Package ‘msd16s’

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Version 0.108.0
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 (&gt;= 2.10), Biobase, metagenomeSeq,
URL http://www.cbcb.umd.edu/research/projects/GEMS-pathogen-discovery
biocViews ExperimentData, SequencingData, MicrobiomeData
NeedsCompilation no

R topics documented:

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msd16s-package  Curated dataset of many healthy and moderate-to-severe diarrhetic 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

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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 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: Dysentery (1) non-dysentery (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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