

Analyzing metabarcoding data with DADA2

We're going to follow a metabarcoding formation we give in France. This formation is called MetaBiodiv:

<https://github.com/ANF-MetaBioDiv/course-material>

In order to download the zip of the formation, click on the green button code and download ZIP.

This formation goes beyond the scope of ASIAME. Nonetheless, you'll find very useful scripts and lectures you may need in the future:

<https://anf-metabiodiv.github.io/course-material/>

For the purpose of ASIAME, please follow the instructions of paragraph 1 in here:

https://anf-metabiodiv.github.io/course-material/practicals/preprocessing_dada2.html

Please check that your version of R is up to date, it should be 4.2 or higher. You can see this in the console window when you open Rstudio.

Please install also the following packages (you just have to copy paste the following lines and run them in the coding window of Rstudio):

```
#install packages
install.packages(BiocManager)
BiocManager::install("ape")
BiocManager::install("base")
BiocManager::install("betapart")
BiocManager::install("Biostrings")
BiocManager::install("ComplexHeatmap")
BiocManager::install("corrplot")
BiocManager::install("dada2")
BiocManager::install("DECIPHER")
BiocManager::install("devtools")
BiocManager::install("digest")
BiocManager::install("dplyr")
BiocManager::install("ecodist")
BiocManager::install("fpc")
BiocManager::install("FSA")
BiocManager::install("ggplot2")
BiocManager::install("ggpmisc")
BiocManager::install("ggpubr")
BiocManager::install("ggrepel")
BiocManager::install("grid")
BiocManager::install("gridExtra")
BiocManager::install("GUniFrac")
BiocManager::install("here")
BiocManager::install("knitr")
```

```
BiocManager::install("microbiome")
BiocManager::install("microbiomeMarker")
BiocManager::install("MicrobiotaProcess")
BiocManager::install("modEvA")
BiocManager::install("NbClust")
BiocManager::install("parallel")
BiocManager::install("patchwork")
BiocManager::install("PCAtools")
BiocManager::install("phangorn")
BiocManager::install("phyloseq")
BiocManager::install("plotly")
BiocManager::install("plyr")
BiocManager::install("RColorBrewer")
BiocManager::install("renv")
BiocManager::install("rmarkdown")
BiocManager::install("stats")
BiocManager::install("tidyverse")
BiocManager::install("treemap")
BiocManager::install("treemapify")
BiocManager::install("vegan")
BiocManager::install("zCompositions")
```

If you have any problem downloading the formation zip or in installing the packages, please let me or Niño know.