Package 'msd16s'

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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

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Contents

| 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))
```

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