Package 'PoTRA'

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Type Package

Title PoTRA: Pathways of Topological Rank Analysis

Version 1.8.2

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Description The PoTRA analysis is based on topological ranks of genes in biological pathways. Po-
TRA can be used to detect pathways involved in disease (Li, Liu & Dinu, 2018). We use PageR-
ank to measure the relative topological ranks of genes in each biological pathway, then se-
lect hub genes for each pathway, and use Fishers Exact test to determine if the num-
ber of hub genes in each pathway is altered from normal to cancer (Li, Liu & Dinu, 2018). Alter-
natively, if the distribution of topological ranks of gene in a pathway is altered between nor-
mal and cancer, this pathway might also be involved in can-
cer (Li, Liu & Dinu, 2018). Hence, we use the Kolmogorov–Smirnov test to detect path-
ways that have an altered distribution of topological ranks of genes between two pheno-
types (Li, Liu & Dinu, 2018). PoTRA can be used with the KEGG, Reactome, SM-
PDB and PharmGKB, Panther, PathBank, etc databases from the devel graphite library.

License LGPL

Encoding UTF-8

LazyData false

Depends R (>= 3.6.0), stats, BiocGenerics, org.Hs.eg.db, igraph,
graph, graphite

Imports

biocViews GraphAndNetwork, StatisticalMethod, GeneExpression,
DifferentialExpression, Pathways, Reactome, Network, KEGG,
PathBank, Panther

RoxygenNote 6.1.1

Suggests BiocStyle, knitr, rmarkdown, colr, metap, repmis

VignetteBuilder knitr

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R topics documented:

PoTRA   *PoTRA.corN*

Description

The PoTRA analysis is based on topological ranks of genes in biological pathways. PoTRA can be used to detect pathways involved in disease. The PoTRA package contains one function for creating the PoTRA results object.

Usage

```
PoTRA.corN(mydata, genelist, Num.sample.normal, Num.sample.case, Pathway.database, PR.quantile)
```

Arguments

mydata	Dataframe that contains rownames consisting of entrez gene identifiers and columns representing normals and samples from gene expression data.
genelist	Dataframe that consists of a single column of entrez gene identifiers (the same as those found in the rownames(mydata)).
Num.sample.normal	
	Represents normal samples in the mydata dataframe.
Num.sample.case	
	Represents case samples in the mydata dataframe.
Pathway.database	
	Object contains gene lists from KEGG, Reactome, PathBank, Panther and PharmGKB databases, and these are made available through the devel graphite library.
PR.quantile	Object contains the percentile of PageRank scores as a cutoff for hub genes, the recommended percentile is 0.95.

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