



# ggClusterNet 2: An R package for microbial co-occurrence networks and associated indicator correlation patterns.

Tao Wen<sup>1</sup>, Yong-Xin Liu<sup>2</sup>, Lanlan Liu<sup>1</sup>, Guoqing Niu<sup>1</sup>, Zhexu Ding<sup>1</sup>, Xinyang Teng<sup>1</sup>, Jie Ma<sup>3</sup>, Ying Liu<sup>3</sup>, Shengdie Yang<sup>1</sup>, Penghao Xie<sup>1</sup>, Tianjiao Zhang<sup>1,3</sup>, Lei Wang<sup>4</sup>, Zhanyuan Lu<sup>3</sup>, Qirong Shen<sup>1</sup>, Jun Yuan<sup>1</sup>



<sup>1</sup>Jiangsu Provincial Key Lab for Organic Solid Waste Utilization, Jiangsu Collaborative Innovation Center for Solid Organic Wastes, Educational Ministry Engineering Center of Resource-saving fertilizers, Key Laboratory of Green Intelligent Fertilizer Innovation, Nanjing Agricultural University, Nanjing, China

<sup>2</sup>Genome Analysis Laboratory of the Ministry of Agriculture and Rural Affairs, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China

<sup>3</sup>Inner Mongolia Academy of Agricultural and Animal Husbandry Sciences, Key Laboratory of Black Soil Protection and Utilization (Hohhot), Ministry of Agriculture and Rural Affairs, Inner Mongolia Key Laboratory of Degradation Farmland Ecological Restoration and Pollution Control, Hohhot, China

<sup>4</sup>National Agricultural Experimental Station for Agricultural Environment, Luhe, Jiangsu Academy of Agricultural Sciences, Nanjing, China

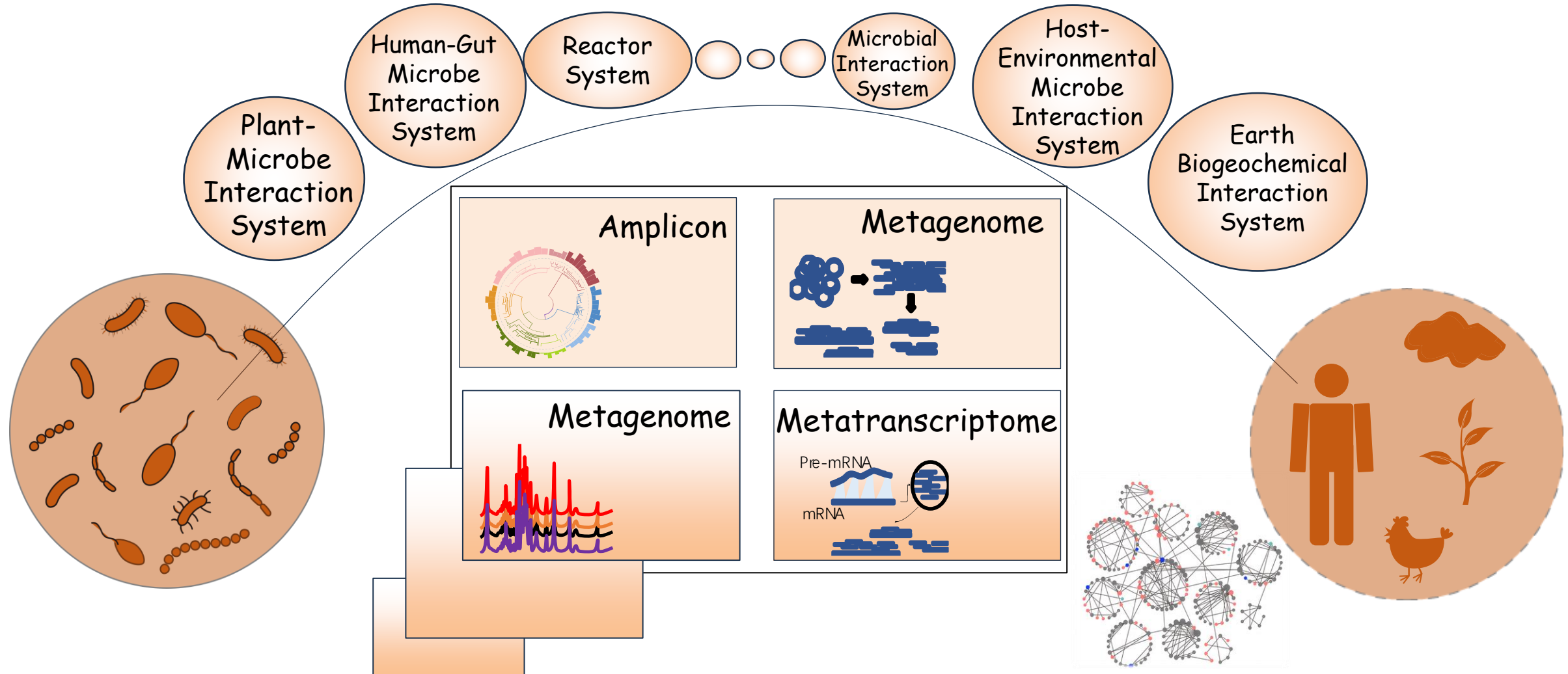
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# Introduction

Microorganisms predominantly exist in complex communities, where cooperative and competitive interactions are crucial in biogeochemical cycles, human health, animal nutrition, and plant stress resistance



# Highlights

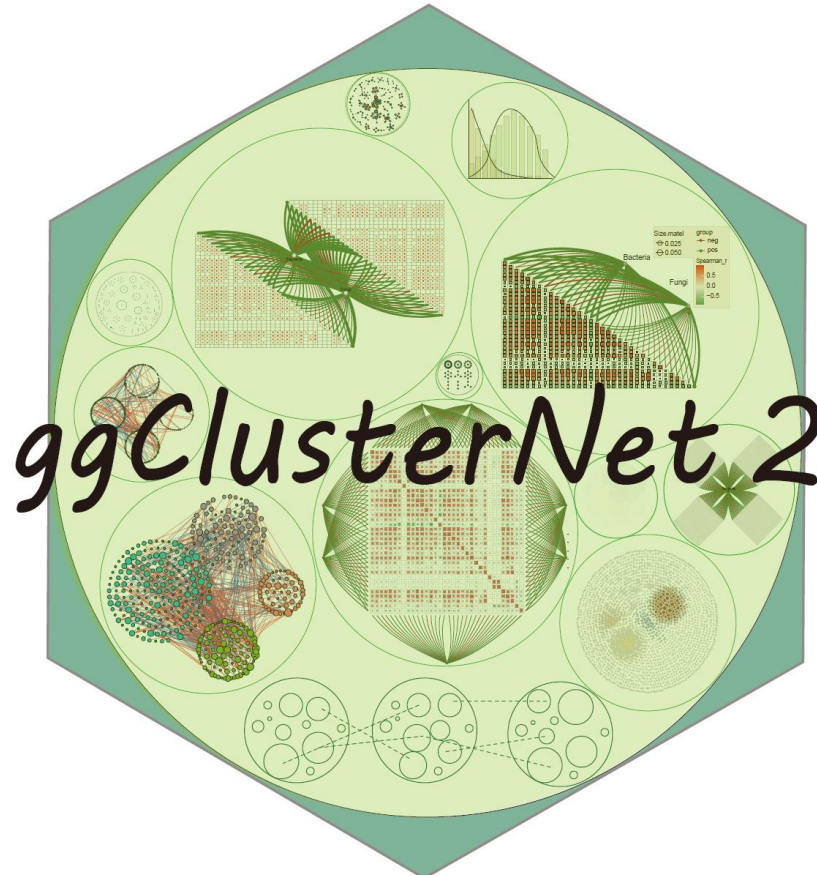
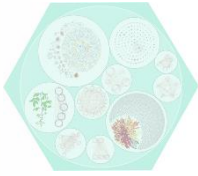


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ggClusterNet: An R package for microbiome network analysis and modularity-based multiple network layouts

Tao Wen, Penghao Xie, Shengdie Yang, Guoqing Niu, Xiaoyu Liu, Zhexu Ding, Chao Xue, Yong-Xin Liu, Qirong Shen, Jun Yuan



Releases 1

ggClusterNet v.2.00 (2025.2) **Latest**  
last week

<https://github.com/taowenmicro/ggClusterNet>



Microbial ecological network visualization clustering

104 stars 46 forks 5 watching 1 Branch 1 Tag Activity

Public repository

master Go to file + Code

Introduced a comprehensive microbial co-occurrence network analysis pipeline.

Enhanced network analysis workflow tailored for complex experimental designs and diverse data types.

Enhanced visualization of microbiomes and their correlated environmental or host-associated indicators.

Introduced various visualization algorithms for transkingdom and multi-omics interaction networks.

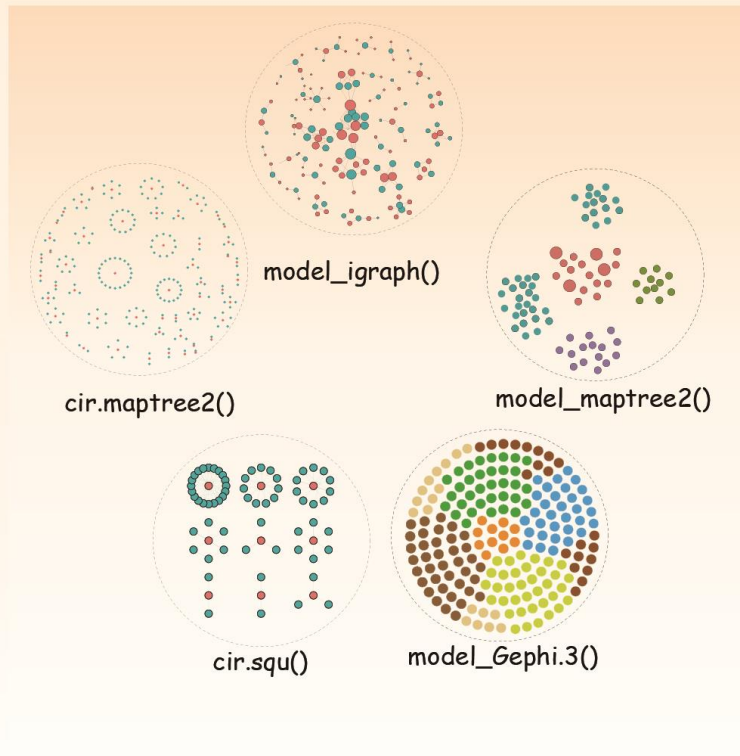


# Overview of ggClusterNet 2

## Microbial Network Analysis

## Cross-domain and Multi-omics Network Analysis

## Microbial Association Analysis with Other Indicators



### 1. Network Computation and Construction

### 2. Network Layout and Visualization

### 3. Network and Node Properties

### 4. Multi-network Comparison and Statistical Testing

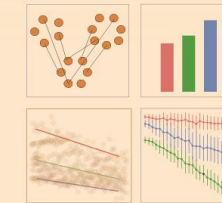
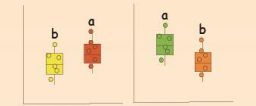
### 5. Network Stability

### 6. Module Analysis and Comparison

`network.pip()`  
`Facet.network()`  
`corBionetwork.st()`

`module.compare.m()`  
`Robustness.Targeted.removal()`  
`negative.correlation.ratio()`  
`natural.con.microp()`

`net_properties.4()`  
`netproperties.sample()`  
`node_properties()`



`module_display.2()`  
`module_alpha()`  
`module_composition()`  
`module.cor.netproperties()`

`module.compare.net.pip()`

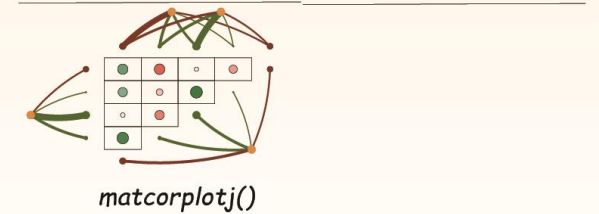
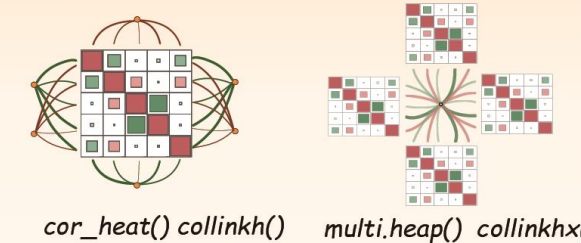
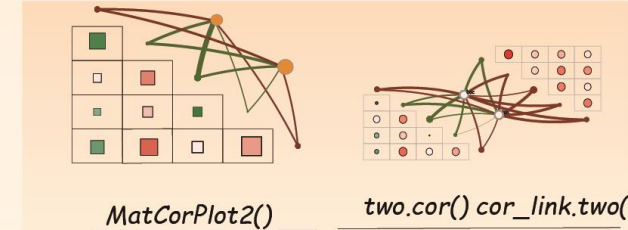
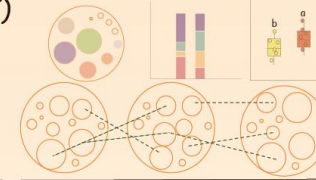
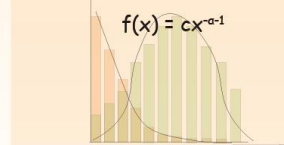


Figure 1. Microbiome network analysis using ggClusterNet 2.



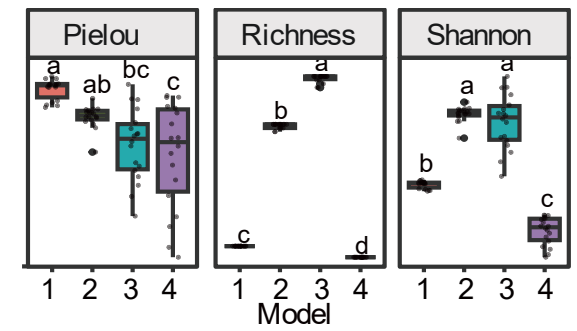
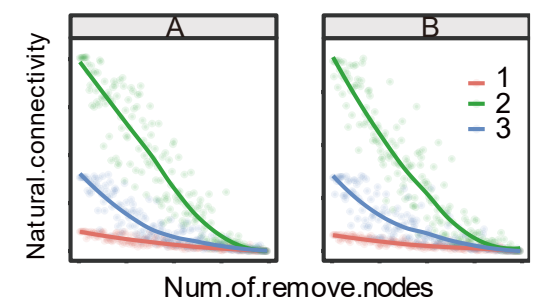
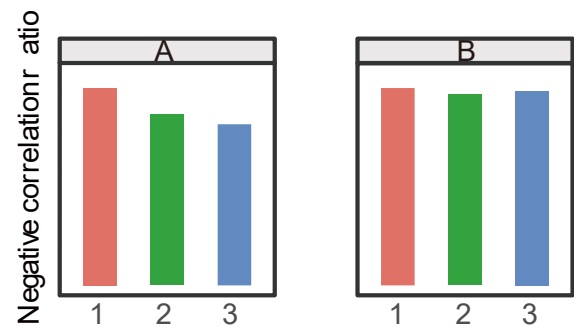
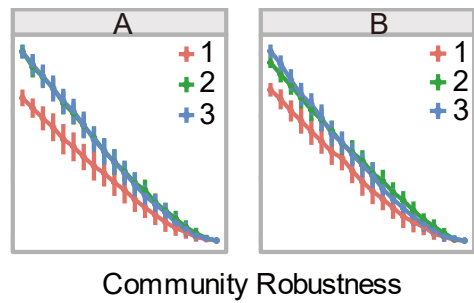
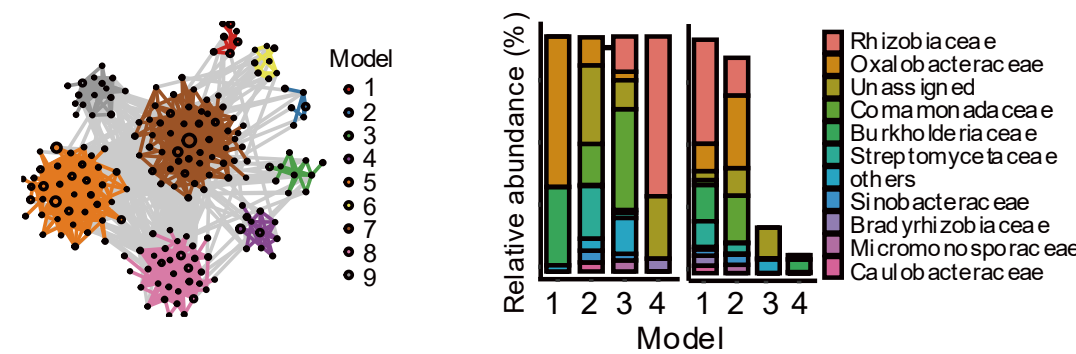
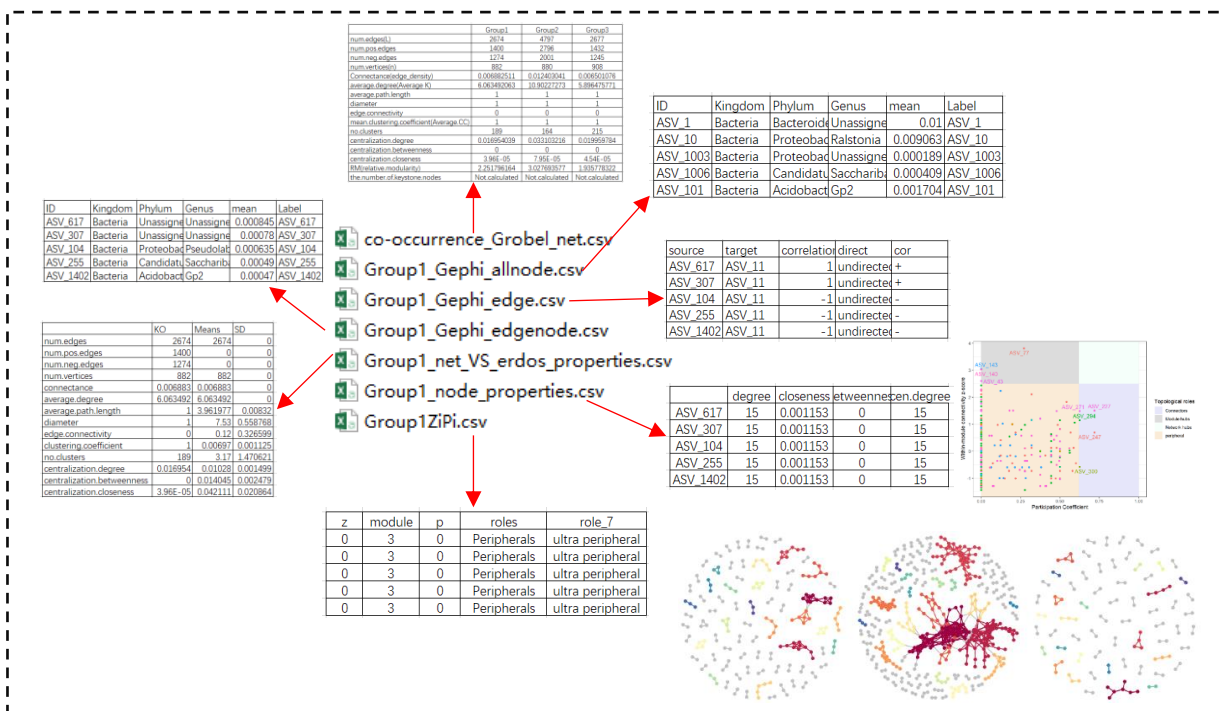
# Design and implementation of the microbial network analysis pipeline



## - network.pip()

- streamlined pipeline by sequentially executing downstream functions

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

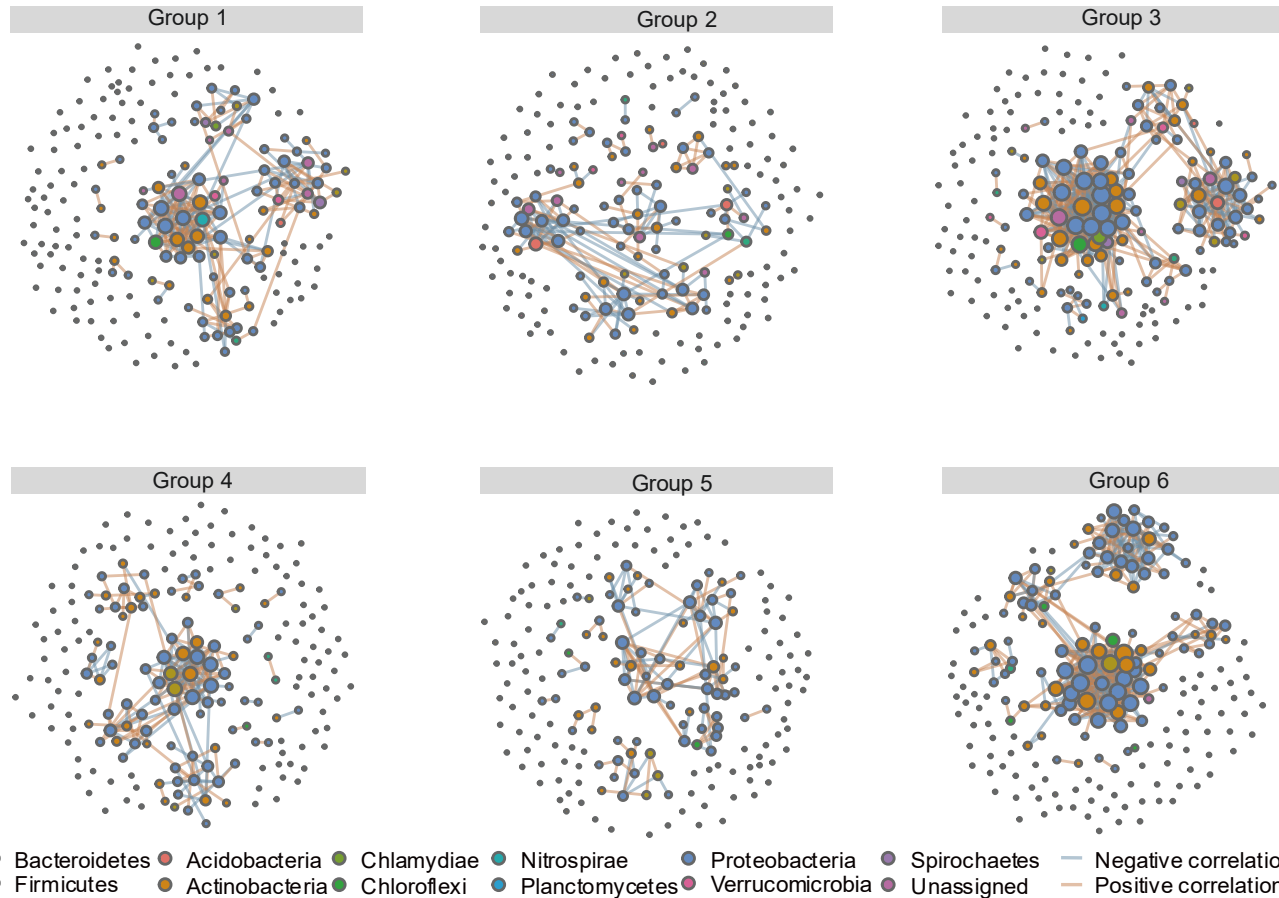




# Design and implementation of the microbial network analysis pipeline

## ★ - Facet.network()

- maintain uniform color, size, and aesthetic scaling across numerous network graphs.



```

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
  
```

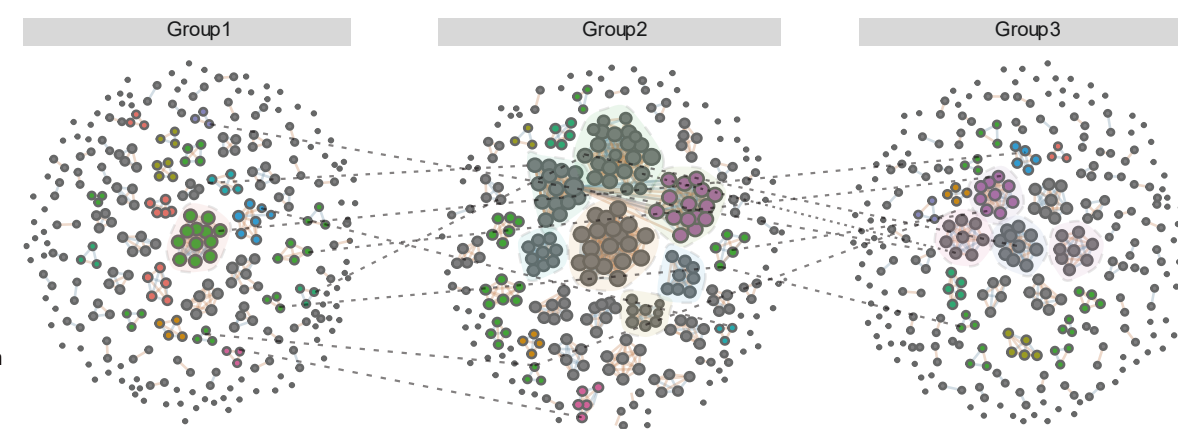


Figure 2. Proposed comprehensive microbiome network analysis pipeline

# Transkingdom network analysis of data from microbiome, multi-omics, and other correlated indicators

Transkingdom networks integrate microbiome, multi-omics, and correlated indicators to study microbial-host interactions and multi-omics correlations

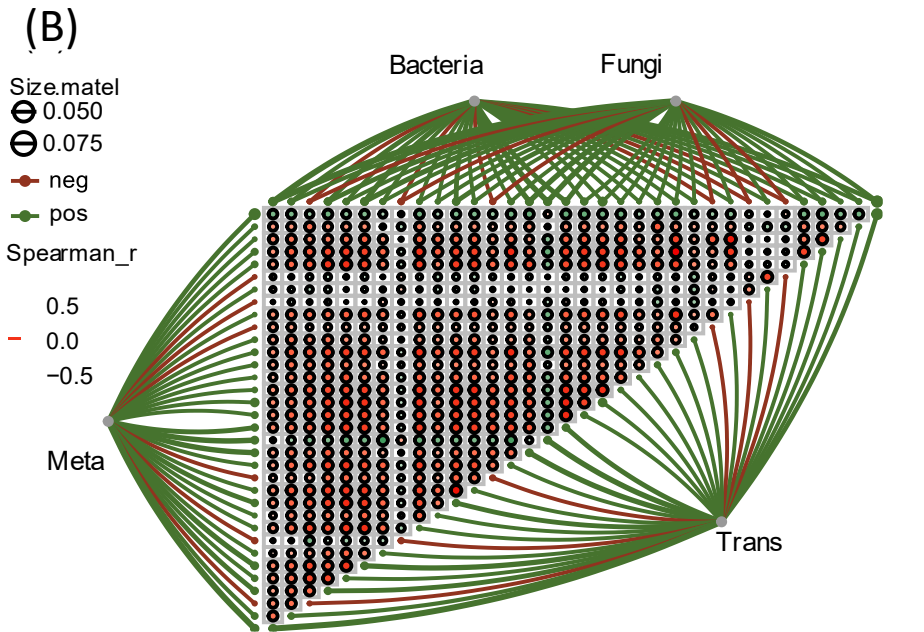
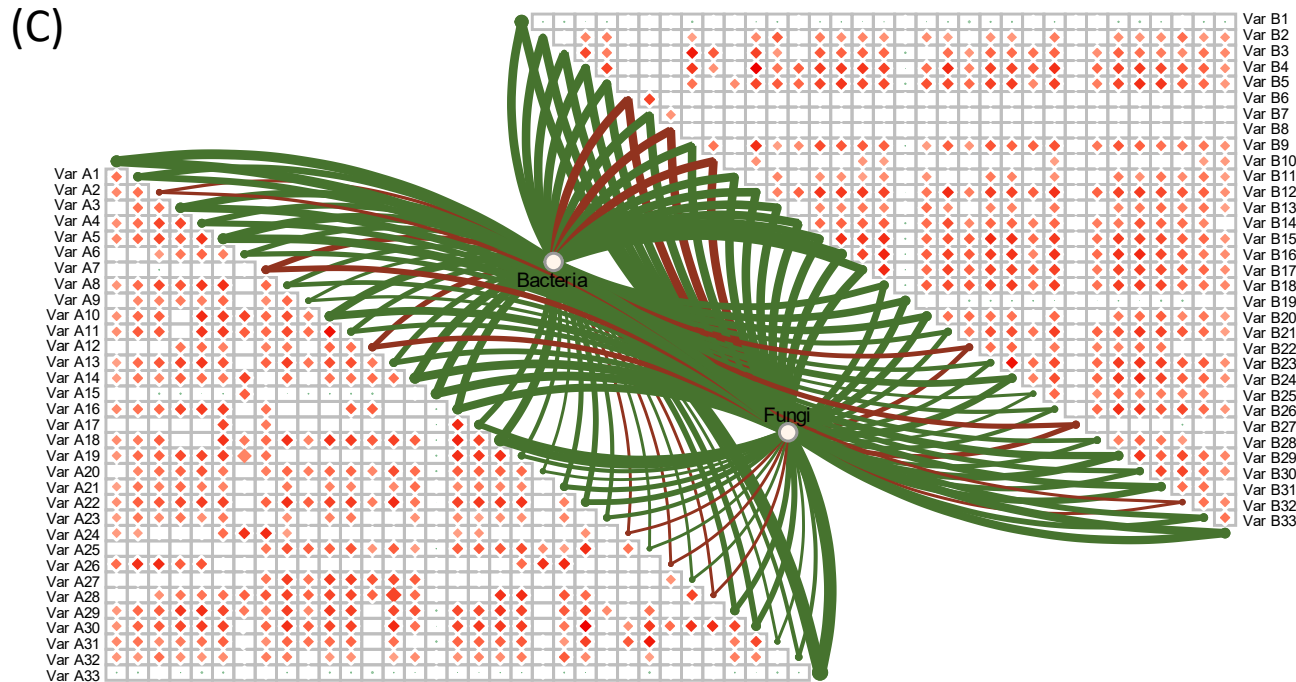
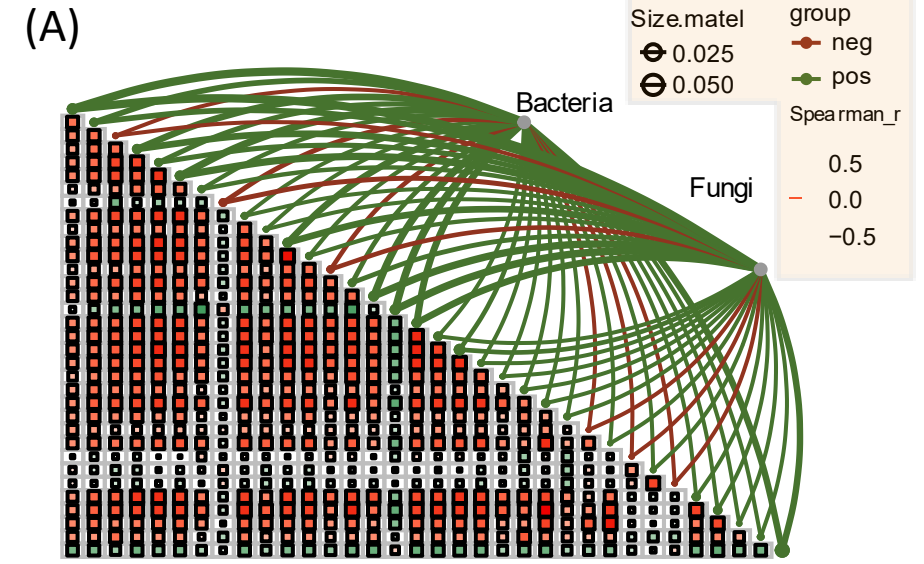
MatCorPlot2()

multi.heap()

matcorplotj()

collinkhx()

two.cor()





# Transkingdom network analysis of data from microbiome, multi-omics, and other correlated indicators

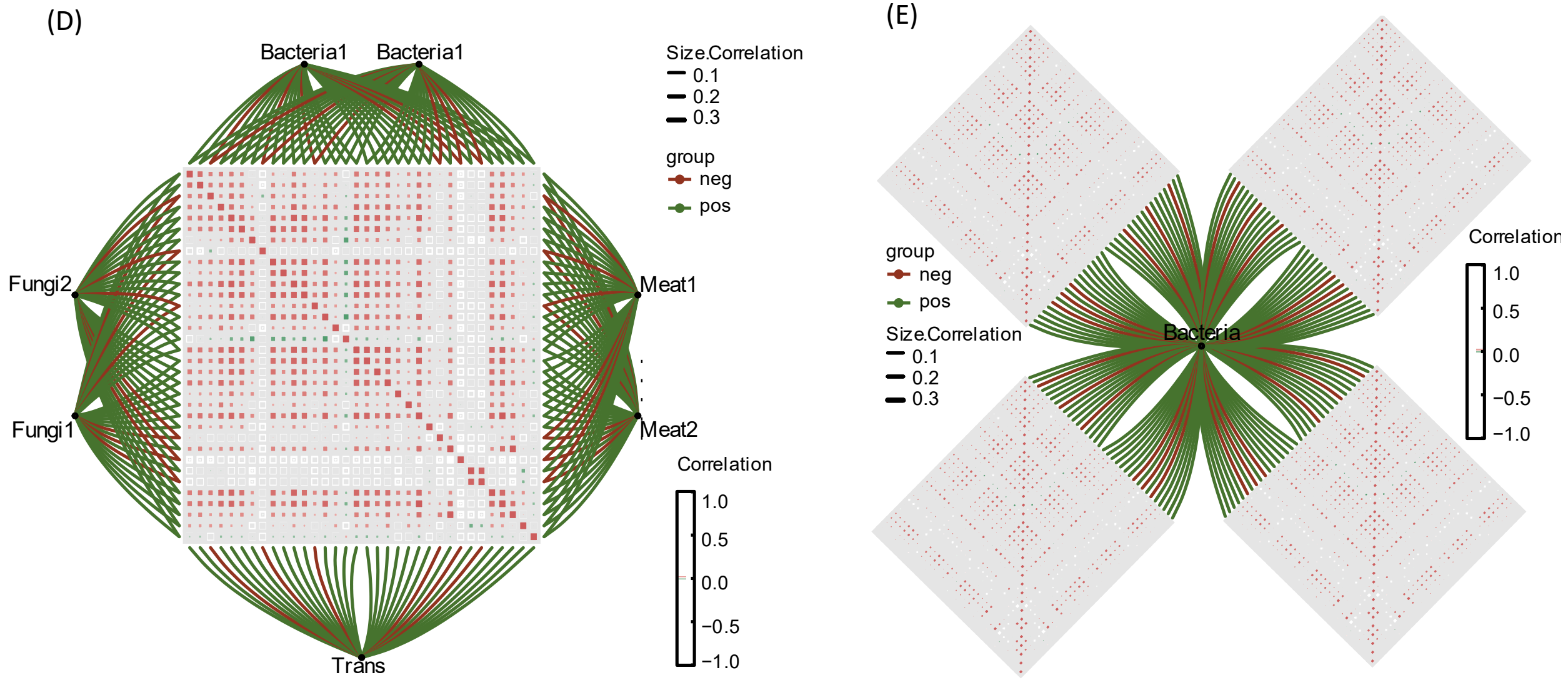
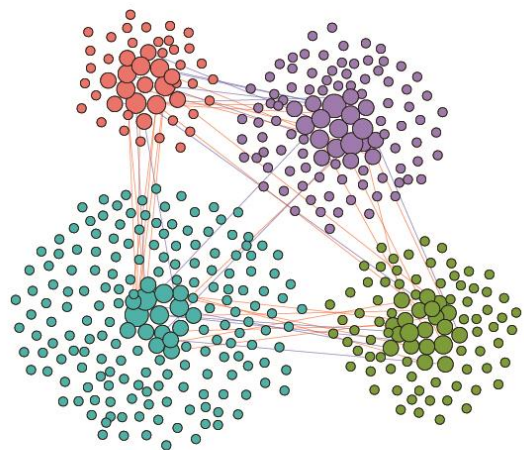


Figure 3. Correlation between multi-omics data and various indicators.

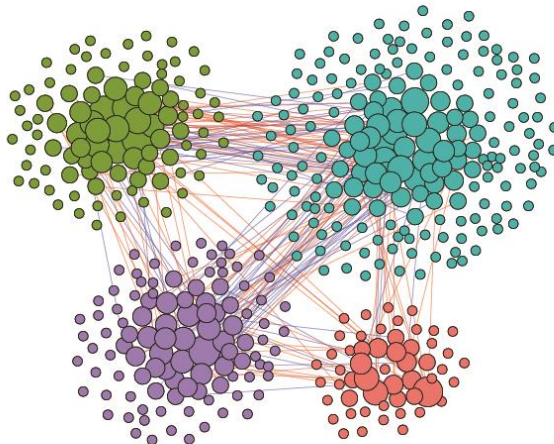


# Transkingdom microbial co-occurrence network analysis with adaptive visualization frameworks

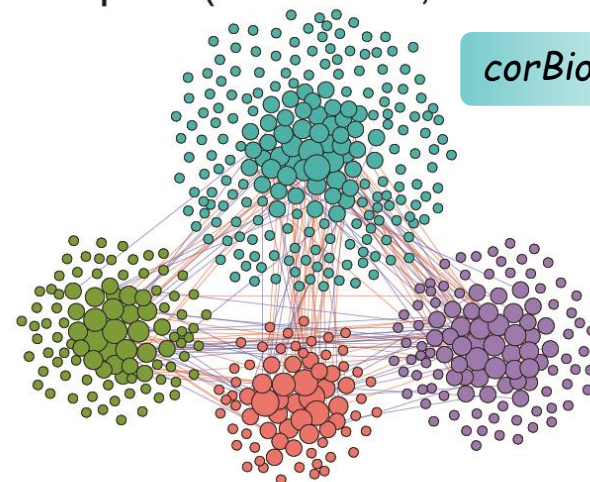
(A) Example 1: (nodes: 80; links: 63)



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



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

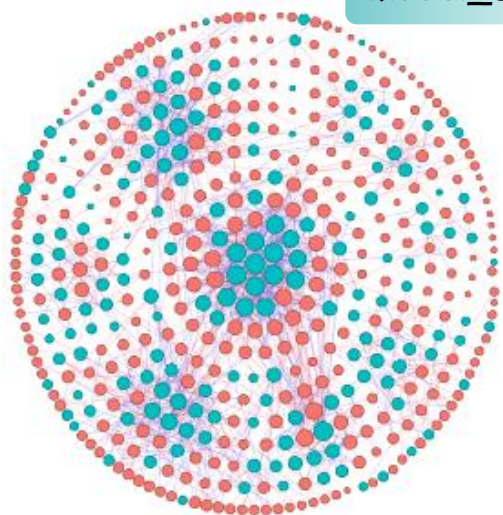


`corBionetwork.st()`

● Compounds    ● Meta    ● Micro    ● RNA    — Negative correlation    — Positive correlation

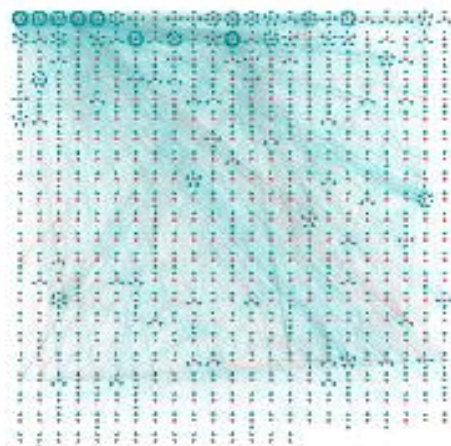
(B)

`model_Gephi.2()`



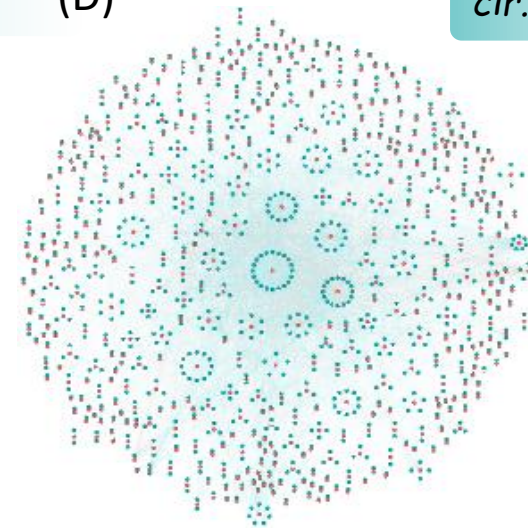
(C)

`cir.squ()`



(D)

`cir.maptree2()`



# Transkingdom microbial co-occurrence network analysis with adaptive visualization frameworks

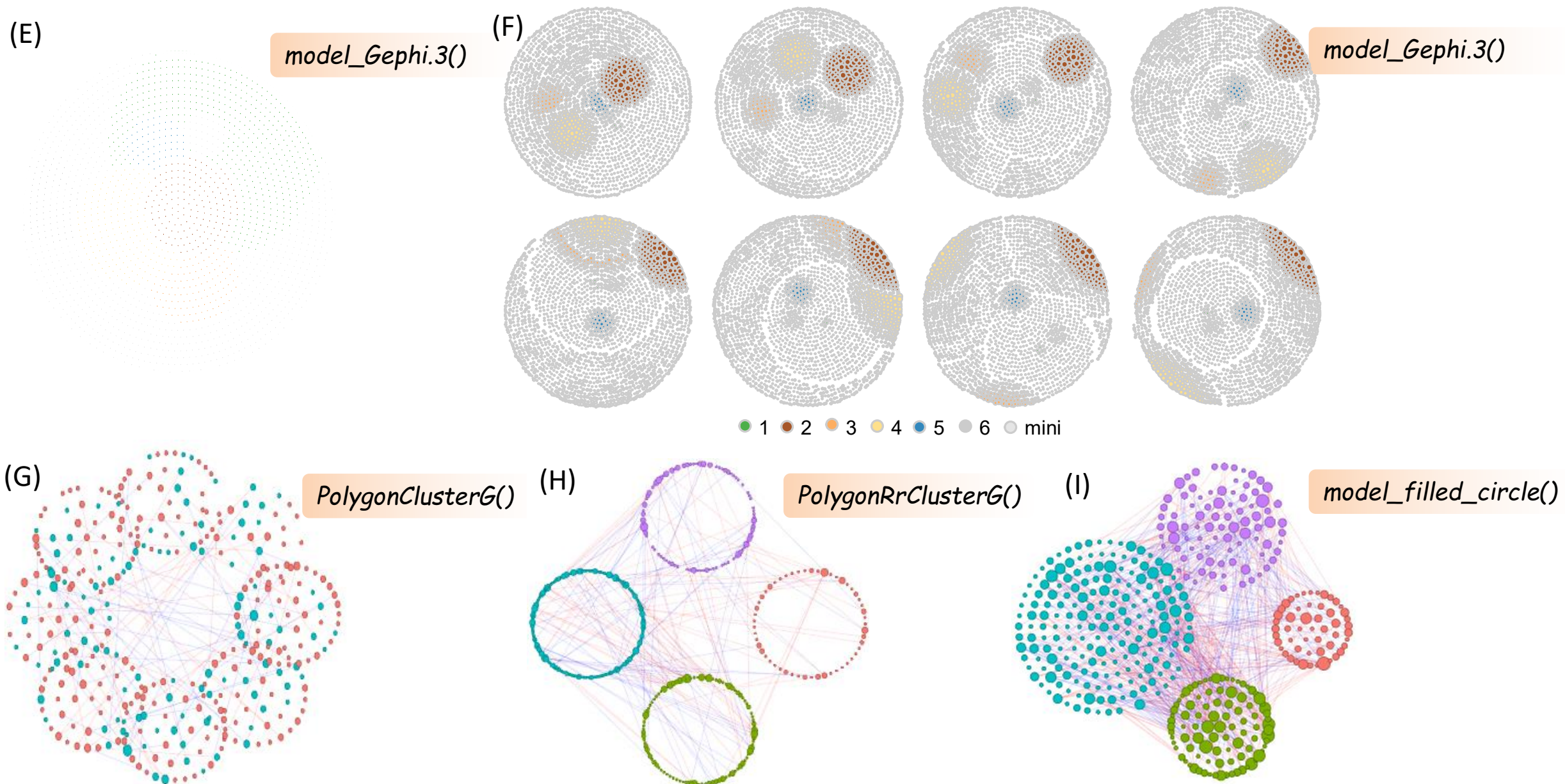


Figure 4 Latest version of ggClusterNet 2 updates the transkingdom network analysis pipeline

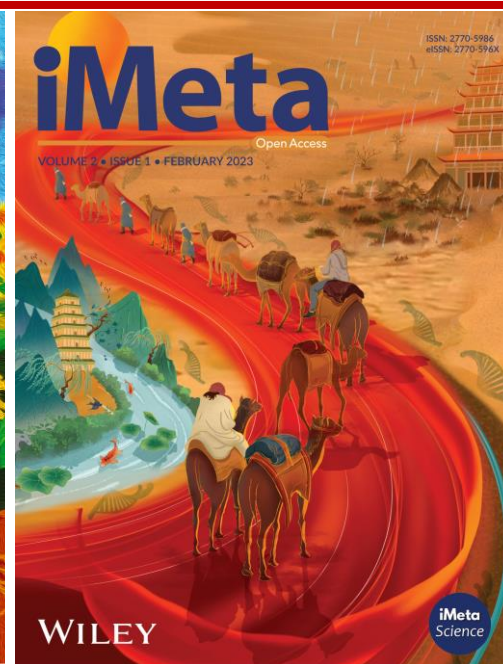


# Summary

- ❑ The ggClusterNet 2 update comprehensively addresses current research demands in microbiome and related indicator network analysis.
- ❑ It introduces an extensive set of network analysis functions, enhancing convenience for researchers using networks to explore relevant research questions.
- ❑ ggClusterNet 2 actively responds to the increasing demand for network analysis in multi-factor, multi-treatment, transkingdom interactions, and multi-omics integrative studies.
- ❑ The ggClusterNet 2 R package is open-source and available on GitHub: <https://github.com/taowenmicro/ggClusterNet>


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<https://doi.org/10.1002/imt2.70041>



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