Package 'msd16s'

March 29, 2021

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Version 1.10.0		
License Artistic-2.0		
Title Healthy and moderate to sev	vere diarrhea 16S expression data	
moderate-to-severe diarrheti	expression data from 992 healthy and c samples used in 'Diarrhea in come countries leads to large-scale obiota composition'.	
LazyData yes		
Depends R (>= 2.10), Biobase, m	netagenomeSeq,	
biocViews ExperimentData, Sequ		
git_url https://git.bioconductor.or	g/packages/msd16s	
git_branch RELEASE_3_12		
git_last_commit 270ed4c		
git_last_commit_date 2020-10-2	7	
Date/Publication 2021-03-29		
R topics documented:		
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	rated dataset of many healthy and moderate-to-severe diarretic gut 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 taxanomic units) by DNAClust.

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Author(s)

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References

Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition.

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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)

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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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