Package 'msd16s'

November 10, 2026

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

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

Version 1.32.0

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_23

git_last_commit cbe0564

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

Contents

msd16s-package 2
msd16s 2

Index **4**

`msd16s-package` *Curated dataset of many healthy and moderate-to-severe diarretic gut 16s samples on the 454 FLEX platform.*

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 (operatonal taxanomic 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` *Curated dataset of many healthy and moderate-to-severe diarretic gut 16s samples on the 454 FLEX platform.*

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://dnaclust.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