# Package 'MetaPhOR' 

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## Type Package

Title Metabolic Pathway Analysis of RNA
Version 1.4.0
Description MetaPhOR was developed to enable users to assess metabolic dysregulation using tran-scriptomic-level data (RNA-sequencing and Microarray data) and produce publicationquality 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 pvalues.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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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 RCy 3 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 DESeq 2 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 $c(l o g$ 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"))
```


## Description

MetaPhOR was developed to enable users to assess metabolic dysregulation using transcriptomiclevel 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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```
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 <br> 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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