

# Package ‘MetaPhOR’

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**Type** Package

**Title** Metabolic Pathway Analysis of RNA

**Version** 1.13.0

**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.

**License** Artistic-2.0

**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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bubblePlot	<i>Create a Bubble Plot for Individual Samples</i>
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### 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
labelsizesize	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",
            labelsizesize = .85)
```

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

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cytoPath

*Map Differentially Expressed Genes to Dysregulated Pathways*

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### 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"))
```

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datasummary

*MetaPhOR: Metabolic Pathway Analysis of RNA*

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**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)**

**Maintainer:** Emily Isenhardt <emily.isenhardt@roswellpark.org>

Authors:

- Spencer Rosario

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metaHeatmap

*Create a Heatmap for Comparing Multiple Samples*

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**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)
```

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pathwayAnalysis      *Metabolic Pathway Analysis of RNAseq Data*

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## 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 bootstrapping 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
```

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`pathwayList`*List Available Metabolic rWikiPathways*

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**Description**

List Available Metabolic rWikiPathways

**Usage**

```
pathwayList()
```

**Value**

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

**Examples**

```
pathwayList()
```

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