

# Package ‘ReactomeGSA’

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**Type** Package

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

**Version** 1.23.0

**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, tidyr

**Suggests** devtools, knitr, ReactomeGSA.data, rmarkdown, scatter, scan, scRNAseq, scuttle, Seurat (>= 3.0), SingleCellExperiment, testthat

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---

|             |                    |
|-------------|--------------------|
| 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 expression_values or from sample_data.                               |
| comparison_group_1 | character. Name of the first group within comparison_factor to use for the comparison.                                                                                                          |
| comparison_group_2 | character. Name of the second group within comparison_factor to use for the comparison.                                                                                                         |
| sample_data        | data.frame (optional) data.frame containing the sample metadata of the expression_values. Depending on the object type of expression_values, this information can also be extracted from there. |
| additional_factors | vector. Vector of additional sample properties that are used as blocking factors (if supported by the chosen analysis method) in the gene set analysis.                                         |
| overwrite          | boolean. If set to TRUE, datasets with the same name will be overwritten                                                                                                                        |
| ...                | Additional parameters passed to downstream functions. See the respective documentation of whether any additional parameters are supported.                                                      |

## Value

The [ReactomeAnalysisRequest](#) object with the added dataset

## See Also

Other add\_dataset methods: [add\\_dataset, ReactomeAnalysisRequest, DGEList-method](#), [add\\_dataset, ReactomeAnalysisRequest, ExpressionSet-method](#), [add\\_dataset, ReactomeAnalysisRequest, data.frame-method](#), [add\\_dataset, ReactomeAnalysisRequest, matrix-method](#)

## 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

|                    |                                                                                                                                                                   |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| request            | ReactomeAnalysisRequest.                                                                                                                                          |
| expression_values  | data.frame. In this case, the sample_data must be set.                                                                                                            |
| name               | character. Name of the dataset. This must be unique within one request.                                                                                           |
| type               | character. The type of the dataset. Get available types using <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, ExpressionS](#), [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**

|                    |                                                                                                                                                                                                 |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| request            | ReactomeAnalysisRequest.                                                                                                                                                                        |
| expression_values  | DGEList 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.                                                                                                          |
| 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, 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 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, 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

|                                 |                                                                                                                                                                                              |
|---------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>request</code>            | ReactomeAnalysisRequest.                                                                                                                                                                     |
| <code>expression_values</code>  | ExpressionSet. 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.                                                                                         |

|                    |                                                                                                                                                                                                 |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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, 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**

|                                 |                                                                                                                                                                                                                                                       |
|---------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>request</code>            | <code>ReactomeAnalysisRequest</code> .                                                                                                                                                                                                                |
| <code>expression_values</code>  | <code>matrix</code> . 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>        | <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, ExpressionS](#), [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**

|                                       |                                                                                                                                                                  |
|---------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>object</code>                   | The object containing the single-cell RNA-sequencing data.                                                                                                       |
| <code>use_interactors</code>          | If set (default), protein-protein interactors from IntAct are used to extend Reactome pathways.                                                                  |
| <code>include_disease_pathways</code> | If set, disease pathways are included as well. Disease pathways in Reactome follow a different annotation approach and can therefore lead to inaccurate results. |

|                               |                                                                                                                           |
|-------------------------------|---------------------------------------------------------------------------------------------------------------------------|
| create_reactome_visualization | If set, the interactive visualization in Reactome's PathwayBrowser is created.                                            |
| create_reports                | If set, PDF and Microsoft Excel reports are created. Links to these report files are send to the supplied e-mail address. |
| report_email                  | The e-mail address to which reports should be sent to.                                                                    |
| verbose                       | If set, additional status messages are printed.                                                                           |
| ...                           | Parameters passed to the specific implementation. Detailed documentations can be found there.                             |

## Details

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

## Value

A [ReactomeAnalysisResult](#) object.

## Examples

```
# 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, 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**

|                                            |                                                                                                                                                                  |
|--------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>object</code>                        | The Seurat object containing the single cell RNA-sequencing data.                                                                                                |
| <code>use_interactors</code>               | If set (default), protein-protein interactors from IntAct are used to extend Reactome pathways.                                                                  |
| <code>include_disease_pathways</code>      | If set, disease pathways are included as well. Disease pathways in Reactome follow a different annotation approach and can therefore lead to inaccurate results. |
| <code>create_reactome_visualization</code> | If set, the interactive visualization in Reactome's PathwayBrowser is created.                                                                                   |
| <code>create_reports</code>                | If set, PDF and Microsoft Excel reports are created. Links to these report files are sent to the supplied e-mail address.                                        |
| <code>report_email</code>                  | The e-mail address to which reports should be sent to.                                                                                                           |
| <code>verbose</code>                       | If set, additional status messages are printed.                                                                                                                  |
| <code>assay</code>                         | By default, the "RNA" assay is used, which contains the original read counts.                                                                                    |
| <code>slot</code>                          | The slot in the Seurat object to use. Default and recommended approach is to use the raw counts.                                                                 |
| <code>...</code>                           | 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**

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

---

**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 (defaultl 46 chars.) |

**Value**

The list of adapted names

---

|                      |                                                             |
|----------------------|-------------------------------------------------------------|
| checkRequestValidity | <i>Check's if a ReactomeAnalysisRequest object is valid</i> |
|----------------------|-------------------------------------------------------------|

---

**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 | <i>check_reactome_url</i> |
|--------------------|---------------------------|

---

### 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 | <i>Convert the Reactome JSON result to a ReactomeAnalysisResult object</i> |
|-------------------------|----------------------------------------------------------------------------|

---

### 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 | <i>Converts a data.frame to a string representation</i> |
|----------------------|---------------------------------------------------------|

---

**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 | <i>fetch_public_data</i> |
|-------------------|--------------------------|

---

**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 <a href="#">find_public_datasets</a> 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 | <i>find_public_datasets</i> |
|----------------------|-----------------------------|

---

## 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 [generate\\_pseudo\\_bulk\\_data](#) 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 |
| <i>Generate metadata</i>             |

---

**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 | <i>get_fc_for_dataset</i> |
|--------------------|---------------------------|

---

**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 | <i>get_is_sig_dataset</i> |
|--------------------|---------------------------|

---

**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 | <i>get_public_species</i> |
|--------------------|---------------------------|

---

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

### 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 | <i>Retrieves the result of the submitted analysis using</i><br><i>perform_reactome_analysis</i> |
|------------------------------|-------------------------------------------------------------------------------------------------|

---

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

**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**

|                           |                                                                                                                                                                                                              |
|---------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>analysis_id</code>  | The running analysis' id                                                                                                                                                                                     |
| <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 list containing the id, status (can be "running", "complete", "failed"), description, and completed (numeric between 0 - 1)

---

`get_reactome_data_types`

*ReactomeGSA supported data types*

---

**Description**

ReactomeGSA supported data types

**Usage**

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

**Arguments**

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

|      |                                                                                       |
|------|---------------------------------------------------------------------------------------|
| 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)
```

---

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)
```

---

|                |                       |
|----------------|-----------------------|
| is_gsva_result | <i>is_gsva_result</i> |
|----------------|-----------------------|

---

**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 | <i>load_public_dataset</i> |
|---------------------|----------------------------|

---

**Description**

Loads a public dataset that was found through the [find\\_public\\_datasets](#) function. The dataset is returned as a Biobase ExpressionSet object.

**Usage**

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

**Arguments**

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

**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 | <i>open_reactome</i> |
|---------------|----------------------|

---

**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  |
| <i>open_reactome - ReactomeAnalysisResult</i> |

---

**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 | <i>plot_correlations</i> |
|-------------------|--------------------------|

---

## Description

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

## Usage

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

## Arguments

**x** ReactomeAnalysisResult. The result object to use as input

**hide\_non\_sig** If set, non-significant pathways are not shown.

## Value

A list of ggplot2 plot objects representing one plot per combination

## See Also

Other ReactomeAnalysisResult functions: [get\\_result\(\)](#), [names, ReactomeAnalysisResult-method](#), [open\\_reactome\(\)](#), [pathways\(\)](#), [plot\\_gsva\\_heatmap\(\)](#), [plot\\_gsva\\_pathway\(\)](#), [plot\\_heatmap\(\)](#), [plot\\_volcano\(\)](#), [reactome\\_links\(\)](#), [result\\_types\(\)](#)

## Examples

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

# create the correlation plots
```

```
plot_objs <- plot_correlations(griss_melanoma_result)

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

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

---

```
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 | <i>plot_gsva_heatmap</i> |
|-------------------|--------------------------|

---

## 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 | <i>plot_gsva_pathway</i> |
|-------------------|--------------------------|

---

**Description**

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

**Usage**

```
plot_gsva_pathway(object, pathway_id, ...)
```

**Arguments**

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

---

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

---

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

---

### 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**

|             |                                                                                                   |
|-------------|---------------------------------------------------------------------------------------------------|
| 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 are passed to prcomp                                                        |

**Value**

A ggplot2 object representing the plot.

**Examples**

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

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

---

plot\_heatmap

*plot\_heatmap*


---

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

*result\_types*


---

### Description

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

### Usage

```
result_types(x)
```

### Arguments

x                      [ReactomeAnalysisResult](#).

### Value

A character vector of result types.

### See Also

Other [ReactomeAnalysisResult](#) functions: [get\\_result\(\)](#), [names](#), [ReactomeAnalysisResult-method](#), [open\\_reactome\(\)](#), [pathways\(\)](#), [plot\\_correlations\(\)](#), [plot\\_gsva\\_heatmap\(\)](#), [plot\\_gsva\\_pathway\(\)](#), [plot\\_heatmap\(\)](#), [plot\\_volcano\(\)](#), [reactome\\_links\(\)](#)

### Examples

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

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

---

result\_types, [ReactomeAnalysisResult-method](#)
*ReactomeAnalysisResult - result\_types*


---

### Description

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

**Usage**

```
## 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 <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\_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  |
| <i>ReactomeAnalysisRequest - 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**

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

**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 | <i>split SCE Object with random pooling</i> |
|------------------|---------------------------------------------|

---

**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

---

split\_variable

*split Seurat object by variable*


---

### 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 | <i>split Seurat object by random pooling</i> |
|-----------------------|----------------------------------------------|

---

**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 | <i>split SCE Object by variable</i> |
|--------------------|-------------------------------------|

---

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

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