

# ETEC 16S dataset

May 1, 2018

This data package contains the data used in the analyses found in "Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic *Escherichia coli* and subsequent ciprofloxacin treatment". DNA was amplified using 'universal' primers targeting the V1-V2 region of the 16S rRNA gene (small subunit of the ribosome) in bacteria - 338R (5'- CATGCTGCCTCCCGTAGGAGT -3') and 27F (5'- AGAGTTTGATCCTGGCTCAG -3'). Both forward and reverse primers had a 5 prime portion specific for use with 454 GS-FLX Titanium sequencing technology and the forward primers contained a barcode between the Titanium and gene specific region, so that samples could be pooled to a multiplex level of 132 samples per instrument run.

16S rRNA gene sequencing was performed for all available stool samples. After sequencing, 124 samples passed quality controls, corresponding to data from 5 volunteers with the most unambiguous cases of diarrhea during the study (54 samples) and 7 volunteers without diarrheal symptoms who had the most stool samples (78 samples). The raw data have been submitted to NCBI under project ID: PRJNA298336.

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 `?etec16s` describes the example dataset.

## 1 The Data

We start by loading the library and the data.

```
> suppressMessages(library(metagenomeSeq))
> library(etec16s)
> data(etec16s)
```

This will load the `etec16s` object of class `MRExperiment`. As described in the `metagenomeSeq` vignette, `print` (or `show`) will display summary information.

```
> etec16s
```

```

MRexperiment (storageMode: environment)
assayData: 6423 features, 124 samples
  element names: counts
protocolData: none
phenoData
  sampleNames: 2 3 ... 333 (124 total)
  varLabels: SubjectID Dose ... AntibPrev (7 total)
  varMetadata: labelDescription
featureData
  featureNames: 3 5 ... 148089 (6423 total)
  fvarLabels: OTU.ID Center ... Species (8 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:

```

The data in `etec16s` is the substrate for the analysis described in "Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic *Escherichia coli* and subsequent ciprofloxacin treatment". 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(etec16s)
```

```

An object of class 'AnnotatedDataFrame'
  sampleNames: 2 3 ... 333 (124 total)
  varLabels: SubjectID Dose ... AntibPrev (7 total)
  varMetadata: labelDescription

```

```
> head(pData(etec16s))
```

	SubjectID	Dose	Day	AnyDayDiarrhea	Diarrhea	AntiGiven	AntibPrev
2	E01JH0003	2 x 10 <sup>6</sup> cfu	-1	0	0	0	0
3	E01JH0004	2 x 10 <sup>6</sup> cfu	-1	1	0	0	0
8	E01JH0011	2 x 10 <sup>6</sup> cfu	-1	1	0	0	0
10	E01JH0013	2 x 10 <sup>6</sup> cfu	-1	0	0	0	0
12	E01JH0016	2 x 10 <sup>6</sup> cfu	-1	1	0	0	0
13	E01JH0017	2 x 10 <sup>5</sup> cfu	-1	1	0	0	0

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

```
> featureData(etec16s)
```

```
An object of class 'AnnotatedDataFrame'
  featureNames: 3 5 ... 148089 (6423 total)
  varLabels: OTU.ID Center ... Species (8 total)
  varMetadata: labelDescription
```

```
> head(fData(etec16s))
```

	OTU.ID	Center	Phylum	Class	Order
3	3	130_6133	Bacteroidetes	Bacteroidia	Bacteroidales
5	5	14_1391	Bacteroidetes	Bacteroidia	Bacteroidales
10	10	111_7283	Bacteroidetes	Bacteroidia	Bacteroidales
11	11	130_1817	Bacteroidetes	Bacteroidia	Bacteroidales
13	13	82_8248	Bacteroidetes	Bacteroidia	Bacteroidales
14	14	131_3769	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales
		Family	Genus	Species	
3		Bacteroidaceae	Bacteroides	Bacteroides vulgatus	
5		Bacteroidaceae	Bacteroides	Bacteroides uniformis	
10		Bacteroidaceae	Bacteroides	Bacteroides uniformis	
11		Bacteroidaceae	Bacteroides	Bacteroides vulgatus	
13		Bacteroidaceae	Bacteroides	Bacteroides ovatus	
14		Akkermansiaceae	Akkermansia	Akkermansia muciniphila	

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

```
> head(MRcounts(etec16s[,1:10]))
```

	2	3	8	10	12	13	16	20	21	24
3	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0
10	0	0	0	0	0	0	1	0	0	0
11	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0

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

```
> etec16s_day84 = etec16s[,which(pData(etec16s)$Day == 84)]
> etec16s_day84
```

```
MRexperiment (storageMode: environment)
assayData: 6423 features, 12 samples
  element names: counts
protocolData: none
phenoData
```

```
sampleNames: 306 307 ... 333 (12 total)
varLabels: SubjectID Dose ... AntibPrev (7 total)
varMetadata: labelDescription
featureData
featureNames: 3 5 ... 148089 (6423 total)
fvarLabels: OTU.ID Center ... Species (8 total)
fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:
```