

# Package ‘MetaPhOR’

July 4, 2025

**Type** Package

**Title** Metabolic Pathway Analysis of RNA

**Version** 1.11.0

**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

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

**git\_branch** devel

**git\_last\_commit** cf1b531

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-07-03

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## Contents

|                           |          |
|---------------------------|----------|
| bubblePlot . . . . .      | 2        |
| cytoPath . . . . .        | 3        |
| datasummary . . . . .     | 3        |
| metaHeatmap . . . . .     | 4        |
| pathwayAnalysis . . . . . | 5        |
| pathwayList . . . . .     | 6        |
| <b>Index</b>              | <b>7</b> |

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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, labelsizesize = 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)

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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()
```

# Index

`bubblePlot`, [2](#)

`cytoPath`, [3](#)

`datasummary`, [3](#)

`metaHeatmap`, [4](#)

`MetaPhOR (datasummary)`, [3](#)

`MetaPhOR-package (datasummary)`, [3](#)

`pathwayAnalysis`, [5](#)

`pathwayList`, [6](#)