Package ‘MicrobiomeBenchmarkData’

May 16, 2024

Title Datasets for benchmarking in microbiome research
Version 1.6.0
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.
License Artistic-2.0
LazyData false
Depends R (>= 4.2), SummarizedExperiment, TreeSummarizedExperiment
Imports BiocFileCache, tools, S4Vectors, ape, utils
Suggests rmarkdown, knitr, BiocStyle, testthat (>= 3.0.0), mia, ggplot2, tidyr, dplyr, magrittr, tibble, purrr
biocViews ExperimentData, MicrobiomeData, ReproducibleResearch, SequencingData
BugReports https://github.com/waldronlab/MicrobiomeBenchmarkData/issues
BiocType ExperimentData
Encoding UTF-8
Roxygen list(markdown = TRUE)
RoxygenNote 7.2.1
VignetteBuilder knitr
Config/testthat/edition 3
git_url https://git.bioconductor.org/packages/MicrobiomeBenchmarkData
git_branch RELEASE_3_19
git_last_commit 9b47f6c
assembleTreeSummarizedExperiment

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.

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**.getResourcePath**

### Get resource path

**Description**

`.getResource` downloads the count matrix and stores 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  

Description

getSampleMetadata returns sampleMetadata.

Usage

getSampleMetadata()

Value

A data frame with sample metadata.

getBenchmarkData  

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.
## Example 1

datasets_names <- getBenchmarkData()
datasets_names

## Example 2

dataset <- getBenchmarkData(
    "HMP_2012_16S_gingival_V35_subset", dryrun = FALSE
)
dataset[[1]]

---

### removeCache

#### Description

removeCache removes all files saved in the cache.

#### Usage

```r
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

```r
## Remove cache
removeCache()
```
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.
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