

Package ‘msd16s’

February 3, 2026

Maintainer Joseph N. Paulson <jpaulson@umiacs.umd.edu>

Author Joseph N. Paulson, Hector Corrada Bravo, Mihai Pop

Version 1.30.0

License Artistic-2.0

Title Healthy and moderate to severe diarrhea 16S expression data

Description Gut 16S sequencing expression data from 992 healthy and moderate-to-severe diarrhetic samples used in 'Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition'.

LazyData yes

Depends R (>= 2.10), Biobase, metagenomeSeq,

URL <http://www.cbcb.umd.edu/research/projects/GEMS-pathogen-discovery>

biocViews ExperimentData, SequencingData, MicrobiomeData

git_url <https://git.bioconductor.org/packages/msd16s>

git_branch RELEASE_3_22

git_last_commit ace6bd3

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-03

Contents

msd16s-package	2
msd16s	2
Index	4

msd16s-package	<i>Curated dataset of many healthy and moderate-to-severe diarrhetic gut 16s samples on the 454 FLEX platform.</i>
----------------	--

Description

Data used in 'Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition'. Measurements are number of reads clustered into OTUs (operational taxonomic units) by DNAClust.

Author(s)

Joseph N. Paulson

References

Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition.

msd16s	<i>Curated dataset of many healthy and moderate-to-severe diarrhetic gut 16s samples on the 454 FLEX platform.</i>
--------	--

Description

Data used in 'Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition'. Measurements are number of reads annotated for a particular cluster within a given sample followed by filtering. Sequencing was performed on the 454 Flex platform.

format

Data is stored as an `MRexperiment-class` object. Using `MRcounts` one can obtain the 16S count matrix produced using using DNAClust (<http://dnacrust.sourceforge.net/>). The `pData` function accesses a data frame with the following columns:

Type: Status of samples: Case, Control

Country: Country of origin

Age: Month

AgeFactor: Month group

Dysentery: Dysentteric (1) non-dysenterric (0) indicator

The `fData` function accesses a data frame with the following columns:

OTU: OTU cluster id

Taxonomy: Full taxonomic profile

superkingdom: superkingdom

phylum: phylum

class: class
order: order
family: family
genus: genus
species: species
clusterCenter: The OTU cluster's representative sequence

Author(s)

Joseph N. Paulson

References

'Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition'

See Also

[MRexperiment-class](#) for the class definition, [cumNorm](#) to normalize the counts.

Examples

```
data(msd16s)
head(pData(msd16s))
head(fData(msd16s))
```

Index

* **datasets**

msd16s, [2](#)

cumNorm, [3](#)

msd16s, [2](#)

msd16s-package, [2](#)