



microeco 2: 一个用于微生物组学数据下游分析的综合性 R 语言包

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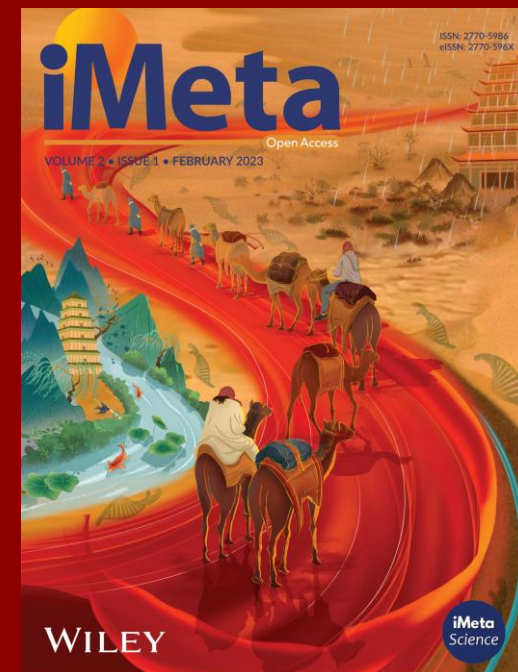
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Chi Liu, Xiangzhen Li, Felipe R. P. Mansoldo, Tong Chen, Fanzheng Meng, Ruixiang Tang, Siyu Zhou, et al. 2026. microeco 2: A Comprehensive R Package for Downstream Analysis of Microbiome Omics Data. *iMeta* 5: e70132.

<https://doi.org/10.1002/imt2.70132>

microeco: Version 2.0 Key Enhancements & Ecosystem

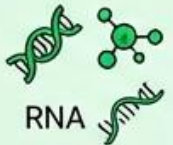
Version 2.0
Enhanced

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 

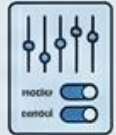
Need: Integrated and Flexible System

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



亮点

- ◆ microeco 软件包第二版整合了更多分析方法类别与算法。
- ◆ 本版本对代码完成重构，构建了逻辑更完善的程序架构。
- ◆ 该软件包可支持复杂宏基因组生物学信息等数据的下游分析。



microeco v2.0的主要更新内容

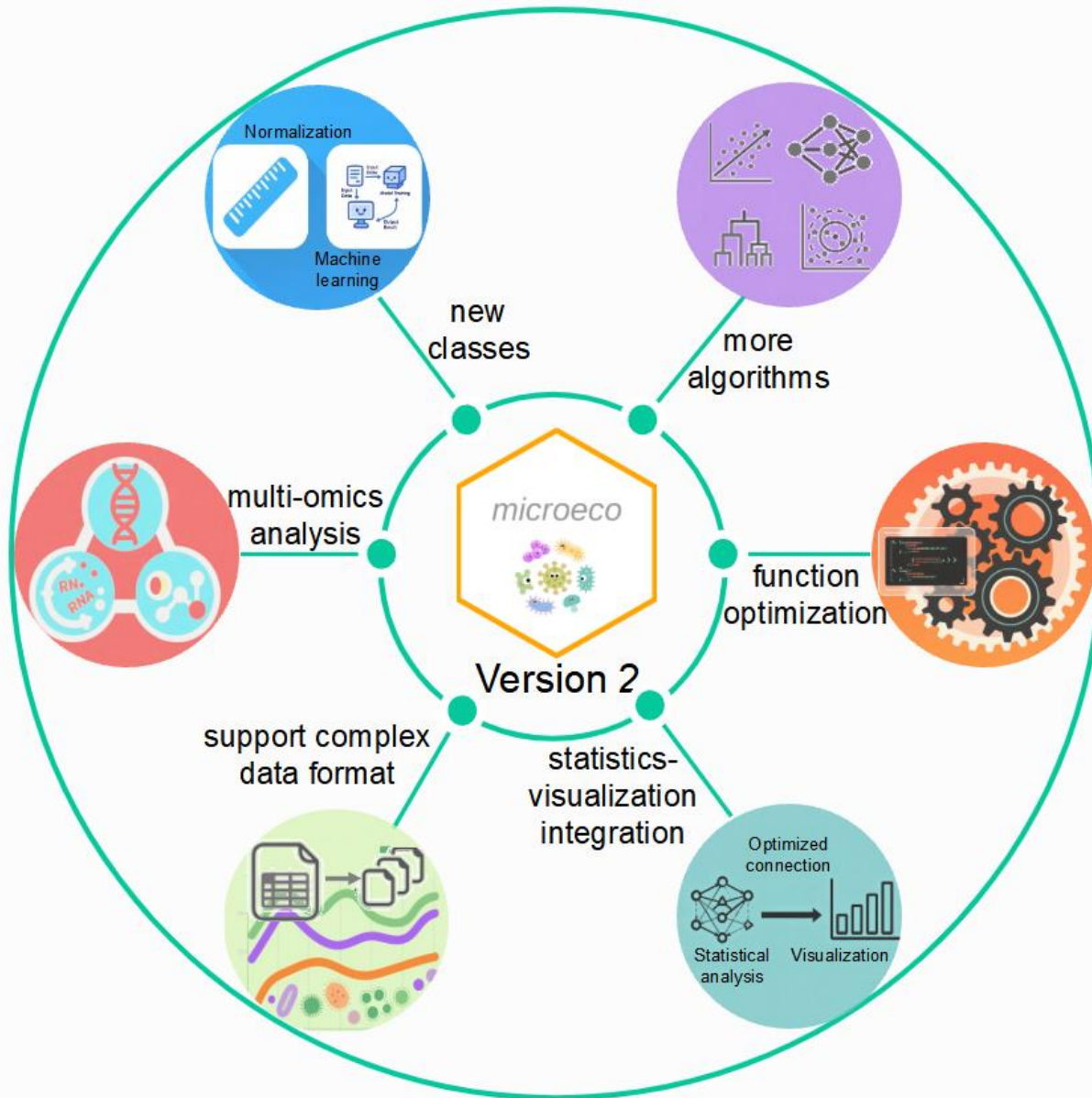


图1 microeco 包第二版主要升级内容的概要图。



microeco v2.0体系的设计框架

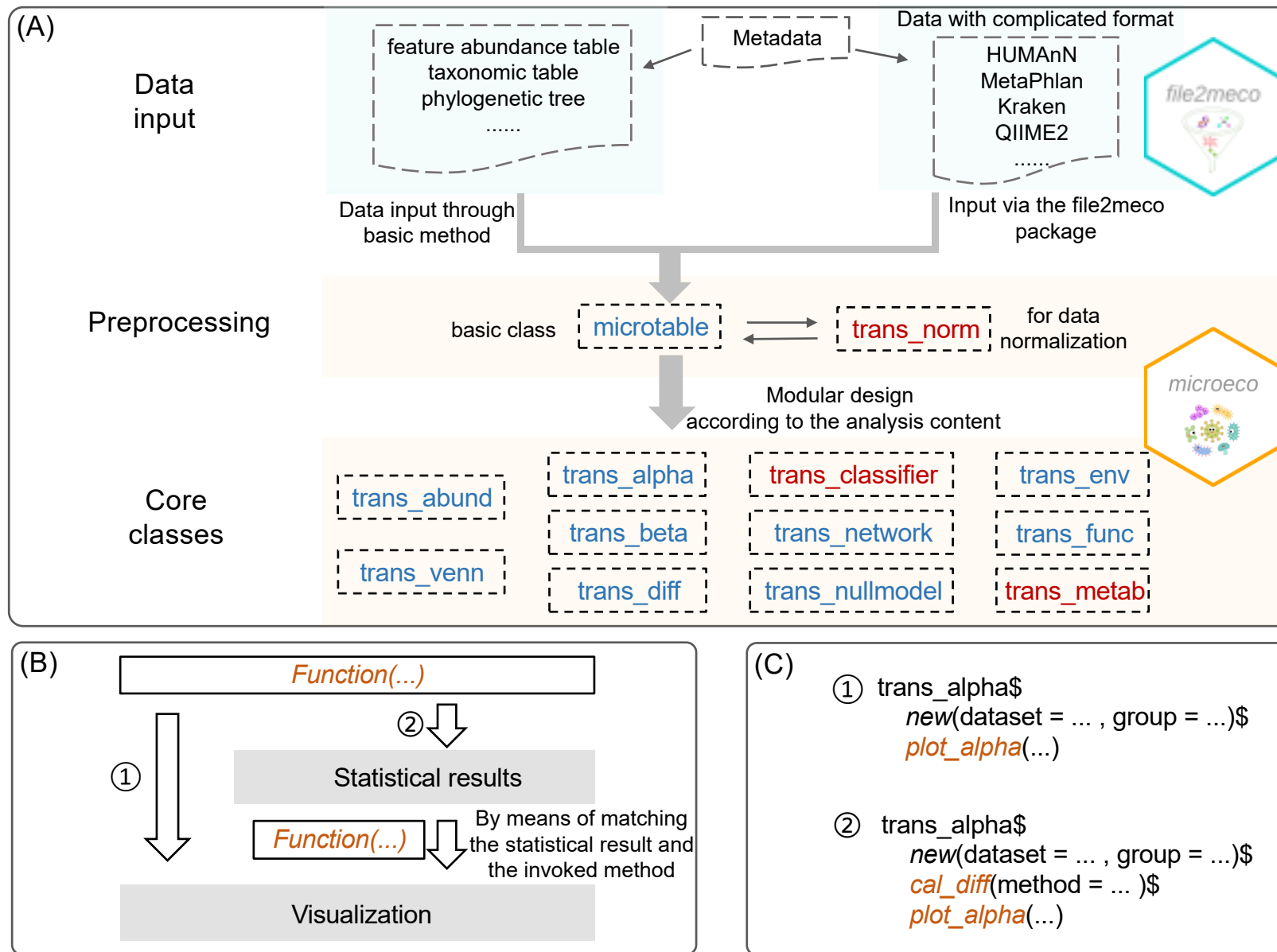


图2 microeco 包第二版的设计框架与逻辑。



函数体系

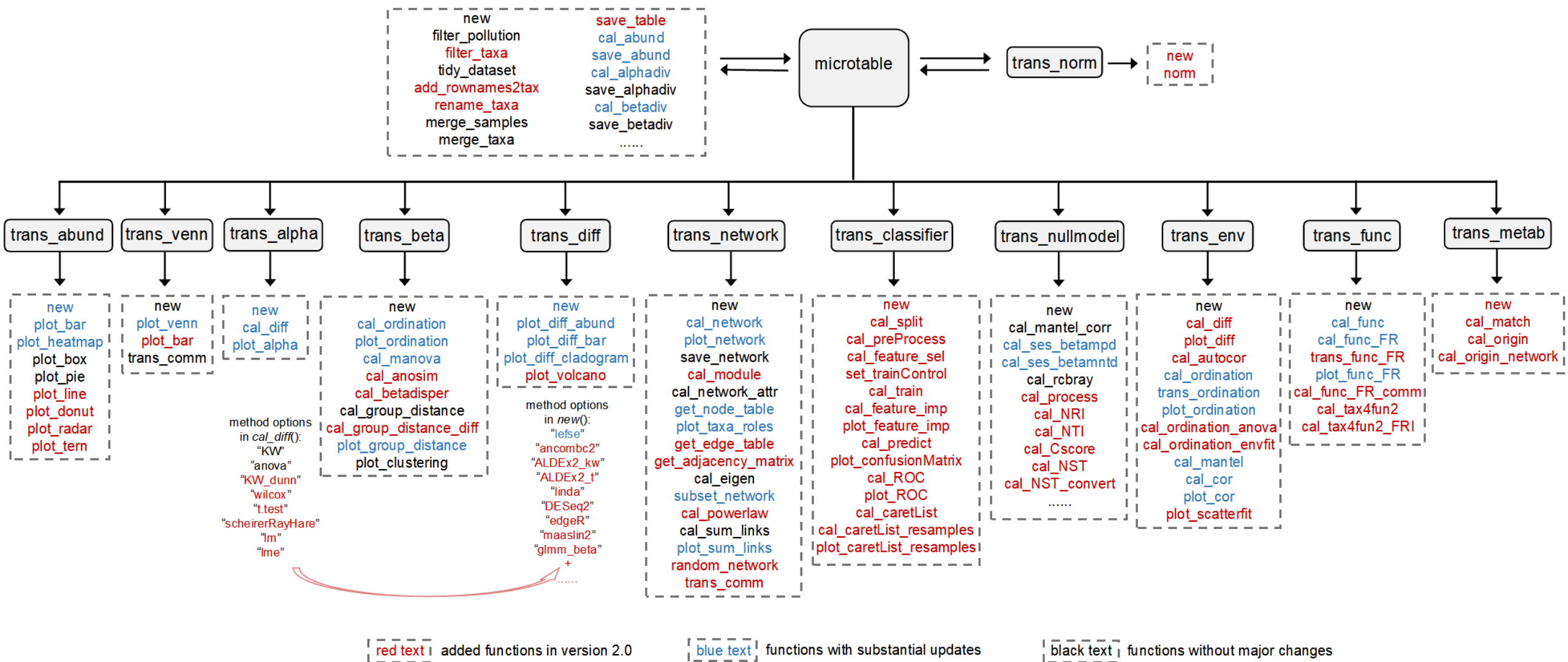


图3 microeco 包第二版中的主要函数。

解析MetaCyc代谢通路丰度数据

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)

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

图4 使用 file2meco 和 microeco 包解析 MetaCyc 通路丰度文件的流程图。

多组学数据的分析流程示例

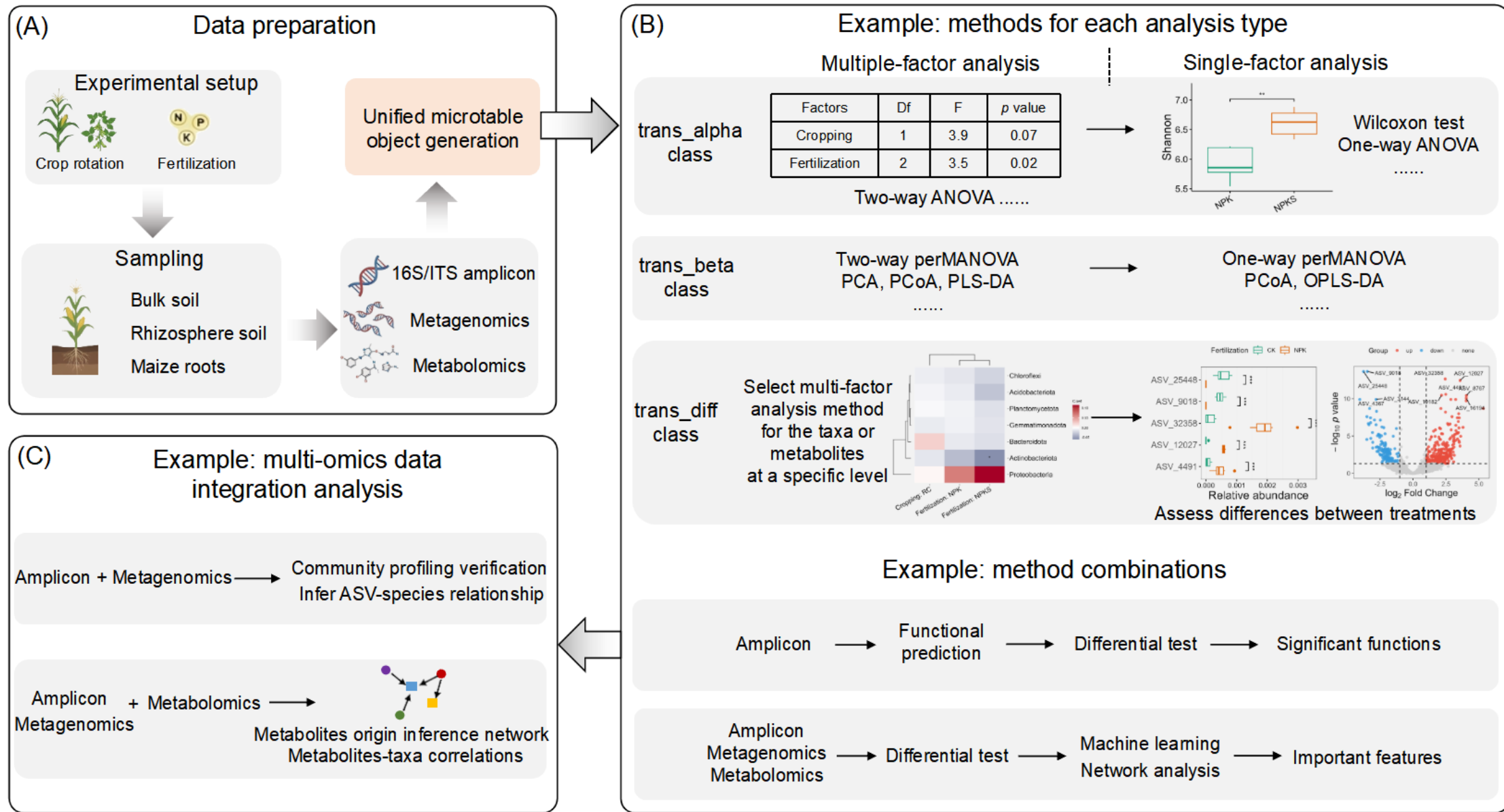
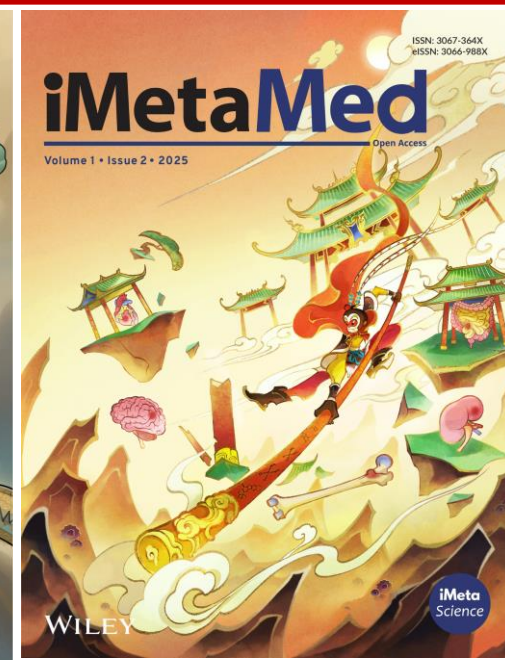
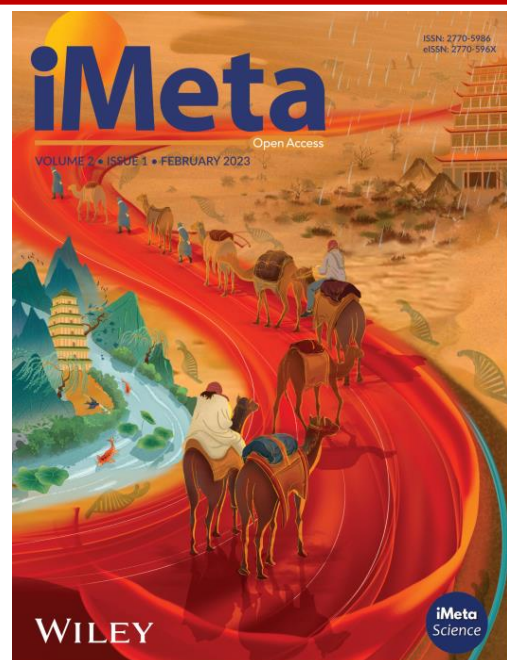


图5 基于真实实验数据的示例性分析流程示意图。

总结

- ❑ microeco 2.0 版本较初始版本实现了大幅更新，提升了设计一致性与方法覆盖范围。
- ❑ 结合其扩展包，microeco 为微生物组研究多个领域的组学数据提供了稳定且一体化的下游分析框架。
- ❑ 计划基于 shiny 包与 microeco 2.0 开发一款交互式分析工具，帮助初学者高效学习并使用 microeco 包开展组学分析。
- ❑ 库网站: <https://github.com/ChiLiubio/microeco>

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iMeta(宏)期刊由宏科学创办，对标**Cell**的生物/医学综合期刊，**SCIE**、**PubMed**收录，影响因子(IF)44.4，位列全球第47，中国第4，**分区表生物学1区Top**，外审平均21天，投稿至发表中位数87天(比同水平期刊快3倍)，欢迎高影响力的研究、方法和综述投稿，CNS外审稿件可带意见和回复转投。

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