Package: MetaPhOR (via r-universe)

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Type Package

Title Metabolic Pathway Analysis of RNA

Version 1.7.0

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

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/MetaPhOR

RemoteRef HEAD

RemoteSha bd8ea30e3a3e755109bc34059b798f1c01dd4dda

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)
```

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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
```

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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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