

Moderate-to-Severe diarrhea 16S dataset

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This data package contains the information used to run the analyses found in "Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition". Measurements are the number of reads annotated for a particular cluster within a given sample followed by filtering. Sequencing was performed on the 454 Flex platform. Data is stored as an `MRExperiment`-class object. The count matrix was generated using DNAClust (<http://dnaclust.sourceforge.net/>). For more details please refer to the paper.

The help file `?msd16s` describes the example dataset.

1 The Data

We start by loading the library and the data.

```
> suppressMessages(library(metagenomeSeq))
> library(msd16s)
> data(msd16s)
```

This will load the `msd16s` object of class `MRExperiment`. As described in the `metagenomeSeq` vignette, `print` (or `show`) will display summary information.

```
> msd16s

MRExperiment (storageMode: environment)
assayData: 26044 features, 992 samples
  element names: counts
protocolData: none
phenoData
  sampleNames: 100259 100262 ... 602385 (992 total)
  varLabels: Type Country ... Dysentery (5 total)
  varMetadata: labelDescription
featureData
  featureNames: 54 94 ... 276421 (26044 total)
```

```

fvarLabels: superkingdom phylum ... clusterCenter (10 total)
fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:

```

The data in `msd16s` is the substrate for the analysis described in "Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition". Included in the `MRexperiment` object are the counts, phenotype and feature information.

The phenotype information can be accessed with the `phenoData` and `pData` methods:

```
> phenoData(msd16s)
```

```

An object of class 'AnnotatedDataFrame'
sampleNames: 100259 100262 ... 602385 (992 total)
varLabels: Type Country ... Dysentery (5 total)
varMetadata: labelDescription

```

```
> head(pData(msd16s))
```

	Type	Country	Age	AgeFactor	Dysentery
100259	Case	Gambia	14	[12,18)	1
100262	Control	Gambia	24	[24,60)	0
100267	Case	Gambia	17	[12,18)	0
100274	Case	Gambia	36	[24,60)	0
100275	Case	Gambia	29	[24,60)	0
100277	Case	Gambia	29	[24,60)	0

The feature information including cluster representative sequence can be accessed with the `featureData` and `fData` methods:

```
> featureData(msd16s)
```

```

An object of class 'AnnotatedDataFrame'
featureNames: 54 94 ... 276421 (26044 total)
varLabels: superkingdom phylum ... clusterCenter (10 total)
varMetadata: labelDescription

```

```
> head(fData(msd16s))
```

	superkingdom	phylum	class	order	family
54	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae
94	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae
113	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae

```

117 Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae
145 Bacteria Bacteroidetes Bacteroidia Bacteroidales Prevotellaceae
202 Bacteria Bacteroidetes Bacteroidia Bacteroidales Bacteroidaceae
      genus species OTU
54 Lactobacillus Lactobacillus sp. TSK G32-2 54
94 Lactobacillus Lactobacillus sp. TSK G32-2 94
113 Lactobacillus Lactobacillus sp. TSK G32-2 113
117 Lactobacillus Lactobacillus sp. TSK G32-2 117
145 Prevotella Prevotella sp. DJF_RP53 145
202 Bacteroides Bacteroides fragilis 202

```

```

54 ;cellular organisms;Bacteria;Firmicutes;Bacilli;Lactobacil
94 ;cellular organisms;Bacteria;Firmicutes;Bacilli;Lactobacil
113 ;cellular organisms;Bacteria;Firmicutes;Bacilli;Lactobacil
117 ;cellular organisms;Bacteria;Firmicutes;Bacilli;Lactobacil
145 ;cellular organisms;Bacteria;Bacteroidetes/Chlorobi group;Bacteroidetes;Bacteroidia
202 ;cellular organisms;Bacteria;Bacteroidetes/Chlorobi group;Bacteroidetes;Bacteroid

```

```

54 CATGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCGATCAACCTCTCAGTTCGGCTACGTATCATCAO
94 CATGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCGATCAACCTCTCA
113 CATGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCGATCAACC
117 CATGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTCCCAATGTGGCCGATCAAC
145 CATGCTGCCTCCCGTAGGAGTTTGGACCGTGTCTCAGTTCCAATGTGGGGG
202 CATGCTGCCTCCCGTAGGAGTTTGGACCGTGTCTCAGT

```

The raw or normalized counts matrix can be accessed with the `MRcounts` function:

```
> head(MRcounts(msd16s[,1:10]))
```

```

      100259 100262 100267 100274 100275 100277 100291 100292 100293 100294
54      0      0      0      0      0      0      0      0      0      0
94      0      0      0      0      0      0      0      0      0      0
113     0      0      0      0      0      0      0      0      0      0
117     0      0      0      0      0      0      0      0      0      0
145     0      0      0      0      0      0      0      0      0      0
202     0      0      0      0      0      0      0      0      0      0

```

Using this class, the object can be easily subsetted, for example:

```
> msd16s_bangladesh = msd16s[,pData(msd16s)$Country == "Bangladesh"]
> msd16s_bangladesh
```

```
MRexperiment (storageMode: environment)
assayData: 26044 features, 206 samples
```

```
    element names: counts
protocolData: none
phenoData
  sampleNames: 600002 600005 ... 602385 (206 total)
  varLabels: Type Country ... Dysentery (5 total)
  varMetadata: labelDescription
featureData
  featureNames: 54 94 ... 276421 (26044 total)
  fvarLabels: superkingdom phylum ... clusterCenter (10 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:
```