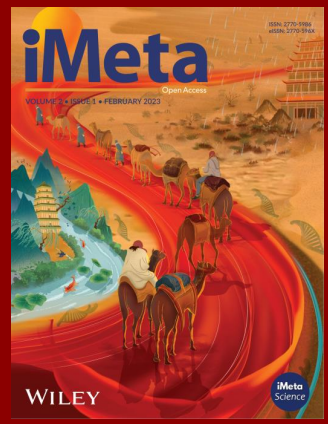
# ggClusterNet 2：一款用于微生物共现网络构建及其关联指标相关性模式分析的R语言工具包



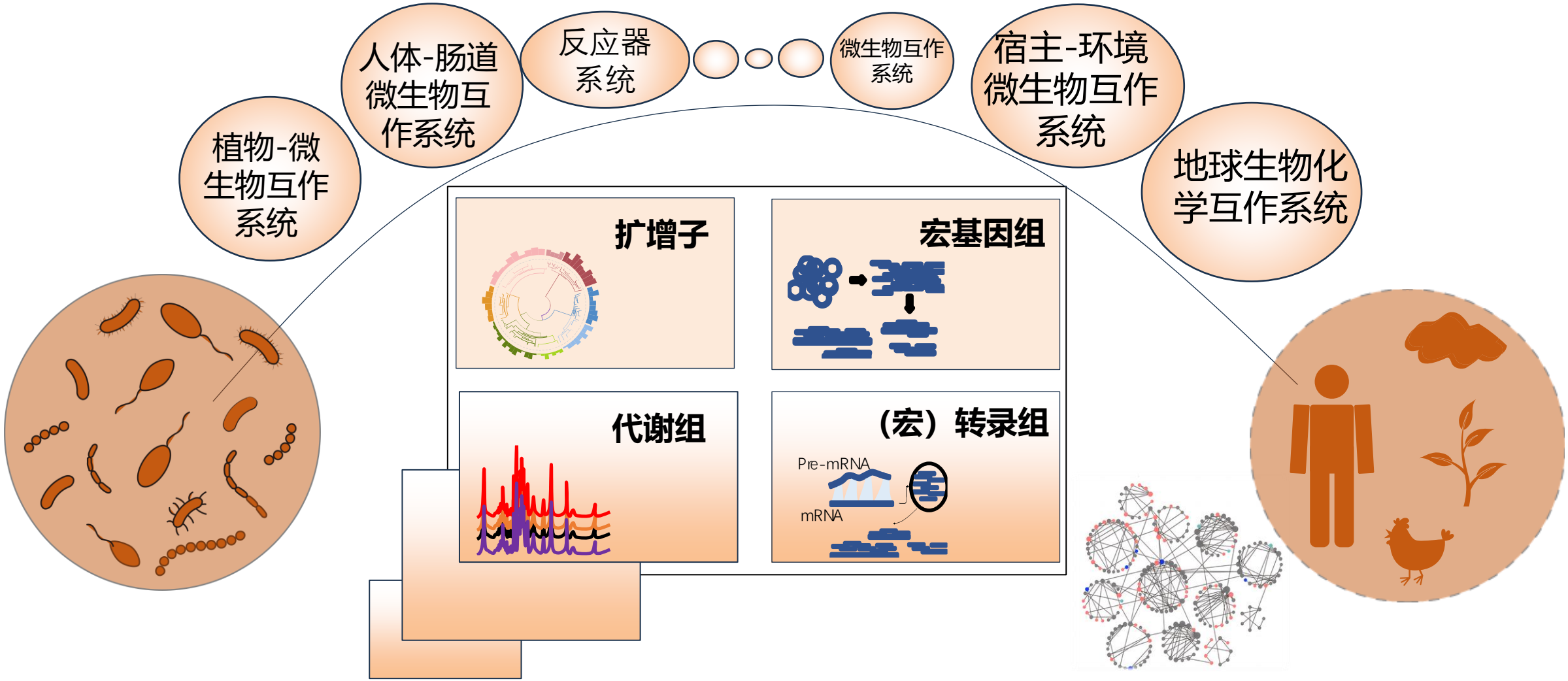

文涛[1]，刘永鑫[2]，刘兰兰[1]，牛国庆[1]，丁哲旭[1]，滕昕洋[1]，马婕[3]，刘莹[3]，杨盛蝶[1]，谢鹏昊[1]，张天娇[1,3]，王磊[4]，路战远[3]，沈其荣[1]，袁军[1]

[1]南京农业大学，江苏省固体有机废弃物资源化高技术研究重点实验室，江苏省有机固体废弃物资源化协同创新中心，教育部资源节约型肥料工程研究中心，绿色智能肥料创新农业农村部重点实验室
[2]中国农业科学院深圳农业基因组研究所， 农业农村部农业基因数据分析重点实验室
[3]内蒙古自治区农牧业科学院，农业农村部黑土地保护与利用重点实验室，内蒙古自治区退化农田生态修复与污染治理重点实验室
[4]江苏省农业科学院，国家农业科学农业环境六合观测实验站

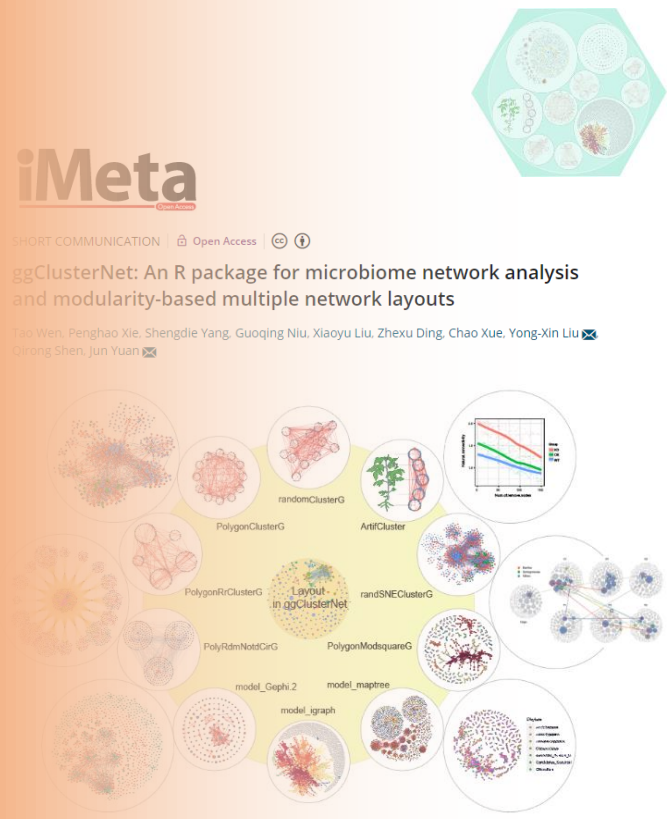
Tao Wen, Yong-Xin Liu, Lanlan Liu, Guoqing Niu, Zhexu Ding, Xinyang Teng, Jie Ma, *et al*. 2025. ggClusterNet 2: An R package for microbial co-occurrence networks and associated indicator correlation patterns. ***iMeta*** 4: e70041. https://doi.org/10.1002/imt2.70041

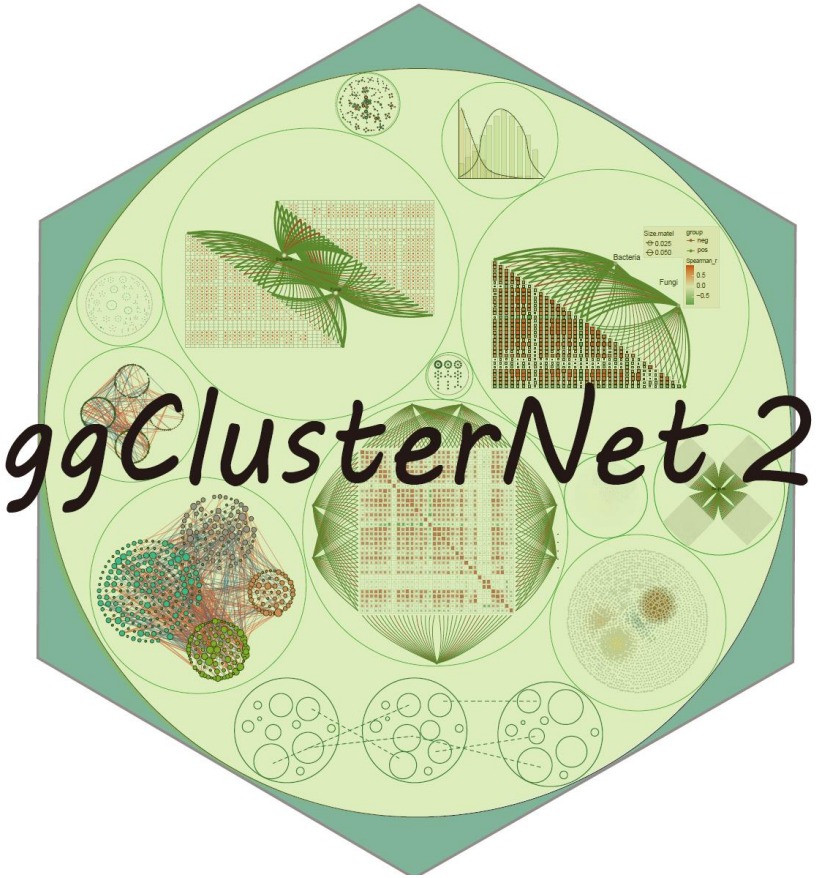
# 简介

地球上微生物往往是以复杂群落的形式存在的，其合作与竞争相互作用对生物地球化学循环、人类健康、动物营养和植物抗逆性等过程至关重要。



# 亮点



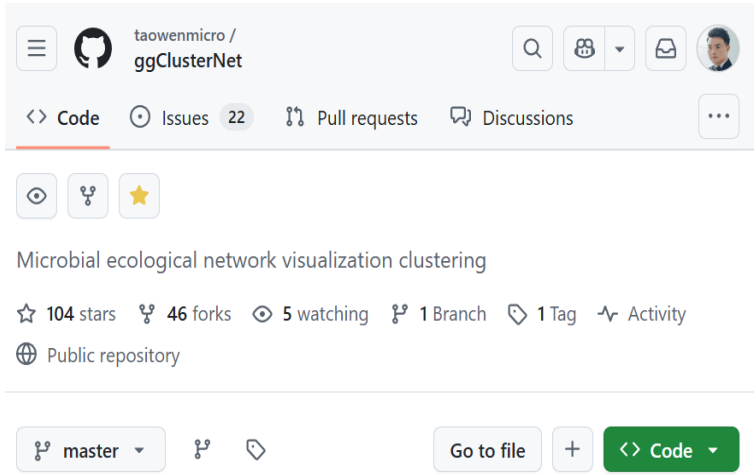




Releases 1

ggClusterNet v.2.00 (2025.2) Latest

last week

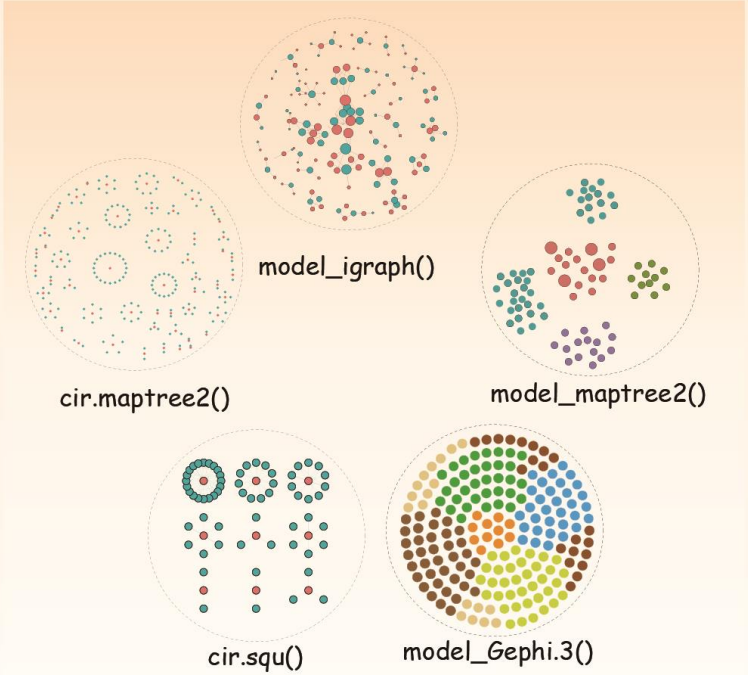
https://github.com/taowenmicro/ggClusterNet




- ggClusterNet 2 推荐并设计了一套丰富的微生物共现性网络分析流程
- ggClusterNet 2 优化了复杂设计和多类型数据下的网络分析过程和展示
- ggClusterNet 2 增加了微生物组同其他关联环境或宿主指标的优化展示
- ggClusterNet 2 增加了多种适用于跨界，多组学互作的网络可视化布局算法

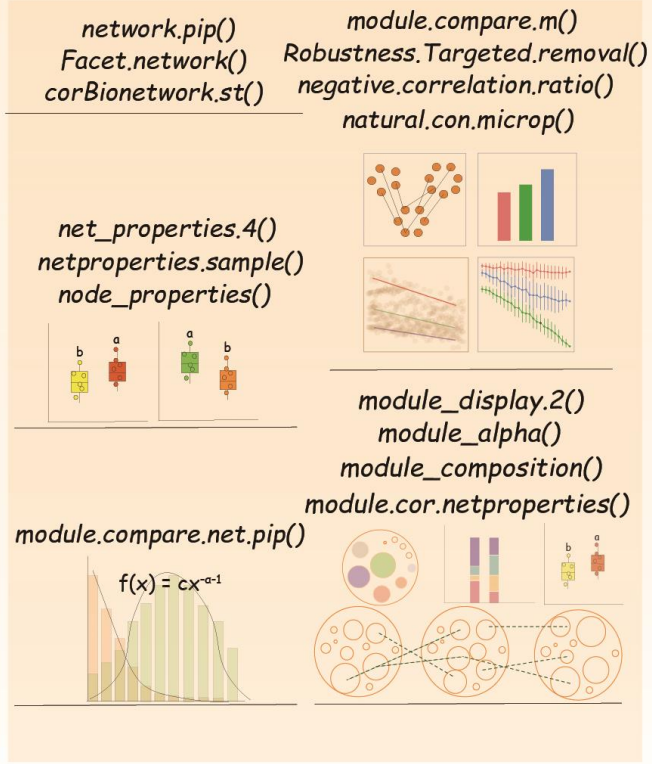
# ggClusterNet 2 概述

## Microbial Network Analysis




## Cross-domain and Multi-omics Network Analysis

1. Network Computation and Construction
2. Network Layout and Visualization
3. Network and Node Properties
4. Multi-network Comparison and Statistical Testing
5. Network Stability
6. Module Analysis and Comparison




## Microbial Association Analysis with Other Indicators

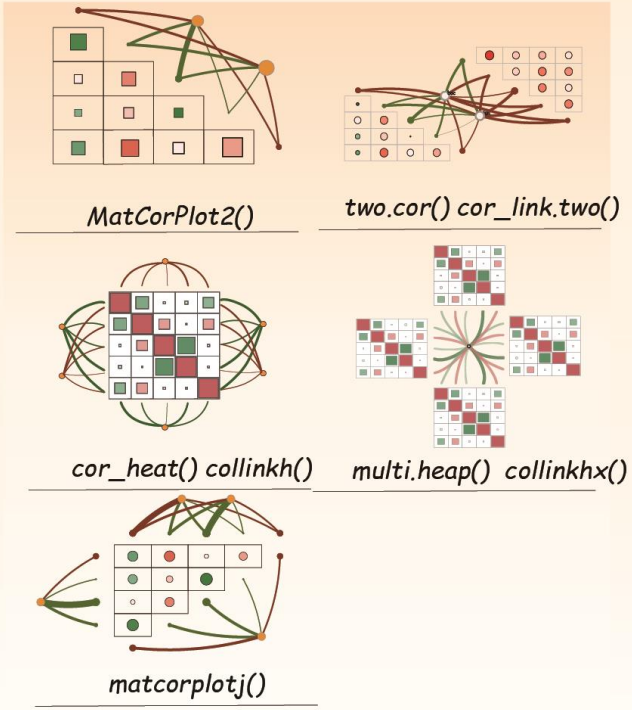
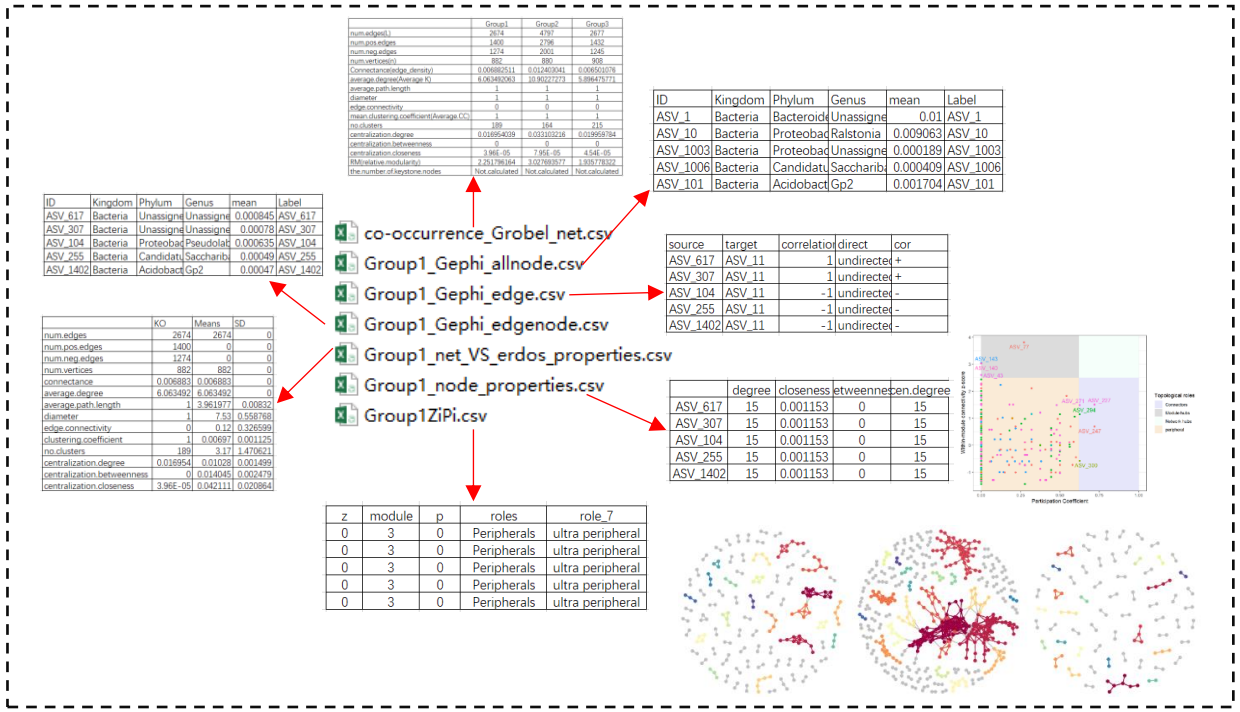


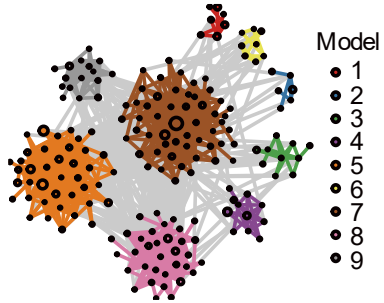

图1. 基于*ggClusterNet 2* 的微生物组网络分析

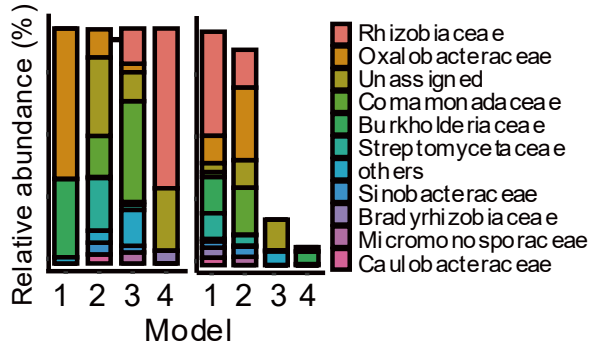
# 微生物网络的分析流程设计与分析

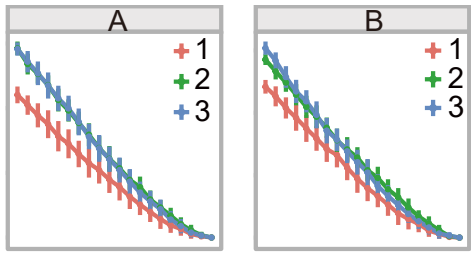
- ***network.pip()***
  - 将各类分析功能整合为标准化分析流程

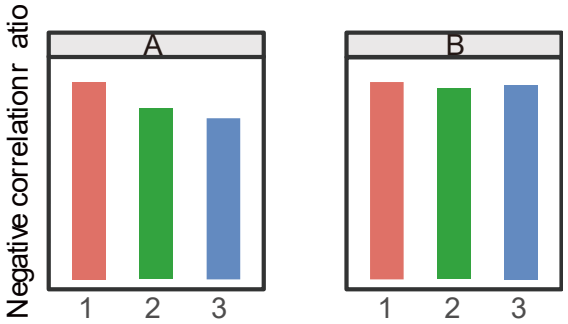
```
tab.r = network.pip(  ps = ps,
                      zipi = TRUE,
                      big = FALSE,
                      select_layout = FALSE,
                      layout_net = "model_maptree2",
                      ram.net = TRUE
                      R=100,
                      ncpus = 1  )
```

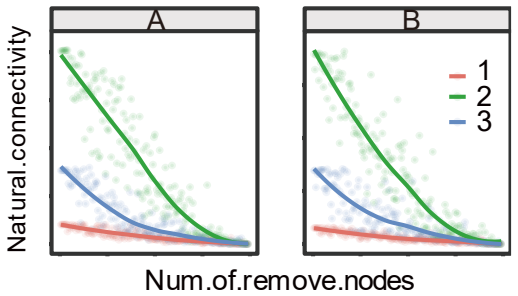


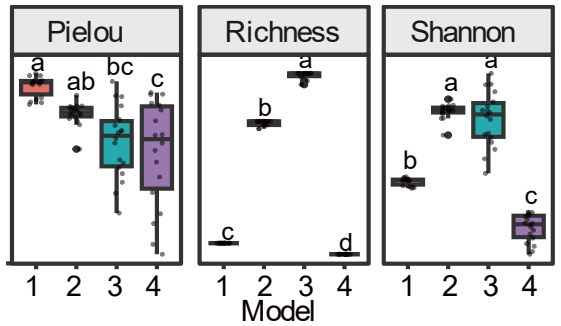



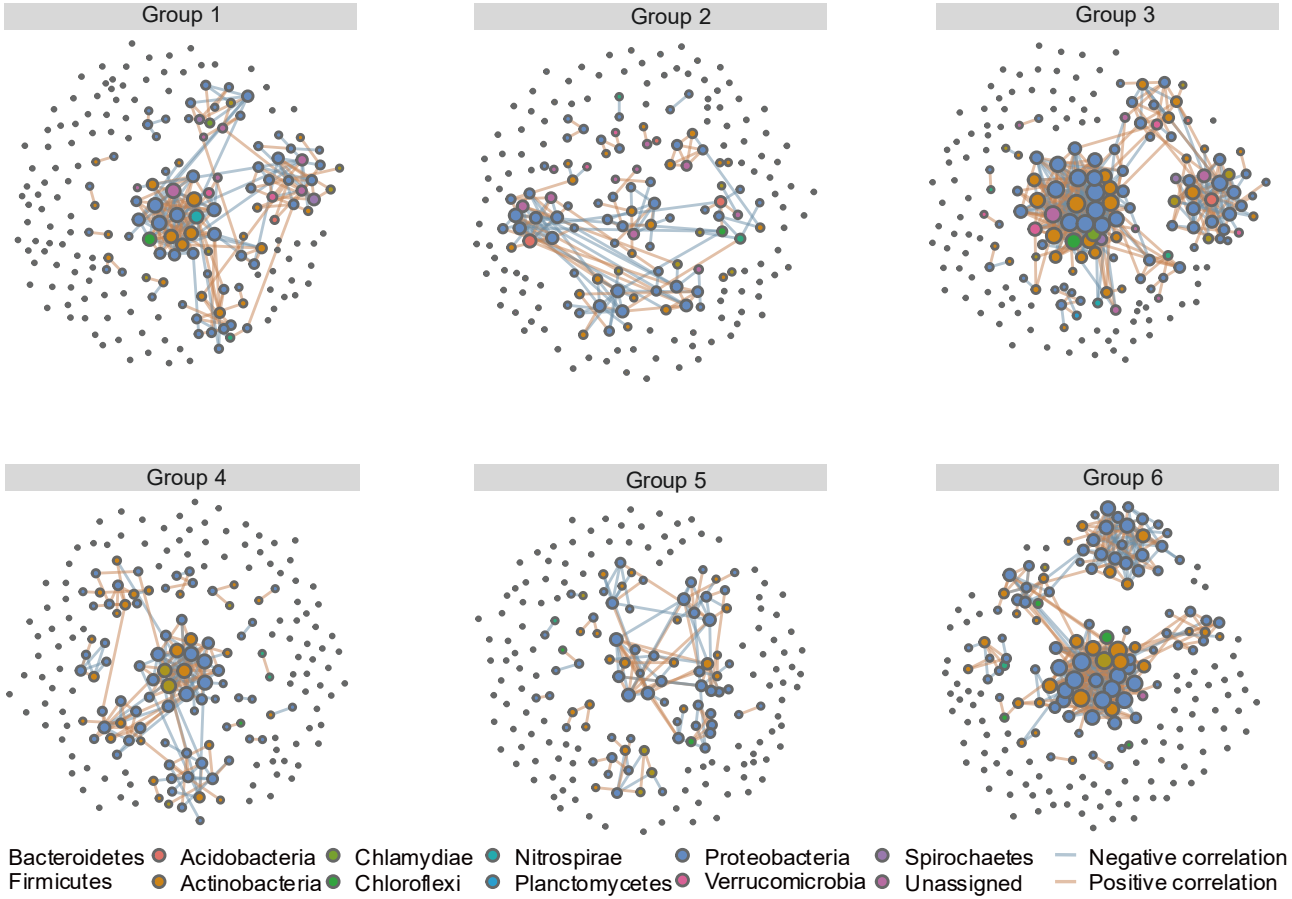



# 微生物网络的分析流程设计与分析

- ***Facet.network()***
  - 确保大批量网络图的颜色、大小与其他标尺映射统一

```
library(tidyverse)
library(ggClusterNet)
library(phyloseq)
library(igraph)
ps.st = readRDS("./ps_TS.rds")
ps.st
res = Facet.network(
  ps.st= ps.st,  g1 = "Group",g2 = "space",g3 = "time",
  ord.g1 = c("WT","KO","OE"),ord.g2 = c("B","R") ,
  ord.g3 = c("T1","T2","T3") ,order = "time", fill = "Phylum",
  size = "igraph.degree", layout_net = "model_maptree2",
  r.threshold=0.8,p.threshold=0.01,method = "spearman",
  select_layout = TRUE,clu_method = "cluster_fast_greedy",
  maxnode = 5)
p = res[[1]]
p
```



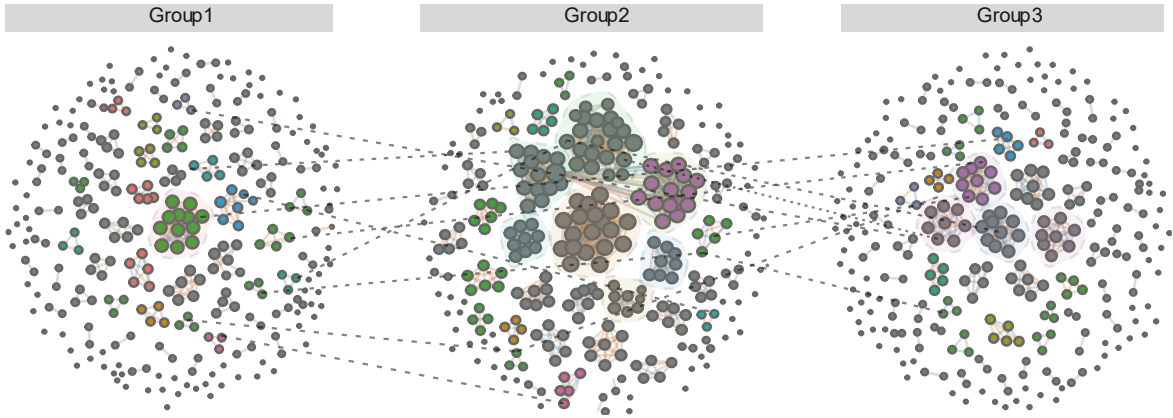




图2. 微生物组网络分析流程

# 微生物组、多组学及相关指标的跨界网络分析

跨界网络整合微生物组、多组学及关联指标，用于研究微生物-宿主互作与多组学关联。

MatCorPlot2()

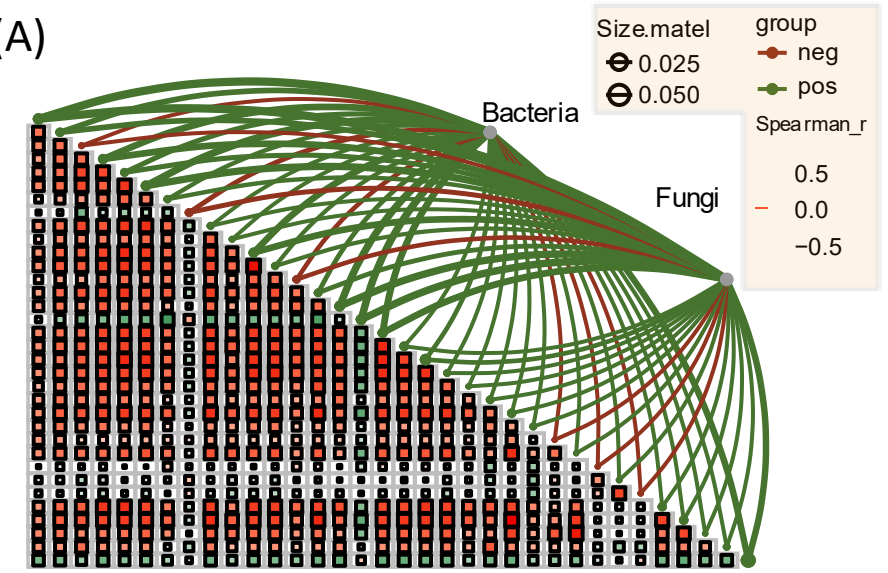
multi.heap()

matcorplotj()

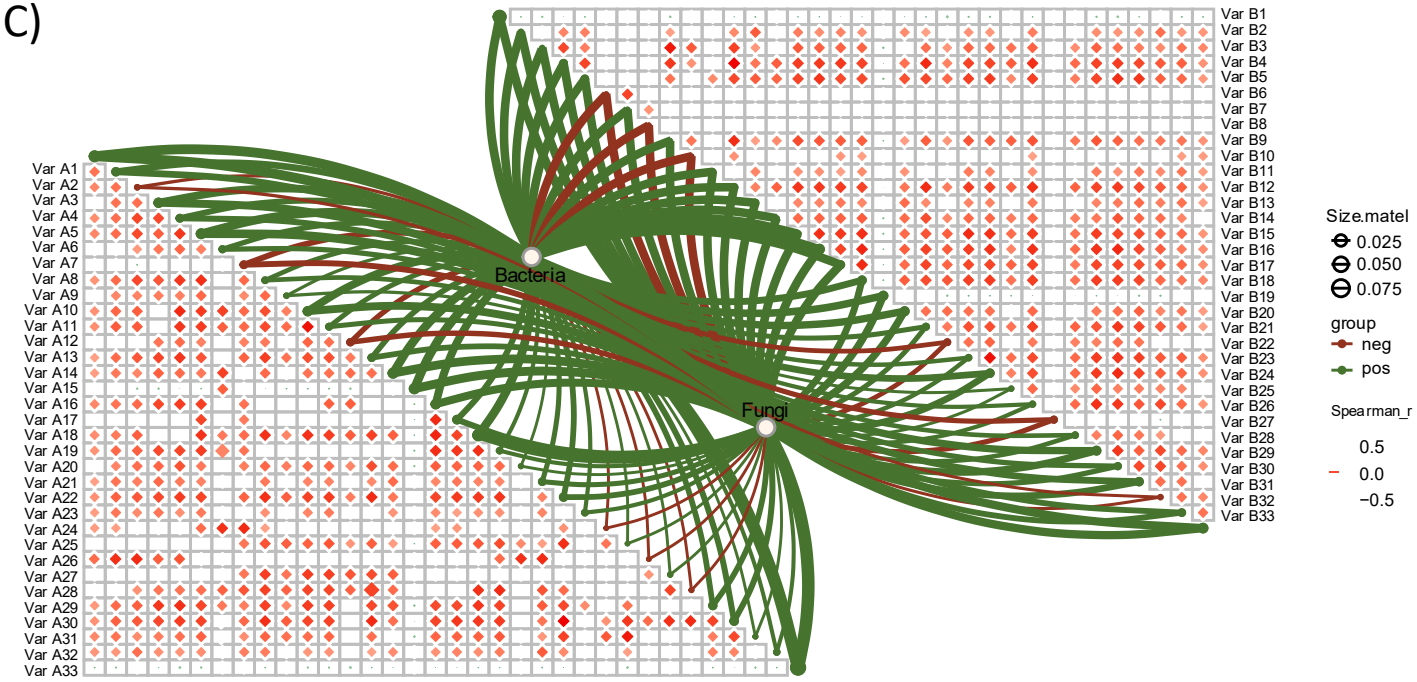
collinkhx()

two.cor()

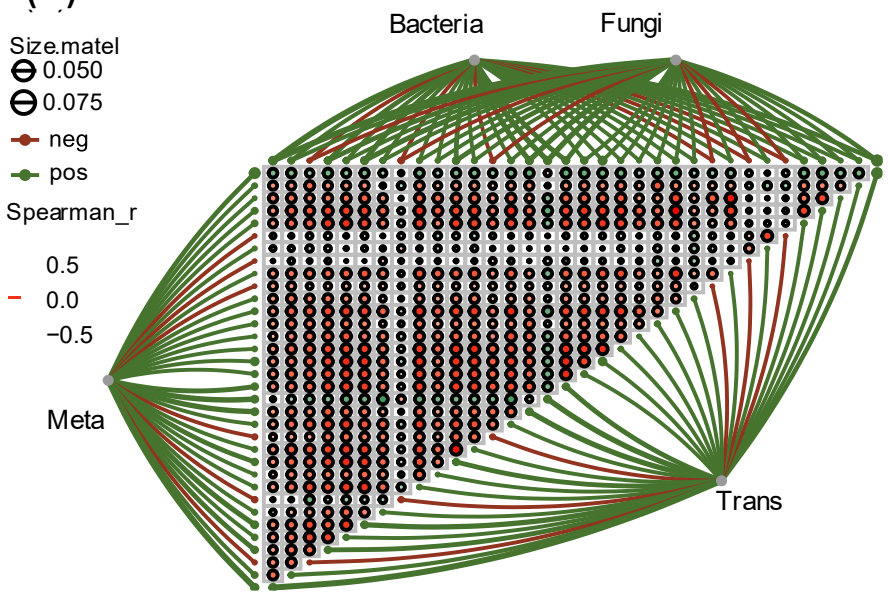
(A)




(C)




(B)



# 微生物组、多组学及相关指标的跨界网络分析

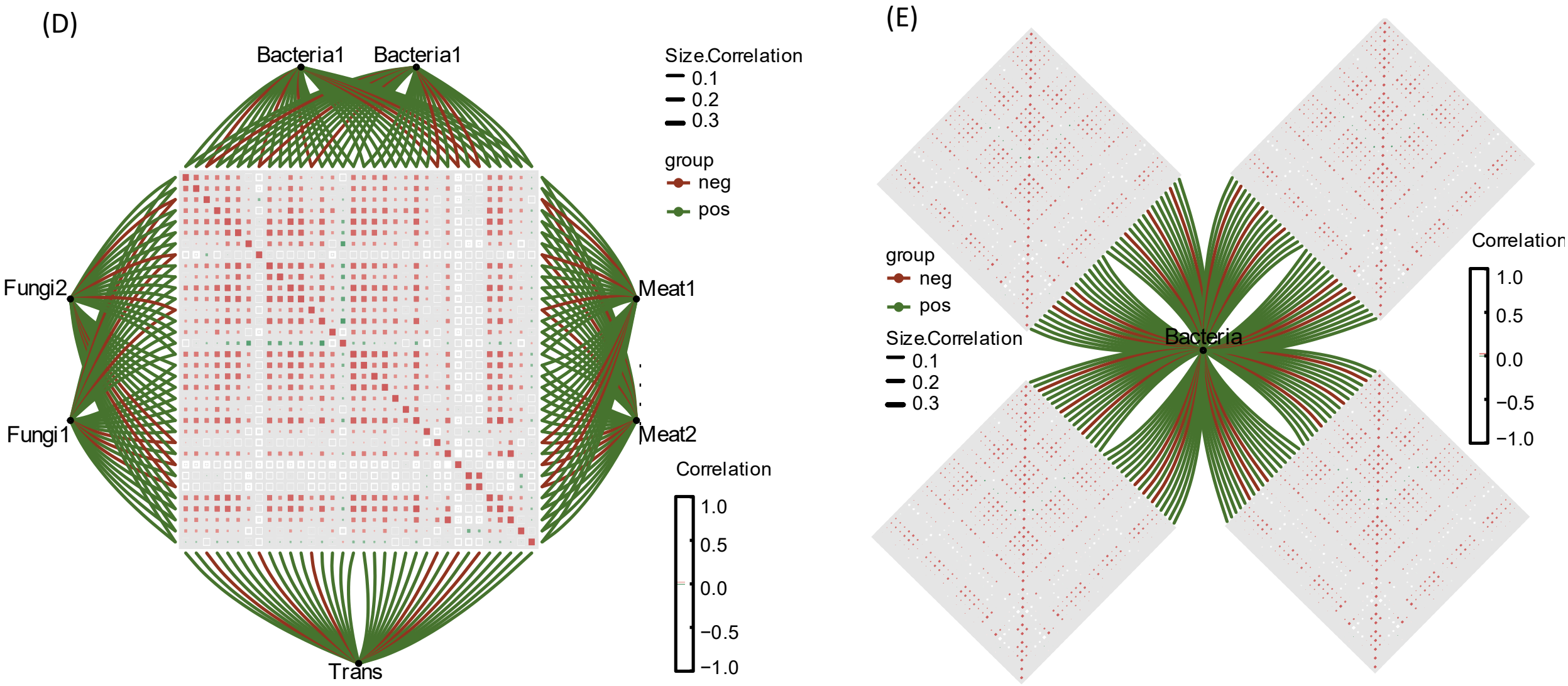



图3. 多组学数据与各类指标的相关性分析

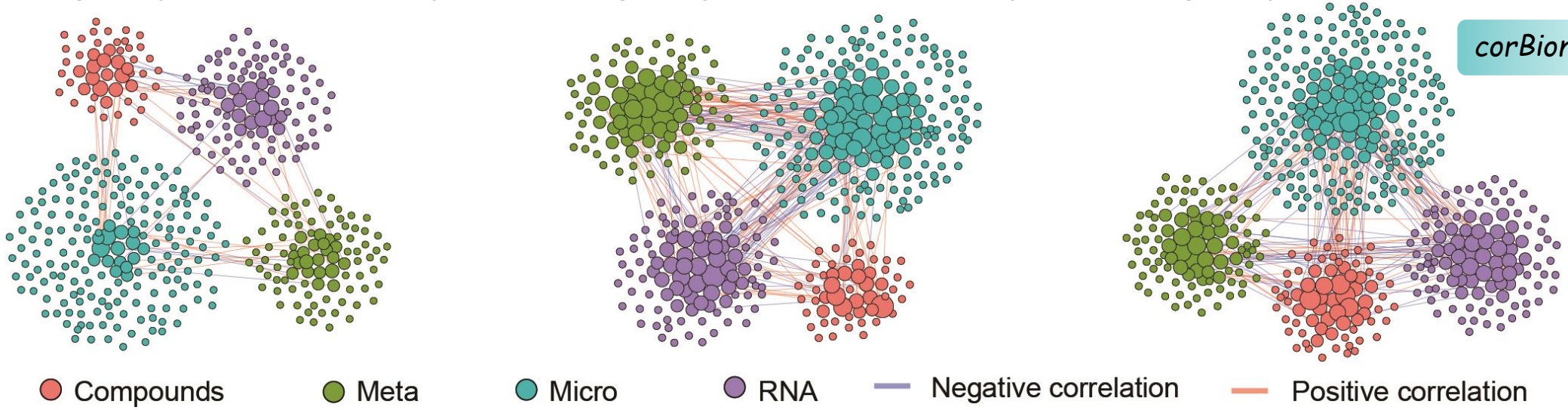
# 微生物跨域共现性网络分析与适应性可视化布局算法

(A) Example 1: (nodes: 80; links: 63)

Example 2: (nodes: 175; links: 224)

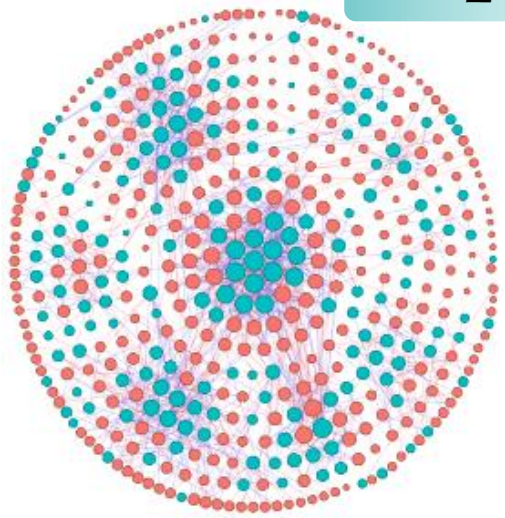
Example 3: (nodes: 146; links: 132)

corBionetwork.st()



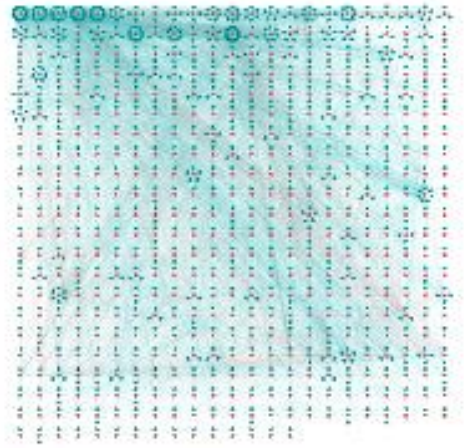

(B)

model_Gephi.2()



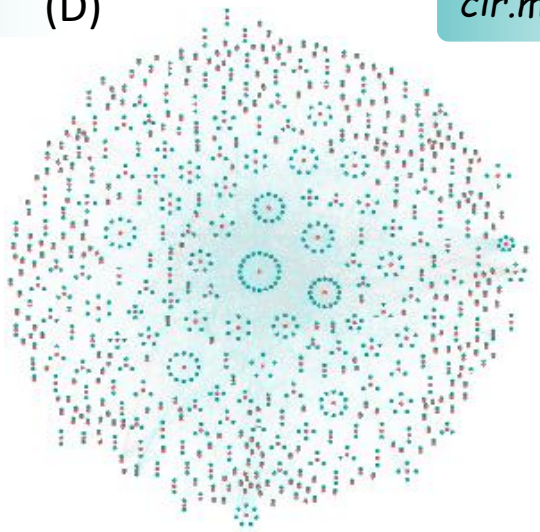
(C)

cir.squ()



(D)

cir.maptree2()



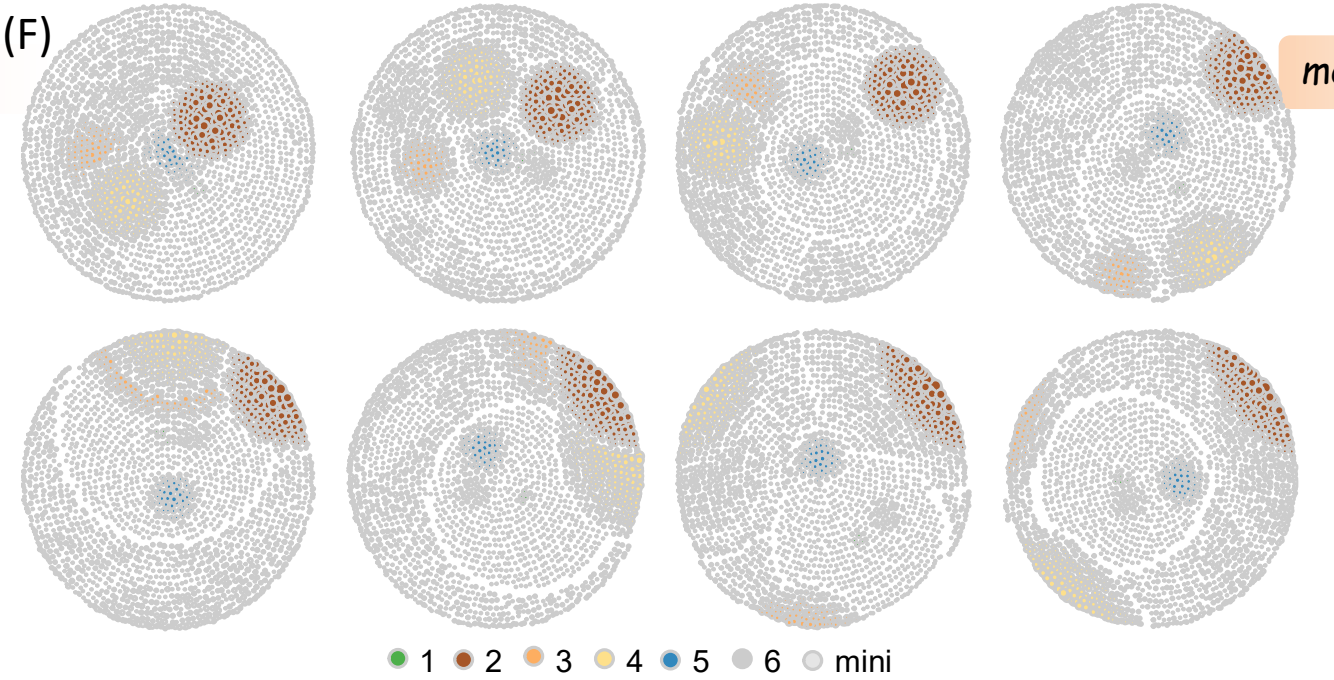
# 微生物跨域共现性网络分析与适应性可视化布局算法

(E)

model_Gephi.3()

(F)

model_Gephi.3()




(G)

PolygonClusterG()

(H)

PolygonRrClusterG()

(I)

model_filled_circle()

图4. *ggClusterNet 2* 中跨域网络分析流程更新和可视化布局算法优化升级

# 总结

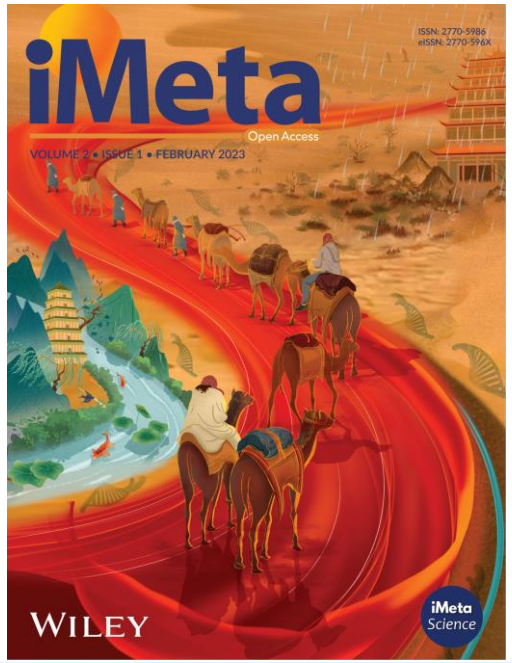
- *ggClusterNet 2* 更新全面满足了当前微生物组及相关指标网络分析的研究需求；
- 引入了一套广泛的网络分析功能，为研究者利用网络探索相关科学问题提供了更高便捷性；
- *ggClusterNet 2* 积极响应多因素、多处理、跨界互作及多组学整合研究中日益增长的网络分析需求，通过新增分析功能并优化现有功能，保持与相关研究领域快速发展的同步；
- *ggClusterNet 2*的R包为开源项目，可通过GitHub获取（https://github.com/taowenmicro/ggClusterNet）

Tao Wen, Yong-Xin Liu, Lanlan Liu, Guoqing Niu, Zhexu Ding, Xinyang Teng, Jie Ma, *et al*. 2025. ggClusterNet 2: An R package for microbial co-occurrence networks and associated indicator correlation patterns. ***iMeta*** 4: e70041. https://doi.org/10.1002/imt2.70041

# *iMeta*: 整合宏组学重新认识生命和环境科学

iMeta WILEY








"***iMeta***"(影响因子**23.8**)由威立、宏科学和千名华人科学家出版的期刊，主编刘双江和傅静远教授。
收稿范围：任何领域高影响力的研究、方法和综述，重点关注生物技术、生物信息和微生物组等;
影响力：SCIE/WOS、PubMed、Google、Scopus收录，**IF 23.8**位列JCR微生物学研究期刊全球第一;
时效性：外审平均21天；投稿至发表中位数57天;
"***iMetaOmics***" 主编赵方庆和于君教授，定位IF>10的高水平交叉学科综合期刊，欢迎投稿!

主页: http://www.imeta.science
出版社: https://wileyonlinelibrary.com/journal/imeta

office@imeta.science
imetaomics@imeta.science

投稿: https://wiley.atyponrex.com/journal/IMT2
https://wiley.atyponrex.com/journal/IMO2

宣传片

iMeta