Package 'SurprisalAnalysis'

April 21, 2024

Title Surprisal Analysis

Version 0.1

Description This package applies surprisal analysis on transcriptomics data.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Imports ggplot2,
tidyr,
dplyr,
matlib,
org.Mm.eg.db,
org.Hs.eg.db,
clusterProfiler,
AnnotationDbi,
tidyverse

R topics documented:

GO_analysis_surprisal_analysis

Perform Gene ontology analysis on a pattern of interest

Description

Perform Gene ontology analysis on a pattern of interest

Usage

```
GO_analysis_surprisal_analysis(
  transcript_weights,
  percentile_GO,
  lambda_no,
  key_type = "SYMBOL",
  flip = FALSE,
  species.db = org.Hs.eg.db,
  top_GO_terms = 15
)
```

Arguments

transcript_weights
    a dataframe containing the weight of transcripts in each pattern

percentile_GO	the percentile of transcript to be used for GO analysis, for example 95 will run GO on transcripts in the 95th percentile and above
lambda_no	the lambda pattern the user is interested in analyzing
key_type	type of transcripts which can be either SYMBOL, ENTREZID, ENSEMBL, or PROBEID
flip	a boolean variable which can either be true or false, if it is set to true, the lambda values will be multipled by -1
species.db	the type of species used for GO analysis, by default set to Homo sapiens, can be either org.Hs.eg.db or org.Mm.eg.db
top_GO_terms	number of GO terms returns, by default set to 15

Value

the important GO terms related to a lambda gene pattern

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  plot_lambda   *Plot lambda values over time*

Description

Plot lambda values over time

Usage

```
plot_lambda(lambda_values, lambda_no)
```

Arguments

lambda_values	dataframe containing lambda values
lambda_no	the pattern number of interest

Value

a plot showing lambda values over time

| surprisal_analysis | *This function performs surprisal analysis on transcriptomics data* |

Description

This function performs surprisal analysis on transcriptomics data

Usage

```
surprisal_analysis(input.data)
```

Arguments

input.data   transcriptomics data stores as dataframe

Value

a list containing the lambda values and corresponding weights of transcripts stored

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