

# Package ‘PoTRA’

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**Type** Package

**Title** PoTRA: Pathways of Topological Rank Analysis

**Version** 1.13.0

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**Description** The PoTRA analysis is based on topological ranks of genes in biological pathways. PoTRA can be used to detect pathways involved in disease (Li, Liu & Dinu, 2018). We use PageRank to measure the relative topological ranks of genes in each biological pathway, then select hub genes for each pathway, and use Fishers Exact test to determine if the number of hub genes in each pathway is altered from normal to cancer (Li, Liu & Dinu, 2018). Alternatively, if the distribution of topological ranks of gene in a pathway is altered between normal and cancer, this pathway might also be involved in cancer (Li, Liu & Dinu, 2018). Hence, we use the Kolmogorov–Smirnov test to detect pathways that have an altered distribution of topological ranks of genes between two phenotypes (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

**git\_url** <https://git.bioconductor.org/packages/PoTRA>

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PoTRA	<i>PoTRA.corN</i>
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### 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

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

### Author(s)

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