

# Package ‘msd16s’

July 4, 2024

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

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

**Version** 1.24.0

**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\_19

**git\_last\_commit** 3fe4af0

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-07-04

## Contents

msd16s-package . . . . .	2
msd16s . . . . .	2

<b>Index</b>	<b>4</b>
--------------	----------

---

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://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](#)