

# Tutorial for R microeco package (v0.14.0)

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2023-02-10



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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.

