

Installations:

We will be using the miaverse R package for this tutorial (<https://microbiome.github.io/>)
To install the needed packages simply do:

```
BiocManager::install("microbiome/mia")
```

Data:

The data can be loaded from the mia package itself, we will be using the GlobalPatterns dataset, which comes from this this: <https://www.pnas.org/doi/full/10.1073/pnas.1000080107>, which looked at the the microbial communities from 25 environmental samples and three known ``mock communities" at an average depth of 3.1 million reads per sample in order to identify global patterns of 16S rRNA diversity at a depth of millions of sequences per sample (Caporaso, 2010).

To access the data all you need to do is:

```
library(mia)  
data("GlobalPatterns", package="mia")
```

To both test that you have correctly installed the package, and have the wanted data, simply print out GlobalPatterns:

```
GlobalPatterns
```

And make sure that this is the result you get:

```
## class: TreeSummarizedExperiment  
## dim: 19216 26  
## metadata(0):  
## assays(1): counts  
## rownames(19216): 549322 522457 ... 200359 271582  
## rowData names(7): Kingdom Phylum ... Genus Species  
## colnames(26): CL3 CC1 ... Even2 Even3  
## colData names(7): X.SampleID Primer ... SampleType Description  
## reducedDimNames(0):  
## mainExpName: NULL  
## altExpNames(0):  
## rowLinks: a LinkDataFrame (19216 rows)  
## rowTree: 1 phylo tree(s) (19216 leaves)  
## colLinks: NULL  
## colTree: NULL
```