



microeco 2: A comprehensive R package for downstream analysis of microbiome omics data

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Introduction

microeco: Version 2.0 Key Enhancements & Ecosystem

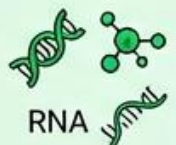
Version 2.0
Enhanced

Data & Experimental Challenges

- 1 Increasing Data Complexity:**
Amplicon vs. Metagenomic
Formats 
- 2 Complex Experimental Designs:**
Multiple factors,
time points, studies 
- 3 Analysis Method Proliferation:**
Hundreds of specialized
methods & tools 

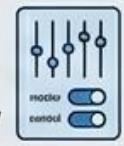
Need: Integrated and Flexible System

Enhanced Modular Architecture

- 1 Advanced R6 Core:**
Flexible, object-oriented,
new classes added 
- 2 Multi-Omics Suite:**
Metagenomics,
Transcriptomics,
Metabolomics 
- 3 Refined Workflows:**
Improved connectivity
between stats & visualization 

'Comprehensive Overhaul & Refinement'

Ecosystem & Workflow Integration

- 1 Flexible Data Parsing:**
Parsing for complex
metagenomic data files 
- 2 Unified Parameters:**
Overhauled parameter
system for consistency 
- 3 Broad Tool Compatibility:**
Support for integrating
new analytical methods
& multi-omics tools 

120,000+

Cumulative Downloads

4,000+

Peak Monthly Downloads

1,600+

Scientific Publications

5 Years

Continuous Maintenance

- ◆ The second version of the microeco package integrates more method categories and algorithms.
- ◆ The code has been refactored for a more logically sound architecture.
- ◆ The package supports downstream analyses of complex metagenomic bioinformatics data.



Overview of microeco v2.0

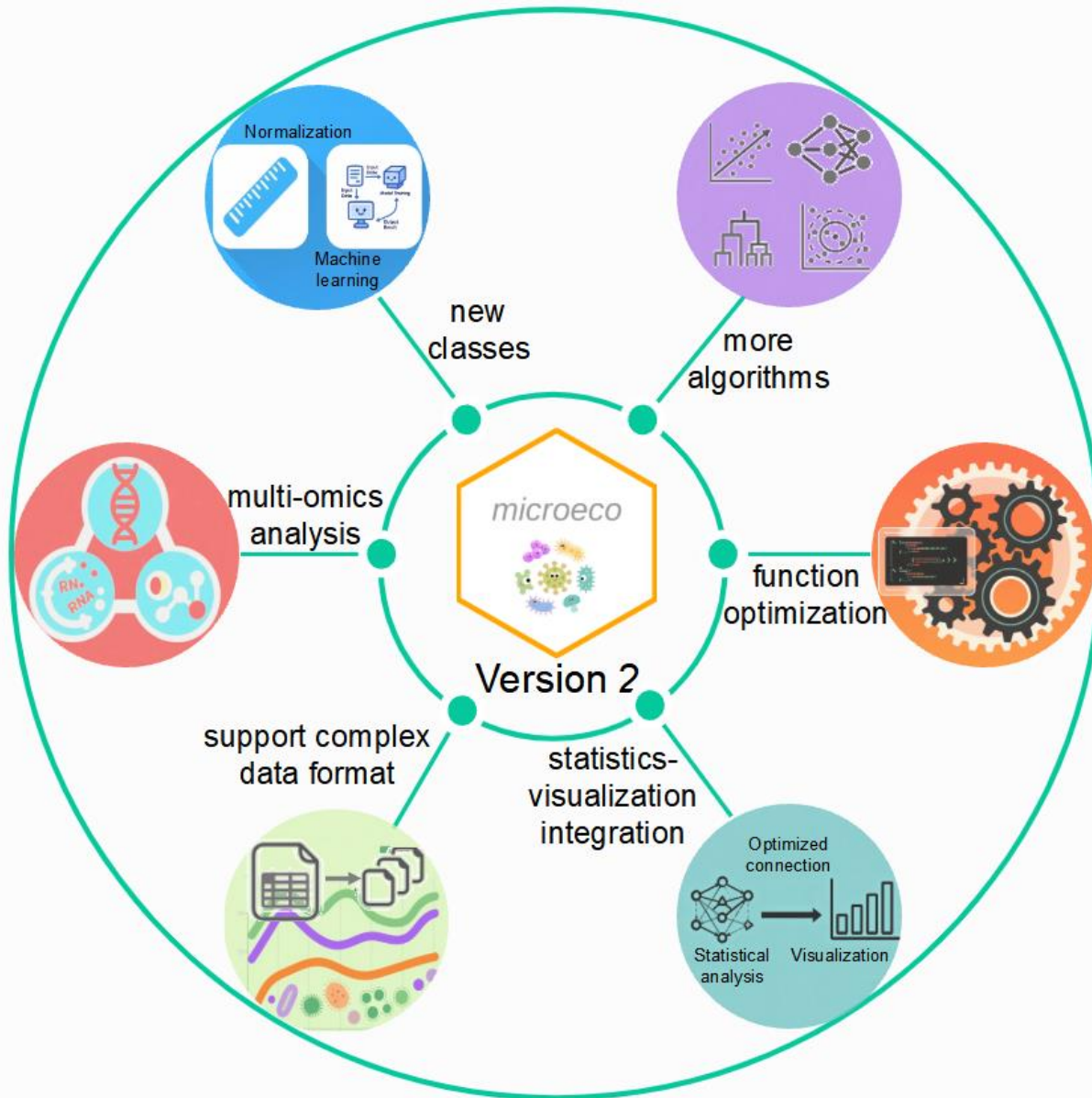


Figure 1 A summary diagram of the main upgraded contents of the second version of the microeco package.



Design framework of microeco v2.0

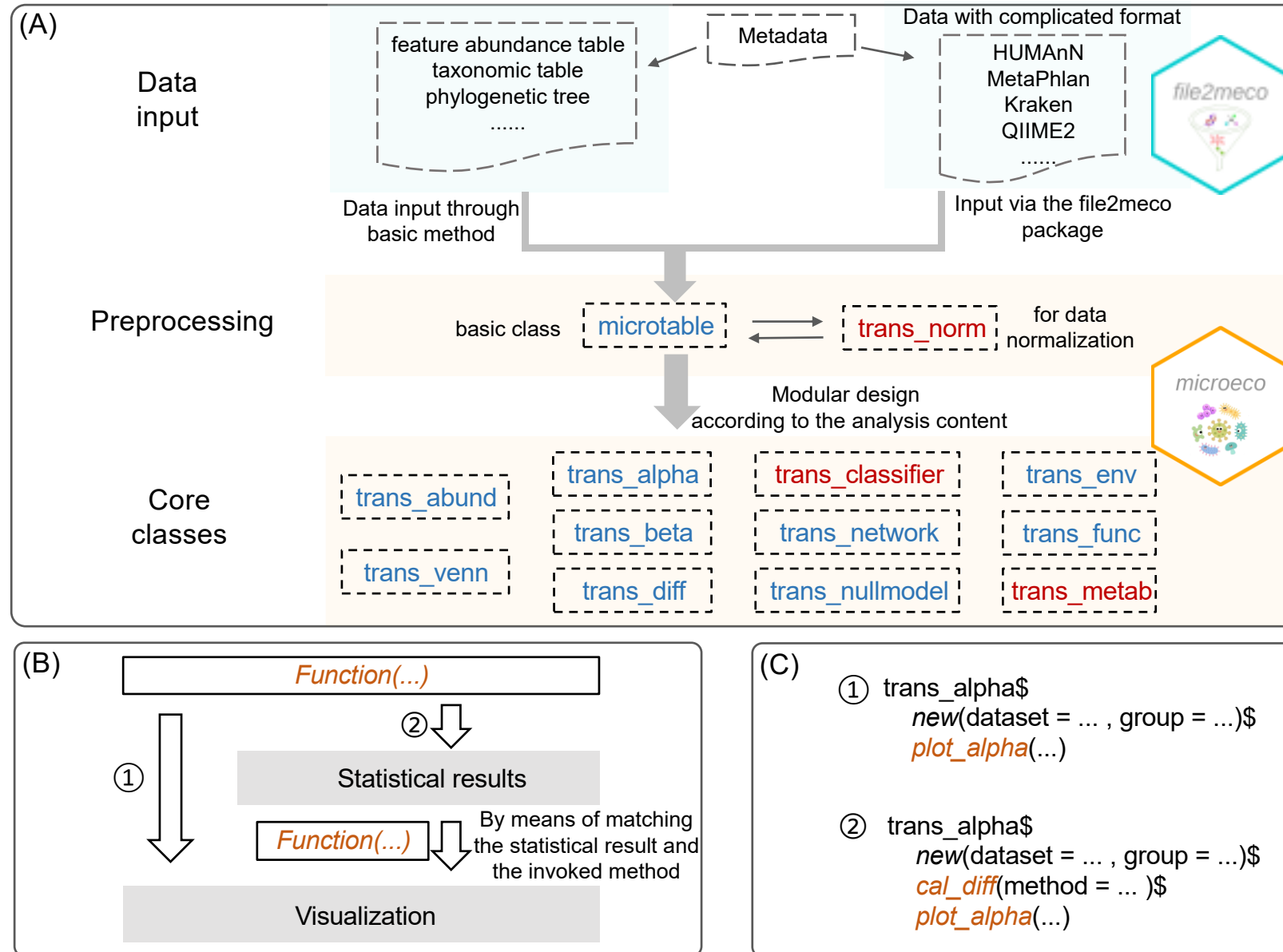


Figure 2 Design framework and logic of the second version of the microeco package.



Function system

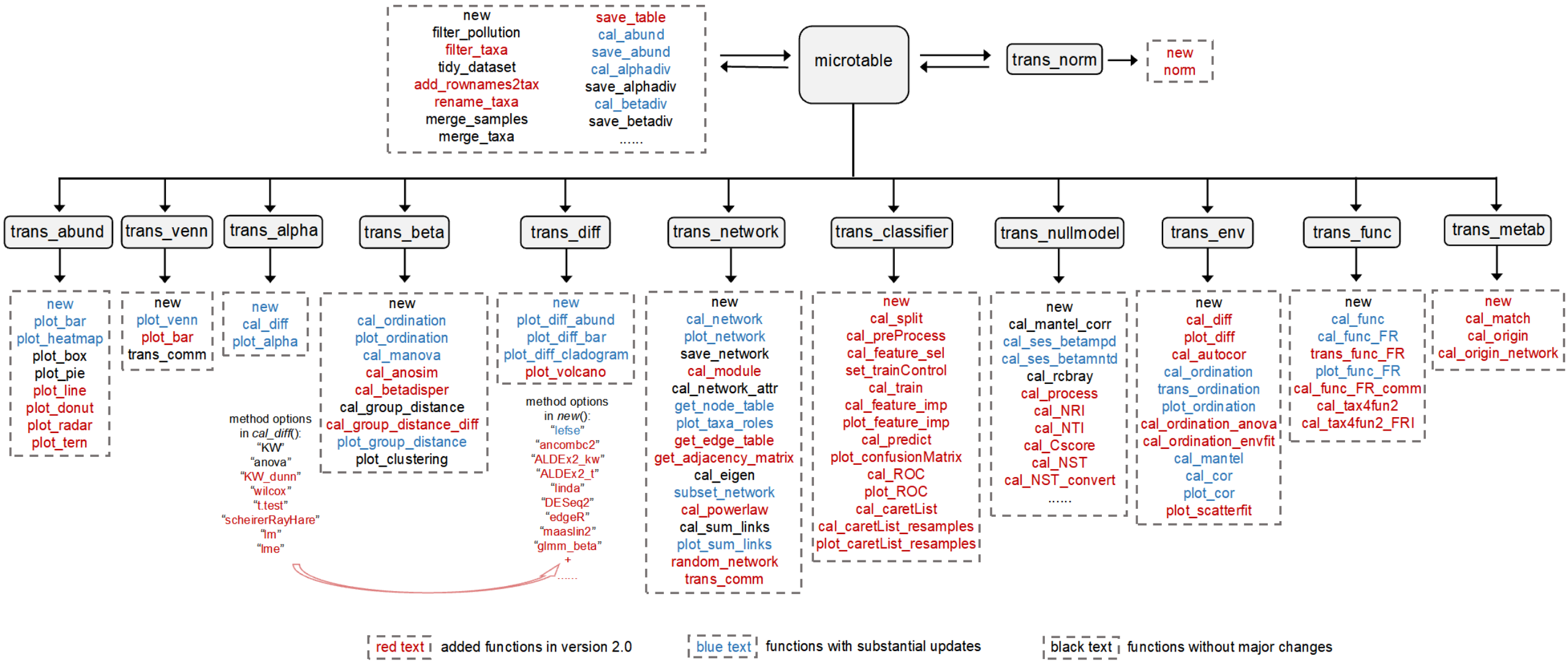


Figure 3 Main functions in the second-version microeco package.



Flowchart: parsing MetaCyc pathway abundances

I : MetaCyc abundance file

	S1	S2
PWY0-1338	88	66
PWY0-1338 g__Enterobacter.s__Enterobacter_mori	32	5
PWY0-1338 g__Pantoea.s__Pantoea_sesami	3	0
PWY0-1338 unclassified	53	61

II : resulting *otu_table* (*microtable* object)

	S1	S2
PWY0-1338 g__Enterobacter.s__Enterobacter_mori	32	5
PWY0-1338 g__Pantoea.s__Pantoea_sesami	3	0
PWY0-1338 unclassified	53	61

remove redundant data (Step 1)

(Step 4)

(Step 5)

III: resulting *tax_table* (*microtable* object)

	Superclass1	Superclass2	pathway	Kingdom	...	Genus	Species
PWY0-1338 g__Enterobacter.s__Enterobacter_mori	Biosynthesis&&Detoxification	Cell Structure Biosynthesis&&Antibiotic Resistance	polymyxin resistance	k__Bacteria	...	g__Enterobacter	s__Enterobacter_mori
PWY0-1338 g__Pantoea.s__Pantoea_sesami	Biosynthesis&&Detoxification	Cell Structure Biosynthesis&&Antibiotic Resistance	polymyxin resistance	k__Bacteria	...	g__Pantoea	s__Pantoea_sesami
PWY0-1338 unclassified	Biosynthesis&&Detoxification	Cell Structure Biosynthesis&&Antibiotic Resistance	polymyxin resistance	unclassified	...	unclassified	unclassified

split the content based on '&&'

Function: *cal_abund*(select_cols = 1, rel = FALSE) (Step 4)

IV: resulting *taxa_abund* list (*microtable* object), including tables like V and VI

	S1	S2
Biosynthesis	88	66
Detoxification	88	66
...	...	...

V : abundances at the Superclass1 level

Function: *cal_abund*(select_cols = c("Superclass1", "Genus"), rel = FALSE) (Step 5)

	S1	S2
Biosynthesis g__Enterobacter	32	5
Biosynthesis g__Pantoea	3	0
Biosynthesis unclassified	53	61
Detoxification g__Enterobacter	32	5
Detoxification g__Pantoea	3	0
...	...	...

VI: abundances at the joint Superclass1 and Genus levels

Figure 4 Flowchart for parsing the MetaCyc pathway abundance file with the file2meco and microeco packages.

Case: analysis workflow of multi-omics data

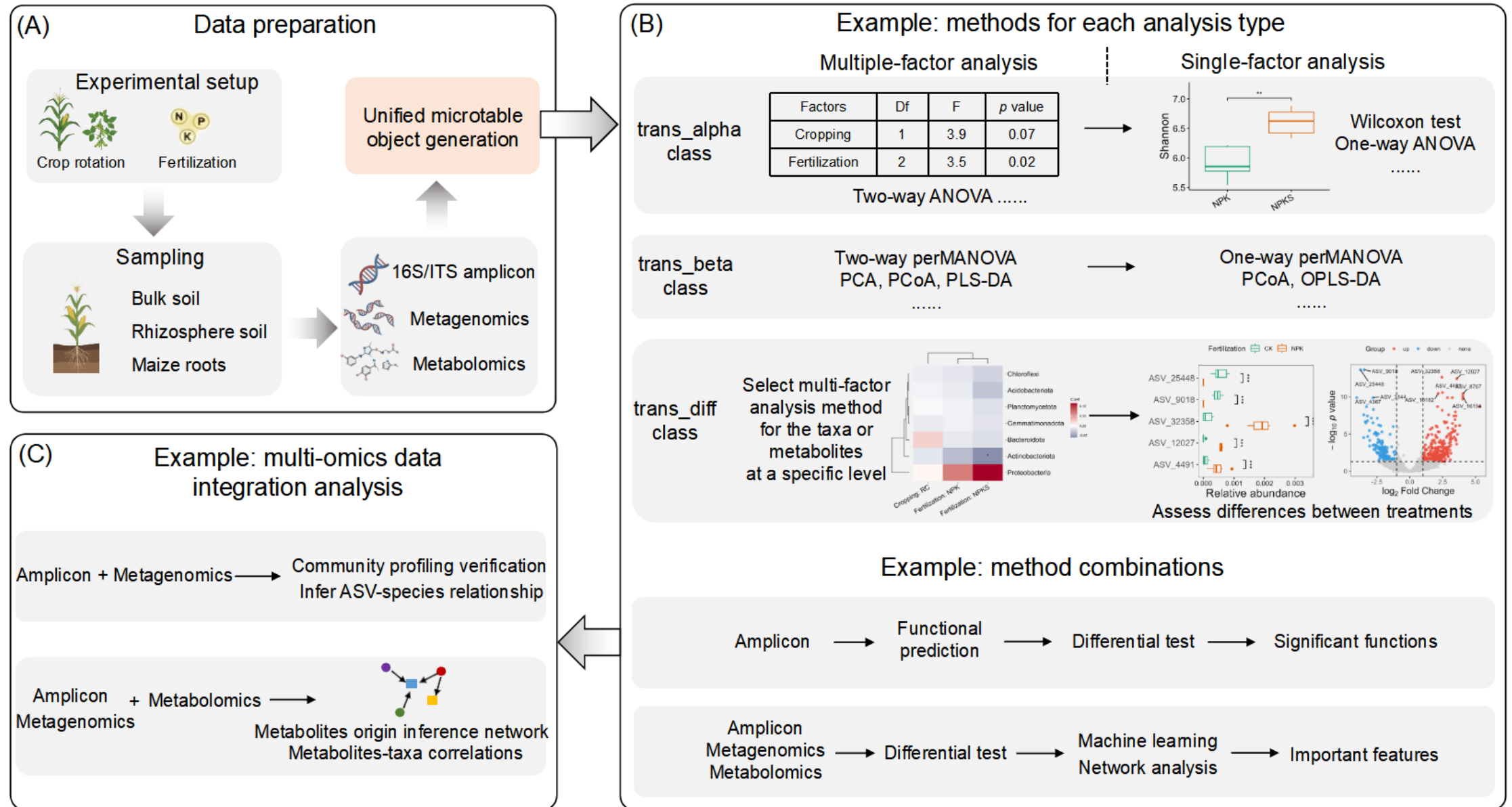


Figure 5 Schematic diagram of an exemplary analysis workflow based on actual experimental data.



Summary

- ❑ The microeco package version 2.0 represents a substantial update compared to its initial release, improving both design coherence and methodological coverage.
- ❑ Together with its extension packages, microeco offers a robust and integrated downstream analytical framework for omics data across diverse areas of microbiome research.
- ❑ We plan to develop an interactive analytical tool built upon the shiny package and microeco 2.0, designed to help beginners learn and apply the microeco package for omics analyses efficiently.
- ❑ Website: <https://github.com/ChiLiubio/microeco>

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