

Package: isoformic (via r-universe)

October 11, 2024

Title Isoformic: isoform-level biological interpretation of transcriptomic data

Version 0.1.1.9000

Description Isoform-level biological interpretation of transcriptomic data.

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Imports cli, dplyr, forcats, fs, ggplot2, glue, readr, rlang, stringr, tibble, tidyr, withr, SummarizedExperiment, MultiAssayExperiment, fgsea, fishpond, vroom

Suggests knitr, rmarkdown, viridis, curl, testthat (>= 3.0.0)

VignetteBuilder knitr

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

URL <https://github.com/luciorq/isoformic>,
<https://luciorq.github.io/isoformic/>

BugReports <https://github.com/luciorq/isoformic/issues>

Config/testthat/edition 3

Repository <https://luciorq.r-universe.dev>

RemoteUrl <https://github.com/luciorq/isoformic>

RemoteRef HEAD

RemoteSha 3c711b1930f94b3f0f88d80d81c2315f8e2e3cbe

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check_mae_isoformic_is_list
Check if Isoformic mae have a list isoformic slot

Description

Check if Isoformic mae have a list isoformic slot

Usage

check_mae_isoformic_is_list(mae)

check_mae_isoformic_tx_to_gene
Check if Isoformic mae have a tx_to_gene

Description

Check if Isoformic mae have a tx_to_gene

Usage

check_mae_isoformic_tx_to_gene(mae)

`check_se_metadata_level_length`*Check if content of metadata level slot is a string.*

Description

Check if content of metadata level slot is a string.

Usage`check_se_metadata_level_length(se)`

`check_se_metadata_level_type`*Check if content of metadata level slot is a string.*

Description

Check if content of metadata level slot is a string.

Usage`check_se_metadata_level_type(se)`

`create_isoformic_mae_from_se`*Create Isoformic Object from SummarizedExperiment*

Description

Create Isoformic Object from SummarizedExperiment

Usage`create_isoformic_mae_from_se(se_tx, se_gene, tx_to_gene = NULL)`**Arguments**

<code>se_tx</code>	SummarizedExperiment object containing transcript-level differential expression analysis results.
<code>se_gene</code>	SummarizedExperiment object containing gene-level differential expression analysis results.

download_reference *Download Reference Files From GENCODE*

Description

This function facilitates the downloading of reference files from the GENCODE database. It supports downloading GTF, GFF, and transcriptome FASTA files for human and mouse genomes. The function ensures that the correct version and file type are downloaded and handles directory creation and file existence checks to avoid redundant downloads.

Usage

```
download_reference(
  version = "46",
  reference = "gencode",
  organism = c("human", "mouse"),
  file_type = c("gtf", "gff", "fasta"),
  output_path = "data-raw",
  timeout_limit = 3600,
  method = "auto"
)
```

Arguments

version	Character with the version string. For mouse references, the letter 'M' in the version string is mandatory.
reference	Character indicating the source of the reference file. One of "gencode" or "mane". Defaults to "gencode". NOTE: "mane" is not implemented yet.
organism	Character indicating the organism. For GENCODE, this can only "human" or "mouse".
file_type	Character indicating the type of file to download. One of "gtf", "gff", or "fasta". Defaults to "gtf". NOTE: "fasta" refers to the transcriptome FASTA.
output_path	Character specifying the directory where the downloaded file will be saved. Defaults to "data-raw".
timeout_limit	Numeric value specifying the time in seconds for the download limit. This argument takes precedence over <code>base::options("timeout")</code> . Defaults to 3600 seconds (1 Hour).
method	Character specifying the method used by <code>utils::download.file()</code> . Defaults to "auto"

Value

A character string with the full path to the downloaded file.

is_deg_sig	<i>Add Differential Gene Expression Results to Transcript Table</i>
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Description

Add Differential Gene Expression Results to Transcript Table

Usage

```
is_deg_sig(DegsigVector, DET_table)
```

join_DEG_DET	<i>Merge Gene and Transcript Level Differential Expression Tables</i>
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Description

Merge Gene and Transcript Level Differential Expression Tables

Usage

```
join_DEG_DET(DEG_tab, DET_final_tab, logfc_cut, pval_cut)
```

make_tx_to_gene	<i>Create Transcript to Gene Relationship Table</i>
-----------------	---

Description

This function can extract a transcript to gene relationship table from GENCODE annotation files, such as the transcriptome FASTA and GFF3 or GTF annotation files.

Usage

```
make_tx_to_gene(file_path, file_type = "fasta")
```

Arguments

file_path	Path to file containing the reference.
file_type	Character indicating the type of file to download. One of "gtf", "gff", or "fasta". Defaults to "gtf". NOTE: "fasta" refers to the transcriptome FASTA.

modify_lnc_ranges	<i>Edit the lncRNA start and end table Table of lncRNA starts and ends plus a value to add</i>
-------------------	--

Description

Edit the lncRNA start and end table Table of lncRNA starts and ends plus a value to add

Usage

```
modify_lnc_ranges(lncRNA_start_end, value_to_add)
```

Arguments

lncRNA_start_end	Genomic position where the lncRNA annotation Starts.
value_to_add	Value to add to the lncRNA annotation.

plot_log2FC	<i>Plot Log2 Fold-Change Results</i>
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Description

Plot Log2 Fold-Change Results

Usage

```
plot_log2FC(DEG_DET_table, selected_gene, custom_colors = NULL)
```

plot_tx_context	<i>Plot Transcript Genomic Context</i>
-----------------	--

Description

This function plots the genomic context of all transcripts of given genes.

Usage

```
plot_tx_context(exon_table, custom_colors = NULL)
```

Arguments

exon_table	a tibble with exon information. Must contain columns tx_id, exon_left, and exon_right.
custom_colors	a vector of colors to use for each transcript. If not provided, the function will use the default colors. Actually, this argument is *NOT implemented yet .

plot_tx_expr	<i>Plot Transcript per gene expression</i>
--------------	--

Description

Plot Transcript per gene expression

Usage

```
plot_tx_expr(genes_to_plot, profile_data)
```

Arguments

genes_to_plot	a character vector with gene names
profile_data	tibble output from prepare_profile_data

Value

a ggplot object

prepare_annotation	<i>Prepare Annotation</i>
--------------------	---------------------------

Description

Prepare annotation to be imported as rowRanges and rowData for both Genes, Transcripts and Exons based Position Annotation Table. From a GTF or GFF3 annotation file.

Usage

```
prepare_annotation(file_path, file_type = c("gtf", "gff"))
```

Arguments

file_path	Path to annotation file.
file_type	Character indicating the type of file to download. One of "gtf" or "gff". Defaults to "gtf".

```
prepare_exon_annotation
```

Prepare Exon based Position Annotation Table

Description

Prepare Exon based Position Annotation Table

Usage

```
prepare_exon_annotation(gene_name, file_path, file_type = c("gff"))
```

Arguments

file_path	Path to annotation file.
file_type	Character indicating the type of file to download. One of "gtf", "gff", or "fasta". Defaults to "gtf". NOTE: "fasta" refers to the transcriptome FASTA.
gene_names	String or vector of gene names to extract.

```
prepare_profile_data
```

Prepare Data for Profile Plot

Description

Prepare Data for Profile Plot

Usage

```
prepare_profile_data(
  txi_gene = NULL,
  txi_transcript,
  sample_metadata,
  tx_to_gene,
  de_result_gene,
  de_result_transcript,
  var,
  var_levels,
  gene_col = "gene_name",
  tx_col = "transcript_name",
  pvalue_cutoff = 0.05,
  lfc_cutoff = 1,
  use_fdr = TRUE
)
```


Value

a tibble with data to plot.

run_enrichment	<i>Run Functional Analysis</i>
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Description

Run Functional Analysis

Usage

```
run_enrichment(det_df, genesets_list, pval_cutoff = 0.05, lfc_cutoff = 1)
```

Arguments

det_df	data.frame with differential expression of transcripts
genesets_list	list of gene sets to be used in the enrichment analysis
pval_cutoff	p-value cutoff for the enrichment analysis
lfc_cutoff	log2 fold change cutoff for the enrichment analysis

run_swish_pairwise	<i>Run Swish Differential Expression</i>
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Description

Run swish method for a SummarizedExperiment with inferential replicates.

Usage

```
run_swish_pairwise(se, contrast_var = "condition", ...)
```

Arguments

se	SummarizedExperiment object.
contrast_var	column name from colData(se).
...	Additional arguments passed to fishpond::swish().

Value

SummarizedExperiment object.

se_experiment_level *Return SummarizedExperiment Experiment Level*

Description

Check level of quantification for

Usage

```
se_experiment_level(se)
```

Arguments

se object of class SummarizedExperiment.
type String containing one of c("txp", "gene").

validate_isoformic_mae
 Validate Isoformic Object

Description

Validate if MultiAssayExperiment object is compatible with{isoformic}. Also, validates if {isoformic} preparation steps have been executed for the object.

Usage

```
validate_isoformic_mae(mae)
```

Arguments

mae MultiAssayExperiment object to be validated.

Value

MultiAssayExperiment object with valid {isoformic} slots.

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