Package ‘MicrobiomeProfiler’

April 6, 2024

Title  An R/shiny package for microbiome functional enrichment analysis
Version 1.8.0
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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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

maxGSSize = 500,
qvalueCutoff = 0.2

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 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)
```

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**

```r
data(Rat_data)
k0 <- enrichKO(Rat_data)
head(k0)
```

---

**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)
mda <- enrichMDA(microbiota_taxlist)
head(mda)
```
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)
k0 <- enrichModule(Rat_data)
head(k0)
enrichSMPDB

Metabolism enrichment analysis for microbiome data

Description

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**

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

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

Examples
data(microbiota_taxlist)
Psoriasis_data

Example data: a vector of 134 significantly different functional COGs between Psoriasis patients and controls

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)

Rat_data

Example data: a vector of 91 KEGG Orthologies (KOs) showing significant associations with weaning weight

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**

```r
describe 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**

```r
if (interactive()) {run_MicrobiomeProfiler()}
```
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