Package ‘MicrobiomeProfiler’

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Title An R/shiny package for microbiome functional enrichment analysis

Version 1.10.0

Description
This is an R/shiny package to perform functional enrichment analysis for microbiome data. This package was based on clusterProfiler. Moreover, MicrobiomeProfiler support KEGG enrichment analysis, COG enrichment analysis, Microbe-Disease association enrichment analysis, Metabo-Pathway analysis.

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URL https://github.com/YuLab-SMU/MicrobiomeProfiler/

BugReports https://github.com/YuLab-SMU/MicrobiomeProfiler/issues

Imports clusterProfiler (>= 4.5.2), config, DT, enrichplot, golem, gson, methods, magrittr, shiny (>= 1.6.0), shinyWidgets, shinycustomloader, htmltools, ggplot2, graphics, stats, utils

Encoding UTF-8

biocViews Microbiome, Software, Visualization,KEGG

RoxygenNote 7.2.3

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Config/testthat/edition 3

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Contents

MicrobiomeProfiler-package .................................................. 2
enrichCOG ........................................................................ 2
enrichHMDB ....................................................................... 3
enrichKO .......................................................................... 4
enrichMBKEGG ................................................................. 5
enrichMDA ......................................................................... 6
enrichModule ...................................................................... 7
enrichSMPDB ..................................................................... 8
gson_cpd ........................................................................... 9
gson_enzyme ..................................................................... 9
gson_KO ............................................................................ 9
gson_module ...................................................................... 10
microbiota_taxlist ............................................................... 10
Psoriasis_data .................................................................... 11
Rat_data ............................................................................. 11
run_MicrobiomeProfiler ..................................................... 12

Index .................................................................................. 13

MicrobiomeProfiler-package

*Functional enrichment analysis for microbiome data*

Description

The package implements an shiny application for functional enrichment analysis and visualization of microbiome studies.

enrichCOG

*COG enrichment analysis for microbiome data*

Description

COG enrichment analysis for microbiome data

Usage

enrichCOG(
       gene,  
dtype = "category",  
pvalueCutoff = 0.05,  
pAdjustMethod = "BH",  
universe,  
minGSSize = 10,
enrichHMDB

```r
maxGSSize = 500,
qvalueCutoff = 0.2
)
```

**Arguments**

- `gene` a vector of COG ids.
- `dtype` one of "category", "pathway"
- `pvalueCutoff` adjusted p value cutoff on enrichment tests to report.
- `pAdjustMethod` one of "holm" ,"hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
- `universe` universe background genes. If missing, use the all COGs.
- `minGSSize` minimal size of genes annotated by KEGG term for testing.
- `maxGSSize` maximal size of genes annotated for testing.
- `qvalueCutoff` qvalue cutoff on enrichment tests to report.

**Value**

A enrichResult instance.

**Examples**

```r
data(Psoriasis_data)
cog <- enrichCOG(Psoriasis_data,dtype="category")
```

---

**enrichHMDB**

*Metabolism enrichment analysis for microbiome data*

**Description**

Metabolism enrichment analysis for microbiome data

**Usage**

```r
enrichHMDB(
  metabo_list,
pvalueCutoff = 0.05,
pAdjustMethod = "BH",
universe,
minGSSize = 10,
maxGSSize = 500,
qvalueCutoff = 0.2
)
```
Arguments

- **metabo_list**: a vector of metabolites in HMDB.ID
- **pvalueCutoff**: adjusted pvalue cutoff on enrichment tests to report.
- **pAdjustMethod**: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
- **universe**: universe background genes. If missing, use HMDB db.
- **minGSSize**: minimal size of genes annotated by KEGG term for testing.
- **maxGSSize**: maximal size of genes annotated for testing.
- **qvalueCutoff**: qvalue cutoff on enrichment tests to report.

Value

A enrichResult instance.

Examples

```r
x1 <- c("HMDB0000001","HMDB0000005","HMDB0000008")
x2 <- enrichHMDB(x1)
```

---

**enrichKO**  
**KO enrichment for microbiome data**

Description

KO enrichment for microbiome data

Usage

```r
enrichKO(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)
```

Arguments

- **gene**: a vector of K gene id (e.g. K00001) or EC id (e.g. 1.1.1.27).
- **pvalueCutoff**: adjusted pvalue cutoff on enrichment tests to report.
- **pAdjustMethod**: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
- **universe**: universe background genes. If missing, use all K genes.
- **minGSSize**: minimal size of genes annotated by KEGG term for testing.
- **maxGSSize**: maximal size of genes annotated for testing.
- **qvalueCutoff**: qvalue cutoff on enrichment tests to report.
enrichMBKEGG

Value

A enrichResult instance.

Examples

data(Rat_data)
ko <- enrichKO(Rat_data)
head(ko)

enrichMBKEGG  Metabolism enrichment analysis for microbiome data

Description

Metabolism enrichment analysis for microbiome data

Usage

enrichMBKEGG(
  metabo_list,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)

Arguments

metabo_list  a vector of metabolites in KEGG.ID
pvalueCutoff  adjusted pvalue cutoff on enrichment tests to report.
pAdjustMethod  one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
universe  universe background genes. If missing, use KEGG as default.
minGSSize  minimal size of genes annotated by KEGG term for testing.
maxGSSize  maximal size of genes annotated for testing.
qvalueCutoff  qvalue cutoff on enrichment tests to report.

Value

A enrichResult instance.
Examples

```r
mblist3 <- c("C00019","C00020","C00022")
mb3 <- enrichMBKEGG(mblist3)
head(mb3)
```

---

enrichMDA  
Microbe-Disease associations enrichment analysis

Description

Microbe-Disease associations enrichment analysis

Usage

```r
enrichMDA(
  microbe_list,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)
```

Arguments

- `microbe_list`: a vector of microbe ncbi tax ids.
- `pvalueCutoff`: adjusted pvalue cutoff on enrichment tests to report.
- `pAdjustMethod`: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
- `universe`: universe background genes. If missing, use disbiome as default.
- `minGSSize`: minimal size of genes annotated by KEGG term for testing.
- `maxGSSize`: maximal size of genes annotated for testing.
- `qvalueCutoff`: qvalue cutoff on enrichment tests to report.

Value

A enrichResult instance.

Examples

```r
data(microbiota_taxlist)
mda <- enrichMDA(microbiota_taxlist)
head(mda)
```
**Description**

Module enrichment for microbiome data

**Usage**

```r
enrichModule(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)
```

**Arguments**

- `gene`: a vector of K gene id (e.g. K00001).
- `pvalueCutoff`: adjusted pvalue cutoff on enrichment tests to report.
- `pAdjustMethod`: one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
- `universe`: universe background genes. If missing, use all K genes.
- `minGSSize`: minimal size of genes annotated by KEGG term for testing.
- `maxGSSize`: maximal size of genes annotated for testing.
- `qvalueCutoff`: qvalue cutoff on enrichment tests to report.

**Value**

A enrichResult instance.

**Examples**

```r
data(Rat_data)
ko <- enrichModule(Rat_data)
head(ko)
```
Metabolism enrichment analysis for microbiome data

Usage

enrichSMPDB(
  metabo_list,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)

Arguments

  metabo_list         a vector of metabolites in smpdb Metabolite.ID
  pvalueCutoff        adjusted pvalue cutoff on enrichment tests to report.
  pAdjustMethod       one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
  universe            universe background genes. If missing, use SMPDB db.
  minGSSize           minimal size of genes annotated by KEGG term for testing.
  maxGSSize           maximal size of genes annotated for testing.
  qvalueCutoff        qvalue cutoff on enrichment tests to report.

Value

A enrichResult instance.

Examples

smp <- enrichSMPDB(c("PW_C000164","PW_C000078","PW_C000040"))
head(smp)
### gson_cpd

**Description**

Download compound annotation of the latest version of KEGG pathway and stored in a 'GSON' object.

**Usage**

```r
gson_cpd()
```

**Value**

A 'GSON' object

---

### gson_enzyme

**Description**

Download compound annotation of the latest version of KEGG pathway to enzyme and stored in a 'GSON' object.

**Usage**

```r
gson_enzyme()
```

**Value**

A 'GSON' object

---

### gson_KO

**Description**

Download KO annotation of the latest version of KEGG pathway and stored in a 'GSON' object.

**Usage**

```r
gson_KO()
```

**Value**

A 'GSON' object
gson_module

**Description**

Download compound annotation of the latest version of KEGG Module and stored in a `GSON` object.

**Usage**

```r
gson_module(db = "ko")
```

**Arguments**

- `db`
  - `ko` or `enzyme`

**Value**

- a `GSON` object

---

**microbiota_taxlist**

**Example data**: a vector of 54 bacterial genera tested for significantly between T2D metformin samples

**Description**

This example data was reported on Forslund K, et al. 2016 (doi: 10.1038/nature15766) and used for Microbe-Disease Association analysis.

**Format**

- a vector with 54 genera tax ids

**References**

[https://www.nature.com/articles/nature15766](https://www.nature.com/articles/nature15766)

**Examples**

```r
data(microbiota_taxlist)
```
<table>
<thead>
<tr>
<th><strong>Psoriasis_data</strong></th>
<th><strong>Example data:</strong> a vector of 134 significantly different functional COGs between Psoriasis patients and controls</th>
</tr>
</thead>
</table>

**Description**
This example data was reported on Xiao S, et al. 2021 (doi: 10.3389/fcimb.2021.605825) and used for COG enrichment analysis.

**Format**
a vector with 134 COGs

**Value**

**Examples**
data(Psoriasis_data)

<table>
<thead>
<tr>
<th><strong>Rat_data</strong></th>
<th><strong>Example data:</strong> a vector of 91 KEGG Orthologies (KOs) showing significant associations with weaning weight</th>
</tr>
</thead>
</table>

**Description**
This example data was reported on Fang S, et al. 2019 (doi: 10.1111/1751-7915.13485) and used for KEGG enrichment analysis.

**Format**
a vector with 91 KEGG Orthologies (KOs)

**References**

**Examples**
data(Rat_data)
Description

Run the Shiny Application

Usage

run_MicrobiomeProfiler(
  onStart = NULL,
  options = list(),
  enableBookmarking = NULL,
  uiPattern = "/",
  ...
)

Arguments

onStart

A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global.R file can be used for this purpose.

options

Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app.

enableBookmarking

Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to enableBookmarking(). See enableBookmarking() for more information on bookmarking your app.

uiPattern

A regular expression that will be applied to each GET request to determine whether the ui should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.

... arguments to pass to golem_opts. See '\golem::get_golem_options' for more details.

Value

Shiny application object.

Examples

if (interactive()) {run_MicrobiomeProfiler()}
Index

*data*

  microbiota_taxlist, 10
  Psoriasis_data, 11
  Rat_data, 11

enableBookmarking(), 12
enrichCOG, 2
enrichHMDB, 3
enrichKO, 4
enrichMBKEGG, 5
enrichMDA, 6
enrichModule, 7
enrichSMPDB, 8

gson_cpd, 9
gson_enzyme, 9
gson_KO, 9
gson_module, 10

MicrobiomeProfiler
  (MicrobiomeProfiler-package), 2
MicrobiomeProfiler-package, 2
microbiota_data (microbiota_taxlist), 10
microbiota_taxlist, 10

Psoriasis_data, 11

Rat_data, 11
run_MicrobiomeProfiler, 12