

Package: BioPathNet (via r-universe)

June 29, 2024

Type Package

Title BioPathNet: Three Pod Analysis System

Version 0.2.0

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Description This package aims to provide a simple interface to perform the Three Pod Analysis of RNASeq dataset. In addition, this also provides utility functions to perform the individual components.

License GPL-3

Encoding UTF-8

LazyData true

LazyDataCompression xz

Suggests testthat

RoxygenNote 7.2.3

Imports magrittr, tibble, readr, stringr, purrr, methods, fgsea, enrichR, rlang, stats, dplyr, tidyr

Collate 'classes.R' 'BPNList.R' 'EnrichRResult.R' 'GSEAResult.R' 'LEResult.R' 'S4methods.R' 'data.R' 'do_enrichr_pod.R' 'do_gsea_pod.R' 'do_leading_pod.R' 'get_revigo_output.R' 'prepare_data.R'

Depends R (>= 2.10)

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

RemoteUrl <https://github.com/CogDisResLab/BioPathNet>

RemoteRef HEAD

RemoteSha 1d92af3bc0df623714bb5d2864752d98492ae59e

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BPNList	<i>Construct a BPNList object</i>
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Description

Construct a BPNList object

Usage

```
BPNList(input, gsea, enrichr, ilincs, leading, revigo, integrated)
```

Arguments

input	tbl_df A tibble with the differentially expressed genes
gsea	GSEAResult An object containing the GSEA results
enrichr	EnrichRResult An object containing the EnrichR results
ilincs	iLINCSResult An object containing the iLINCS results
leading	LEResult An object containing the Leading Edge Analysis results
revigo	RevigoResult An object containing the Revigo results
integrated	IntegratedResult An object containing the Integrated results

Value

A BPNList object

Examples

TRUE

BPNList-class*BPNList-class: The BioPathNet Core Class*

Description

This class takes care of the entire analysis infrastructure of the BioPathNet analysis. This class is created with inputting a list of differentially expressed genes and then stores the subsequently generated results.

Value

An object of class BPNList

Slots

`input` tbl_df. A tibble with Two columns of gene names and logfc values and optionally a p-value column

`gsea` GSEAResult. An instance of [GSEAResult-class](#) class storing the results GSEA Analysis

`enrichr` EnrichRResult. An instance of [EnrichRResult-class](#) class storing the results EnrichR Analysis

`ilincs` iLINCSResult. An instance of [iLINCSResult-class](#) class storing the results iLINCS Analysis

`leading` LEResult. An instance of [LEResult-class](#) class storing the results Leading Edge Analysis

`revigo` RevigoResult. An instance of [RevigoResult-class](#) class storing the results Revigo Analysis

`integrated` IntegratedResult. An instance of [IntegratedResult-class](#) class storing the results after integrating the three components

Examples

TRUE

do_enrichr_pod *Perform the EnrichR Analysis*

Description

This function takes in a BPNList object and returns a BPNList object with the enrichr slot updated with process EnrichR Results

Usage

```
do_enrichr_pod(bpn, alpha = 0.05, lower = NULL, upper = NULL, useFDR = TRUE)
```

Arguments

bpn	BPNList An object of class BPNList created from prepare_data
alpha	numeric The Alpha value for statistical significance. Defaults to 0.05.
lower	numeric The cutoff for down-regulated genes. If not specified, it takes the bottom 10% of the
upper	numeric The cutoff for up-regulated genes. If not specified, it takes the top 10% of the dataset
useFDR	logical Whether to filter by adjusted p-value

Details

This function takes in a BPNList object and returns a BPNList object with the enrichr slot updated with process EnrichR Results.

Value

An object of class BPNList with its enrichr slot populated with the results

Examples

```
TRUE
```

do_gsea_pod

*Perform the Geneset Enrichment Analysis***Description**

This function takes a BPNList object and performs a Geneset Enrichment Analysis and returns a BPNList object with the results of the GSEA

Usage

```
do_gsea_pod(
  bpn,
  species = "hsapiens",
  gmtfile = NULL,
  lower = NULL,
  upper = NULL,
  alpha = 0.05,
  minSize = 15,
  maxSize = 500,
  rankWithSignificance = FALSE,
  useFDR = TRUE
)
```

Arguments

bpn	BPNList An object of class BPNList created from prepare_data
species	character One of the species for which we provide current GMT pathways. Currently the valid species are hsapiens, mmusculus and rnorvegicus. Cannot be specified along with gmtfile
gmtfile	character A full path to a GMT File you would like to use. Cannot be specified along with species
lower	numeric The cutoff for down-regulated genes. If not specified, it takes the bottom 10% of the dataset
upper	numeric The cutoff for up-regulated genes. If not specified, it takes the top 10% of the dataset
alpha	numeric The Alpha value for statistical significance. Defaults to 0.05.
minSize	numeric The minimum number of genes that should be in a pathway for it to be included in the analysis
maxSize	numeric The maximum number of genes that should be in a pathway for it to be included in the analysis
rankWithSignificance	logical Whether to rank genes using p-values
useFDR	logical Whether to filter by adjusted p-value

Details

This function takes a BPNList object and performs a Geneset Enrichment Analysis and returns a BPNList object with the results of the GSEA

Value

An object of class BPNList with its gsea slot populated with the results

Examples

```
TRUE
```

do_leading_pod	<i>Perform Leading Edge Gene Analysis</i>
----------------	---

Description

This method takes in a bpn object and performs a leading edge analysis to identify the genes that are driving the majority of pathways.

Usage

```
do_leading_pod(bpn)
```

Arguments

bpn An object of class BPNList. Must have the gsea analysis completed beforehand.

Value

An object of class BPNList with its leading slot populated with the results

Examples

```
TRUE
```

`EnrichRResult`*Construct an EnrichRResult object*

Description

Construct an EnrichRResult object

Usage

```
EnrichRResult(  
  up_results,  
  down_results,  
  upreg,  
  downreg,  
  alpha,  
  upper,  
  lower,  
  dbs,  
  useFDR  
)
```

Arguments

<code>up_results</code>	<code>tbl_df</code> A tibble of enrichment results from the upregulated genes
<code>down_results</code>	<code>tbl_df</code> A tibble of enrichment results from the downregulated genes
<code>upreg</code>	<code>tbl_df</code> A tibble of up-regulated genes
<code>downreg</code>	<code>tbl_df</code> A tibble of down-regulated genes
<code>alpha</code>	numeric Alpha level of significance
<code>upper</code>	numeric Upper threshold for up-regulated genes
<code>lower</code>	numeric Lower threshold for down-regulated genes
<code>dbs</code>	character a vector of the databases used for the enrichment analysis
<code>useFDR</code>	logical Whether to filter by adjusted p-value

Value

an object of class `EnrichRResult`

Examples

```
TRUE
```

EnrichRResult-class *EnrichRResult-class: Class storing EnrichR Results*

Description

This class stores the input parameters and results of the Gene Set Enrichment Analysis.

Value

an object of class EnrichRResult

Slots

alpha numeric. The Alpha threshold for significance
threshold_up numeric. The logfc threshold for up-regulated genes
threshold_down numeric. The logfc threshold for down-regulated genes
upregulated_genes tbl_df. The up-regulated genes from the input DEG tibble
downregulated_genes tbl_df. The down-regulated genes from the input DEG tibble
dbs_used character. A vector of the databases used from enrichR
up_enrichr tbl_df. Enriched pathways in up-regulated genes
down_enrichr tbl_df. Enriched pathways in down-regulated genes
sig_up_enrichr tbl_df. Significant enriched pathways in up-regulated genes
sig_down_enrichr tbl_df. Significant enriched pathways in down-regulated genes
num_upreg numeric. Number of up-regulated genes
num_downreg numeric. Number of down-regulated genes
num_up_enrichr numeric. Number of enriched pathways in up-regulated genes
num_down_enrichr numeric. Number of enriched pathways in down-regulated genes
num_sig_up_enrichr numeric. Number of significant enriched pathways in up-regulated genes
num_sig_down_enrichr numeric. Number of significant enriched pathways in down-regulated genes
empty logical. A simple check for whether or not the object is empty

Examples

TRUE

get_revigo_output *Perform Revigo enrichment analysis*

Description

Perform Revigo enrichment analysis

Usage

```
get_revigo_output(input_data)
```

Arguments

input_data A dataframe containing GO IDs and associated p-values

Value

A dataframe containing the Revigo Enrichment analysis

Examples

```
TRUE
```

GSEAResult *Construct a GSEAResult Object*

Description

Construct a GSEAResult Object

Usage

```
GSEAResult(results, pathways, lower, upper, alpha, upreg, downreg, useFDR)
```

Arguments

results	tbl_df A tibble with the results from fgsea
pathways	list A list of vectors with gene sets
lower	numeric Lower threshold for down-regulated genes
upper	numeric Upper threshold for up-regulated genes
alpha	numeric Alpha level of significance
upreg	tbl_df A tibble of up-regulated genes
downreg	tbl_df A tibble of down-regulated genes
useFDR	logical Whether to filter by adjusted p-value

Value

an object of class GSEAResult

Examples

TRUE

GSEAResult-class

GSEAResult-class: Class storing GSEA Results

Description

This class stores the input parameters and results of the Gene Set Enrichment Analysis.

Value

an object of class GSEAResult

Slots

alpha numeric. The Alpha threshold for significance
 threshold_up numeric. The logfc threshold for up-regulated genes
 threshold_down numeric. The logfc threshold for down-regulated genes
 upregulated_genes tbl_df. The up-regulated genes from the input DEG tibble
 pathways tbl_df. The pathways we used, either built-in or user-supplied
 downregulated_genes tbl_df. The down-regulated genes from the input DEG tibble
 pos_enriched tbl_df. The positively enriched pathways
 neg_enriched tbl_df. The negatively enriched pathways
 sig_pos_enriched tbl_df. Significant positively enriched pathways
 sig_neg_enriched tbl_df. Significant positively enriched pathways
 num_upreg numeric. Number of up-regulated genes
 num_downreg numeric. Number of down-regulated genes
 num_tested numeric. Number of pathways tested
 num_pos_enriched numeric. Number of positively enriched pathways
 num_neg_enriched numeric. Number of negatively enriched pathways
 num_sig_pos_enriched numeric. Number of significant positively enriched pathways
 num_sig_neg_enriched numeric. Number of significant negatively enriched pathways
 empty logical. A simple check for whether or not the object is empty

Examples

TRUE

 hsapiens

List of pathways and associated genes in homo sapiens

Description

The processed form of the October 2020 Pathway annotation containing every pathway annotated with the associated genes in humans. This uses the Symbol annotation from BaderLab.

Usage

hsapiens

Format

A list

Source

http://download.baderlab.org/EM_Genesets/October_01_2020/Human/symbol/Human_GO_AllPathways_with_GO_iea_October_01_2020_symbol.gmt

 iLINCSResult-class

iLINCSResult-class: Class storing iLINCS Results

Description

This class stores the result of the results from iLINCS

Value

an object of class iLINCSResult

Slots

threshold_up numeric. LFC threshold for up-regulated genes

threshold_down numeric. LFC threshold for down-regulated genes

threshold_pval numeric. P Value threshold for genes.

threshold_similarity numeric. Similarity threshold

l1000_subset tbl_df. Subset of L1000 genes in the dataset

upregulated_genes tbl_df. L1000 genes up-regulated in dataset

downregulated_genes tbl_df. L1000 genes down-regulated in dataset

ilincs_query_signature tbl_df. Complete iLINCS Query signature

all_perturbagens tbl_df. Complete list returned from iLINCS of perturbagens

`filtered_perturbagens` `tbl_df`. Filtered list of perturbagens by the similarity threshold
`num_genes_l1000` numeric. Number of L1000 genes in dataset
`num_genes_upregulated` numeric. Number of up-regulated L1000 genes in dataset
`num_genes_downregulated` numeric. Number of down-regulated L1000 genes in dataset
`num_all_perturbagens` numeric. Number of all perturbagens returned by iLINCS
`num_filtered_perturbagens` numeric. Number of filtered perturbagens returned by iLINCS
`empty` logical. A simple check for whether or not the object is empty

Examples

TRUE

`IntegratedResult-class`

IntegratedResult-class: Class containing Integrated results

Description

`IntegratedResult-class`: Class containing Integrated results

Value

and object of class `IntegratedResults`

Slots

`placeholder` numeric.

`empty` logical. A simple check for whether or not the object is empty

Examples

TRUE

leading_edge	<i>Extract Leading Edge Genes from GSEA Results</i>
--------------	---

Description

Extract Leading Edge Genes from GSEA Results

Usage

```
leading_edge(gsea, direction)
```

Arguments

gsea	an object of class GSEAResult
direction	one of "up" or "down"

Value

A tibble with the leading edge genes and associated pathways

Examples

```
TRUE
```

LEResult	<i>Construct an LEResult object</i>
----------	-------------------------------------

Description

Construct an LEResult object

Usage

```
LEResult(leading_up, leading_down)
```

Arguments

leading_up	tbl_df. A dataframe with the results of all the leading edge genes from upregulated genes
leading_down	tbl_df. A dataframe with the results of all the leading edge genes from down-regulated genes

Value

An object of class LEResult

Examples

TRUE

LEResult-class	<i>LEResult-class: Class containing Leading Edge Analysis results</i>
----------------	---

Description

LEResult-class: Class containing Leading Edge Analysis results

Value

an object of class LEResult

Slots

leading_up tbl_df. A tibble with the results of LE analysis for the upregulated pathways
 leading_down tbl_df. A tibble with the results of LE analysis for the downregulated pathways
 count_leading_up tbl_df. A tibble with the counts of LE genes for the upregulated pathways
 count_leading_down tbl_df. A tibble with the counts of LE genes for the downregulated pathways
 num_leading_up numeric. Number of LE genes for the upregulated pathways
 num_leading_down numeric. Number of LE genes for the downregulated pathways
 empty logical. A simple check for whether or not the object is empty

Examples

TRUE

load_pathways	<i>Load Pathways data</i>
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Description

Load Pathways data

Usage

load_pathways(species)

Arguments

species The species. Can be hsapiens, mmusculus or rnorvegicus

Value

The loaded pathways
importFrom utils data

Examples

TRUE

mmusculus

List of pathways and associated genes in mus musculus

Description

The processed form of the October 2020 Pathway annotation containing every pathway annotated with the associated genes in mice. This uses the Symbol annotation from BaderLab.

Usage

mmusculus

Format

A list

Source

http://download.baderlab.org/EM_Genesets/October_01_2020/Mouse/symbol/Mouse_GO_AllPathways_with_GO_iea_October_01_2020_symbol.gmt

prepare_data

Prepare the data for downstream analysis

Description

This function takes vectors of gene names, log Fold-change values and optionally p-values and formats them into a tibble for downstream analysis.

Usage

```
prepare_data(genes, logfc, pvalues = NULL)
```

Arguments

genes a character vector of gene names
logfc a numeric vector of log fold-change values
pvalues (optional) a numeric vector of p-values

Details

The function returns an object of class BPNList that will update as the analysis proceeds

Value

An object of class BPNList with the following slot set:
input

Examples

TRUE

RevigoResult-class *RevigoResult-class: Class containing results from Revigo*

Description

RevigoResult-class: Class containing results from Revigo

Value

and object of class RevigoResult

Slots

placeholder numeric.

empty logical. A simple check for whether or not the object is empty

Examples

TRUE

rnorvegicus *List of pathways and associated genes in rattus norvegicus*

Description

The processed form of the October 2020 Pathway annotation containing every pathway annotated with the associated genes in rats. This uses the Symbol annotation from BaderLab.

Usage

rnorvegicus

Format

A list

Source

http://download.baderlab.org/EM_Genesets/October_01_2020/MRat/symbol/Rat_GO_AllPathways_with_GO_iea_October_01_2020_symbol.gmt

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