Package ‘MetaPhOR’

April 1, 2025

Type Package

Title Metabolic Pathway Analysis of RNA

Version 1.8.0

Description MetaPhOR was developed to enable users to assess metabolic dysregulation using transcriptomic-level data (RNA-sequencing and Microarray data) and produce publication-quality figures. A list of differentially expressed genes (DEGs), which includes fold change and p value, from DESeq2 or limma, can be used as input, with sample size for MetaPhOR, and will produce a data frame of scores for each KEGG pathway. These scores represent the magnitude and direction of transcriptional change within the pathway, along with estimated p-values.MetaPhOR then uses these scores to visualize metabolic profiles within and between samples through a variety of mechanisms, including: bubble plots, heatmaps, and pathway models.

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Encoding UTF-8

RoxygenNote 7.2.1

Imports utils, ggplot2, ggrepel, stringr, pheatmap, grDevices, stats, clusterProfiler, RecordLinkage, RCy3

Depends R (>= 4.2.0)

biocViews Metabolomics, RNASeq, Pathways, GeneExpression, DifferentialExpression, KEGG, Sequencing, Microarray

Suggests BiocStyle, knitr, rmarkdown, kableExtra

VignetteBuilder knitr

LazyData false

SystemRequirements Cytoscape (>= 3.9.0) for the cytoPath() examples

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Contents

`bubblePlot` *Create a Bubble Plot for Individual Samples*

Description

Create a Bubble Plot for Individual Samples

Usage

```
bubblePlot(scorelist, labeltext, labelsize = 0.25)
```

Arguments

`scorelist`	dataframe(1) the output of Pathway Analysis fun
`labeltext`	character(1) what to label points by: LogFC or Pval
`labelsize`	numeric(1) size of text labels for points

Value

bubblePlot() returns a bubble plot using pathway scores, pval, logfc

Examples

```
brca <- read.csv(system.file("extdata/BRCA_Scores.csv",
                    package = "MetaPhOR"),
                    header = TRUE,
                    row.names = 1)

#Bubble Plot Labeled By P Value
bubblePlot(scorelist = brca,
            labeltext = "Pval",
            labelsize = .85)

#Bubble Plot Labeled by LogFC
bubblePlot(scorelist = brca,
            labeltext = "LogFC",
            labelsize = .85)
```

`cytoPath` *Map Differentially Expressed Genes to Dysregulated Pathways*

Description

requires the package RCy3 and a local instance of Cytoscape

Usage

```
cytoPath(
    pathway,
    DEGpath,
    figpath,
    genename,
    headers = c("log2FoldChange", "padj")
)
```

Arguments

`pathway`	character, the name of the pathway to be visualized
`DEGpath`	character, the path to a DEG file by DESeq2 or limma
`figpath`	character, the path to which the figure will be saved
`genename`	character, column name with HUGO Gene Names in DEG file
`headers`	character vector of length 2 in the form c(log fold change col name, adjusted p value col name)

Value

cytoPath() Returns a Cytoscape figure of DEG data on rWikiPathways

Examples

```
cytoPath(pathway = "Tryptophan Metabolism",
        DEGpath = system.file("extdata/BRCA_DEGS.csv", package = "MetaPhOR"),
        figpath = file.path(tempdir(), "example_map"),
        genename = "X",
        headers = c("logFC", "adj.P.Val"))
```

`datasummary` *MetaPhOR: Metabolic Pathway Analysis of RNA*

Description

MetaPhOR was developed to enable users to assess metabolic dysregulation using transcriptomic-level data (RNA-sequencing and Microarray data) and produce publication-quality figures. A list of differentially expressed genes (DEGs), which includes fold change and p value, from DESeq2 or limma, can be used as input, with sample size for MetaPhOR, and will produce a data frame of scores for each KEGG pathway. These scores represent the magnitude and direction of transcriptional change within the pathway, along with estimated p-values. MetaPhOR then uses these scores to visualize metabolic profiles within and between samples through a variety of mechanisms, including: bubble plots, heatmaps, and pathway models.

Author(s)

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- Spencer Rosario

`metaHeatmap` *Create a Heatmap for Comparing Multiple Samples*

Description

Create a Heatmap for Comparing Multiple Samples

Usage

```
metaHeatmap(scorelist, samplenames, pvalcut = 0.05)
```

Arguments

`scorelist`	list of outputs from pathwayAnalysis()
`samplenames`	vector of samples names for axis labels
`pvalcut`	numeric, the p val over which pathways will not be included

Value

metaHeatmap() returns a heatmap of significant dysregulated pathways

for each sample included

Examples

```
brca <- read.csv(system.file("extdata/BRCA_Scores.csv",
            package = "MetaPhOR"), header = TRUE, row.names = 1)

ovca <- read.csv(system.file("extdata/OVCA_Scores.csv",
            package = "MetaPhOR"), header = TRUE, row.names = 1)

prad <- read.csv(system.file("extdata/PRAD_Scores.csv",
            package = "MetaPhOR"), header = TRUE, row.names = 1)

all.scores <- list(brca, ovca, prad)
```

```
names <- c("BRCA", "OVCA", "PRAD")

metaHeatmap(scorelist = all.scores,
            samplenames = names,
            pvalcut = 0.05)
```

`pathwayAnalysis` *Metabolic Pathway Analysis of RNAseq Data*

Description

Metabolic Pathway Analysis of RNAseq Data

Usage

```
pathwayAnalysis(
    DEGpath,
    genename,
    sampsize,
    iters = 1e+05,
    headers = c("log2FoldChange", "padj")
)
```

Arguments

`DEGpath`	character, the path to a txt or csv DEG file
`genename`	character, column name with HUGO Gene Names in DEG file
`sampsize`	numeric, the sample size of the experiment to be analyzed
`iters`	numeric, the number of iterations of resampling to perform in bootstrapping
`headers`	character vector of length2 in the form c(log fold change col name, adjusted p value col name)

Value

pathwayAnalysis() returns a dataframe of pathway scores and pvals

Examples

```
#iterations (iters) of resampling in bootstraping set to 30,000 for speed
#100,000 iterations recommended for improved power

set.seed(1234)

scores <- pathwayAnalysis(
                DEGpath = system.file("extdata/BRCA_DEGS.csv",
                                      package = "MetaPhOR"),
                genename = "X",
                sampsize = 1095,
                iters = 30000,
                headers = c("logFC", "adj.P.Val"))
scores
```

`pathwayList` *List Available Metabolic rWikiPathways*

Description

List Available Metabolic rWikiPathways

Usage

```
pathwayList()
```

Value

pathwayList() returns a list of rWikiPathways for use in CytoPath()

Examples

```
pathwayList()
```

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