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

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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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