Package ‘msd16s’

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Version 1.22.0
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
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R topics documented:

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

Index 4
msd16s-package

Curated dataset of many healthy and moderate-to-severe diarrheic 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 (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

Curated dataset of many healthy and moderate-to-severe diarrheic 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**: Dysenteric (1) non-dysenteric (0) indicator

The `fData` function accesses a data frame with the following columns:

- **OTU**: OTU cluster id
msd16s

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