

Package: MicrobiomeProfiler (via r-universe)

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Title An R/shiny package for microbiome functional enrichment analysis

Version 1.19.2

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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Depends R (>= 4.2.0)

Imports clusterProfiler (>= 4.5.2), enrichit (>= 0.2.2), config, digest, DT, enrichplot, golem, gson, methods, magrittr, jsonlite, shiny (>= 1.6.0), shinyWidgets, shinycustomloader, htmltools, ggplot2, graphics, stats, utils, yulab.utils

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

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available_datasets	<i>List configured external datasets</i>
--------------------	--

Description

List configured external datasets

Usage

```
available_datasets(include_remote = FALSE)
```

Arguments

include_remote whether to fetch remote manifests and include remote version metadata.

Value

A data.frame describing configured datasets and cache status.

clear_dataset_cache	<i>Remove cached external dataset artifacts</i>
---------------------	---

Description

Remove cached external dataset artifacts

Usage

```
clear_dataset_cache(dataset = NULL)
```

Arguments

dataset optional dataset key. If omitted, remove all cached datasets.

Value

Invisibly returns TRUE when cache removal completes.

dataset_cache_info	<i>Summarize the local external data cache</i>
--------------------	--

Description

Summarize the local external data cache

Usage

```
dataset_cache_info(dataset = NULL)
```

Arguments

dataset optional dataset key. If omitted, return all cached datasets.

Value

A data.frame with one row per cached dataset version.

download_dataset	<i>Download an external dataset into the local cache</i>
------------------	--

Description

Download an external dataset into the local cache

Usage

```
download_dataset(dataset, refresh = FALSE)
```

Arguments

dataset	dataset key registered in the external data registry.
refresh	whether to force a fresh download even if a valid cached artifact already exists.

Value

A list with cache metadata for the downloaded dataset.

enrichBugSigDB	<i>BugSigDB enrichment analysis for microbiome data</i>
----------------	---

Description

BugSigDB enrichment analysis for microbiome data

Usage

```
enrichBugSigDB(
  microbe_list,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe = NULL,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  refresh = FALSE
)
```

Arguments

microbe_list	a vector of microbe NCBI taxonomy ids.
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
universe	universe background microbes. If missing, use the BugSigDB dataset background.
minGSSize	minimal size of microbes annotated by a signature term for testing.
maxGSSize	maximal size of microbes annotated by a signature term for testing.
qvalueCutoff	qvalue cutoff on enrichment tests to report.
refresh	whether to force a fresh download of the remote artifact.

Value

An `enrichResult` instance.

Examples

```
## Not run:
taxa <- c("1224", "1236", "91347")
enrichBugSigDB(taxa)

## End(Not run)
```

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 = NULL,
  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")
```

enrichEggNOG

eggNOG-based KEGG pathway enrichment for microbiome data

Description

eggNOG-based KEGG pathway enrichment for microbiome data

Usage

```
enrichEggNOG(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe = NULL,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  refresh = FALSE
)
```

Arguments

gene	a vector of eggNOG orthologous group identifiers.
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
universe	background eggNOG orthologous groups. If missing, use the eggNOG dataset background.
minGSSize	minimal size of pathway gene sets for testing.
maxGSSize	maximal size of pathway gene sets for testing.
qvalueCutoff	qvalue cutoff on enrichment tests to report.
refresh	whether to force a fresh download of the remote eggNOG artifact.

Value

An `enrichResult` instance.

Examples

```
## Not run:
eggnog_obj <- MicrobiomeProfiler::mp_eggnog_gson()
gsid2gene <- methods::slot(eggnog_obj, "gsid2gene")
pathway_sizes <- sort(table(gsid2gene$gsid))
pathway_id <- names(pathway_sizes[pathway_sizes >= 3])[1]
og <- head(unique(gsid2gene[gsid2gene$gsid == pathway_id, "gene"]), 3)
enrichEggNOG(og, minGSSize = 1)

## End(Not run)
```

enrichHMDB

Metabolism enrichment analysis for microbiome data

Description

Metabolism enrichment analysis for microbiome data

Usage

```
enrichHMDB(
  metabo_list,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe = NULL,
  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("HMDB00000001", "HMDB00000005", "HMDB00000008")
x2 <- enrichHMDB(x1)
```

enrichKO

KO enrichment for microbiome data

Description

KO enrichment for microbiome data

Usage

```
enrichKO(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe = NULL,
  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 = NULL,
  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 <- c("C00019", "C00020", "C00022")
mb3 <- enrichMBKEGG(mblist3)
head(mb3)
```

enrichMDA

Microbe-Disease associations enrichment analysis

Description

Microbe-Disease associations enrichment analysis

Usage

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

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.
refresh	whether to force a fresh download of the remote Disbiome artifact.

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 = NULL,  
  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 = NULL,  
  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)
```

gseCOG

*COG GSEA enrichment analysis for microbiome data***Description**

COG GSEA enrichment analysis for microbiome data

Usage

```

gseCOG(
  geneList,
  dtype = "category",
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  seed = FALSE
)

```

Arguments

geneList	a vector of COG ids with values.
dtype	one of "category", "pathway"
nPerm	number of permutations.
exponent	exponent of weighting.
minGSSize	minimal size of genes annotated by KEGG term for testing.
maxGSSize	maximal size of genes annotated for testing.
pvalueCutoff	pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.

seed random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see `enrichit::gsea()` for details.

Value

A `gseaResult` instance.

`gseEggNOG`

GSEA with eggNOG-based KEGG pathway annotations

Description

GSEA with eggNOG-based KEGG pathway annotations

Usage

```
gseEggNOG(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  refresh = FALSE,
  seed = FALSE
)
```

Arguments

<code>geneList</code>	order ranked <code>geneList</code> .
<code>exponent</code>	weight of each step.
<code>minGSSize</code>	minimal size of each <code>geneSet</code> for analyzing.
<code>maxGSSize</code>	maximal size of genes annotated for testing.
<code>pvalueCutoff</code>	pvalue Cutoff.
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
<code>refresh</code>	whether to force a fresh download of the remote eggNOG artifact.
<code>seed</code>	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A gseaResult instance.

Examples

```
## Not run:
eggnog_obj <- MicrobiomeProfiler::mp_eggnog_gson()
gsid2gene <- methods::slot(eggnog_obj, "gsid2gene")
pathway_sizes <- sort(table(gsid2gene$gsid))
pathway_id <- names(pathway_sizes[pathway_sizes >= 3])[1]
og <- head(unique(gsid2gene[gsid2gene$gsid == pathway_id, "gene"]), 3)
geneList <- c(2.5, 1.2, -1.8)
names(geneList) <- og
gseEggNOG(geneList, minGSSize = 1)

## End(Not run)
```

gseHMDB

Metabolism GSEA enrichment analysis for microbiome data

Description

Metabolism GSEA enrichment analysis for microbiome data

Usage

```
gseHMDB(
  metabo_list,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  seed = FALSE
)
```

Arguments

metabo_list a vector of metabolites in HMDB.ID with values
nPerm number of permutations.

exponent	exponent of weighting.
minGSSize	minimal size of genes annotated by KEGG term for testing.
maxGSSize	maximal size of genes annotated for testing.
pvalueCutoff	pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.
seed	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A `gseaResult` instance.

gseKO

KO GSEA enrichment for microbiome data

Description

KO GSEA enrichment for microbiome data

Usage

```
gseKO(
  geneList,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  seed = FALSE
)
```

Arguments

geneList	a vector of K gene id (e.g. K00001) or EC id (e.g. 1.1.1.27) with values.
nPerm	number of permutations.
exponent	exponent of weighting.
minGSSize	minimal size of genes annotated by KEGG term for testing.
maxGSSize	maximal size of genes annotated for testing.
pvalueCutoff	pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.
seed	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A `gseaResult` instance.

gseMBKEGG

Metabolism GSEA enrichment analysis for microbiome data

Description

Metabolism GSEA enrichment analysis for microbiome data

Usage

```
gseMBKEGG(
  metabo_list,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
```

```

minPerm = 101,
maxPerm = 1e+05,
pvalThreshold = 0.1,
verbose = TRUE,
seed = FALSE
)

```

Arguments

metabo_list	a vector of metabolites in KEGG.ID with values
nPerm	number of permutations.
exponent	exponent of weighting.
minGSSize	minimal size of genes annotated by KEGG term for testing.
maxGSSize	maximal size of genes annotated for testing.
pvalueCutoff	pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.
seed	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A `gseaResult` instance.

gseMDA

Microbe-Disease associations GSEA enrichment analysis

Description

Microbe-Disease associations GSEA enrichment analysis

Usage

```
gseMDA(
  microbe_list,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  refresh = FALSE,
  seed = FALSE
)
```

Arguments

<code>microbe_list</code>	a vector of microbe ncbi tax ids with values.
<code>nPerm</code>	number of permutations.
<code>exponent</code>	exponent of weighting.
<code>minGSSize</code>	minimal size of genes annotated by KEGG term for testing.
<code>maxGSSize</code>	maximal size of genes annotated for testing.
<code>pvalueCutoff</code>	pvalue cutoff on enrichment tests to report.
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
<code>method</code>	one of "multilevel", "fgsea", "bioc".
<code>adaptive</code>	whether to use adaptive permutation.
<code>minPerm</code>	minimal number of permutations.
<code>maxPerm</code>	maximal number of permutations.
<code>pvalThreshold</code>	pvalue threshold for adaptive permutation.
<code>verbose</code>	whether to show progress.
<code>refresh</code>	whether to force a fresh download of the remote Disbiome artifact.
<code>seed</code>	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A `gseaResult` instance.

gseModule

*Module GSEA enrichment for microbiome data***Description**

Module GSEA enrichment for microbiome data

Usage

```
gseModule(
  geneList,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  seed = FALSE
)
```

Arguments

geneList	a vector of K gene id (e.g. K00001) with values.
nPerm	number of permutations.
exponent	exponent of weighting.
minGSSize	minimal size of genes annotated by KEGG term for testing.
maxGSSize	maximal size of genes annotated for testing.
pvalueCutoff	pvalue cutoff on enrichment tests to report.
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.

seed random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see `enrichit::gsea()` for details.

Value

A `gseaResult` instance.

gseSMPDB

Metabolism GSEA enrichment analysis for microbiome data

Description

Metabolism GSEA enrichment analysis for microbiome data

Usage

```
gseSMPDB(
  metabo_list,
  nPerm = 1000,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  method = "multilevel",
  adaptive = FALSE,
  minPerm = 101,
  maxPerm = 1e+05,
  pvalThreshold = 0.1,
  verbose = TRUE,
  seed = FALSE
)
```

Arguments

<code>metabo_list</code>	a vector of metabolites in <code>smddb</code> <code>Metabolite.ID</code> with values
<code>nPerm</code>	number of permutations.
<code>exponent</code>	exponent of weighting.
<code>minGSSize</code>	minimal size of genes annotated by KEGG term for testing.
<code>maxGSSize</code>	maximal size of genes annotated for testing.
<code>pvalueCutoff</code>	pvalue cutoff on enrichment tests to report.
<code>pAdjustMethod</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

method	one of "multilevel", "fgsea", "bioc".
adaptive	whether to use adaptive permutation.
minPerm	minimal number of permutations.
maxPerm	maximal number of permutations.
pvalThreshold	pvalue threshold for adaptive permutation.
verbose	whether to show progress.
seed	random seed for reproducibility, set to a number (or TRUE to use a fixed default seed) to make the result reproducible, or FALSE (default) to draw a random seed on each run, so results may vary between runs. The underlying permutation engine uses its own RNG seeded with this value; see <code>enrichit::gsea()</code> for details.

Value

A `gseaResult` instance.

<code>gson_cpd</code>	<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

<code>gson_enzyme</code>	<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	<i>gson_module</i>
-------------	--------------------

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

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 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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