

# Package ‘msd16s’

October 18, 2017

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**Version** 0.110.0

**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

**NeedsCompilation** no

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

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

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

**Examples**

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