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

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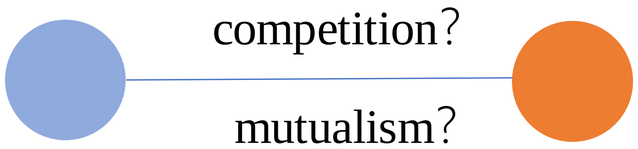
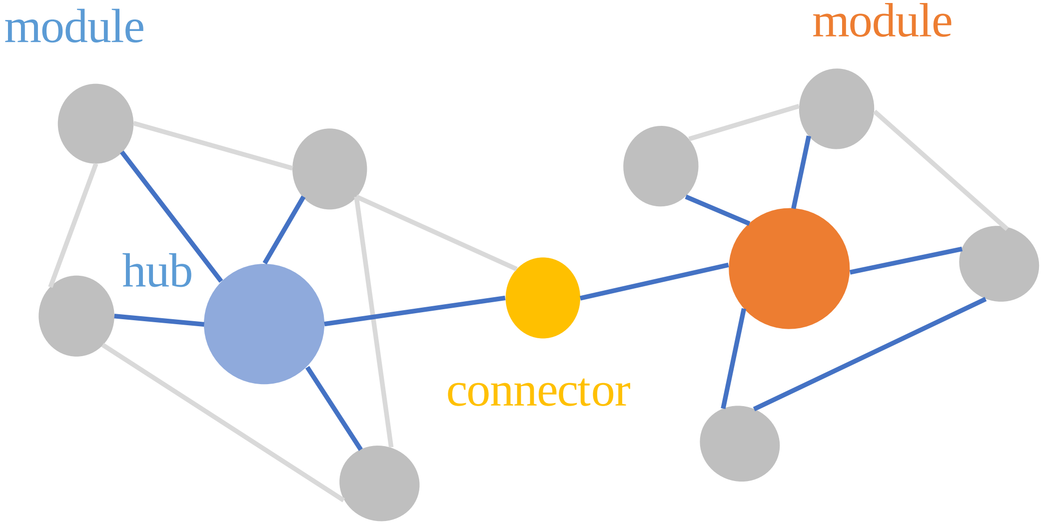
The application of network analysis on microbiome

Network analysis is able to reveal the complex inter-interactions of different bacterial species in microbial ecology study, and are important for research of gut microbiome-human/animal health, soil microbiome-plant health, environmental microbiome-Earth’s biogeochemicalcycles etc.





Explore the potential microbe interaction

Search the key hub in the microbial community

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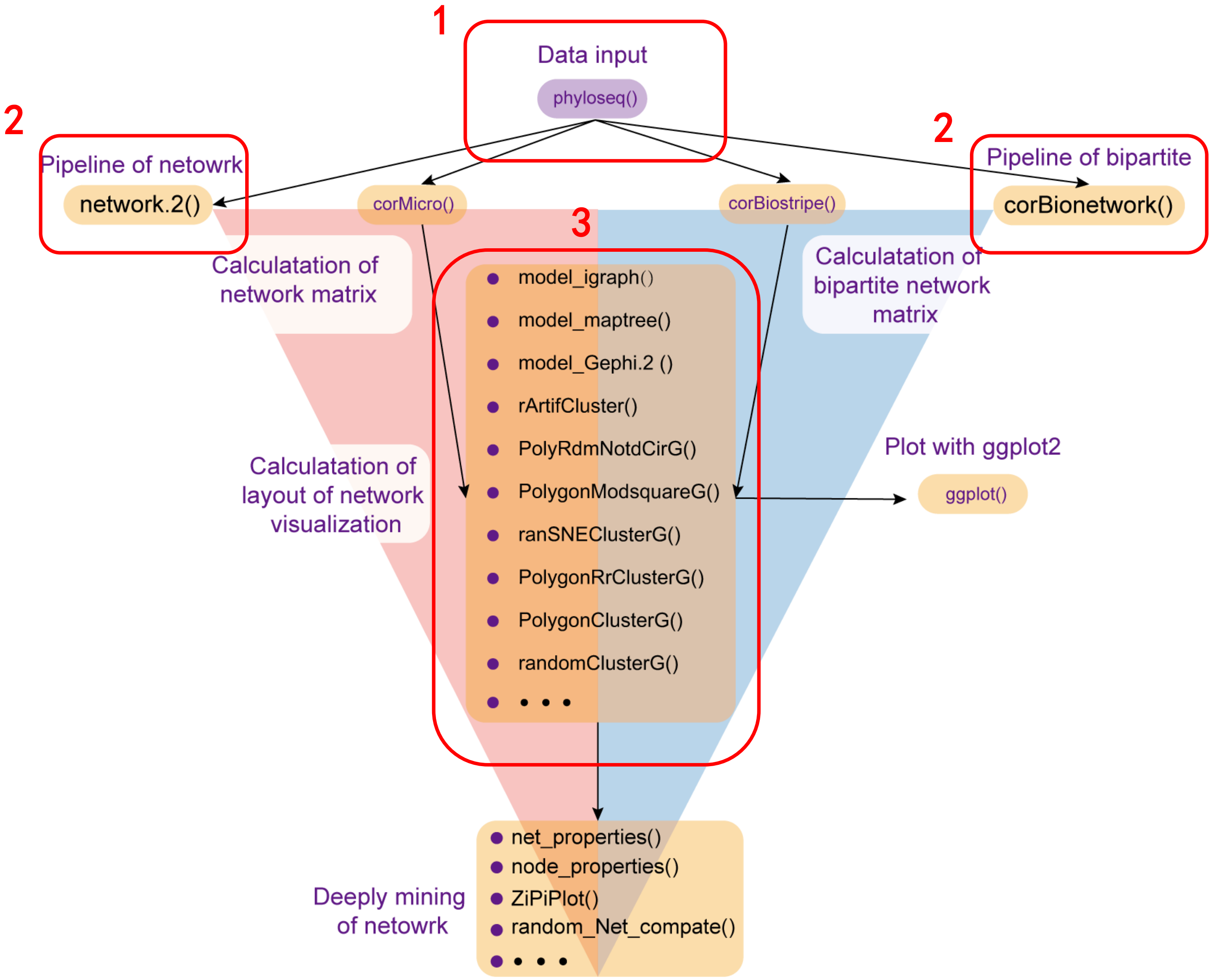
The disadvantages of network analysis tool

The tool for network analysis included Cytoscape, Gephi, R packages (igraph、ggraph、network etc)

- Ease of use
  - The tools of network analysis has tedious steps and is not easily reproducible
  - The lack of rapidly visual and mining tool for network deeply mining
  - A not enough flexible network mining and result reanalysis.
  - Large network mining and visualization with more than 1000 microbes were difficult

- Aesthetics
  - A critical challenge for the visualization of biological networks is to layout the network in a manner more familiar to a biologist.
  - mining module information in network mining and visualization
  - The lack of multigroup network visualization and comparisons

The workflow and function of ggClusterNet



ggCLusterNet consists of two major operations:

- network and bipartite network mining
- multiple network layout algorithms for visualization

- **Network mining**: network properties, calculate nodes properties, and the role of a node according to modules

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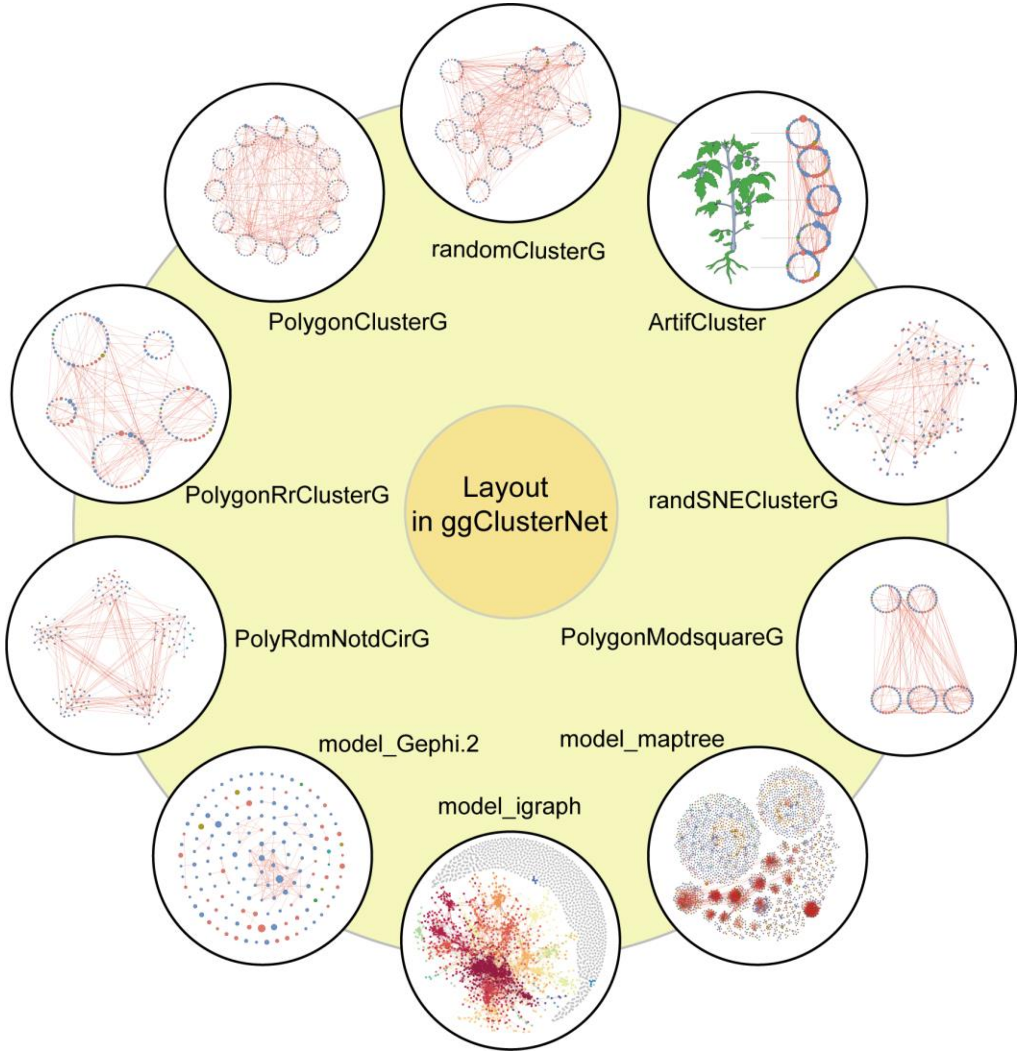
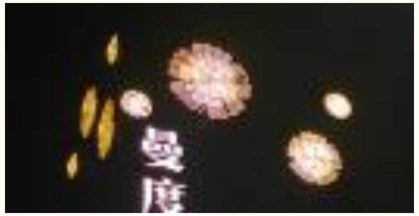
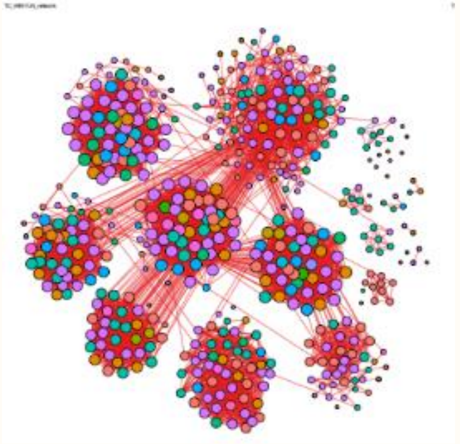
Ten layout algorithms of network visualization in ggClusterNet



The story for developing the layout algorithms of “**model_maptree**”





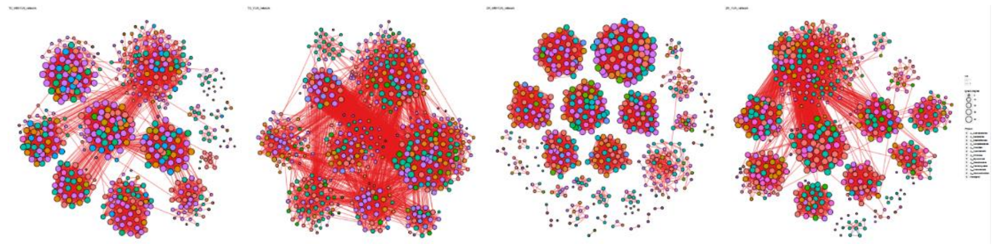
The workflow of the pipeline

① Network construction

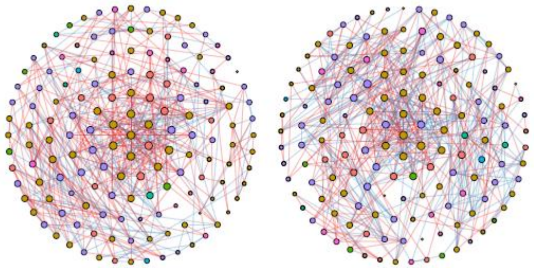
② calculatation of network properties and nodes properties

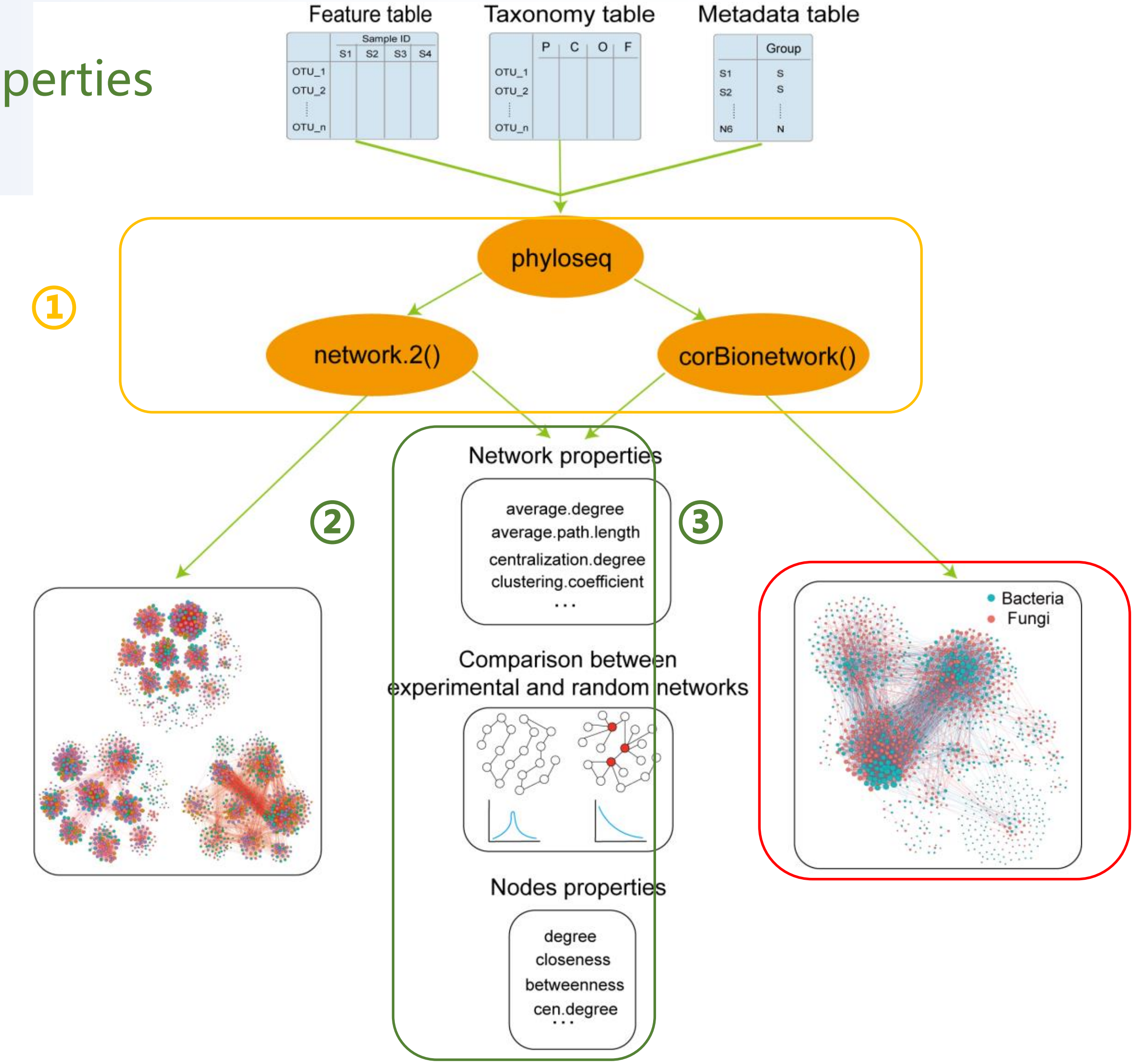
③ layout algorithms and network visualization

1 using the layout algorithms of "model_maptree" for multiple network visualization:



2 using the layout algorithms of "model_Gephi.2" for multiple network visualization:




Feature table

Taxonomy table

Metadata table

①

phyloseq

network.2()

corBionetwork()

②

③

Network properties

average.degree
average.path.length
centralization.degree
clustering.coefficient
…

Comparison between experimental and random networks

Nodes properties

degree
closeness
betweenness
cen.degree
…

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