

Package ‘bugsigdbr’

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Version 1.0.1

Title R-side access to published microbial signatures from BugSigDB

Description The bugsigdbr package implements convenient access to bugsigdb.org from within R/Bioconductor. The goal of the package is to facilitate import of BugSigDB data into R/Bioconductor, provide utilities for extracting microbe signatures, and enable export of the extracted signatures to plain text files in standard file formats such as GMT.

URL <https://github.com/waldronlab/bugsigdbr>

BugReports <https://github.com/waldronlab/bugsigdbr/issues>

Depends R (>= 4.1)

Imports BiocFileCache, vroom, utils

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

License GPL-3

VignetteBuilder knitr

biocViews DataImport, GeneSetEnrichment, Metagenomics, Microbiome

Encoding UTF-8

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R topics documented:

browseSignature	2
browseTaxon	3
extractTaxLevel	3
getSignatures	4
importBugSigDB	5
restrictTaxLevel	6
writeGMT	7
Index	8

browseSignature	<i>Displaying BugSigDB signatures pages in a web browser</i>
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Description

Functionality for programmatically displaying microbe signatures on BugSigDB signature pages.

Usage

```
browseSignature(sname)
```

Arguments

sname character. Signature name. Expected to start with a prefix of the form "bsdb:<X>/<Y>/<Z>_" encoding the corresponding BugSigDB signature ID.

Value

The URL of the selected BugSigDB signature page. If interactive, opens the URL in the default web browser.

References

BugSigDB: <https://bugsigdb.org>

Examples

```
sname <- "bsdb:215/1/1_eczema:infant-with-eczema_vs_healthy-control_UP"
browseSignature(sname)
```

`browseTaxon`*Displaying BugSigDB taxon pages in a web browser*

Description

Functionality for programmatically displaying BugSigDB taxon pages.

Usage

```
browseTaxon(tax.id)
```

Arguments

`tax.id` character. NCBI taxonomy ID.

Value

The URL of the selected BugSigDB taxon page. If interactive, opens the URL in the default web browser.

References

BugSigDB: <https://bugsigdb.org>

Examples

```
# BugSigDB taxon page for Escherichia coli  
browseTaxon("562")
```

`extractTaxLevel`*Extract specific taxonomic levels from a microbe signature*

Description

Functionality for extracting specific taxonomic levels (such as genus and species) from a microbe signature containing taxonomic clades in MetaPhlAn format.

Usage

```
extractTaxLevel(  
  sig,  
  tax.id.type = c("metaphlan", "taxname"),  
  tax.level = "mixed",  
  exact.tax.level = TRUE  
)
```

Arguments

<code>sig</code>	character. Microbe signature containing taxonomic clades in MetaPhlAn format.
<code>tax.id.type</code>	Character. Taxonomic ID type of the returned microbe sets. Either "metaphlan" (default) or "taxname".
<code>tax.level</code>	character. Either "mixed" or any subset of c("kingdom", "phylum", "class", "order", "family", "genus", "species"). This full vector is equivalent to "mixed".
<code>exact.tax.level</code>	logical. Should only the exact taxonomic level specified by <code>tax.level</code> be returned? Defaults to TRUE. If FALSE, a more general <code>tax.level</code> is extracted for microbes given at a more specific taxonomic level.

Value

a character vector storing taxonomic clades restricted to chosen taxonomic level(s).

References

BugSigDB: <https://bugsigdb.org>

Examples

```
ord <- "k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales"
sig <- c("f__Lactobacillaceae|g__Lactobacillus",
        "f__Aerococcaceae|g__Abiotrophia|s__Abiotrophia defectiva",
        "f__Lactobacillaceae|g__Limosilactobacillus|s__Limosilactobacillus mucosae")
sig <- paste(ord, sig, sep = "|")
sig <- extractTaxLevel(sig, tax.level = "genus")
sig <- extractTaxLevel(sig, tax.level = "genus", exact.tax.level = FALSE)
sig <- extractTaxLevel(sig,
                       tax.id.type = "taxname",
                       tax.level = "genus",
                       exact.tax.level = FALSE)
```

getSignatures

Obtain microbe signatures from BugSigDB

Description

Functionality for obtaining microbe signatures from BugSigDB

Usage

```
getSignatures(
  df,
  tax.id.type = c("ncbi", "metaphlan", "taxname"),
  tax.level = "mixed",
```

```

    exact.tax.level = TRUE,
    min.size = 1
  )

```

Arguments

<code>df</code>	data.frame storing BugSigDB data. Typically obtained via <code>importBugSigDB</code> .
<code>tax.id.type</code>	Character. Taxonomic ID type of the returned microbe sets. Either "ncbi" (default), "metaphlan", or "taxname".
<code>tax.level</code>	character. Either "mixed" or any subset of c("kingdom", "phylum", "class", "order", "family", "genus"). This full vector is equivalent to "mixed".
<code>exact.tax.level</code>	logical. Should only the exact taxonomic level specified by <code>tax.level</code> be returned? Defaults to TRUE. If FALSE, a more general <code>tax.level</code> is extracted for microbes given at a more specific taxonomic level.
<code>min.size</code>	integer. Minimum signature size. Defaults to 1, which will filter out empty signature. Use <code>min.size = 0</code> to keep empty signatures.

Value

a list of microbe signatures. Each signature is a character vector of taxonomic IDs depending on the chosen `tax.id.type`.

References

BugSigDB: <https://bugsigdb.org>

See Also

`importBugSigDB`

Examples

```

df <- importBugSigDB()
sigs <- getSignatures(df)

```

`importBugSigDB`

Obtain published microbial signatures from bugsigdb.org

Description

Obtain published microbial signatures from bugsigdb.org

Usage

```
importBugSigDB(cache = TRUE)
```

Arguments

cache logical. Should a locally cached version used if available? Defaults to TRUE.

Value

a `data.frame`.

References

BugSigDB: <https://bugsigdb.org>

Examples

```
df <- importBugSigDB()
```

<code>restrictTaxLevel</code>	<i>Restrict microbe signatures to specific taxonomic levels</i>
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Description

Functionality for restricting microbe signatures to specific taxonomic levels such as genus and species.

Usage

```
restrictTaxLevel(df, tax.level = "mixed", exact.tax.level = TRUE, min.size = 1)
```

Arguments

`df` `data.frame` storing BugSigDB data. Typically obtained via `importBugSigDB`.

`tax.level` character. Either "mixed" or any subset of `c("kingdom", "phylum", "class", "order", "family", "genus", "species")`. This full vector is equivalent to "mixed".

`exact.tax.level` logical. Should only the exact taxonomic level specified by `tax.level` be returned? Defaults to TRUE. If FALSE, a more general `tax.level` is extracted for microbes given at a more specific taxonomic level.

`min.size` integer. Minimum signature size. Defaults to 1, which will filter out empty signatures. Use `min.size = 0` to keep empty signatures.

Value

a `data.frame` with microbe signature columns restricted to chosen taxonomic level(s).

References

BugSigDB: <https://bugsigdb.org>

See Also

importBugSigDB

Examples

```
df <- importBugSigDB()
df <- restrictTaxLevel(df, tax.level = "genus")
```

writeGMT

Write microbe signatures to file in GMT format

Description

Functionality for writing microbe signatures to file in GMT format.

Usage

```
writeGMT(sigs, gmt.file)
```

Arguments

sigs A list of microbe signatures (character vectors of taxonomic IDs).
gmt.file character. Path to output file in GMT format.

Value

none, writes to file.

References

GMT file format: http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data_formats

Examples

```
bsdb <- importBugSigDB()
sigs <- getSignatures(bsdb)
writeGMT(sigs, gmt.file = "signatures.gmt")
file.remove("signatures.gmt")
```

Index

browseSignature, [2](#)
browseTaxon, [3](#)

data.frame, [6](#)

extractTaxLevel, [3](#)

getSignatures, [4](#)

importBugSigDB, [5](#), [5](#), [6](#)

restrictTaxLevel, [6](#)

writeGMT, [7](#)