Package 'DiffExp'

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Title Runs different methods of differential expression analysis

Version 0.2.3

Description Runs different methods of differential expression analysis

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

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

Depends R (>= 3.5.0)

Suggests testthat

R topics documented:

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get_contrast_condition_B_minus_A_factors_interaction
                              Build a list of character contrasts of B-A for an interacting variable.

Description

Build a list of character contrasts of B-A for an interacting variable.

Usage

```
get_contrast_condition_B_minus_A_factors_interaction(
  condition,
  interaction,
  cond_name = "condition",
  inte_name = "interaction",
  level_B_cond = NULL,
  level_A_cond = NULL,
  cond_main_effect = T,
  inte_main_effect = F
)
```

Arguments

condition	the factor vector of condition values
interaction	the factor vector of interaction values
cond_name	the name of the condition variable
inte_name	the name of the interaction variable
level_B_cond	the B level to be contrasted with A
level_A_cond	the A level to be contrasted with B
cond_main_effect	
	is the condition a main effect
inte_main_effect	
	is the interaction a main effect

Author(s)

Yoann Pradat

---

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

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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

---

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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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

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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

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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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tcga_brca   *RNA-seq and clinical data for TCGA BRCA Stage I patients.*

Description

Data from the reanalysis of RNA-seq files by Zheng et al. 2019. The clinical data were taken from the GDC data portal and the cBio data portal. Both the RNA-seq data and the clinical data are public access. The samples were chosen so that

1. all samples are Stage I
2. all samples are Female
3. all samples have complete clinical data

Usage

```
data(tcga_brca)
```

Format

A `SummarizedExperiment` object with 58,288 genes and 98 samples.

assays A `SimpleList` with just one "counts" matrix

colData A `DFrame` with 98 rows and 8 columns

rowData A `DFrame` with 58,288 rows and 2 columns

metadata An empty list

elementMetadata Alias for `rowData`

Details

This selection was performed only to keep this example data set small and may not be suitable for meaningful analyses.

Source

RNA-seq source: https://stanfordmedicine.app.box.com/s/lu703xuaulfz02vgd2lunxnvt4mfvo3q. cBioPortal BRCA Pan-cancer Atlas https://www.cbioportal.org/study/summary?id=brca_tcga_pan_can_atlas_2018. GDC legacy archive clinical BRCA https://portal.gdc.cancer.gov/legacy-archive/files/735bc5ff-86d1-421a-8693-6e6f92055563

References

Hong Zheng, Kevin Brennan, Mikel Hernaez, Olivier Gevaert, Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples, GigaScience, Volume 8, Issue 12, December 2019, giz145, https://doi.org/10.1093/gigascience/giz145

Examples

```
data(tcga_brca)
```

Index