Package 'MicrobiomeBenchmarkData'

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Title Datasets for benchmarking in microbiome research

Version 1.10.0

Description The MicrobiomeBenchmarkData package provides functionality to access microbiome datasets suitable for benchmarking. These datasets have some biological truth, which allows to have expected results for comparison. The datasets come from various published sources and are provided as TreeSummarizedExperiment objects. Currently, only datasets suitable for benchmarking differential abundance methods are available.

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LazyData false

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Imports BiocFileCache, tools, S4Vectors, ape, utils

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biocViews ExperimentData, MicrobiomeData, ReproducibleResearch, SequencingData

BugReports https://github.com/waldronlab/MicrobiomeBenchmarkData/issues

URL https://github.com/waldronlab/MicrobiomeBenchmarkData, http://waldronlab.io/MicrobiomeBenchmarkData/

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Author Samuel Gamboa [aut, cre] (ORCID:
<https://orcid.org/0000-0002-6863-7943>),
Levi Waldron [aut] (ORCID: <https://orcid.org/0000-0003-2725-0694>),
Marcel Ramos [ctb]

Maintainer Samuel Gamboa <Samuel.Gamboa.Tuz@gmail.com>

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`.assembleTreeSummarizedExperiment`
Assemble TreeSummarizedExperiment

Description

`.assembleTreeSummarizedExperiment` assembles a TreeSummarizedDataset taking as input the name of the dataset and the URL. This is a helper function for the `getBenchmarkData` function.

Usage

```
.assembleTreeSummarizedExperiment(x)
```

Arguments

`dat_name`	A character string with the name of the dataset.
`dat_url`	A character string with the URL from Zenodo.

Value

A TreeSummarizedExperiment

.getCache *Get cache*

Description

.getCache creates or loads a cache to store files downloaded through the MicrobiomeBenchmarkData package.

Usage

```
.getCache()
```

Value

A BiocFileCache object.

.getResourcePath *Get resource path*

Description

.getResource downloads the count matrix and store it in the cache.

Usage

```
.getResourcePath(resource, suffix)
```

Arguments

resource_name	A character string with the name of the dataset.
resource_url	A character string with the URL from Zenodo.

Value

A character string containing the path to the count matrix in the cache.

.getSampleMetadata *Get sample metadata*

Description

.getSampleMetadata returns sampleMetadata.

Usage

```
.getSampleMetadata()
```

Value

A data frame with sample metadata.

getBenchmarkData *Get dataset*

Description

getBenchmarkData imports datasets as TreeSummarizedExperiment objects.

Usage

```
getBenchmarkData(x, dryrun = TRUE)
```

Arguments

x	A character vector with the name(s) of the dataset(s). If empty and dryrun = TRUE, it returns a message with the names of the available datasets. If empty and dryrun = FALSE, it returns a list of TreeSummarizedExperiments with all of the datasets.
dryrun	If TRUE, only returns a message and invisibly returns the names of the datasets as a character vector. If FALSE, it returns the TreeSummarizedExperiment datasets indicated in the argument 'x'.

Value

A list of TreeSummarizedExperiments when dryrun = FALSE. A data frame with the datasets characteristics when dryrun = TRUE.

Examples

```
## Example 1
datasets_names <- getBenchmarkData()
datasets_names

## Example 2
dataset <- getBenchmarkData(
    "HMP_2012_16S_gingival_V35_subset", dryrun = FALSE
)
dataset[[1]]
```

MicrobiomeBenchmarkData

MicrobiomeBenchmarkData

Description

The MicrobiomeBenchmarkData provide functions for accessing various microbiome datasets with biological ground truth.

Author(s)

Maintainer: Samuel Gamboa <Samuel.Gamboa.Tuz@gmail.com> (ORCID)

Authors:

- Levi Waldron (ORCID)

Other contributors:

- Marcel Ramos [contributor]

See Also

Useful links:

- https://github.com/waldronlab/MicrobiomeBenchmarkData
- http://waldronlab.io/MicrobiomeBenchmarkData/
- Report bugs at https://github.com/waldronlab/MicrobiomeBenchmarkData/issues

removeCache *Remove cache*

Description

removeCache removes all files saved in the cache.

Usage

```
removeCache(ask = interactive())
```

Arguments

ask	If TRUE, a prompt will appear asking the user to confirm removal of cache. Default value is given by the interactive function.

Value

NULL The cache and all of its contents are removed.

Examples

```
## Remove cache
removeCache()
```

sampleMetadata *sampleMetadata*

Description

A data frame with the combined metadata of all of the samples in the datasets provided through the MicrobiomeBenchmarkData package.

Usage

```
data("sampleMetadata", package = "MicrobiomeBenchMarkData")
```

Format

A data.frame.

scml *SCML: spike-in-based calibration to total microbial load*

Description

The scml function applies the spike-in-based calibration to total microbial load (SCML) method to

Usage

```
scml(tse, bac = c("s", "r", "a"))
```

Arguments

tse	A treeSummarizedExperiment from the getBenchmarkData function.
bac	A character. One of the following options: s = Salinibacter ruber (AF323500), r = Rhizobium radiobacter (AB247615), a, = Alicyclobacillus acidiphilus (AB076660)

Value

A TreeSummarizedExperiment with SCML data instead of counts.

Examples

```
tse <- getBenchmarkData("Stammler_2016_16S_spikein", dryrun = FALSE)[[1]]
tseSCML <- scml(tse, bac = "s")
```

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