Tutorials for R

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I will post here a few tutorials for different types of analysis of microbial communities. For each of these of these tutorials there will be a detailed explanation as a pdf file created with Rmd.

- Introduction to R : https://github.com/vaulot/R_tutorials/tree/master/introduction
- Plot data from culture experiments (cell abundance vs. time) : https://github.com/vaulot/R_tutorials/tree/master/cultures
- Visualization and analysis of metabarcode data with phyloseq : https://github.com/vaulot/R_tutorials/tree/master/phyloseq

Please post any question or issues here : https://github.com/vaulot/R_tutorials/issues

Prerequisites to be installed to run these tutorials

- R : https://pbil.univ-lyon1.fr/CRAN/
- R studio : https://www.rstudio.com/products/rstudio/download/#download
- Download and install the following libraries by running under R studio the following lines

```
install.packages("dplyr")      # To manipulate dataframes
install.packages("tidyr")      # To manipulate dataframes
install.packages("readxl")     # To read Excel files into R

install.packages("ggplot2")    # for high quality graphics
install.packages("maps")       # to make maps
install.packages("gridExtra") # for grids


install.packages("treemap")    # for treemaps

install.packages("FactoMineR") # multivariate analysis
install.packages("plotrix" )   # needed for standard error


source("https://bioconductor.org/biocLite.R")
biocLite('phyloseq')           # metabarcode data analysis
biocLite("Biostrings")         # manipulate sequences
```

Step by step instructions

- Introduction to R : https://github.com/vaulot/R_tutorials/blob/master/introduction/R_introduction_tutorial.pdf
- Plot and process culture data : https://github.com/vaulot/R_tutorials/blob/master/cultures/R_tutorial_cultures.pdf
- Phyloseq analysis of metabarcode data : https://github.com/vaulot/R_tutorials/blob/master/phyloseq/Phyloseq_tutorial.pdf