <code>expression_values</code> . Depending on the object type of <code>expression_values</code> , 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](#)

**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, data.frame-method  
*add\_dataset - data.frame*

---

**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**

|                                 |   |
|---------------------------------|---|
| <code>request</code>            | ReactomeAnalysisRequest.  |
| <code>expression_values</code>  | data.frame. In this case, the <code>sample_data</code> must be set.   |
| <code>name</code>               | character. Name of the dataset. This must be unique within one request.   |
| <code>type</code>               | character. The type of the dataset. Get available types using <a href="#">get_reactome_data_types</a>   |
| <code>comparison_factor</code>  | character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from <code>expression_values</code> or from <code>sample_data</code> .                                |
| <code>comparison_group_1</code> | character. Name of the first group within <code>comparison_factor</code> to use for the comparison.   |
| <code>comparison_group_2</code> | character. Name of the second group within <code>comparison_factor</code> to use for the comparison.  |
| <code>sample_data</code>        | data.frame (optional) data.frame containing the sample metadata of the <code>expression_values</code> . Depending on the object type of <code>expression_values</code> , this information can also be extracted from there. |
| <code>additional_factors</code> | vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.   |
| <code>overwrite</code>          | boolean. If set to TRUE, datasets with the same name will be overwritten  |
| <code>...</code>                | 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\(\)](#), [add\\_dataset,ReactomeAnalysisRequest,DGEList-method](#), [add\\_dataset,ReactomeAnalysisRequest,EList-method](#), [add\\_dataset,ReactomeAnalysisRequest,ExpressionSet-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,DGEList-method  
*add\_dataset - DGEList*

---

## 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

|                                 |   |
|---------------------------------|---|
| <code>request</code>            | ReactomeAnalysisRequest.  |
| <code>expression_values</code>  | DGEList Here, the <code>sample_data</code> is automatically extracted from the <code>expression_values</code> object unless <code>sample_data</code> is specified as well.  |
| <code>name</code>               | character. Name of the dataset. This must be unique within one request.   |
| <code>type</code>               | character. The type of the dataset. Get available types using <a href="#">get_reactome_data_types</a>   |
| <code>comparison_factor</code>  | character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from <code>expression_values</code> or from <code>sample_data</code> .                                |
| <code>comparison_group_1</code> | character. Name of the first group within <code>comparison_factor</code> to use for the comparison.   |
| <code>comparison_group_2</code> | character. Name of the second group within <code>comparison_factor</code> to use for the comparison.  |
| <code>sample_data</code>        | data.frame (optional) data.frame containing the sample metadata of the <code>expression_values</code> . Depending on the object type of <code>expression_values</code> , this information can also be extracted from there. |
| <code>additional_factors</code> | vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.   |
| <code>overwrite</code>          | boolean. If set to TRUE, datasets with the same name will be overwritten  |
| <code>...</code>                | 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\(\)](#), [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"))
```

---

add\_dataset,ReactomeAnalysisRequest,EList-method  
*add\_dataset - EList*

---

## Description

Adds a dataset to the analysis request

## Usage

```
## 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 automaticall 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 <a href="#">get_reactome_data_types</a>   |
| comparison_factor  | character. The name of the sample property to use for the main comparison. The sample properties are either retrieved from <code>expression_values</code> or from <code>sample_data</code> .                                |
| comparison_group_1 | character. Name of the first group within <code>comparison_factor</code> to use for the comparison.   |
| comparison_group_2 | character. Name of the second group within <code>comparison_factor</code> to use for the comparison.  |
| sample_data        | data.frame (optional) data.frame containing the sample metadata of the <code>expression_values</code> . Depending on the object type of <code>expression_values</code> , 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\(\)](#), [add\\_dataset, ReactomeAnalysisRequest, DGEList-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"))

```

---

add\_dataset,ReactomeAnalysisRequest,ExpressionSet-method  
*add\_dataset - ExpressionSet*

---

## 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 automaticall 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 <a href="#">get_reactome_data_types</a>   |
| 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.  |

|                                 |   |
|---------------------------------|---|
| <code>comparison_group_2</code> | character. Name of the second group within <code>comparison_factor</code> to use for the comparison.  |
| <code>sample_data</code>        | <code>data.frame</code> (optional) <code>data.frame</code> containing the sample metadata of the <code>expression_values</code> . Depending on the object type of <code>expression_values</code> , this information can also be extracted from there. |
| <code>additional_factors</code> | vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.   |
| <code>overwrite</code>          | boolean. If set to <code>TRUE</code> , datasets with the same name will be overwritten  |
| <code>...</code>                | 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\(\)](#), [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  
*add\_dataset - matrix*

---

## Description

Adds a dataset to the analysis request

## Usage

```
## 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.   |
| type               | character. The type of the dataset. Get available types using <a href="#">get_reactome_data_types</a>   |
| 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()`, `add_dataset,ReactomeAnalysisRequest,DGEList-method`, `add_dataset,ReactomeAnalysisRequest,EList-method`, `add_dataset,ReactomeAnalysisRequest,ExpressionSet-method`, `add_dataset,ReactomeAnalysisRequest,data.frame-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"))
```

---

analyse\_sc\_clusters    *analyse\_sc\_clusters*

---

**Description**

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

**Usage**

```
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 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.  |
| ...                           | 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 GSEA analysis
gsva_result <- analyse_sc_clusters(jerby_b_cells, verbose = FALSE)
```

---

analyse\_sc\_clusters, Seurat-method  
*analyse\_sc\_clusters - Seurat*

---

## Description

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

## Usage

```
## 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)
```

---

analyse\_sc\_clusters, SingleCellExperiment-method  
*analyse\_sc\_clusters - SingleCellExperiment*

---

## Description

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

## Usage

```
## 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 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.   |
| cell_ids                      | A factor specifying the group to which each cell belongs. For example, <code>object\$cluster</code> . Alternatively, a string specifying the metadata field's name may be passed. |
| ...                           | Parameters passed to <code>scater</code> 's <code>aggregateAcrossCells</code> 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

```
# 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)
```

---

break\_names

*break\_names*

---

### Description

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

### Usage

```
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     *fetch\_public\_data*

---

### Description

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

### Usage

```
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     *find\_public\_datasets*

---

### Description

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

### Usage

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

**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 <a href="#">get_public_species</a> . 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 <a href="http://your.service:1234">http://your.service:1234</a> ) |

**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
```

---

|                   |                          |
|-------------------|--------------------------|
| generate_metadata | <i>generate_metadata</i> |
|-------------------|--------------------------|

---

**Description**

The pseudobulk data is generated using the [generate\\_pseudo\\_bulk\\_data](#) function.

**Usage**

```
generate_metadata(pseudo_bulk_data)
```

**Arguments**

|                  |   |
|------------------|---|
| pseudo_bulk_data | Pseudobulk data generated from the <a href="#">generate_pseudo_bulk_data</a> function |
|------------------|---|

**Value**

Metadata table for later use

**See Also**

[generate\\_pseudo\\_bulk\\_data](#) for generating pseudobulk data.

**Examples**

```
# Example pseudobulk data
pseudo_bulk_data <- data.frame(
  sample1_groupA = c(10, 20, 30),
  sample2_groupA = c(15, 25, 35),
  sample3_groupB = c(5, 10, 15)
)

# Generate metadata from pseudobulk data
metadata <- generate_metadata(pseudo_bulk_data)
```

---

generate\_metadata,data.frame-method  
*Generate metadata*

---

**Description**

Generate metadata

**Usage**

```
## S4 method for signature 'data.frame'
generate_metadata(pseudo_bulk_data)
```

**Arguments**

pseudo\_bulk\_data  
Pseudobulk data generated from the [generate\\_pseudo\\_bulk\\_data](#) function

**Value**

Returns metadata table for later use

---

```
generate_pseudo_bulk_data
      generate_pseudo_bulk_data
```

---

## Description

generate\_pseudo\_bulk\_data

## Usage

```
generate_pseudo_bulk_data(
  object,
  group_by = NULL,
  split_by = "random",
  k_variable = 4
)
```

## Arguments

|            |  |
|------------|--|
| object     | The Seurat or SingleCellExperiment object to analyse.  |
| group_by   | entry in metadata table, based on these cluster annotation pseudo bulk is performed  |
| split_by   | variable -> split by a variable within the metadata; k must be a string random -> splits based on a random number; k must be a number Louvain, Louvain_multilevel, SLM, Leiden -> subclusters k must be a list with [resolution, cluster_1, cluster_2] |
| k_variable | variable dependent on the split_by   |

## Value

returns pseudo bulk generated data

## Examples

```
#using SCE object
library("scrNaseq")
SCE_OBJECT <- ZeiselBrainData()
# generating pseudo bulk data using the SCE object above,
# and clustering level level1class from the metadata

# generate pseudo bulk data based on random subsampling
SCE_RESULT_RANDOM <- generate_pseudo_bulk_data(SCE_OBJECT,
                                              group_by = "level1class",
                                              split_by = "random",
                                              k_variable = 5)

# generate pseudo bulk data based on variable within the metadata
```



```
SCE_RESULT_VARIABLE <- generate_pseudo_bulk_data(SCE_OBJECT, "level1class","variable","tissue")
```

---

```
generate_pseudo_bulk_data,Seurat-method  
generate_pseudo_bulk_data - Seurat
```

---

## Description

Generate Pseudo Bulk Data for Seurat Objects

## Usage

```
## S4 method for signature 'Seurat'  
generate_pseudo_bulk_data(  
  object,  
  group_by = NULL,  
  split_by = "random",  
  k_variable = 4  
)
```

## Arguments

|            |  |
|------------|--|
| object     | The object to analyse.   |
| group_by   | entry in metadata table, based on these cluster annotation pseudo bulk is performed  |
| split_by   | variable -> split by a variable within the metadata; k must be a string random -> splits based on a random number; k must be a number Louvain, Louvain_multilevel, SLM, Leiden -> subclusters k must be a list with [resolution, cluster_1, cluster_2] |
| k_variable | variable dependent on the split_by   |

## Value

returns pseudo bulk generated data

---

```
generate_pseudo_bulk_data, SingleCellExperiment-method
      generate_pseudo_bulk_data - SingleCellExperiment
```

---

**Description**

generate\_pseudo\_bulk\_data - SingleCellExperiment

**Usage**

```
## S4 method for signature 'SingleCellExperiment'
generate_pseudo_bulk_data(
  object,
  group_by = NULL,
  split_by = "random",
  k_variable = 4
)
```

**Arguments**

|            |  |
|------------|--|
| object     | The SingleCellExperiment object to analyse.  |
| group_by   | entry in metadata table, based on these cluster annotation pseudo bulk is performed  |
| split_by   | variable -> split by a variable within the metadata; k must be a string random -> splits based on a random number; k must be a number subclustering [resolution, cluster_1, cluster_2] |
| k_variable | variable dependent on the split_by   |

**Value**

returns pseudo bulk generated data

---

```
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) |

**Value**

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

---

get\_fc\_for\_dataset      *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      *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= $p \leq 0.05$ , 1= $p < 0.01$

---

get\_public\_species     *get\_public\_species*

---

**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)
```

**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**

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

**Arguments**

|                            |  |
|----------------------------|--|
| <code>print_types</code>   | If set to TRUE (default) a (relatively) nice formatted version of the result is printed.   |
| <code>return_result</code> | If set to TRUE, the result is returned as a data.frame (see below)   |
| <code>reactome_url</code>  | 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 <code>http://your.service:1234</code> ) |

**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` *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

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

## 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[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")
```

---

`get_result`

*get\_result*

---

**Description**

Retrieves a result from a [ReactomeAnalysisResult](#) object.

**Usage**

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

**Arguments**

|                   |   |
|-------------------|---|
| <code>x</code>    | ReactomeAnalysisResult.   |
| <code>type</code> | the type of result. Use <a href="#">result_types</a> to retrieve all available types. |
| <code>name</code> | the name of the result. Use <a href="#">names</a> 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  
*ReactomeAnalysisResult - get\_result*

---

**Description**

Retrieves a result from a [ReactomeAnalysisResult](#) object.

**Usage**

```
## S4 method for signature 'ReactomeAnalysisResult'
get_result(x, type, name)
```

**Arguments**

|      |   |
|------|---|
| x    | ReactomeAnalysisResult.   |
| type | the type of result. Use <a href="#">result_types</a> to retrieve all available types. |
| name | the name of the result. Use <a href="#">names</a> 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)
```

---

|                             |                             |
|-----------------------------|-----------------------------|
| <code>is_gsva_result</code> | <code>is_gsva_result</code> |
|-----------------------------|-----------------------------|

---

**Description**

`is_gsva_result`

**Usage**

```
is_gsva_result(object)
```

**Arguments**

`object`            A [ReactomeAnalysisResult](#) object

**Value**

Boolean indicating whether the object is a GSVa result.

---

`load_public_dataset`    *load\_public\_dataset*

---

### 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

|                            |  |
|----------------------------|--|
| <code>dataset_entry</code> | The entry of the respective dataset as returned by the <a href="#">find_public_datasets</a> function.  |
| <code>verbose</code>       | If set to TRUE, status messages and a status bar are displayed.  |
| <code>reactome_url</code>  | 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 <code>http://your.service:1234</code> ) |

### Value

The loaded data as an ExpressionSet object.

### Examples

```
# 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  
*ReactomeAnalysisResult - names*

---

### 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                    *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**

```
## 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**

```
# 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)
```

---

pathways

*pathways*

---

**Description**

Combines and returns the pathways of all analysed datasets.

**Usage**

```
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)
```

---

pathways,ReactomeAnalysisResult-method  
*ReactomeAnalysisResult - pathways*

---

## Description

Combines and returns the pathways of all analysed datasets.

## Usage

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

## Arguments

|              |  |
|--------------|--|
| request      | <a href="#">ReactomeAnalysisRequest</a> 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 <code>http://your.service:1234</code> ) |

## Value

The analysis' result



## 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"))

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

---

plot\_correlations      *plot\_correlations*

---

## 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 GSVAs).

## 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]])`
```

---

`plot_correlations, ReactomeAnalysisResult-method`  
*plot\_correlations - ReactomeAnalysisResult*

---

**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**

```
## 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      *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

|                |   |
|----------------|---|
| object         | The <a href="#">ReactomeAnalysisResult</a> 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**

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

# perform the GSEA 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_heatmap, ReactomeAnalysisResult-method`

*plot\_gsva\_heatmap - ReactomeAnalysisResult function*

---

**Description**

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

**Usage**

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

**Arguments**

|                |   |
|----------------|---|
| object         | The <a href="#">ReactomeAnalysisResult</a> 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 GSEA 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      *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 GSEA 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_pathway, ReactomeAnalysisResult-method`  
*ReactomeAnalysisResult - plot\_gsva\_pathway*

---

**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 GSEA 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*

---

**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 <a href="#">ReactomeAnalysisResult</a> 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**

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

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

---

```
plot_gsva_pca, ReactomeAnalysisResult-method
plot_gsva_pca - ReactomeAnalysisResult
```

---

**Description**

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

**Usage**

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

**Arguments**

|                          |   |
|--------------------------|---|
| <code>object</code>      | A <a href="#">ReactomeAnalysisResult</a> object containing a ssGSEA result                        |
| <code>pathway_ids</code> | A character vector of pathway ids. If set, only these pathways will be used for the PCA analysis. |
| <code>...</code>         | Additional parameters are passed to <code>prcomp</code>   |

**Value**

A `ggplot2` object representing the plot.

**Examples**

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

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



---

|              |                     |
|--------------|---------------------|
| plot_heatmap | <i>plot_heatmap</i> |
|--------------|---------------------|

---

## Description

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

## 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-method  
*plot\_heatmap - ReactomeAnalysisResult*

---

### Description

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

### Usage

```
## 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

```
# 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\_volcano

*plot\_volcano*

---

## 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)`
```

---

plot\_volcano, ReactomeAnalysisResult-method  
*ReactomeAnalysisResult - plot\_volcano*

---

## 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, 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)`
```

---

```
print,ReactomeAnalysisRequest-method
      print - ReactomeAnalysisRequest
```

---

### Description

Shows a [ReactomeAnalysisRequest](#) object summary.

### Usage

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

### Arguments

|     |   |
|-----|---|
| x   | <a href="#">ReactomeAnalysisRequest</a> |
| ... | 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)
```

---

```
print,ReactomeAnalysisResult-method  
    print - ReactomeAnalysisResult
```

---

**Description**

Displays basic information about the [ReactomeAnalysisResult](#) object.

**Usage**

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

**Arguments**

|     |                         |
|-----|-------------------------|
| x   | ReactomeAnalysisResult. |
| ... | Not used                |

**Value**

character classname of the object

**Examples**

```
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**

```
ReactomeAnalysisRequest(method)
```

```
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**

```
# 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)
```



---

|                |                       |
|----------------|-----------------------|
| reactome_links | <i>reactome_links</i> |
|----------------|-----------------------|

---

### Description

Displays detailed information about the result visualizations in Reactome.

### Usage

```
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

```
# 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)
```

---

reactome\_links, ReactomeAnalysisResult-method  
*ReactomeAnalysisResult - reactome\_links*

---

## 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)
```

---

|                |                       |
|----------------|-----------------------|
| remove_dataset | <i>remove_dataset</i> |
|----------------|-----------------------|

---

**Description**

Remove the dataset from the [ReactomeAnalysisRequest](#) object.

**Usage**

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

**Arguments**

|              |  |
|--------------|--|
| x            | The <a href="#">ReactomeAnalysisRequest</a> to remove the dataset from |
| dataset_name | character The dataset's name   |

**Value**

The updated [ReactomeAnalysisRequest](#)

---

|   |
|---|
| remove_dataset, ReactomeAnalysisRequest-method  |
| <i>remove_dataset - ReactomeAnalysisRequest</i> |

---

**Description**

Remove the dataset from the [ReactomeAnalysisRequest](#) object.

**Usage**

```
## S4 method for signature 'ReactomeAnalysisRequest'  
remove_dataset(x, dataset_name)
```

**Arguments**

|              |  |
|--------------|--|
| x            | The <a href="#">ReactomeAnalysisRequest</a> to remove the dataset from |
| dataset_name | character The dataset's name   |

**Value**

The updated [ReactomeAnalysisRequest](#)

---

|              |                     |
|--------------|---------------------|
| result_types | <i>result_types</i> |
|--------------|---------------------|

---

**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)
```

---

|   |  |
|---|--|
| result_types, ReactomeAnalysisResult-method | <i>ReactomeAnalysisResult - result_types</i> |
|---|--|

---

**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**

```
## 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**

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

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

---

set\_method

*set\_method*

---

**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)
```

---

set\_method,ReactomeAnalysisRequest-method  
*set\_method - ReactomeAnalysisRequest*

---

### Description

Set the analysis method used by the [ReactomeAnalysisRequest](#)

### Usage

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

### Arguments

|         |   |
|---------|---|
| request | The <a href="#">ReactomeAnalysisRequest</a> to adjust   |
| method  | The name of the method to use. Use <a href="#">get_reactome_methods</a> 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 | <i>set_parameters</i> |
|----------------|-----------------------|

---

## 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

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

## Arguments

|         |  |
|---------|--|
| request | The <a href="#">ReactomeAnalysisRequest</a> to set the parameters for.   |
| ...     | Any name / value pair to set a parameter (see example). For a complete list of available parameters use <a href="#">get_reactome_methods</a> |

## 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")
```

---

set\_parameters,ReactomeAnalysisRequest-method

*ReactomeAnalysisRequest - 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

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

## Arguments

|         |  |
|---------|--|
| request | The <a href="#">ReactomeAnalysisRequest</a> to set the parameters for.   |
| ...     | Any name / value pair to set a parameter (see example). For a complete list of available parameters use <a href="#">get_reactome_methods</a> |

## 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  
  print - ReactomeAnalysisRequest
```

---

**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  
  show - ReactomeAnalysisResult
```

---

**Description**

Displays basic information about the [ReactomeAnalysisResult](#) object.

**Usage**

```
## 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)
```

---

split\_clustering            *method implementation subclustering*

---

**Description**

method implementation subclustering

**Usage**

```
split_clustering(seurat_object, group_by, res, alg, cluster1, cluster2)
```

**Arguments**

seurat\_object    The Seurat object to analyse.  
group\_by        entry in metadata table, based on these cluster annotation pseudo bulk is performed  
res             The clustering resolution to use.  
alg             Seurat subclustering algorithm id  
cluster1        cluster to subcluster  
cluster2        cluster to subcluster

**Value**

returns pseudo bulk generated data

---

split\_random\_sce      *split SCE Object with random pooling*

---

**Description**

split SCE Object with random pooling

**Usage**

```
split_random_sce(sce_object, group_by, k_variable)
```

**Arguments**

|            |   |
|------------|---|
| sce_object | The SingleCellExperiment object to analyse.   |
| group_by   | entry in metadata table, based on these cluster annotation pseudo bulk is performed |
| k_variable | number of pools that should be created  |

**Value**

returns pseudo bulk generated data

---

split\_subclustering\_sce  
*split SCE Object with random pooling*

---

**Description**

split SCE Object with random pooling

**Usage**

```
split_subclustering_sce(  
  sce_object,  
  group_by,  
  resolution,  
  subcluster_ref,  
  subcluster_comp  
)
```

**Arguments**

|                 |   |
|-----------------|---|
| sce_object      | The SingleCellExperiment object to analyse.   |
| group_by        | entry in metadata table, based on these cluster annotation pseudo bulk is performed |
| resolution      | resolution  |
| subcluster_ref  | cluster to subcluster as areference   |
| subcluster_comp | cluster to subcluster for comparison  |

**Value**

returns pseudo bulk generated data

---

|                       |  |
|-----------------------|--|
| <i>split_variable</i> | <i>split Seurat object by variable</i> |
|-----------------------|--|

---

**Description**

split Seurat object by variable

**Usage**

```
split_variable(seurat_object, group_by, k_variable)
```

**Arguments**

|               |   |
|---------------|---|
| seurat_object | The Seurat object to analyse.   |
| group_by      | entry in metadata table, based on these cluster annotation pseudo bulk is performed |
| k_variable    | variable dependent on the split_by -> meta data entry                               |

**Value**

returns pseudo bulk generated data

---

split\_variable\_random *split Seurat object by random pooling*

---

**Description**

split Seurat object by random pooling

**Usage**

```
split_variable_random(seurat_object, group_by, k_variable)
```

**Arguments**

|               |   |
|---------------|---|
| seurat_object | The Seurat object to analyse.   |
| group_by      | entry in metadata table, based on these cluster annotation pseudo bulk is performed |
| k_variable    | number of random pools  |

**Value**

returns pseudo bulk generated data

---

split\_variable\_sce *split SCE Object by variable*

---

**Description**

split SCE Object by variable

**Usage**

```
split_variable_sce(sce_object, group_by, k_variable)
```

**Arguments**

|            |   |
|------------|---|
| sce_object | The SingleCellExperiment object to analyse.   |
| group_by   | entry in metadata table, based on these cluster annotation pseudo bulk is performed |
| k_variable | variable for sub setting must be in the metadata                                    |

**Value**

returns pseudo bulk generated data

---

```
start_reactome_analysis
```

*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      | <a href="#">ReactomeAnalysisRequest</a> 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 <code>http://your.service:1234</code> ) |

## 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

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  
    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 http 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 example <code>http://your.service:1234</code> ) |

# Index

- \* **Reactome Service functions**
  - get\_reactome\_data\_types, 30
  - get\_reactome\_methods, 31
- \* **ReactomeAnalysisResult functions**
  - get\_result, 32
  - names, ReactomeAnalysisResult-method, 36
  - open\_reactome, 36
  - pathways, 38
  - plot\_correlations, 41
  - plot\_gsva\_heatmap, 43
  - plot\_gsva\_pathway, 45
  - plot\_heatmap, 49
  - plot\_volcano, 51
  - reactome\_links, 57
  - result\_types, 60
- \* **add\_dataset methods**
  - add\_dataset, 4
  - add\_dataset, ReactomeAnalysisRequest, data.frame-method, 5
  - add\_dataset, ReactomeAnalysisRequest, DGEList-method, 7
  - add\_dataset, ReactomeAnalysisRequest, EList-method, 9
  - add\_dataset, ReactomeAnalysisRequest, ExpressionSet-method, 11
  - add\_dataset, ReactomeAnalysisRequest, matrix-method, 13
- add\_dataset, 4, 7, 8, 10, 12, 14, 31
- add\_dataset, ReactomeAnalysisRequest, data.frame-method, 5
- add\_dataset, ReactomeAnalysisRequest, DGEList-method, 7
- add\_dataset, ReactomeAnalysisRequest, EList-method, 9
- add\_dataset, ReactomeAnalysisRequest, ExpressionSet-method, 11
- add\_dataset, ReactomeAnalysisRequest, matrix-method, 13
- analyse\_sc\_clusters, 14
- analyse\_sc\_clusters, Seurat-method, 16
- analyse\_sc\_clusters, SingleCellExperiment-method, 17
- break\_names, 18
- check\_reactome\_url, 19
- checkRequestValidity, 19
- convert\_reactome\_result, 20
- data\_frame\_as\_string, 20
- fetch\_public\_data, 21
- find\_public\_datasets, 21, 21, 35
- generate\_metadata, 22
- generate\_metadata, data.frame-method, 23
- generate\_pseudo\_bulk\_data, 22, 23, 24
- generate\_pseudo\_bulk\_data, Seurat-method, 25
- generate\_pseudo\_bulk\_data, SingleCellExperiment-method, 26
- get\_dataset\_loading\_status, 26
- get\_id\_for\_dataset, 27
- get\_is\_sig\_dataset, 27
- get\_public\_species, 22, 28
- get\_reactome\_analysis\_result, 28, 55
- get\_reactome\_analysis\_status, 28, 29
- get\_reactome\_data\_types, 4, 6, 8, 10, 11, 13, 30, 32
- get\_reactome\_methods, 30, 31, 61–64
- get\_result, 32, 36–39, 42, 44–47, 49–52, 56–58, 60, 61
- get\_result, ReactomeAnalysisResult-method, 33
- is\_gsva\_result, 34
- load\_public\_dataset, 35



- names, [32](#), [33](#), [56](#)
- names, ReactomeAnalysisResult-method, [36](#)
- open\_reactome, [33](#), [34](#), [36](#), [36](#), [38](#), [39](#), [42](#), [44–47](#), [49–52](#), [56–58](#), [60](#), [61](#)
- open\_reactome, ReactomeAnalysisResult-method, [37](#)
- pathways, [33](#), [34](#), [36–38](#), [38](#), [42](#), [44–47](#), [49–52](#), [56–58](#), [60](#), [61](#)
- pathways, ReactomeAnalysisResult-method, [39](#)
- perform\_reactome\_analysis, [28](#), [40](#), [55](#), [70](#)
- plot\_correlations, [33](#), [34](#), [36–39](#), [41](#), [44–47](#), [49–52](#), [57](#), [58](#), [60](#), [61](#)
- plot\_correlations, ReactomeAnalysisResult-method, [42](#)
- plot\_gsva\_heatmap, [33](#), [34](#), [36–39](#), [42](#), [43](#), [46](#), [47](#), [49–52](#), [57](#), [58](#), [60](#), [61](#)
- plot\_gsva\_heatmap, ReactomeAnalysisResult-method, [44](#)
- plot\_gsva\_pathway, [33](#), [34](#), [36–39](#), [42](#), [44](#), [45](#), [45](#), [49–52](#), [57](#), [58](#), [60](#), [61](#)
- plot\_gsva\_pathway, ReactomeAnalysisResult-method, [46](#)
- plot\_gsva\_pca, [47](#)
- plot\_gsva\_pca, ReactomeAnalysisResult-method, [48](#)
- plot\_heatmap, [33](#), [34](#), [36–39](#), [42](#), [44–47](#), [49](#), [51](#), [52](#), [57](#), [58](#), [60](#), [61](#)
- plot\_heatmap, ReactomeAnalysisResult-method, [50](#)
- plot\_volcano, [33](#), [34](#), [36–39](#), [42](#), [44–47](#), [49](#), [50](#), [51](#), [57](#), [58](#), [60](#), [61](#)
- plot\_volcano, ReactomeAnalysisResult-method, [52](#)
- print, ReactomeAnalysisRequest-method, [53](#)
- print, ReactomeAnalysisResult-method, [54](#)
- reactome\_links, [33](#), [34](#), [36–39](#), [42](#), [44–47](#), [49–52](#), [56](#), [57](#), [60](#), [61](#)
- reactome\_links, ReactomeAnalysisResult-method, [58](#)
- ReactomeAnalysisRequest, [4–6](#), [8](#), [10](#), [12](#), [14](#), [40](#), [53](#), [54](#), [59](#), [61–65](#), [70](#)
- ReactomeAnalysisResult, [15](#), [17](#), [18](#), [20](#), [32–34](#), [36](#), [43](#), [45–48](#), [54](#), [60](#), [65](#)
- ReactomeAnalysisResult (ReactomeAnalysisResult-class), [55](#)
- ReactomeAnalysisResult-class, [55](#)
- remove\_dataset, [59](#)
- remove\_dataset, ReactomeAnalysisRequest-method, [59](#)
- result\_types, [32–34](#), [36–39](#), [42](#), [44–47](#), [49–52](#), [56–58](#), [60](#)
- result\_types, ReactomeAnalysisResult-method, [60](#)
- set\_method, [61](#)
- set\_method, ReactomeAnalysisRequest-method, [62](#)
- set\_parameters, [31](#), [63](#)
- set\_parameters, ReactomeAnalysisRequest-method, [64](#)
- show, ReactomeAnalysisRequest-method, [65](#)
- show, ReactomeAnalysisResult-method, [65](#)
- split\_clustering, [66](#)
- split\_random\_sce, [67](#)
- split\_subclustering\_sce, [67](#)
- split\_variable, [68](#)
- split\_variable\_random, [69](#)
- split\_variable\_sce, [69](#)
- start\_reactome\_analysis, [29](#), [70](#)
- wait\_for\_loading\_dataset, [71](#)