Package 'mosdef'

July 12, 2025

Title MOSt frequently used and useful Differential Expression Functions

Version 1.5.1

Description This package provides functionality to run a number of tasks in the differential expression analysis workflow. This encompasses the most widely used steps, from running various enrichment analysis tools with a unified interface to creating plots and beautifying table components linking to external websites and databases. This streamlines the generation of comprehensive analysis reports.

Depends R (>= 4.4.0)

Imports DT, ggplot2, ggforce, ggrepel, graphics, grDevices, htmltools, methods, AnnotationDbi, topGO, GO.db, clusterProfiler, goseq, utils, RColorBrewer, rlang, DESeq2, scales, SummarizedExperiment, S4Vectors, stats

Suggests knitr, rmarkdown, macrophage, org.Hs.eg.db, GeneTonic, testthat (>= 3.0.0), TxDb.Hsapiens.UCSC.hg38.knownGene, BiocStyle

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

VignetteBuilder knitr

URL https://github.com/imbeimainz/mosdef

BugReports https://github.com/imbeimainz/mosdef/issues

Config/testthat/edition 3

biocViews GeneExpression, Software, Transcription, Transcriptomics, DifferentialExpression, Visualization, ReportWriting, GeneSetEnrichment, GO

git_url https://git.bioconductor.org/packages/mosdef

git_branch devel

git_last_commit 0964a99

git_last_commit_date 2025-05-01

Repository Bioconductor 3.22

Date/Publication 2025-07-11

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Contents

.info_enrichrun *Printing some info before the enrichment runs*

Description

Printing some info before the enrichment runs

Usage

```
.info_enrichrun(n_de, n_de_selected, de_type, res_de = NULL)
```

Arguments

n_de	Numeric, number of DE genes (in total)
n_de_selected	Character vector, containing the selected DE genes
de_type	Character string, specifying up/down/both direction of DE regulation
res_de	The res_de container as expected in most mosdef functions.

Value

Prints out an informative summary message.

Examples

```
# .info_enrichrun(10, length(c("geneA", "geneB")), "up")
```

buttonifier *Create sets of buttons for gene symbols*

Description

A function to turn Gene Symbols into buttons in an Rmarkdown linking to various portals for further info about these genes.

Usage

```
buttonifier(
  df,
  create_buttons_to = c("PUBMED", "GC", "UNIPROT"),
  col_to_use = "SYMBOL",
  output_format = "DT",
  ens_col = NULL,
  ens_species = NULL
)
```

Arguments

df	A dataframe with at least on column with gene Symbols named: SYMBOL
create_buttons_to	At least one of: "GC", "NCBI", "GTEX", "UNIPROT", "dbPTM", "HPA" "PUBMED"
col_to_use	name of the columns were the gene symbols are stored. Default is SYMBOL
output_format	a parameter deciding which output format to return, either a "DT" (DT::datatable(), recommended), or a simple dataframe ("DF"). In the latter case it is important that if the data is visualized with the DT::datatable function the parameter escape must be set to FALSE
ens_col	Character string, name of the columns were the ENSEMBL IDs are stored.
ens_species	The species you are working with to link to the correct gene on ENSEMBL

Details

Current supported portals are: GeneCards, NCBI, GTEx, Uniprot, dbPTM, Human Protein Atlas

Value

A data.frame or a DT::datatable object with columns adding HTML objects that link to websites with further information on the genes in question.

Examples

```
data(res_de_macrophage, package = "mosdef")

res_de <- res_macrophage_IFNg_vs_naive
res_df <- deresult_to_df(res_de)

## Subsetting for quicker run
res_df <- res_df[1:100, ]
buttonifier(res_df)

buttonifier(res_df,
  create_buttons_to = c("NCBI", "HPA"),
  ens_col = "id",
  ens_species = "Homo_sapiens"
)
```

---

create_link_dbPTM *Link to dbPTM database*

Description

Link to dbPTM database

Usage

```
create_link_dbPTM(val)
```

Arguments

val	Character, the gene symbol

Value

HTML for an action button

Examples

```
create_link_dbPTM("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_dbPTM(res_macrophage_IFNg_vs_naive$SYMBOL)
```

---

create_link_ENSEMBL *Link to ENSEMBL database*

Description

Link to ENSEMBL database

Usage

```
create_link_ENSEMBL(val, species = "Mus_musculus")
```

Arguments

val	Character, the gene symbol
species	The species to be analyzed e.g "Mus_musculus"

Value

HTML for an action button

Examples

```
create_link_ENSEMBL("ENSMUSG00000024406")

data(res_de_macrophage, package = "mosdef")
rownames(res_macrophage_IFNg_vs_naive) <- create_link_ENSEMBL(
  rownames(res_macrophage_IFNg_vs_naive))
```

create_link_GeneCards *Link to the GeneCards database*

Description

Link to the GeneCards database

Usage

```
create_link_GeneCards(val)
```

Arguments

val	Character, the gene symbol of interest

Value

HTML for an action button

Examples

```
 create_link_GeneCards("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
   create_link_GeneCards(res_macrophage_IFNg_vs_naive$SYMBOL)
```

create_link_GO *Link to AMIGO database*

Description

Link to AMIGO database

Usage

```
create_link_GO(val)
```

Arguments

val	Character, the GOID

Value

HTML for an action button

Examples

```
create_link_GO("GO:0008150")
```

create_link_GTEX *Link to the GTEx Portal*

Description

Link to the GTEx Portal

Usage

```
create_link_GTEX(val)
```

Arguments

val	Character, the gene symbol of interest

Value

HTML for an action button

Examples

```
create_link_GTEX("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_GTEX(res_macrophage_IFNg_vs_naive$SYMBOL)
```

create_link_HPA *Link to the Human Protein Atlas*

Description

Link to the Human Protein Atlas

Usage

```
create_link_HPA(val)
```

Arguments

val	Character, the gene symbol

Value

HTML for an action button

Examples

```
create_link_HPA("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_HPA(res_macrophage_IFNg_vs_naive$SYMBOL)
```

create_link_NCBI *Link to NCBI database*

Description

Link to NCBI database

Usage

```
create_link_NCBI(val)
```

Arguments

val	Character, the gene symbol

Value

HTML for an action button

Examples

```
create_link_NCBI("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_NCBI(res_macrophage_IFNg_vs_naive$SYMBOL)
```

create_link_PubMed *Link to Pubmed*

Description

Link to Pubmed

Usage

```
create_link_PubMed(val)
```

Arguments

val	Character, the gene symbol

Value

HTML for an action button

Examples

```
create_link_PubMed("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_PubMed(res_macrophage_IFNg_vs_naive$SYMBOL)
```

create_link_UniProt *Link to UniProt database*

Description

Link to UniProt database

Usage

```
create_link_UniProt(val)
```

Arguments

val	Character, the gene symbol

Value

HTML for an action button

Examples

```
create_link_UniProt("Oct4")

data(res_de_macrophage, package = "mosdef")
res_macrophage_IFNg_vs_naive$SYMBOL <-
  create_link_UniProt(res_macrophage_IFNg_vs_naive$SYMBOL)
```

deresult_to_df *Generate a table from the* DESeq2 *results*

Description

Generate a tidy table with the results of DESeq2

Usage

```
deresult_to_df(res_de, FDR = NULL)
```

Arguments

res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
FDR	Numeric value, specifying the significance level for thresholding adjusted p-values. Defaults to NULL, which would return the full set of results without performing any subsetting based on FDR.

Value

A tidy data.frame with the results from differential expression, sorted by adjusted p-value. If FDR is specified, the table contains only genes with adjusted p-value smaller than the value.

Examples

```
library("DESeq2")
library("macrophage")
data(res_de_macrophage, package = "mosdef")
head(res_macrophage_IFNg_vs_naive)
res_df <- deresult_to_df(res_macrophage_IFNg_vs_naive)
head(res_df)
```

`de_table_painter` *DE table painter*

Description

Beautifying the aspect and looks of a DE results table

Usage

```
de_table_painter(
  res_de,
  rounding_digits = NULL,
  signif_digits = NULL,
  up_DE_color = "darkred",
  down_DE_color = "navyblue",
  logfc_column = "log2FoldChange",
  basemean_column = "baseMean",
  lfcse_column = "lfcSE",
  stat_column = "stat",
  pvalue_column = "pvalue",
  padj_column = "padj"
)
```

Arguments

`res_de`	An object containing the results of the Differential Expression analysis workflow (e.g. `DESeq2`, `edgeR` or `limma`). Currently, this can be a `DESeqResults` object created using the `DESeq2` framework. Or a data frame obtained from such an object through `deresult_to_df()`
`rounding_digits`	Numeric value, specifying the number of digits to round the numeric values of the DE table (except the p-values)
`signif_digits`	Numeric value, specifying the number of significant digits to display for the p-values in the DE table
`up_DE_color`	Character string, specifying the color to use for coloring the bar of upregulated genes.
`down_DE_color`	Character string, specifying the color to use for coloring the bar of downregulated genes.
`logfc_column`	Character string, defining the name of the column in which to find the log2 fold change.

basemean_column
: Character string, defining the name of the column in which to find the average expression value.

lfcse_column
: Character string, defining the name of the column in which to find the standard error of the log2 fold change.

stat_column
: Character string, defining the name of the column in which to find the values of the test statistic.

pvalue_column
: Character string, defining the name of the column in which to find the unadjusted p-values.

padj_column
: Character string, defining the name of the column in which to find the adjusted p-values.

Details

Feeding on the classical results of DE workflows, this function formats and tries to prettify the representation of the key values in it.

Value

A `datatable` object, ready to be rendered as a widget inside an analysis Rmarkdown report.

Examples

```
data(res_de_macrophage, package = "mosdef")
de_table_painter(res_macrophage_IFNg_vs_naive,
                 rounding_digits = 3,
                 signif_digits = 5)

## It is also possible to pass the "buttonified" table,
res_df_small <- deresult_to_df(res_macrophage_IFNg_vs_naive)[1:100, ]

buttonified_df <- buttonifier(res_df_small,
                              create_buttons_to = c("NCBI", "HPA"),
                              ens_col = "id",
                              ens_species = "Homo_sapiens",
                              output_format = "DF"
)

de_table_painter(buttonified_df,
                 rounding_digits = 3,
                 signif_digits = 5)
```

---

de_volcano *Generates a volcano plot using ggplot2*

Description

This function generates a base volcanoplot for differentially expressed genes that can then be expanded upon using further ggplot functions.

Usage

```
de_volcano(
  res_de,
  mapping = "org.Mm.eg.db",
  logfc_cutoff = 0,
  FDR = 0.05,
  draw_FDR_line = FALSE,
  labeled_genes = 30
)
```

Arguments

res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
mapping	Which org.XX.eg.db package to use for annotation - select according to the species
logfc_cutoff	A numeric value that sets the cutoff for the xintercept argument of ggplot. Defaults to 0.
FDR	The pvalue threshold to us for counting genes as de and therefore also where to draw the line in the plot. Default is 0.05
draw_FDR_line	Logical, whether to draw a line at the p-value corresponding to the specified FDR. Defaults to FALSE.
labeled_genes	A numeric value describing the amount of genes to be labeled. This uses the Top(x) highest differentially expressed genes

Value

A ggplot2 volcano plot object that can be extended upon by the user

Examples

```
library("ggplot2")
library("RColorBrewer")
library("ggrepel")
library("DESeq2")
library("org.Hs.eg.db")

data(res_de_macrophage, package = "mosdef")

p <- de_volcano(res_macrophage_IFNg_vs_naive,
  logfc_cutoff = 1,
  labeled_genes = 20,
  mapping = "org.Hs.eg.db"
)

p
```

geneinfo_to_html *Information on a gene*

Description

Assembles information, in HTML format, regarding a gene symbol identifier

Usage

```
geneinfo_to_html(gene_id, res_de = NULL, col_to_use = "SYMBOL")
```

Arguments

gene_id	Character specifying the gene identifier for which to retrieve information
res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework. If not provided, the experiment-related information is not shown, and only some generic info on the identifier is displayed. The information about the gene is retrieved by matching on the SYMBOL column, which should be provided in res_de.
col_to_use	The column of your res_de object containing the gene symbols. Default is "SYMBOL"

Details

Creates links to the NCBI and the GeneCards databases

Value

HTML content related to a gene identifier, to be displayed in web applications (or inserted in Rmd documents)

Examples

```
geneinfo_to_html("ACTB")
geneinfo_to_html("Pf4")
```

gene_plot *Plot expression values for a gene*

Description

Plot expression values (e.g. normalized counts) for a gene of interest, grouped by experimental group(s) of interest

Usage

```
gene_plot(
  de_container,
  gene,
  intgroup = NULL,
  assay = "counts",
  annotation_obj = NULL,
  normalized = TRUE,
  transform = TRUE,
  labels_display = TRUE,
  labels_repel = TRUE,
  plot_type = "auto",
  return_data = FALSE
)
```

Arguments

de_container	An object containing the data for a Differential Expression workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqDataSet object, normally obtained after running your data through the DESeq2 framework.
gene	Character, specifies the identifier of the feature (gene) to be plotted
intgroup	A character vector of names in colData(de_container) to use for grouping. Note: the vector components should be categorical variables. Defaults to NULL, which which would then select the first column of the colData slot.
assay	Character, specifies with assay of the de_container object to use for reading out the expression values. Defaults to "counts".
annotation_obj	A data.frame object with the feature annotation information, with at least two columns, gene_id and gene_name.
normalized	Logical value, whether the expression values should be normalized by their size factor. Defaults to TRUE, applies when assay is "counts"
transform	Logical value, corresponding whether to have log scale y-axis or not. Defaults to TRUE.
labels_display	Logical value. Whether to display the labels of samples, defaults to TRUE.
labels_repel	Logical value. Whether to use ggrepel's functions to place labels; defaults to TRUE
plot_type	Character, one of "auto", "jitteronly", "boxplot", "violin", or "sina". Defines the type of geom_ to be used for plotting. Defaults to auto, which in turn chooses one of the layers according to the number of samples in the smallest group defined via intgroup
return_data	Logical, whether the function should just return the data.frame of expression values and covariates for custom plotting. Defaults to FALSE.

Details

The result of this function can be fed directly to plotly::ggplotly() for interactive visualization, instead of the static ggplot viz.

Value

A ggplot object

Examples

```
library("macrophage")
library("DESeq2")
library("org.Hs.eg.db")

# dds object
data(gse, package = "macrophage")
dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
# dds_macrophage <- DESeq(dds_macrophage)

# annotation object
anno_df <- data.frame(
  gene_id = rownames(dds_macrophage),
  gene_name = mapIds(org.Hs.eg.db,
    keys = rownames(dds_macrophage),
    column = "SYMBOL",
    keytype = "ENSEMBL"
  ),
  stringsAsFactors = FALSE,
  row.names = rownames(dds_macrophage)
)

gene_plot(
  de_container = dds_macrophage,
  gene = "ENSG00000125347",
  intgroup = "condition",
  annotation_obj = anno_df
)
```

`get_annotation_orgdb` *Get an annotation data frame from org db packages*

Description

Get an annotation data frame from org db packages

Usage

```
get_annotation_orgdb(
  de_container,
  orgdb_package,
  id_type,
  key_for_genenames = "SYMBOL"
)
```

Arguments

`de_container`	An object containing the data for a Differential Expression workflow (e.g. `DESeq2`, `edgeR` or `limma`). Currently, this can be a `DESeqDataSet` object, normally obtained after running your data through the `DESeq2` framework.

orgdb_package — Character string, named as the org.XX.eg.db package which should be available in Bioconductor

id_type — Character, the ID type of the genes as in the row names of the de_container, to be used in the call to AnnotationDbi::mapIds()

key_for_genenames — Character, corresponding to the column name for the key in the orgDb package containing the official gene name (often called gene symbol). This parameter defaults to "SYMBOL", but can be adjusted in case the key is not found in the annotation package (e.g. for org.Sc.sgd.db).

Value

A data frame to be used for annotation of genes, with the main information encoded in the gene_id and gene_name columns.

Examples

```
library("macrophage")
library("DESeq2")
library("org.Hs.eg.db")

# dds object
data(gse, package = "macrophage")
dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)

anno_df <- get_annotation_orgdb(dds_macrophage, "org.Hs.eg.db", "ENSEMBL")

head(anno_df)
```

---

get_expr_values *Get expression values*

Description

Extract expression values, with the possibility to select other assay slots

Usage

```
get_expr_values(
  de_container,
  gene,
  intgroup,
  assay = "counts",
  normalized = TRUE
)
```

Arguments

de_container	An object containing the data for a Differential Expression workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqDataSet object, normally obtained after running your data through the DESeq2 framework.
gene	Character, specifies the identifier of the feature (gene) to be extracted
intgroup	A character vector of names in colData(de_container) to use for grouping.
assay	Character, specifies with assay of the de_container object to use for reading out the expression values. Defaults to "counts".
normalized	Logical value, whether the expression values should be normalized by their size factor. Defaults to TRUE, applies when assay is "counts"

Value

A tidy data.frame with the expression values and covariates for further processing

Examples

```
library("macrophage")
library("DESeq2")
library("org.Hs.eg.db")
library("AnnotationDbi")

# dds object
data(gse, package = "macrophage")
dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
# dds_macrophage <- DESeq(dds_macrophage)

df_exp <- get_expr_values(
  de_container = dds_macrophage,
  gene = "ENSG00000125347",
  intgroup = "condition"
)
head(df_exp)
```

---

go_to_html *Information on a Gene Ontology identifier*

Description

Assembles information, in HTML format, regarding a Gene Ontology identifier

Usage

```
go_to_html(go_id, res_enrich = NULL)
```

Arguments

go_id	Character, specifying the GeneOntology identifier for which to retrieve information
res_enrich	A data.frame object, storing the result of the functional enrichment analysis. If not provided, the experiment-related information is not shown, and only some generic info on the identifier is displayed.

Details

Also creates a link to the AmiGO database

Value

HTML content related to a GeneOntology identifier, to be displayed in web applications (or inserted in Rmd documents)

Examples

```
go_to_html("GO:0002250")
go_to_html("GO:0043368")
```

---

go_volcano *Generates a volcano plot using ggplot2 This function generates a base volcano plot highlighting genes associated with a certain GOterm that can then be expanded upon using further ggplot functions.*

Description

Generates a volcano plot using ggplot2 This function generates a base volcano plot highlighting genes associated with a certain GOterm that can then be expanded upon using further ggplot functions.

Usage

```
go_volcano(
  res_de,
  res_enrich,
  mapping = "org.Hs.eg.db",
  term_index,
  logfc_cutoff = 1,
  FDR = 0.05,
  draw_FDR_line = FALSE,
  col_to_use = NULL,
  enrich_col = "genes",
  gene_col_separator = ",",
  down_col = "black",
  up_col = "black",
  highlight_col = "tomato",
  n_overlaps = 20
)
```

Arguments

res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
res_enrich	A enrichment result object created by for example using run_topGO()
mapping	Which org.XX.eg.db package to use for annotation - select according to the species
term_index	The location (row) of your GO term of interest in your enrichment result
logfc_cutoff	A numeric value that sets the cutoff for the xintercept argument of ggplot
FDR	The pvalue threshold to us for counting genes as de and therefore also where to draw the line in the plot. Default is 0.05
draw_FDR_line	Logical, whether to draw a line at the p-value corresponding to the specified FDR. Defaults to FALSE.
col_to_use	The column in your differential expression results containing your gene symbols. If you don't have one it is created automatically
enrich_col	column name from your res_enrich where the genes associated with your GOterm are stored (for example see the run_topGO() result in mosdef)
gene_col_separator	The separator used to split the genes. If you used topGO or goseq this is a "," which is the default. (For an example see the run_topGO() result in mosdef) If you used clusterProfiler this has to be set to "/". (For example see the run_cluPro() result in mosdef)
down_col	The colour for your downregulated genes, default is "gray"
up_col	The colour for your upregulated genes, default is "gray"
highlight_col	The colour for the genes associated with your GOterm default is "tomato"
n_overlaps	Number of overlaps ggrepel is supposed to allow when labeling (for more info check ggrepel documentation)

Value

A ggplot2 volcano plot object that can be extended upon by the user

Examples

```
library("org.Hs.eg.db")

data(res_de_macrophage, package = "mosdef")
data(res_enrich_macrophage_topGO, package = "mosdef")

p <- go_volcano(
  res_macrophage_IFNg_vs_naive,
  res_enrich = res_enrich_macrophage_topGO,
  term_index = 1,
  logfc_cutoff = 1,
  mapping = "org.Hs.eg.db",
  n_overlaps = 20
)

p
```

map_to_color *Maps numeric values to color values*

Description

Maps numeric continuous values to values in a color palette

Usage

```
map_to_color(x, pal, symmetric = TRUE, limits = NULL)
```

Arguments

x	A character vector of numeric values (e.g. log2FoldChange values) to be converted to a vector of colors
pal	A vector of characters specifying the definition of colors for the palette, e.g. obtained via RColorBrewer::brewer.pal()
symmetric	Logical value, whether to return a palette which is symmetrical with respect to the minimum and maximum values - "respecting" the zero. Defaults to TRUE.
limits	A vector containing the limits of the values to be mapped. If not specified, defaults to the range of values in the x vector.

Value

A vector of colors, each corresponding to an element in the original vector

Examples

```
a <- 1:9
pal <- RColorBrewer::brewer.pal(9, "Set1")
map_to_color(a, pal)
plot(a, col = map_to_color(a, pal), pch = 20, cex = 4)

b <- 1:50
pal2 <- grDevices::colorRampPalette(
  RColorBrewer::brewer.pal(name = "RdYlBu", 11)
)(50)
plot(b, col = map_to_color(b, pal2), pch = 20, cex = 3)
```

mosdef-pkg *mosdef: mostly useful differential expression functions*

Description

mostly useful differential expression functions

Details

This package provides functionality to run a number of tasks in the differential expression analysis workflow. This encompasses the most widely used steps, from running various enrichment analysis tools with a unified interface to creating plots and beautifying table components linking to external websites and databases. This streamlines the generation of comprehensive analysis reports.

Author(s)

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See Also

Useful links:

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

`mosdef_de_container_check` *A function checking if your* `de_container` *contains everything you need*

Description

A function checking if your `de_container` contains everything you need

Usage

```
mosdef_de_container_check(de_container, verbose = FALSE)
```

Arguments

`de_container`	An object containing the data for a Differential Expression workflow (e.g. `DESeq2`, `edgeR` or `limma`). Currently, this can be a `DESeqDataSet` object, normally obtained after running your data through the `DESeq2` framework.
`verbose`	Logical, whether to add messages telling the user which steps were taken.

Value

An invisible `NULL` after performing the checks

Examples

```
library("macrophage")
library("DESeq2")
data(gse, package = "macrophage")

dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
# dds_macrophage <- DESeq(dds_macrophage)

mosdef_de_container_check(dds_macrophage)
```

---

mosdef_res_check *A function checking if your res_de contains everything you need*

Description

A function checking if your res_de contains everything you need

Usage

```
mosdef_res_check(res_de, verbose = FALSE)
```

Arguments

res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
verbose	Logical, whether to add messages telling the user which steps were taken

Value

An invisible NULL after performing the checks

Examples

```
data(res_de_macrophage, package = "mosdef")

mosdef_res_check(res_macrophage_IFNg_vs_naive)
```

pair_corr *Pairwise scatter plot matrix and correlation plot of counts*

Description

Pairwise scatter plot matrix and correlation plot of counts

Usage

```
pair_corr(df, log = TRUE, method = "pearson", use_subset = TRUE)
```

Arguments

df	A data frame, containing the (raw/normalized/transformed) counts
log	Logical, whether to convert the input values to log2 (with addition of a pseudo-count). Defaults to TRUE.
method	Character string, one of pearson (default), kendall, or spearman as in cor
use_subset	Logical value. If TRUE, only 1000 values per sample will be used to speed up the plotting operations.

Value

A plot with pairwise scatter plots and correlation coefficients

Examples

```
library("macrophage")
library("DESeq2")
data(gse, package = "macrophage")
## dds object
dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
dds_macrophage <- estimateSizeFactors(dds_macrophage)

## Using just a subset for the example
pair_corr(counts(dds_macrophage, normalized = TRUE)[1:100, 1:8])
```

plot_ma *MA-plot from base means and log fold changes*

Description

MA-plot from base means and log fold changes, in the ggplot2 framework, with additional support to annotate genes if provided.

Usage

```
plot_ma(
  res_de,
  FDR = 0.05,
  point_alpha = 0.2,
  sig_color = "red",
  annotation_obj = NULL,
  draw_y0 = TRUE,
  hlines = NULL,
  title = NULL,
  xlab = "mean of normalized counts - log10 scale",
  ylim = NULL,
  add_rug = TRUE,
  intgenes = NULL,
  intgenes_color = "steelblue",
  labels_intgenes = TRUE,
  labels_repel = TRUE
)
```

Arguments

res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
FDR	Numeric value, the significance level for thresholding adjusted p-values
point_alpha	Alpha transparency value for the points (0 = transparent, 1 = opaque)
sig_color	Color to use to mark differentially expressed genes. Defaults to red
annotation_obj	A data.frame object, with row.names as gene identifiers (e.g. ENSEMBL ids) and a column, gene_name, containing e.g. HGNC-based gene symbols. Optional
draw_y0	Logical, whether to draw the horizontal line at y=0. Defaults to TRUE.
hlines	The y coordinate (in absolute value) where to draw horizontal lines, optional
title	A title for the plot, optional
xlab	X axis label, defaults to "mean of normalized counts - log10 scale"
ylim	Vector of two numeric values, Y axis limits to restrict the view
add_rug	Logical, whether to add rug plots in the margins
intgenes	Vector of genes of interest. Gene symbols if a symbol column is provided in res_de, or else the identifiers specified in the row names
intgenes_color	The color to use to mark the genes on the main plot.
labels_intgenes	Logical, whether to add the gene identifiers/names close to the marked plots
labels_repel	Logical, whether to use ggrepel::geom_text_repel for placing the labels on the features to mark

Details

The genes of interest are to be provided as gene symbols if a symbol column is provided in res_de, or else by using the identifiers specified in the row names

Value

An object created by ggplot

Examples

```
data(res_de_macrophage, package = "mosdef")

plot_ma(res_macrophage_IFNg_vs_naive, FDR = 0.05, hlines = 1)

plot_ma(res_macrophage_IFNg_vs_naive,
  FDR = 0.1,
  intgenes = c(
    "ENSG00000103196", # CRISPLD2
    "ENSG00000120129", # DUSP1
    "ENSG00000163884", # KLF15
    "ENSG00000179094" # PER1
  )
)
```

---

res_enrich_macrophage_cluPro

A sample enrichment object

Description

A sample enrichment object, generated in the mosdef and clusterProfiler framework

Format

An enrichResult object

Details

This enrichment object is on the data from the macrophage package

Specifically, this set of enrichment results was created using the Biological Process ontology, mapping the gene identifiers through the org.Hs.eg.db package.

Source

Details on how this object has been created are included in the create_mosdef_data.R script, included in the (installed) inst/scripts folder of the mosdef package. This is also available at https://github.com/imbeimainz/mosdef/blob/devel/inst/scripts/create_mosdef_data.R

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

res_macrophage_IFNg_vs_naive

`res_enrich_macrophage_goseq` *A sample enrichment object*

Description

A sample enrichment object, generated in the `mosdef` and `goseq` framework

Format

A `data.frame` object

Details

This enrichment object is on the data from the `macrophage` package

Specifically, this set of enrichment results was created using the Biological Process ontology, mapping the gene symbol identifiers through the `org.Hs.eg.db` package - the gene length information is retrieved by the internal routines of `goseq`.

Source

Details on how this object has been created are included in the `create_mosdef_data.R` script, included in the (installed) `inst/scripts` folder of the `mosdef` package. This is also available at https://github.com/imbeimainz/mosdef/blob/devel/inst/scripts/create_mosdef_data.R

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

res_macrophage_IFNg_vs_naive

`res_enrich_macrophage_topGO` *A sample enrichment object*

Description

A sample enrichment object, generated in the `mosdef` and `topGO` framework

Format

A `data.frame` object

Details

This enrichment object is on the data from the macrophage package.

Specifically, this set of enrichment results was created using the Biological Process ontology, mapping the gene symbol identifiers through the org.Hs.eg.db package.

Source

Details on how this object has been created are included in the create_mosdef_data.R script, included in the (installed) inst/scripts folder of the mosdef package. This is also available at https://github.com/imbeimainz/mosdef/blob/devel/inst/scripts/create_mosdef_data.R

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

res_macrophage_IFNg_vs_naive

---

res_macrophage_IFNg_vs_naive

A sample DESeqResults *object*

Description

A sample DESeqResults object, generated in the DESeq2 framework

Format

A DESeqResults object

Details

This DESeqResults object is on the data from the macrophage package. This result set has been created by setting the design to ~line + condition to detect the effect of the condition while accounting for the different cell lines included.

Specifically, this object contains the differences between the IFNg vs naive samples, testing against a logFC threshold of 1 for robustness.

Source

Details on how this object has been created are included in the create_mosdef_data.R script, included in the (installed) inst/scripts folder of the mosdef package. This is also available at https://github.com/imbeimainz/mosdef/blob/devel/inst/scripts/create_mosdef_data.R

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.

`run_cluPro` *Extract functional terms enriched in the DE genes, based on clusterProfiler*

Description

A wrapper for extracting functional GO terms enriched in a list of (DE) genes, based on the algorithm and the implementation in the clusterProfiler package

Usage

```
run_cluPro(
  de_container = NULL,
  res_de = NULL,
  de_genes = NULL,
  bg_genes = NULL,
  top_de = NULL,
  FDR_threshold = 0.05,
  min_counts = 0,
  mapping = "org.Hs.eg.db",
  de_type = "up_and_down",
  keyType = "SYMBOL",
  verbose = TRUE,
  ...
)
```

Arguments

`de_container`	An object containing the data for a Differential Expression workflow (e.g. `DESeq2`, `edgeR` or `limma`). Currently, this can be a `DESeqDataSet` object, normally obtained after running your data through the `DESeq2` framework.
`res_de`	An object containing the results of the Differential Expression analysis workflow (e.g. `DESeq2`, `edgeR` or `limma`). Currently, this can be a `DESeqResults` object created using the `DESeq2` framework.
`de_genes`	A vector of (differentially expressed) genes
`bg_genes`	A vector of background genes, e.g. all (expressed) genes in the assays
`top_de`	numeric, how many of the top differentially expressed genes to use for the enrichment analysis. Attempts to reduce redundancy. Assumes the data is sorted by padj (default in DESeq2).
`FDR_threshold`	The pvalue threshold to us for counting genes as de. Default is 0.05
`min_counts`	numeric, min number of counts a gene needs to have to be included in the geneset that the de genes are compared to. Default is 0, recommended only for advanced users.
`mapping`	Which `org.XX.eg.db` package to use for annotation - select according to the species
`de_type`	One of: 'up', 'down', or 'up_and_down' Which genes to use for GOterm calculations

keyType	Gene format to input into enrichGO from clusterProfiler. If res_de and de_container are used use "SYMBOL" for more information check the enrichGO documentation
verbose	Logical, whether to add messages telling the user which steps were taken
...	Further parameters to use for the clusterProfiler::enrichGO() function from clusterProfiler.

Value

A table containing the computed GO Terms and related enrichment scores.

See Also

clusterProfiler::enrichGO() for the underlying method

Other Enrichment functions: run_goseq(), run_topGO()

Examples

```
library("macrophage")
library("DESeq2")
data(gse, package = "macrophage")

dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
dds_macrophage <- DESeq(dds_macrophage)
data(res_de_macrophage, package = "mosdef")

library("AnnotationDbi")
library("org.Hs.eg.db")
library("clusterProfiler")
CluProde_macrophage <- run_cluPro(
  res_de = res_macrophage_IFNg_vs_naive,
  de_container = dds_macrophage,
  mapping = "org.Hs.eg.db"
)
```

---

run_goseq *Extract functional terms enriched in the DE genes, based on goseq*

Description

A wrapper for extracting functional GO terms enriched in a list of (DE) genes, based on the algorithm and the implementation in the goseq package

Usage

```
run_goseq(
  de_container = NULL,
  res_de = NULL,
  de_genes = NULL,
```

```
  bg_genes = NULL,
  top_de = NULL,
  FDR_threshold = 0.05,
  min_counts = 0,
  genome = "hg38",
  id = "ensGene",
  de_type = "up_and_down",
  testCats = c("GO:BP", "GO:MF", "GO:CC"),
  mapping = "org.Hs.eg.db",
  add_gene_to_terms = TRUE,
  verbose = TRUE
)
```

Arguments

de_container	An object containing the data for a Differential Expression workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqDataSet object, normally obtained after running your data through the DESeq2 framework.
res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
de_genes	A vector of (differentially expressed) genes
bg_genes	A vector of background genes, e.g. all (expressed) genes in the assays
top_de	numeric, how many of the top differentially expressed genes to use for the enrichment analysis. Attempts to reduce redundancy. Assumes the data is sorted by padj (default in DESeq2).
FDR_threshold	The pvalue threshold to us for counting genes as de. Default is 0.05
min_counts	numeric, min number of counts a gene needs to have to be included in the geneset that the de genes are compared to. Default is 0, recommended only for advanced users.
genome	A string identifying the genome that genes refer to, as in the goseq::goseq() function
id	A string identifying the gene identifier used by genes, as in the goseq::goseq() function
de_type	One of: 'up', 'down', or 'up_and_down' Which genes to use for GOterm calculations: upregulated, downregulated or both
testCats	A vector specifying which categories to test for overrepresentation amongst DE genes - can be any combination of "GO:CC", "GO:BP", "GO:MF" & "KEGG"
mapping	Character string, named as the org.XX.eg.db package which should be available in Bioconductor
add_gene_to_terms	Logical, whether to add a column with all genes annotated to each GO term
verbose	Logical, whether to add messages telling the user which steps were taken

Details

Note: the feature length retrieval is based on the goseq::goseq() function, and requires that the corresponding TxDb packages are installed and available

Value

A table containing the computed GO Terms and related enrichment scores

See Also

`goseq::goseq()` for the underlying method

Other Enrichment functions: `run_cluPro()`, `run_topGO()`

Examples

```
library("macrophage")
library("DESeq2")
data(gse, package = "macrophage")

dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
dds_macrophage <- DESeq(dds_macrophage)

data(res_de_macrophage, package = "mosdef")
res_de <- res_macrophage_IFNg_vs_naive
mygo <- run_goseq(
  res_de = res_macrophage_IFNg_vs_naive,
  de_container = dds_macrophage,
  mapping = "org.Hs.eg.db",
  testCats = "GO:BP",
  add_gene_to_terms = TRUE
)

head(mygo)
```

---

run_topGO *Extract functional terms enriched in the DE genes, based on topGO*

Description

A wrapper for extracting functional GO terms enriched in the DE genes, based on the algorithm and the implementation in the topGO package

Usage

```
run_topGO(
  de_container = NULL,
  res_de = NULL,
  de_genes = NULL,
  bg_genes = NULL,
  top_de = NULL,
  FDR_threshold = 0.05,
  min_counts = 0,
  ontology = "BP",
  annot = annFUN.org,
```

```
  mapping = "org.Mm.eg.db",
  gene_id = "symbol",
  full_names_in_rows = TRUE,
  add_gene_to_terms = TRUE,
  de_type = "up_and_down",
  topGO_method2 = "elim",
  do_padj = FALSE,
  verbose = TRUE
)
```

Arguments

de_container	An object containing the data for a Differential Expression workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqDataSet object, normally obtained after running your data through the DESeq2 framework.
res_de	An object containing the results of the Differential Expression analysis workflow (e.g. DESeq2, edgeR or limma). Currently, this can be a DESeqResults object created using the DESeq2 framework.
de_genes	A vector of (differentially expressed) genes
bg_genes	A vector of background genes, e.g. all (expressed) genes in the assays
top_de	numeric, how many of the top differentially expressed genes to use for the enrichment analysis. Attempts to reduce redundancy. Assumes the data is sorted by padj (default in DESeq2).
FDR_threshold	The pvalue threshold to us for counting genes as de. Default is 0.05
min_counts	numeric, min number of counts a gene needs to have to be included in the geneset that the de genes are compared to. Default is 0, recommended only for advanced users.
ontology	Which Gene Ontology domain to analyze: BP (Biological Process), MF (Molecular Function), or CC (Cellular Component)
annot	Which function to use for annotating genes to GO terms. Defaults to annFUN.org
mapping	Which org.XX.eg.db package to use for annotation - select according to the species
gene_id	Which format the genes are provided. Defaults to symbol, could also be entrez or ENSEMBL
full_names_in_rows	Logical, whether to display or not the full names for the GO terms
add_gene_to_terms	Logical, whether to add a column with all genes annotated to each GO term
de_type	One of: 'up', 'down', or 'up_and_down' Which genes to use for GOterm calculations: upregulated, downregulated or both
topGO_method2	Character, specifying which of the methods implemented by topGO should be used, in addition to the classic algorithm. Defaults to elim.
do_padj	Logical, whether to perform the adjustment on the p-values from the specific topGO method, based on the FDR correction. Defaults to FALSE, since the assumption of independent hypotheses is somewhat violated by the intrinsic DAG-structure of the Gene Ontology Terms
verbose	Logical, whether to add messages telling the user which steps were taken

Details

Allowed values assumed by the `topGO_method2` parameter are one of the following: `elim`, `weight`, `weight01`, `lea`, `parentchild`. For more details on this, please refer to the original documentation of the `topGO` package itself

Value

A table containing the computed GO Terms and related enrichment scores

See Also

`topGO::topGOdata-class()` and `topGO::runTest()` for the class objects and underlying methods

Other Enrichment functions: `run_cluPro()`, `run_goseq()`

Examples

```
library("macrophage")
library("DESeq2")
data(gse, package = "macrophage")

dds_macrophage <- DESeqDataSet(gse, design = ~ line + condition)
rownames(dds_macrophage) <- substr(rownames(dds_macrophage), 1, 15)
keep <- rowSums(counts(dds_macrophage) >= 10) >= 6
dds_macrophage <- dds_macrophage[keep, ]
dds_macrophage <- DESeq(dds_macrophage)

data(res_de_macrophage, package = "mosdef")

library("AnnotationDbi")
library("org.Hs.eg.db")
library("topGO")
topgoDE_macrophage <- run_topGO(
  de_container = dds_macrophage,
  res_de = res_macrophage_IFNg_vs_naive,
  ontology = "BP",
  mapping = "org.Hs.eg.db",
  gene_id = "symbol",
)
```

`styleColorBar_divergent` *Style DT color bars*

Description

Style DT color bars for values that diverge from 0.

Usage

```
styleColorBar_divergent(data, color_pos, color_neg)
```

Arguments

data	The numeric vector whose range will be used for scaling the table data from 0-100 before being represented as color bars. A vector of length 2 is acceptable here for specifying a range possibly wider or narrower than the range of the table data itself.
color_pos	The color of the bars for the positive values
color_neg	The color of the bars for the negative values

Details

This function draws background color bars behind table cells in a column, width the width of bars being proportional to the column values *and* the color dependent on the sign of the value.

A typical usage is for values such as `log2FoldChange` for tables resulting from differential expression analysis. Still, the functionality of this can be quickly generalized to other cases - see in the examples.

The code of this function is heavily inspired from styleColorBar, and borrows at full hands from an excellent post on StackOverflow - https://stackoverflow.com/questions/33521828/stylecolorbar-center-and-shift-left-right-dependent-on-sign/33524422#33524422

Value

This function generates JavaScript and CSS code from the values specified in R, to be used in DT tables formatting.

Examples

```
# With a very simple data frame

simplest_df <- data.frame(
  a = c(rep("a", 9)),
  value = c(-4, -3, -2, -1, 0, 1, 2, 3, 4)
)

library("DT")
DT::datatable(simplest_df) |>
  formatStyle(
    "value",
    background = styleColorBar_divergent(
      simplest_df$value,
      scales::alpha("forestgreen", 0.4),
      scales::alpha("gold", 0.4)
    ),
    backgroundSize = "100% 90%",
    backgroundRepeat = "no-repeat",
    backgroundPosition = "center"
  )
```

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