

Package ‘MicrobiomeProfiler’

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Title An R/shiny package for microbiome functional enrichment analysis

Version 1.11.0

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

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MicrobiomeProfiler-package
Functional enrichment analysis for microbiome data

Description

The package implements a 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,
```

```
    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")
```

enrichHMDB

Metabolism enrichment analysis for microbiome data

Description

Metabolism enrichment analysis for microbiome data

Usage

```
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

```
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 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)
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

```
mblast3 <- c("C00019", "C00020", "C00022")
mb3 <- enrichMBKEGG(mblast3)
head(mb3)
```

enrichMDA

Microbe-Disease associations enrichment analysis

Description

Microbe-Disease associations enrichment analysis

Usage

```
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

```
data(microbiota_taxlist)
mda <- enrichMDA(microbiota_taxlist)
head(mda)
```

| | |
|--------------|--|
| enrichModule | <i>Module enrichment for microbiome data</i> |
|--------------|--|

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)  
ko <- enrichModule(Rat_data)  
head(ko)
```

`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

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

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 | <i>gson_enzyme</i> |
|-------------|--------------------|

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 | <i>gson_KO</i> |
|---------|----------------|

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`*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 | <i>Example data: a vector of 134 significantly different functional COGs between Psoriasis patients and controls</i> |
|----------------|--|

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

<https://www.frontiersin.org/articles/10.3389/fcimb.2021.605825/full>

Examples

```
data(Psoriasis_data)
```

| | |
|----------|---|
| Rat_data | <i>Example data: a vector of 91 KEGG Orthologies (KOs) showing significant associations with weaning weight</i> |
|----------|---|

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

<https://sfamjournals.onlinelibrary.wiley.com/doi/10.1111/1751-7915.13485>

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 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 <code>'?golem::get_golem_options'</code> for more details. |

Value

Shiny application object.

Examples

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

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