Package 'DiffExp'

November 18, 2020

Title Runs different methods of differential expression analysis

Version 0.2.0

Description Runs different methods of differential expression analysis

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LazyData true

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

Suggests testthat

R topics documented:

get_contrast_vector *Produce a contrast vector*

Description

Produce a contrast vector

Usage

```
get_contrast_vector(contrast, design, data)
```

Arguments

contrast	a character vector specifying the contrast beween refined beta names (see refine_beta_names
design	a formula specifying the design
data	a data.frame used for building the model matrix

Value

a character vector of refined beta names

Author(s)

Yoann Pradat

References

internal

opts_diffexp *Define the parameters specific to each differential analysis method.*

Description

Define the parameters specific to each differential analysis method.

Usage

```
opts_diffexp(
  alpha = 0.1,
  ncores = 6,
  save_table = T,
  only_significant = T,
  folder_results = "./results",
  use_deseq2 = T,
  use_edgeR = T,
  use_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
use_deseq2	boolean to choose to run DESeq2.
use_edgeR	boolean to choose to run edgeR.
use_limma	boolean to choose to run limma.
...	extra parameters added to the configuration list

Value

a list

Author(s)

Yoann Pradat

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opts_prepro *Define the options for* preprocess_object

Description

See edgeR::filterByExp for more details about the filtering options and edgeR::calcNormFactors for mode details about the normalization options.

Usage

```
opts_prepro(
  design = NULL,
  min_count = 0,
  min_total_count = 15,
  large_n = 10,
  min_prop = 0.7,
  norm_factors_method = c("TMM", "TMMwsp", "RLE", "upperquartile", "none"),
  ...
)
```

Arguments

design	a formula object specifying the design matrix
min_count	min.total.count param of filterByExpr
min_total_count	min.count param of filterByExpr
large_n	large.n param of filterByExpr
min_prop	min.prop param of filterByExpr
norm_factors_method	method argument of calcNormFactors.
...	extra parameters added to the options list

Value

a list

Author(s)

Yoann Pradat

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preprocess_object *Perform preprocessing steps.*

Description

Perform preprocessing steps.

Usage

```
preprocess_object(object, opts)
```

Arguments

object	a SummarizedExperiment object
opts	a named list of options. See opts_prepro

Value

a SummarizedExperiment object

Author(s)

Yoann Pradat

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refine_beta_names *Add references levels to beta names created by* model.matrix

---

Description

Add references levels to beta names created by model.matrix

Usage

```
refine_beta_names(design, data)
```

Arguments

design	a formula specifying the design
data	a data.frame used for building the model matrix

Value

a character vector of refined beta names

Author(s)

Yoann Pradat

References

internal

`run_deseq2` *Run DESEQ2 algorithm.*

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`	a character vector specifying the contrasts (one or multiple beta coefficient) to be used for making tests and building results table.
`opts_algo`	a named list of options specific to DESeq2
`opts_comm`	a named list of options common to all methods

Value

a dataframe of 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` *Run edgeR algorithm.*

Description

Run edgeR algorithm.

Usage

```
run_edgeR(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`	a character vector specifying the contrasts (one or multiple beta coefficient) to be used for making tests and building results table.
`opts_algo`	a named list of options specific to edgeR
`opts_comm`	a named list of options common to all methods

Value

a dataframe of results

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` *Run limma algorithm.*

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

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