

# Package ‘MicrobiomeProfiler’

October 18, 2022

**Title** An R/shiny package for microbiome functional enrichment analysis

**Version** 1.2.0

**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.

**License** GPL-2

**URL** <https://github.com/YuLab-SMU/MicrobiomeProfiler/>

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

**Imports** clusterProfiler (>= 4.0.2), config, DT, enrichplot, golem, magrittr, shiny (>= 1.6.0), shinyWidgets, shinycustomloader, htmltools, ggplot2, graphics, utils

**Encoding** UTF-8

**biocViews** Microbiome, Software, Visualization,KEGG

**RoxygenNote** 7.1.2

**Depends** R (>= 4.1.0)

**Suggests** rmarkdown, knitr, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

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MicrobiomeProfiler-package

*Functional enrichment analysis for microbiome data*

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### Description

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

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bitr\_smpdb

*convert metabolite IDs*

---

### Description

You can choose one id type as input and convert to other id type

### Usage

```
bitr_smpdb(mbid, from_Type, to_Type)
```

### Arguments

mbid	query vector of metabolite ids
from_Type	input id type, character
to_Type	output id type, character

### Value

a dataframe

**Examples**

```
bitr_smpdb(c("HMDB0000538", "HMDB0000161", "HMDB0000045"),
  from_Type = "HMDB.ID", to_Type = "ChEBI.ID")
```

---

enrichCOG

*COG enrichment analysis for microbiome data*

---

**Description**

COG enrichment analysis for microbiome data

**Usage**

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

**Arguments**

gene	a vector of COG 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 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)
```

---

**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

<code>metabo_list</code>	a vector of metabolites in HMDB.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 HMDB 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

```
x1 <- bitr_smpdb(c("PW_C000164", "PW_C000078", "PW_C000040"),  
  from_Type = "Metabolite.ID", to_Type = "HMDB.ID")  
x2 <- enrichHMDB(x1$HMDB.ID)
```

---

`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

<code>gene</code>	a vector of K gene id (e.g. K00001).
<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 all K genes.
<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

```
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

<code>metabo_list</code>	a vector of metabolites in KEGG.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 KEGG as default.
<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

```
mblist3 <- bitr_smpdb(c("PW_C000164", "PW_C000078", "PW_C000040"),  
  from_Type = "Metabolite.ID", to_Type = "KEGG.ID")  
mb3 <- enrichMBKEGG(mblist3$KEGG.ID)  
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**

<code>microbe_list</code>	a vector of microbe ncbi tax ids.
<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 disbiome as default.
<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**

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

---

`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)
```



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microbiota_taxlist	<i>Example data: a vector of 54 bacterial genera tested for significantly between T2D metformin samples</i>
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---

**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	<i>Run the Shiny Application</i>
------------------------	----------------------------------

---

### 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 <a href="#">enableBookmarking()</a> . See <a href="#">enableBookmarking()</a> 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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