Package 'ToPASeq'

October 16, 2018

Version 1.14.1

Date 2018-06-19

Title Topology-based pathway analysis of RNA-seq data

Author Ivana Ihnatova, Eva Budinska, Ludwig Geistlinger

Maintainer Ludwig Geistlinger <ludwig.geistlinger@sph.cuny.edu>

Description Implementation of methods for topology-based pathway analysis of RNA-seq data. This includes Topological Analysis of Pathway Phenotype Association (TAPPA; Gao and Wang, 2007), PathWay Enrichment Analysis (PWEA; Hung et al., 2010), and the Pathway Regulation Score (PRS; Ibrahim et al., 2012).

Depends R(>= 3.5.0), graphite

Imports Rcpp, graph, methods

Suggests BiocStyle, EnrichmentBrowser, airway, knitr, rmarkdown

LinkingTo Rcpp

LazyData yes

License AGPL-3

biocViews GeneExpression, RNASeq, DifferentialExpression, GraphAndNetwork, Pathways, NetworkEnrichment, Visualization

VignetteBuilder knitr

RoxygenNote 6.0.1

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

git_branch RELEASE_3_7

git_last_commit bd4f779

git_last_commit_date 2018-06-19

Date/Publication 2018-10-15

R topics documented:

prs *Pathway regulation score (PRS)*

Description

This function implements the PRS method to analyze pathway enrichment of gene expression data. For PRS, a gene weight correspond to the number of downstream differentially expressed genes.

Usage

```
prs(de, all, pwys, nperm = 1000)

prsWeights(pwy, de, all)
```

Arguments

de	A named numeric vector containing log2 fold-changes of the differentially expressed genes. Recommended names are Entrez gene IDs.
all	A character vector with the gene IDs in the reference set. If the data was obtained from a gene expression experiment, this set will contain all genes measured in the experiment. This vector should contain *all* names of the de argument.
pwys	A linkS4class{PathwayList} containing the pathways that should be analyzed for enrichment.
nperm	Integer. Number of permutations.
pwy	A linkS4class{Pathway} for which the weights should be computed.

Value

A data.frame with normalized score and p-value for each pathway analyzed.

Author(s)

Ivana Ihnatova

References

Ibrahim et al. (2012) A topology-based score for pathway enrichment. J Comput Biol, 19(5):563-73.

See Also

pathways

Examples

```
# pathways
library(graphite)
pwys <- pathways("hsapiens","kegg")[1:10]

# expression data
```

```
all <- nodes(pwys[[1]])
nds <- sample(all, 30)
de <- setNames(rnorm(30), nds)

# executing PRS
prsWeights(pwys[[1]], de, all)
prs(de, all, pwys, nperm=100)
```

Index