

# Package ‘MicrobiomeBenchmarkData’

February 2, 2023

**Title** Datasets for benchmarking in microbiome research

**Version** 1.0.0

**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>

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

**BiocType** ExperimentData

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.1

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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getBenchmarkData	<i>Get dataset</i>
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### 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]]
```

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MicrobiomeBenchmarkData

*MicrobiomeBenchmarkData*

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**Description**

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

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removeCache

*Remove cache*

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**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()
```

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sampleMetadata	<i>sampleMetadata</i>
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**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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