Package 'DeeDeeExperiment'

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

Version 1.2.0

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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Contents

clusterPro_res . . . 3
dd_list_original . . . 3
DeeDeeExperiment-class . . . 4
DeeDeeExperiment-methods . . . 5
DeeDeeExperiment-misc . . . 10
DeeDeeExperiment-pkg . . . 11
de_limma . . . 12
de_named_list . . . 13
dge_exact_IFNg_both . . . 13
dge_exact_IFNg_naive . . . 14
dge_exact_Salm_both . . . 15
dge_exact_Salm_naive . . . 15
dge_lrt_IFNg_both . . . 16
dge_lrt_IFNg_naive . . . 17
dge_lrt_Salm_both . . . 18
dge_lrt_Salm_naive . . . 18
enrichr_res . . . 19
export_result_for_dde . . . 20
fgseaRes . . . 21
gost_res . . . 21
gsea_res . . . 22
IFNg_both . . . 22
IFNg_naive . . . 23
limma_list_for_dde . . . 24
muscat_list_for_dde . . . 25
muscat_res . . . 26
Salm_both . . . 26
Salm_naive . . . 27
supported_fea_formats . . . 28
topGO_results_list . . . 28

Index **29**

clusterPro_res clusterPro_res

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 *dd_list_original*

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 *The DeeDeeExperiment class*

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, muscat).
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 Schwarz, 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

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

object	a DeeDeeExperiment object
FDR	Numeric, sets the significance threshold for subsetting differentially expressed genes based on adjusted p-values. Defaults to 0.05
show_scenario_info	Logical; if TRUE, displays the associated scenario info for each DE contrast, if available. Defaults to FALSE
...	additional argument passed to the summary method. Currently supports: • FDR: Numeric, sets the significance threshold for subsetting differentially expressed genes based on adjusted p-values. Defaults to 0.05 • show_scenario_info: 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 omics analysis results.

Details

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

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See Also

Useful links:

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

---

`de_limma` *A sample* `MArrayLM` *object*

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 IFNg 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 *de_named_list*

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* `DGEExact` *object*

Description

A sample `DGEExact` object, generated with `edgeR`

Format

A `DGEExact` object

Details

This `DGEExact` 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 `DGEExact` 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* DGEExact *object*

Description

A sample DGEExact object, generated with edgeR

Format

A DGEExact object

Details

This DGEExact 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 DGEExact 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 *A sample* DGEExact *object*

Description

A sample DGEExact object, generated with edgeR

Format

A DGEExact object

Details

This DGEExact 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 DGEExact 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* DGEExact *object*

Description

A sample DGEExact object, generated with edgeR

Format

A DGEExact object

Details

This DGEExact 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 DGEExact 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 *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 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 *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 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 *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 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

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

export_result_for_dde *Export DEA/FEA/ASSAY results from a* DeeDeeExperiment *to excel files*

Description

Extracts DEA and/or FEA results stored in a DeeDeeExperiment and writes them to excel files. Each contrast/result is written to a separate sheet. DEA and FEA are written to separate files.

Usage

```
export_result_for_dde(
  x,
  res_type = c("assay", "dea", "fea", "all"),
  res_format = c("minimal", "original"),
  output_dir = getwd(),
  file_name = NULL,
  assay_type = c("counts"),
  force = FALSE
)
```

Arguments

x	A DeeDeeExperiment object containing DEA/FEA results to be extracted
res_type	A character vector indicating the result to extract (i.e. "dea", "fea", "assay") from the corresponding slot If set to "all", DEAs, FEAs, as well as the specified assays are extracted into separate excel files
res_format	A character string specifying the DEA/FEAs output format to be exported (i.e. "minimal" or "original")
output_dir	A character string specifying the directory where the excel file will be written
file_name	Optional character string specifying a file name. If NULL, a default name is generated
assay_type	Optional character vector specifying the assays to export. It defaults to "counts"
force	Logical. If TRUE, an existing file with the same name will be overwritten

Value

An (invisible) character vector of file paths to the exported excel files. The vector may contain one path res_type = "dea" or res_type = "fea" or three paths res_type = "all"

Examples

```
data("de_named_list", package = "DeeDeeExperiment")
data("topGO_results_list", package = "DeeDeeExperiment")
dde <- DeeDeeExperiment(de_results = de_named_list, enrich_results = topGO_results_list)
```

```
export_result_for_dde(dde,
res_type = "dea",
res_format = "minimal", output_dir = tempdir(), force = TRUE)

export_result_for_dde(dde,
res_type = c("dea", "fea"),
res_format = "original", output_dir = tempdir(), force = TRUE)
```

`fgseaRes` `fgseaRes`

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`

`gost_res` `gost_res`

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

---

gsea_res gsea_res

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 *A sample* DESeqResults *object*

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 DEresus: IFNg_naive, Salm_both, Salm_naive

IFNg_naive *A sample* DESeqResults *object*

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 DEresus: IFNg_both, Salm_both, Salm_naive

limma_list_for_dde *Convert a* MArrayLM *object with multiple contrasts into a list of DE results tables compatible with DeeDeeExperiment*

Description

This helper function extracts DE results for each contrast contained in a limma::MArrayLM object and reformats them into a list of standardized data frames suitable for integration in a DeeDeeExperiment object. Each resulting data frame includes renamed columns: logFC to log2FoldChange ,P.Value to pvalue, and adj.P.Val to padj

Usage

```
limma_list_for_dde(fit, number = nrow(fit), sort.by = "none")
```

Arguments

fit	A MArrayLM object, as produced by the limma workflow
number	An integer specifying the maximum number of genes to extract per contrast
sort.by	A character string specifying which statistic to rank the genes by. It must be one of the values accepted by the sort.by argument in the limma::topTable() function. Defaults to "none".

Details

The function assumes that each column in fit$coefficients corresponds to a contrast of interest. The names of the resulting list elements are taken directly from colnames(fit$coefficients). The names in the input object must therefore accurately reflect the intended contrast names.

Value

A named list of DE results tables, one per contrast. Each table contains standardized columns and the list is annotated with metadata indicating its package origin (limma).

See Also

limma::topTable()

Examples

```
data("de_limma", package = "DeeDeeExperiment")
new_limma_list <- limma_list_for_dde(de_limma)
```

`muscat_list_for_dde` *Convert* `muscat::pbDS()` *results into a flat list of data frames compatible with* `DeeDeeExperiment`

Description

This helper function extracts and flattens the nested structure returned by `muscat::pbDS()`, returning one table per contrast–cluster combination. Each resulting data frame will have standardized column names (`log2FoldChange`, `pvalue`, `padj`).

Usage

```
muscat_list_for_dde(res, padj_col = c("p_adj.loc", "p_adj.glb"))
```

Arguments

`res`	A list, typically the output of `muscat::pbDS()` function, containing one or more contrasts
`padj_col`	A character string specifying which adjusted p-value column to extract. It can be either "p_adj.loc" or "p_adj.glb".

Details

The function is intended to simplify the integration of muscat results into a `DeeDeeExperiment` object. It automatically renames columns (`logFC` to `log2FoldChange`, `p_val` to `pvalue`, and the selected adjusted p-value column to `padj`) and annotates the resulting list with metadata about the originating package.

The function checks that each contrast entry contains a valid `table` component as expected from `pbDS()` output. Invalid or empty contrasts are skipped with a warning message. The names of the list elements in `res` must match contrast names found in the `table` slot of each entry.

Value

A named list of data frames

Examples

```
data("muscat_pbDS_res", package = "DeeDeeExperiment")
new_muscat_list <- muscat_list_for_dde(list(`stim-ctrl` = muscat_res))
```

muscat_res muscat_res

Description

A small example object generated with `muscat::pbDS()` ona subset Kang et al. dataset. The results represent DE between stimulated vs control samples.

Format

A `list` structured as returned by `muscat::pbDS()`

Details

The original data were obtained from Kang et al. dataset in `ExperimentHub` and processed using `muscat` workflows. Only a small subset of genes and clusters was retained to reduce object size.

Value

A named `list` of DE results tables compatible with `muscat_list_for_dde`

Salm_both *A sample* `DESeqResults` *object*

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 DEresus: IFNg_both, IFNg_naive, Salm_naive

`Salm_naive` *A sample* `DESeqResults` *object*

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 DEresus: IFNg_both, IFNg_naive, Salm_both

supported_fea_formats *Display available FEA formats*

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

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, 22
IFNg_naive, 23
Salm_both, 26
Salm_naive, 27
∗ **edgeRresus**
dge_exact_IFNg_both, 13
dge_exact_IFNg_naive, 14
dge_exact_Salm_both, 15
dge_exact_Salm_naive, 15
dge_lrt_IFNg_both, 16
dge_lrt_IFNg_naive, 17
dge_lrt_Salm_both, 18
dge_lrt_Salm_naive, 18
∗ **enrich_resus**
clusterPro_res, 3
enrichr_res, 19
fgseaRes, 21
gost_res, 21
gsea_res, 22
topGO_results_list, 28
.DeeDeeExperiment
*(*DeeDeeExperiment-class*)*, 4

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, 3, *19*, *21, 22*, *28*

dd_list_original, 3
de_limma, 12
de_named_list, 13
DeeDeeExperiment, *5*, *10, 11*
DeeDeeExperiment
*(*DeeDeeExperiment-class*)*, 4
DeeDeeExperiment(), *5*, *7*
DeeDeeExperiment-class, 4
DeeDeeExperiment-methods, 5
DeeDeeExperiment-misc, 10
DeeDeeExperiment-package
*(*DeeDeeExperiment-pkg*)*, 11
DeeDeeExperiment-pkg, 11
dge_exact_IFNg_both, 13, *14–19*
dge_exact_IFNg_naive, *14*, 14, *15–19*
dge_exact_Salm_both, *14*, 15, *16–19*
dge_exact_Salm_naive, *14, 15*, 15, *17–19*
dge_lrt_IFNg_both, *14–16*, 16, *17–19*
dge_lrt_IFNg_naive, *14–17*, 17, *18, 19*
dge_lrt_Salm_both, *14–17*, 18, *19*
dge_lrt_Salm_naive, *14–18*, 18

enrichr_res, *3*, 19, *21, 22*, *28*
export_result_for_dde, 20

fgseaRes, *3*, *19*, 21, *22*, *28*

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, *3*, *19*, *21*, 21, *22*, *28*
gsea_res, *3*, *19*, *21*, *22*, 22, *28*

IFNg_both, 22, *23*, *27*
IFNg_naive, *23*, 23, *27*

limma::topTable(), *24*
limma_list_for_dde, 24
linkDEAandFEA
(DeeDeeExperiment-methods), 5
linkDEAandFEA,DeeDeeExperiment-method
(DeeDeeExperiment-methods), 5

muscat_list_for_dde, 25
muscat_res, 26

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, *23*, 26, *27*
Salm_naive, *23*, *27*, 27
show,DeeDeeExperiment-method
(DeeDeeExperiment-misc), 10
summary,DeeDeeExperiment-method
(DeeDeeExperiment-misc), 10
supported_fea_formats, 28

topGO_results_list, *3*, *19*, *21*, *22*, 28