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 article: 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
```