Tutorial for R microeco package (v0.14.0)

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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://github.com/KasperSkytte/ampvis2), MicrobiomeR(https://github.com/vallenderlab/MicrobiomeR), theseus (**?**), rANOMALY (**?**), tidyMicro (**?**), microbial (https://github.com/guokai8/microbial), amplicon (https://github.com/microbiota/amplicon), MicrobiotaProcess (https://github.com/YuLab-SMU/MicrobiotaProcess) and so on. In addition, some web tools associated with R language are also useful for microbial community data analysis, such as Shiny-phyloseq (**?**), MicrobiomeExplorer (**?**), animalcules (**?**) and Namco (**?**). 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.