

Package ‘DiffExp’

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Title Runs different methods of differential expression analysis

Version 0.1.0

Description Runs different methods of differential expression analysis

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LazyData true

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Imports apeglm,
BiocParallel,
DESeq2,
edgeR,
S4Vectors,
SummarizedExperiment

Suggests testthat

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load_to_deseq2	<i>Transform SummarizedExperiment object to DESeq2DataSet object.</i>
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Description

Transform SummarizedExperiment object to [DESeq2DataSet](#) object.

Usage

```
load_to_deseq2(object, design = NULL)
```

Arguments

object	a SummarizedExperiment object
design	a formula or matrix that expresses how the counts for each variable depend on the variables in colData. See DESeqDataSet .

Value

a DESeq2DataSet object

Author(s)

Yoann Pradat

load_to_edgeR	<i>Transform SummarizedExperiment object to DGEList object.</i>
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Description

Transform SummarizedExperiment object to [DGEList](#) object.

Usage

```
load_to_edgeR(object)
```

Arguments

object	a SummarizedExperiment object
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Author(s)

Yoann Pradat

load_to_limma	<i>Transform SummarizedExperiment object to ????</i>
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Description

Transform SummarizedExperiment object to ????

Usage

```
load_to_limma(object)
```

Arguments

object a SummarizedExperiment object

Author(s)

Yoann Pradat

opts_diffexp_default	<i>Define the parameters specific to each differential analysis method.</i>
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Description

Define the parameters specific to each differential analysis method.

Usage

```
opts_diffexp_default(
  alpha = 0.1,
  ncores = 6,
  save_table = T,
  only_significant = T,
  folder_results = "./results",
  run_deseq2 = T,
  run_edgeR = F,
  run_limma = F,
  ...
)
```

Arguments

alpha	fdr level when adjusting for multiple testing.
ncores	number of cores available for doing parallel computations. Used in DESeq.
save_table	boolean to decide whether to save tables in txt files or not
only_significant	boolean to decide whether only significant (FDR) variables are kept in the results tables or not
run_deseq2	boolean to choose to run DESeq2.

run_edgeR	boolean to choose to run edgeR.
run_limma	boolean to choose to run limma.
...	extra parameters added to the configuration list

Author(s)

Yoann Pradat

run_deseq2	<i>Run DESEQ2 algorithm.</i>
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Description

Run DESEQ2 algorithm.

Usage

```
run_deseq2(object, design = NULL, contrasts, opts_algo, opts_comm)
```

Arguments

object	a SummarizedExperiment object
design	a formula specifying the design for the model matrix of DESeq2. Any variable appearing should be present in the colData of object
contrasts	(optional) a character vector specifying the contrasts (one or multiple beta coefficient) to be used for making tests and building results table. If set to NULL, one table for each element of resultsNames(dds) will be built
opts_algo	a named list of options passed to DESeq, results and lfcShrink functions. See DEseq , results , lfcShrink

Value

dataframe with results

Author(s)

Yoann Pradat

References

Love, M.I., Huber, W., Anders, S. (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15:550. <https://doi.org/10.1186/s13059-014-0550-8>

run_edgeR	<i>Run edgeR algorithm.</i>
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Description

Run edgeR algorithm.

Usage

```
run_edgeR(object)
```

Author(s)

Yoann Pradat

References

Robinson MD, McCarthy DJ, Smyth GK (2010). “edgeR: a Bioconductor package for differential expression analysis of digital gene expression data.” *Bioinformatics*, 26(1), 139-140. <https://doi.org/10.1093/bioinformatics/btp616>

McCarthy DJ, Chen Y, Smyth GK (2012). “Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation.” *Nucleic Acids Research*, 40(10), 4288-4297. <https://doi.org/10.1093/nar/gks042>

run_limma	<i>Run limma algorithm.</i>
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Description

Run limma algorithm.

Usage

```
run_limma(object)
```

Author(s)

Yoann Pradat

References

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015). “limma powers differential expression analyses for RNA-sequencing and microarray studies.” *Nucleic Acids Research*, 43(7), e47. <https://doi.org/10.1093/nar/gkv007>

Law, C.W., Chen, Y., Shi, W. et al. voom: precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biol* 15, R29 (2014). <https://doi.org/10.1186/gb-2014-15-2-r29>

save_update_table	<i>Update an existing table with a new table.</i>
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Description

Update an existing table with a new table.

Usage

```
save_update_table(file, tab_new, tags, verbose = T)
```

Arguments

file	path to where the table should be saved
tab_new	a data.frame
tags	named list of tags values to decide between merging and updating if a table already exists at file

Value

a data.frame

Author(s)

Yoann Pradat

update_table	<i>Update an existing table with a new table.</i>
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Description

Update an existing table with a new table.

Usage

```
update_table(tab, tab_new, tags)
```

Arguments

tab	a data.frame
tab_new	a data.frame
tags	named list of tags values to decide between merging and updating

Value

a data.frame

Author(s)

Yoann Pradat

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