

Package ‘DeeDeeExperiment’

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Title DeeDeeExperiment: An S4 Class for managing and exploring omics analysis results

Version 1.0.0

Description DeeDeeExperiment is an S4 class extending the SingleCellExperiment class, designed to integrate and manage omics analysis results. It introduces two dedicated slots to store Differential Expression Analysis (DEA) results and Functional Enrichment Analysis (FEA) results, providing a structured approach for downstream analysis.

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BugReports <https://github.com/imbeimainz/DeeDeeExperiment/issues>

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Contents

clusterPro_res	2
dd_list_original	3
DeeDeeExperiment-class	3
DeeDeeExperiment-methods	5
DeeDeeExperiment-misc	9
DeeDeeExperiment-pkg	10
de_limma	11
de_named_list	11
dge_exact_IFNg_both	12
dge_exact_IFNg_naive	12
dge_exact_Salm_both	13
dge_exact_Salm_naive	14
dge_lrt_IFNg_both	14
dge_lrt_IFNg_naive	15
dge_lrt_Salm_both	16
dge_lrt_Salm_naive	16
enrichr_res	17
fgseaRes	17
gost_res	18
gsea_res	18
IFNg_both	19
IFNg_naive	19
Salm_both	20
Salm_naive	21
supported_fea_formats	21
topGO_results_list	22
Index	23

clusterPro_res	clusterPro_res
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Description

A list of FE results generated with clusterProfiler::enrichGO()

Format

A list of enrichResult objects

Details

A list of FE result for the macrophage data (salmonella vs naive and IFNg vs naive)

Value

A list

See Also

Other enrich_resus: [enrichr_res](#), [fgseaRes](#), [gost_res](#), [gsea_res](#), [topGO_results_list](#)

dd_list_original	<i>dd_list_original</i>
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Description

A list of deedee_prepared DE results.

Format

A list object

Details

documented creation in ... script

Value

A list of DE results

DeeDeeExperiment-class	<i>The DeeDeeExperiment class</i>
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Description

The DeeDeeExperiment class is integrate and manage omics analysis results. It inherits from the SingleCellExperiment class, and additionally stores DE-related/functional enrichment information via dedicated slots and rowData.

Usage

```
DeeDeeExperiment(
  sce = SingleCellExperiment(),
  de_results = NULL,
  enrich_results = NULL
)
```

Arguments

sce	A SingleCellExperiment object, that will be used as a scaffold to store the DE related information.
de_results	A named list of DE results, in any of the formats supported by the package (currently: results from DESeq2, edgeR, limma).
enrich_results	A named list of functional enrichment results. Each element can be either a data.frame (currently supports results from topGO, enrichR, gProfiler, fgsea, gsea, DAVID, and output of GeneTonic shakers), or an enrichResult/gseaResult objects (currently supports clusterProfiler)

Details

The `sce` parameter can be optionally left unspecified. If this is the case, the resulting `DeeDeeExperiment` object will contain as features the ones specified by the provided components of the object supplied via the `de_results` parameter.

The conversion of the components of the `de_results` list will be handled via conversion functions to uniform the names and set of information which will be stored in the returned `DeeDeeExperiment` object. The names of the list will be used to define the contrasts for the different DE analyses included, which will determine the way to access the information stored in the `dea` slot of the `DeeDeeExperiment` object.

The content of the `enrich_results` provided by the user will be validated to ensure that it is properly formatted and correctly named. The FE tool can be automatically detected, and based on that, the appropriate shaking method is used to return a standardized format of the FEA results. The names of the list will be used to attempt to associate each enrichment result with a corresponding DE contrast stored in the `DeeDeeExperiment` object, but it also can be defined by the user.

Since a `DeeDeeExperiment` is also a `SummarizedExperiment` object, it can be seamlessly provided downstream for visualization and in-depth exploration to packages such as `iSEE` or similar.

Value

A `DeeDeeExperiment` object.

Slots

`dea` This slot is designed to hold the DE-related information. This is internally being created upon importing from the list of DE results objects, provided when instantiating the [DeeDeeExperiment](#).

`fea` This slot is designed to hold Functional Enrichment related information.

Author(s)

Najla Abassi, Lea Rothörl, and Federico Marini

Examples

```
data("de_named_list", package = "DeeDeeExperiment")

dde_onlyde <- DeeDeeExperiment(
  de_results = de_named_list
)

# or, with a SE object as support - even without assay data available
library("SummarizedExperiment")

rd_macrophage <- DataFrame(
  gene_id = rownames(de_named_list$ifng_vs_naive)
)
rownames(rd_macrophage) <- rownames(de_named_list$ifng_vs_naive)
se_macrophage_noassays <- SummarizedExperiment(
  assays = SimpleList(),
  rowData = rd_macrophage
)

dde <- DeeDeeExperiment(
```

```

    se_macrophage_noassays,
    de_results = de_named_list
  )

```

DeeDeeExperiment-methods

Methods for [DeeDeeExperiment](#) objects

Description

The [DeeDeeExperiment\(\)](#) class provides a family of methods to get and set DE-related information and functional enrichment results in [DeeDeeExperiment](#) objects.

Usage

```

## S4 method for signature 'DeeDeeExperiment'
getDEAInfo(x)

## S4 replacement method for signature 'DeeDeeExperiment'
getDEAInfo(x) <- value

## S4 method for signature 'DeeDeeExperiment'
getDEANames(x)

## S4 method for signature 'DeeDeeExperiment'
renameDEA(x, old_name, new_name)

## S4 method for signature 'DeeDeeExperiment'
addDEA(x, dea, force = FALSE)

## S4 method for signature 'DeeDeeExperiment'
removeDEA(x, dea_name, remove_linked_fea = FALSE)

## S4 method for signature 'DeeDeeExperiment'
getDEA(
  x,
  dea_name = NULL,
  format = c("minimal", "original"),
  extra_rd = NULL,
  type = c("DFrame", "data.frame"),
  verbose = FALSE
)

## S4 method for signature 'DeeDeeExperiment'
getDEAList(x, format = c("minimal", "original"), verbose = FALSE)

## S4 method for signature 'DeeDeeExperiment'
addScenarioInfo(x, dea_name, info = NULL, force = FALSE)

## S4 method for signature 'DeeDeeExperiment'
getFEAInfo(x)

```

```

## S4 replacement method for signature 'DeeDeeExperiment'
getFEAInfo(x) <- value

## S4 method for signature 'DeeDeeExperiment'
getFEANames(x)

## S4 method for signature 'DeeDeeExperiment'
renameFEA(x, old_name, new_name)

## S4 method for signature 'DeeDeeExperiment'
addFEA(
  x,
  fea,
  de_name = NA_character_,
  fe_name = NULL,
  fea_tool = "auto",
  force = FALSE,
  verbose = FALSE
)

## S4 method for signature 'DeeDeeExperiment'
removeFEA(x, fea_name)

## S4 method for signature 'DeeDeeExperiment'
getFEA(x, fea_name = NULL, format = c("minimal", "original"), verbose = FALSE)

## S4 method for signature 'DeeDeeExperiment'
getFEAList(
  x,
  dea_name = NULL,
  format = c("minimal", "original"),
  verbose = FALSE
)

## S4 method for signature 'DeeDeeExperiment'
linkDEAandFEA(x, dea_name, fea_name, force = FALSE)

```

Arguments

<code>x</code>	A <code>DeeDeeExperiment()</code> object
<code>value</code>	Replacement value for replacement methods.
<code>old_name</code>	A character vector of existing DEA names to be renamed in a <code>DeeDeeExperiment</code> object
<code>new_name</code>	A character vector with new names to assign to existing DEA names in a <code>DeeDeeExperiment</code> object. It must be the same length of <code>old_name</code> , and contains unique values that don't overlap with existing DEA names.
<code>dea</code>	A named list of DE results, in any of the formats supported by the package (currently: results from <code>DESeq2</code> , <code>edgeR</code> , <code>limma</code>).
<code>force</code>	A logical, indicating whether to overwrite results when introducing the same results name. It defaults to <code>FALSE</code> .

dea_name	Character value, specifying the name of the DE analysis to get or remove, or match against (e.g., to fetch associated FEA results), or to which additional context and information can be attached
remove_linked_fea	A logical, specifying whether to remove or not the linked FEA when a DEA results is removed
format	A character string, specifying the DEA/FEAs output format. It takes either "minimal" to return only essential columns (e.g. log2FC, p-value, adjusted p-value for DEAs, or gs_id, gs_description, gs_pvalue, gs_genes... for FEAs), or "original" to return the full result object. It defaults to "minimal"
extra_rd	A character vector of additional columns from rowData(x) to include. It defaults to c("gene_id", "SYMBOL").
type	A character string referring to the type of object returned by getDEA(). It defaults to DFrame, but can also take the value of data.frame
verbose	Logical, whether or not to display warnings. If TRUE, warnings/messages will be displayed. If FALSE, the function runs silently
info	A character vector, containing contextual information about the specified DE analysis. It defaults to NULL
fea	A named list of Functional Enrichment results. Each element can be either a data.frame (currently supports results from topGO, enrichR, gProfiler, fgsea, gsea, DAVID, and output of GeneTonic shakers), or an enrichResult/gseaResult objects (currently supports clusterProfiler)
de_name	A character string to explicitly specify the name of the de result this fea should be linked to. If not provided, the function will attempt to match fea names to de results automatically.
fe_name	A character string giving a name to the FE results.
fea_tool	A character string indicating the FEA tool used. It can take any of the following values : "topGO", "clusterProfiler", "GeneTonic", "DAVID", "gsea", "fgsea", "enrichr", "gProfiler". When not specified, it defaults to "auto" and the tool is inferred automatically based on the input.
fea_name	Character value, specifying the name of the functional enrichment result to add or remove

Details

DEAs

- getDEAInfo and getDEAInfo<- are the methods to get and set the dea information as a whole. These methods return DeeDeeExperiment objects.
- getDEANames returns the names of the available DE contrasts in DeeDeeExperiment objects.
- renameDEA is the method to rename one or multiple DEAs stored in a DeeDeeExperiment object.
- addDEA and removeDEA are used to respectively add or remove DE-results items. These methods also return DeeDeeExperiment objects, with updated content in the dea slot.
- dea and getDEAList retrieve the DEA information, as well as some extra rowData information and provide this as a DataFrame object (for a specific analysis) or as a list, with one element for each reported analysis.

- `addScenarioInfo` is the method to add user defined contextual information for a specific DE analysis. It allows users to attach free-text notes to a specific DEA results that stored in a `DeeDeeExperiment` object. This information can include any other relevant information to help document that DEA scenario. This context is stored in the `dea` slot under the name `scenario_info`, which is not a default element in `dea`.

FEAs

- `getFEAInfo` and `getFEAInfo<-` are the methods to get and set the fea information as a whole. These methods return `DeeDeeExperiment` objects.
- `getFEANames` returns the names of the available enrichment results in `DeeDeeExperiment` objects.
- `renameFEA` is the method to rename one or multiple FEAs stored in a `DeeDeeExperiment` object.
- `addFEA` and `removeFEA` are used to respectively add or remove functional enrichment results items. These methods also return `DeeDeeExperiment` objects, with updated content in the `fea` slot.
- `fea` is the method to retrieve FE results stored in a `DeeDeeExperiment` object for a specific contrast, as a standardized format similar to the output of `GeneTonic` shakers.
- `getFEAList` is the method that retrieves FEA results as a list. if the `dea_name` is indicated, the method will return only FEAs linked to that `dea_name`, otherwise it returns all FEAs in the `fea` slot.
- `linkDEAandFEA` is the method that allows the user to manually link a FEA result to a specific DEA result.
- `show` is the method to nicely print out the information of a `DeeDeeExperiment` object.
- `summary` is the method to print a summary of the available DE and FE results in a `DeeDeeExperiment` object.

Value

Return value varies depending on the individual methods, as described below.

Examples

```
data("de_named_list", package = "DeeDeeExperiment")
data("topGO_results_list", package = "DeeDeeExperiment")
library("SummarizedExperiment")

rd_macrophage <- DataFrame(
  gene_id = rownames(de_named_list$ifng_vs_naive)
)
rownames(rd_macrophage) <- rownames(de_named_list$ifng_vs_naive)
se_macrophage_noassays <- SummarizedExperiment(
  assays = SimpleList(),
  rowData = rd_macrophage
)

# creating a `DeeDeeExperiment`
dde <- DeeDeeExperiment(
  se_macrophage_noassays,
  de_results = de_named_list
)
dde
```



```

new_del <- list(
  ifng2 = de_named_list$ifng_vs_naive,
  ifngsalmo2 = de_named_list$ifngsalmo_vs_naive
)

# add a new (set of) DE result(s)
dde_new <- addDEA(dde, new_del)
dde_new

# removing DEAs
dde_removed <- removeDEA(dde, "ifng_vs_naive")
dde_removed

# add a new (set of) FE result(s)
dde_new <- addFEA(dde, fea = topGO_results_list)

# removing FEAs
dde_rem <- removeFEA(dde_new, "ifng_vs_naive")

# display available DEAs
getDEANames(dde)

# display available FEAs
getFEANames(dde)

# print a summary of the available DEAs and FEAs
summary(dde, FDR = 0.01)

# rename DEA
dde_new <- renameDEA(dde_new,
  old_name = "salmonella_vs_naive",
  new_name = "Salmo_vs_Naive_renamed"
)

# assign DEA to FEA
dde_new <- linkDEAandFEA(dde_new,
  dea_name = "ifngsalmo_vs_naive",
  fea_name = "ifngsalmo_vs_naive"
)

```

DeeDeeExperiment-misc *Miscellaneous DeeDeeExperiment methods*

Description

Miscellaneous methods for the [DeeDeeExperiment](#) class and its descendants that do not fit into any other documentation category such as, for example, show and summary methods.

Usage

```
## S4 method for signature 'DeeDeeExperiment'
```

```
show(object)
```

```
## S4 method for signature 'DeeDeeExperiment'
summary(object, FDR = 0.05, show_scenario_info = FALSE, ...)
```

Arguments

<code>object</code>	a DeeDeeExperiment object
<code>FDR</code>	Numeric, sets the significance threshold for subsetting differentially expressed genes based on adjusted p-values. Defaults to 0.05
<code>show_scenario_info</code>	Logical; if TRUE, displays the associated scenario info for each DE contrast, if available. Defaults to FALSE
<code>...</code>	additional argument passed to the summary method. Currently supports: <ul style="list-style-type: none"> • <code>FDR</code>: Numeric, sets the significance threshold for subsetting differentially expressed genes based on adjusted p-values. Defaults to 0.05 • <code>show_scenario_info</code>: Logical; if TRUE, displays the associated scenario info for each DE contrast, if available.

Value

Returns NULL

DeeDeeExperiment-pkg *DeeDeeExperiment*

Description

DeeDeeExperiment is a an S4 class that allows integrating and managing transcriptomic analysis results.

Details

DeeDeeExperiment is an S4 class extending the SummarizedExperiment framework to facilitate the integration and management of transcriptomic analysis results. It introduces two dedicated slots to store Differential Expression (DE) analysis results and Functional Enrichment analysis outcomes, providing a structured approach for downstream analysis.

Author(s)

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See Also

Useful links:

- <https://github.com/imbeimainz/DeeDeeExperiment>
- Report bugs at <https://github.com/imbeimainz/DeeDeeExperiment/issues>

de_limma	<i>A sample MArrayLM object</i>
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Description

A sample MArrayLM object, generated with limma

Format

A MArrayLM object

Details

This MArrayLM object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with different stimulation conditions, including IFN γ treatment, Salmonella infection, and their combined effects.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample MArrayLM object, generated with limma

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", *Nature Genetics*, January 2018 doi: 10.1038/s41588-018-0046-7.

de_named_list	<i>de_named_list</i>
---------------	----------------------

Description

A named list of DE results, in their original format (from DESeq2, edgeR or limma)

Format

A list object

Details

documented creation in the `create_dataset_example.R` script in the `scripts` package folder

Value

A named list of DE results, in their original format

dge_exact_IFNg_both *A sample DGEEExact object*

Description

A sample DGEEExact object, generated with edgeR

Format

A DGEEExact object

Details

This DGEEExact object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with IFNg to those associated with IFNg and Salmonella.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DGEEExact object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_exact_IFNg_naive *A sample DGEEExact object*

Description

A sample DGEEExact object, generated with edgeR

Format

A DGEEExact object

Details

This DGEEExact object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from naive macrophage to those associated with IFNg.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DGEEExact object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_exact_Salm_both	<i>A sample DGEEExact object</i>
---------------------	----------------------------------

Description

A sample DGEEExact object, generated with edgeR

Format

A DGEEExact object

Details

This DGEEExact object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with Salmonella to those associated with IFNg and Salmonella.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample DGEEExact object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_exact_Salm_naive *A sample DGEEexact object*

Description

A sample DGEEexact object, generated with edgeR

Format

A DGEEexact object

Details

This DGEEexact object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from naive macrophage to those associated with Salmonella.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DGEEexact object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_lrt_IFNg_both *A sample DGELRT object*

Description

A sample DGELRT object, generated with edgeR

Format

A DGELRT object

Details

This DGELRT object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with IFNg to those associated with IFNg and Salmonella.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DGELRT object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_lrt_IFNg_naive	<i>A sample DGELRT object</i>
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Description

A sample DGELRT object, generated with edgeR

Format

A DGELRT object

Details

This DGELRT object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with IFNg to those associated with IFNg and naive.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DGELRT object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_Salm_both](#), [dge_lrt_Salm_naive](#)

dge_lrt_Salm_both	<i>A sample DGELRT object</i>
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Description

A sample DGELRT object, generated with edgeR

Format

A DGELRT object

Details

This DGELRT object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with Salmonella to those associated with IFNg and Salmonella.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample DGELRT object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", *Nature Genetics*, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_naive](#)

dge_lrt_Salm_naive	<i>A sample DGELRT object</i>
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Description

A sample DGELRT object, generated with edgeR

Format

A DGELRT object

Details

This DGELRT object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from naive macrophage to those associated with Salmonella.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample DGELRT object, generated with edgeR

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other edgeRresus: [dge_exact_IFNg_both](#), [dge_exact_IFNg_naive](#), [dge_exact_Salm_both](#), [dge_exact_Salm_naive](#), [dge_lrt_IFNg_both](#), [dge_lrt_IFNg_naive](#), [dge_lrt_Salm_both](#)

enrichr_res	enrichr_res
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Description

A list of FE results generated with enrichr::enrichr()

Format

A list of data.frame objects

Details

A list of FE result for the macrophage data (salmonella vs naive)

Value

A list

See Also

Other enrich_resus: [clusterPro_res](#), [fgseaRes](#), [gost_res](#), [gsea_res](#), [topGO_results_list](#)

fgseaRes	fgseaRes
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Description

A data frame of FE results generated with fgsea::fgsea()

Format

A data.table/data.frame object

Details

Tabular representation of FE result for the macrophage data (IFNg vs naive)

Value

A data.table/data.frame

See Also

Other enrich_resus: [clusterPro_res](#), [enrichr_res](#), [gost_res](#), [gsea_res](#), [topGO_results_list](#)

<code>gost_res</code>	<code>gost_res</code>
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Description

A list of FE results generated with `gprofiler2::gost()`

Format

A list, as returned by `gprofiler2`

Details

A list of FE result for the macrophage data (salmonella vs naive)

Value

A list

See Also

Other enrich_resus: [clusterPro_res](#), [enrichr_res](#), [fgseaRes](#), [gsea_res](#), [topGO_results_list](#)

<code>gsea_res</code>	<code>gsea_res</code>
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Description

An individual set of FE results generated with `clusterProfiler::gseGO()`

Format

A `gseaResult` object

Details

A set of FE results for the macrophage data (IFNg vs naive)

Value

A `gseaResult` object

See Also

Other enrich_resus: [clusterPro_res](#), [enrichr_res](#), [fgseaRes](#), [gost_res](#), [topGO_results_list](#)

IFNg_both	<i>A sample DESeqResults object</i>
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Description

A sample DESeqResults object, generated with DESeq2

Format

A DESeqResults object

Details

This DESeqResults object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from macrophage associated with IFNg to those associated with IFNg and Salmonella.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample DESeqResults object, generated with DESeq2

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other DResus: [IFNg_naive](#), [Salm_both](#), [Salm_naive](#)

IFNg_naive	<i>A sample DESeqResults object</i>
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Description

A sample DESeqResults object, generated with DESeq2

Format

A DESeqResults object

Details

This DESeqResults object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from naive macrophage to those associated with IFNg.

The code to create said object can be found in the folder /inst/scripts in the DeeDeeExperiment package, the file is called generate_data.R.

Value

A sample `DESeqResults` object, generated with `DESeq2`

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", *Nature Genetics*, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other `DResus`: [IFNg_both](#), [Salm_both](#), [Salm_naive](#)

Salm_both	<i>A sample DESeqResults object</i>
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Description

A sample `DESeqResults` object, generated with `DESeq2`

Format

A `DESeqResults` object

Details

This `DESeqResults` object contains the results of a Differential Expression Analysis performed on data from the `macrophage` package, more precisely contrasting the counts from macrophage associated with *Salmonella* to those associated with IFNg and *Salmonella*.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample `DESeqResults` object, generated with `DESeq2`

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", *Nature Genetics*, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other `DResus`: [IFNg_both](#), [IFNg_naive](#), [Salm_naive](#)

Salm_naive	<i>A sample DESeqResults object</i>
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Description

A sample DESeqResults object, generated with DESeq2

Format

A DESeqResults object

Details

This DESeqResults object contains the results of a Differential Expression Analysis performed on data from the macrophage package, more precisely contrasting the counts from naive macrophage to those associated with Salmonella.

The code to create said object can be found in the folder `/inst/scripts` in the `DeeDeeExperiment` package, the file is called `generate_data.R`.

Value

A sample DESeqResults object, generated with DESeq2

References

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", *Nature Genetics*, January 2018 doi: 10.1038/s41588-018-0046-7.

See Also

Other DResus: [IFNg_both](#), [IFNg_naive](#), [Salm_both](#)

supported_fea_formats	<i>Display available FEA formats</i>
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Description

Display available FEA formats

Usage

```
supported_fea_formats()
```

Value

a data.frame of possible FEA input formats

Examples

```
supported_fea_formats()
```

topGO_results_list	topGO_results_list
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Description

A list of FE results generated with `mosdef::topGOtable()`

Format

A list of `data.frame` objects

Details

A list of FE results for the macrophage data

Value

A list

See Also

Other `enrich_resus`: [clusterPro_res](#), [enrichr_res](#), [fgseaRes](#), [gost_res](#), [gsea_res](#)

Index

- * **DEResus**
 - IFNg_both, [19](#)
 - IFNg_naive, [19](#)
 - Salm_both, [20](#)
 - Salm_naive, [21](#)
- * **edgeRresus**
 - dge_exact_IFNg_both, [12](#)
 - dge_exact_IFNg_naive, [12](#)
 - dge_exact_Salm_both, [13](#)
 - dge_exact_Salm_naive, [14](#)
 - dge_lrt_IFNg_both, [14](#)
 - dge_lrt_IFNg_naive, [15](#)
 - dge_lrt_Salm_both, [16](#)
 - dge_lrt_Salm_naive, [16](#)
- * **enrich_resus**
 - clusterPro_res, [2](#)
 - enrichr_res, [17](#)
 - fgseaRes, [17](#)
 - gost_res, [18](#)
 - gsea_res, [18](#)
 - topGO_results_list, [22](#)
- .DeeDeeExperiment
 - (DeeDeeExperiment-class), [3](#)
- addDEA (DeeDeeExperiment-methods), [5](#)
- addDEA, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- addFEA (DeeDeeExperiment-methods), [5](#)
- addFEA, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- addScenarioInfo
 - (DeeDeeExperiment-methods), [5](#)
- addScenarioInfo, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- clusterPro_res, [2](#), [17](#), [18](#), [22](#)
- dd_list_original, [3](#)
- de_limma, [11](#)
- de_named_list, [11](#)
- DeeDeeExperiment, [4](#), [5](#), [9](#), [10](#)
- DeeDeeExperiment
 - (DeeDeeExperiment-class), [3](#)
- DeeDeeExperiment(), [5](#), [6](#)
- DeeDeeExperiment-class, [3](#)
- DeeDeeExperiment-methods, [5](#)
- DeeDeeExperiment-misc, [9](#)
- DeeDeeExperiment-package
 - (DeeDeeExperiment-pkg), [10](#)
- DeeDeeExperiment-pkg, [10](#)
- dge_exact_IFNg_both, [12](#), [13–17](#)
- dge_exact_IFNg_naive, [12](#), [12](#), [13–17](#)
- dge_exact_Salm_both, [12](#), [13](#), [13](#), [14–17](#)
- dge_exact_Salm_naive, [12](#), [13](#), [14](#), [15–17](#)
- dge_lrt_IFNg_both, [12–14](#), [14](#), [15–17](#)
- dge_lrt_IFNg_naive, [12–15](#), [15](#), [16](#), [17](#)
- dge_lrt_Salm_both, [12–15](#), [16](#), [17](#)
- dge_lrt_Salm_naive, [12–16](#), [16](#)
- enrichr_res, [2](#), [17](#), [18](#), [22](#)
- fgseaRes, [2](#), [17](#), [17](#), [18](#), [22](#)
- getDEA (DeeDeeExperiment-methods), [5](#)
- getDEA, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getDEAInfo (DeeDeeExperiment-methods), [5](#)
- getDEAInfo, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getDEAInfo<-
 - (DeeDeeExperiment-methods), [5](#)
- getDEAInfo<- , DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getDEAList (DeeDeeExperiment-methods), [5](#)
- getDEAList, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getDEANames (DeeDeeExperiment-methods), [5](#)
- getDEANames, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getFEA (DeeDeeExperiment-methods), [5](#)
- getFEA, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getFEAInfo (DeeDeeExperiment-methods), [5](#)
- getFEAInfo, DeeDeeExperiment-method
 - (DeeDeeExperiment-methods), [5](#)
- getFEAInfo<-
 - (DeeDeeExperiment-methods), [5](#)

getFEAInfo<- ,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
getFEAList (DeeDeeExperiment-methods), [5](#)
getFEAList,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
getFEANames (DeeDeeExperiment-methods),
 [5](#)
getFEANames,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
gost_res, [2](#), [17](#), [18](#), [18](#), [22](#)
gsea_res, [2](#), [17](#), [18](#), [18](#), [22](#)

IFNg_both, [19](#), [20](#), [21](#)
IFNg_naive, [19](#), [19](#), [20](#), [21](#)

linkDEAandFEA
 (DeeDeeExperiment-methods), [5](#)
linkDEAandFEA,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)

removeDEA (DeeDeeExperiment-methods), [5](#)
removeDEA,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
removeFEA (DeeDeeExperiment-methods), [5](#)
removeFEA,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
renameDEA (DeeDeeExperiment-methods), [5](#)
renameDEA,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)
renameFEA (DeeDeeExperiment-methods), [5](#)
renameFEA,DeeDeeExperiment-method
 (DeeDeeExperiment-methods), [5](#)

Salm_both, [19](#), [20](#), [20](#), [21](#)
Salm_naive, [19](#), [20](#), [21](#)
show,DeeDeeExperiment-method
 (DeeDeeExperiment-misc), [9](#)
summary,DeeDeeExperiment-method
 (DeeDeeExperiment-misc), [9](#)
supported_fea_formats, [21](#)

topGO_results_list, [2](#), [17](#), [18](#), [22](#)