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, MetaboPathway analysis.
License  GPL-2
URL  https://github.com/YuLab-SMU/MicrobiomeProfiler/
BugReports  https://github.com/YuLab-SMU/MicrobiomeProfiler/issues
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Author  Guangchuang Yu [aut, ths] (<https://orcid.org/0000-0002-6485-8781>), Meijun Chen [aut, cre] (<https://orcid.org/0000-0003-2486-8106>)
Maintainer  Meijun Chen <mjchen1996@outlook.com>
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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,
Arguments

gene a vector of COG ids.
dtype one of "category", "pathway"
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 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

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

- **metabo_list**: a vector of metabolites in HMDB.ID
- **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 HMDB db.
- **minGSSize**: minimal size of genes annotated by KEGG term for testing.
- **maxGSSize**: maximal size of genes annotated for testing.
- **qvalueCutoff**: q-value 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

```
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 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 all K genes.
- **minGSSize**: minimal size of genes annotated by KEGG term for testing.
- **maxGSSize**: maximal size of genes annotated for testing.
- **qvalueCutoff**: q-value 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**

```r
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)
dmda <- enrichMDA(microbiota_taxlist)
head(dmda)
```
enrichModule

Module enrichment for microbiome data

Description

Module enrichment for microbiome data

Usage

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

data(Rat_data)
kob <- enrichModule(Rat_data)
head(kob)
enrichSMPDB  
Metabolism enrichment analysis for microbiome data

Description

Metabolism enrichment analysis for microbiome data

Usage

```r
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

```r
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**

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**

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**

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**

gson_module(db = "ko")

**Arguments**

db ko or enzyme

**Value**
a 'GSON' object

---

microbiota_taxlist

**Description**

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

**Format**
a vector with 54 genera tax ids

**References**

https://www.nature.com/articles/nature15766

**Examples**

data(microbiota_taxlist)
<table>
<thead>
<tr>
<th>Psoriasis_data</th>
<th>Example data: 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>Rat_data</th>
<th>Example data: 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)
run_MicrobiomeProfiler

Run the Shiny Application

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 \texttt{enableBookmarking()}. See \texttt{enableBookmarking()} for more information on bookmarking your app.

uiPattern A regular expression that will be applied to each GET request to determine whether the \texttt{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()}
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