

Tutorial for R microeco package (v0.12.0)

Chi Liu, Felipe R. P. Mansoldo, Umer Zeeshan Ijaz, Chenhao Li, Yang Cao, Jarrod J. Scott, Yaoyao

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Chapter 1

Background

R language (?) and its packages ecosystem are wonderful tools for data analysis. In the field of microbial community ecology, many packages can be used for the statistical analysis, such as `vegan` (?), `ape` (?) and `picante` (?). However, with the development of the high-throughput sequencing techniques, the increasing data amount and complexity of studies make the data mining a challenge. There have been some R packages created for the statistics and visualization for microbiome data, such as `phyloseq` (?), `microbiome` (<https://github.com/microbiome/microbiome>), `microbiomeSeq` (<http://www.github.com/umerijaz/microbiomeSeq>), `ampvis2` (<https://madsalbertsen.github.io/ampvis2/reference/index.html>), `MicrobiomeR` (<https://github.com/vallenderlab/MicrobiomeR>), `theseus` (?), `rANOMALY` (?), `MicrobiomeExplorer` (?), `tidyMicro` (?), `microbial` (<https://github.com/guokai8/microbial>), and so on. In addition, some web tools associated with R language are also useful for microbial community data analysis, such as `Shiny-phyloseq` (?), `Mian` (?) and `animalcules` (?). Even so, users still lack a flexible, comprehensive and modularized R package to analyze and manage the data fast and easily. So we created the `microeco` R package (?) for this goal (<https://github.com/ChiLiubio/microeco>). Besides, we also developed the `file2meco` package (<https://github.com/ChiLiubio/file2meco>) for the data input from some famous tools easily and `mecodev` package (<https://github.com/ChiLiubio/mecodev>) for some extending approaches in this field.

