

Package: MicrobiomeBenchmarkData (via r-universe)

October 10, 2026

Title Datasets for benchmarking in microbiome research

Version 1.14.0

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 7.3.2

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libuv1-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:36:32 UTC
RemoteUrl https://github.com/bioc/MicrobiomeBenchmarkData
RemoteRef RELEASE_3_23
RemoteSha 58cbc080e2d0fb0efd33f7beaa07d3d1b055b485

Contents

getBenchmarkData	2
MicrobiomeBenchmarkData	3
removeCache	4
sampleMetadata	4
scml	5
Index	6

getBenchmarkData	<i>Get dataset</i>
------------------	--------------------

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	<i>Remove cache</i>
-------------	---------------------

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	<i>sampleMetadata</i>
----------------	-----------------------

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

<code>tse</code>	A <code>treeSummarizedExperiment</code> from the <code>getBenchmarkData</code> function.
<code>bac</code>	A character. One of the following options: <code>s</code> = <i>Salinibacter ruber</i> (AF323500), <code>r</code> = <i>Rhizobium radiobacter</i> (AB247615), <code>a</code> , = <i>Alicyclobacillus acidiphilus</i> (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")
```

Index

* **datasets**

sampleMetadata, [4](#)

getBenchmarkData, [2](#)

MicrobiomeBenchmarkData, [3](#)

MicrobiomeBenchmarkData-package
(MicrobiomeBenchmarkData), [3](#)

removeCache, [4](#)

sampleMetadata, [4](#)

scml, [5](#)