

# Package ‘ToPASeq’

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**Version** 1.14.1

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**Title** Topology-based pathway analysis of RNA-seq data

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**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>

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prs *Pathway regulation score (PRS)*

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### 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)
```

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