Package 'MicrobiomeProfiler'

August 11, 2022

Title An R/shiny package for microbiome functional enrichment analysis

Version 1.3.0

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 (>= 4.0.2), 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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R topics documented:

`MicrobiomeProfiler-package` *Functional enrichment analysis for microbiome data*

Description

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

`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")
```

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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

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 <- 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

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 <- 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

```
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

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)
```

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)
```

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

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

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

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 '?golem::get_golem_options' for more details.

Value

Shiny application object.

Examples

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

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