

Tutorial for R microeco package (v1.16.0)

2025-11-25

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Chapter 1

Background

R language (?) and its packages ecosystem are wonderful tools for data analysis. In community ecology, a series of packages are available for 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 in microbiome a challenge. There have been some R packages created specifically for the statistics and visualization of 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 microbiome data analysis, such as Shiny-phyloseq (?), MicrobiomeExplorer (?), animalcules (?) and Namco (?). Even so, researchers still lack a flexible, comprehensive and modularized R package to analyze and manage the data fast and easily. Based on this background, we created the R microeco package (??) (<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.

