ggNetView manual documentation

Yue Liu

2026-01-12

Contents

Chapter 1

ggNetView manual documentation

1.1 Introdution

Network analysis has been widely applied in the **life sciences, microbiology, ecology, and agronomy** to quantify interactions among **genes, proteins, metabolites, microorganisms, and environmental factors**. These interactions collectively shape the functioning of biological and ecological systems. Despite its broad adoption, existing tools often face limitations in flexibility, customization, reproducibility, and the generation of publication-ready figures.

To address these challenges, **ggNetView** was developed as an **R package** that integrates **ggplot2, ggraph, and tidygraph** within the **Grammar of Graphics framework**, enabling fully reproducible and highly customizable network visualizations. The package provides deterministic layout algorithms, comprehensive topological analyses, modular coloring schemes, hierarchical annotations, and consistent theming, ensuring standardized and interpretable graphical output.

Although initially designed for applications in **soil science and microbial ecology**, **ggNetView** is broadly applicable to network analyses in `molecular biology`, including **WGCNA and protein–protein interaction (PPI) networks**. By lowering technical barriers in network construction and visualization, **ggNetView** enables researchers across disciplines to efficiently produce reproducible, publication-quality network figures.

1.2   Installation

First, install the required dependencies

```r
# install.packages("BiocManager")
BiocManager::install("WGCNA")

# install.packages("remotes")
remotes::install_github("alserglab/mascarade")
remotes::install_github("zdk123/SpiecEasi")
```

and then install ggNetView.

```r
# install.packages("devtools")
devtools::install_github("Jiawang1209/ggNetView")

# install.packages("pak")
pak::pak("Jiawang1209/ggNetView")
```

1.3   Citation

If you use ggNetView in your research, please cite:

```r
Yue Liu, Chao Wang (2025). ggNetView: An R package for complex biological and ecologica
https://github.com/Jiawang1209/ggNetView
```

1.4   Source Code

The source code for ggNetView is available in the ggNetView repository.

https://github.com/Jiawang1209/ggNetView

1.5   Contact

- Email: Jiawang1209@163.com
- Github: https://github.com/Jiawang1209/ggNetView
- ggNetView-manual: https://jiawang1209.github.io/ggNetView-manual/

Chapter 2

Build graph object

Basic workflow of **ggNetView**

1. Build a **graph object**
2. Understand and manipulate the **graph object**
3. Visualize the network using **layout algorithms**
4. Retrieve **topology** of network

Load R Package

```r
library(tidyverse)
library(ggNetView)
```

2.1 Build graph from matrix

Example data

```r
# Access built-in example datasets in ggNetView

# Raw ASV or OTU table
data("otu_tab")
dim(otu_tab)
```

```
## [1] 2859    18
```

```
otu_tab[1:5, 1:5]
```

```
##        KO1  KO2  KO3  KO4  KO5
## ASV_1 1113 1968  816 1372 1062
## ASV_2 1922 1227 2355 2218 2885
## ASV_3  568  460  899  902 1226
## ASV_4 1433  400  535  759 1287
## ASV_6  882  673  819  888 1475
```

```
# Rarefied ASV or OTU table
data("otu_rare")
dim(otu_rare)
```

```
## [1] 2859    18
```

```
otu_rare[1:5, 1:5]
```

```
##        KO1  KO2  KO3  KO4  KO5
## ASV_1  992 1636  604 1084  806
## ASV_2 1725 1018 1814 1743 2196
## ASV_3  520  389  687  701  932
## ASV_4 1280  328  425  580 1004
## ASV_6  794  557  633  706 1142
```

```
# Relative abundance table of rarefied ASVs or OTUs
data("otu_rare_relative")
dim(otu_rare_relative)
```

```
## [1] 2859    18
```

```
otu_rare_relative[1:5, 1:5]
```

```
##               KO1        KO2        KO3        KO4        KO5
## ASV_1 0.03306667 0.05453333 0.02013333 0.03613333 0.02686667
## ASV_2 0.05750000 0.03393333 0.06046667 0.05810000 0.07320000
## ASV_3 0.01733333 0.01296667 0.02290000 0.02336667 0.03106667
## ASV_4 0.04266667 0.01093333 0.01416667 0.01933333 0.03346667
## ASV_6 0.02646667 0.01856667 0.02110000 0.02353333 0.03806667
```

```
# Taxonomic annotation table of ASVs or OTUs
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859    8
```

```
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##    OTUID  Kingdom  Phylum          Class          Order
##    <chr>  <chr>    <chr>           <chr>          <chr>
## 1 ASV_2   Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 2 ASV_3   Bacteria Verrucomicrobia Spartobacteria Unassigned
## 3 ASV_31  Bacteria Actinobacteria  Actinobacteria Actinomycetales
## 4 ASV_27  Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 5 ASV_9   Bacteria Unassigned      Unassigned     Unassigned
```

Build graph object

```
graph_obj <- build_graph_from_mat(
  mat = otu_rare_relative,
  transfrom.method = "none", #  based your input data
  r.threshold = 0.7,
  p.threshold = 0.05,
  method = "WGCNA",
  cor.method = "pearson",
  proc = "Bonferroni",
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj
```

```
## # A tbl_graph: 213 nodes and 844 edges
## #
## # An undirected simple graph with 29 components
## #
## # Node Data: 213 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>      <dbl>   <dbl> <chr>
## 1 ASV_649  5          5           5           5             27    26.5 Bacter~
```

```
##  2 ASV_705 5          5          5          5          27     26.5 Bacter~
##  3 ASV_12~ 5          5          5          5          27     26.5 Bacter~
##  4 ASV_13~ 5          5          5          5          27     26.5 Bacter~
##  5 ASV_14~ 5          5          5          5          27     26.5 Bacter~
##  6 ASV_14~ 5          5          5          5          27     26.5 Bacter~
##  7 ASV_24~ 5          5          5          5          27     26.5 Bacter~
##  8 ASV_25~ 5          5          5          5          27     26.4 Bacter~
##  9 ASV_28~ 5          5          5          5          27     26.5 Bacter~
## 10 ASV_28~ 5          5          5          5          27     26.5 Bacter~
## # i 203 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 844 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1   194   195  0.959       0.959 Positive
## 2   185   208  0.954       0.954 Positive
## 3   185   213  0.957       0.957 Positive
## # i 841 more rows
```

2.2   Build graph from data frame

Example data

```
# Access built-in example datasets in ggNetView
data("ppi_example")
df = ppi_example$ppi
head(df)
```

```
##   from  to     weight
## 1   A1 D40   9.306533
## 2   A2 D39  11.783920
## 3   A3 D38  23.005025
## 4   A4 D37   7.412060
## 5   A5 D36  18.778894
## 6   A6 D35  16.592965
```

```
node_annotation = ppi_example$annotation
head(node_annotation)
```

```
##    node group
## 1   A1     A
## 2   A2     A
## 3   A3     A
## 4   A4     A
## 5   A5     A
## 6   A6     A
```

Build graph object

```
graph_obj_from_df <- build_graph_from_df(
  df = df,
  node_annotation = node_annotation,
  directed = F,
  module.method = "Fast_greedy",
  top_modules = 15,
  seed = 1115
)

graph_obj_from_df
```

```
## # A tbl_graph: 100 nodes and 50 edges
## #
## # An unrooted forest with 50 trees
## #
## # Node Data: 100 x 9 (active)
##     name  group modularity modularity2 modularity3 Modularity Degree Segree
##     <chr> <chr> <fct>      <fct>       <chr>       <fct>       <dbl>  <dbl>
##  1 C13    C     1          1           1           1               1      1
##  2 C28    C     1          1           1           1               1      1
##  3 C2     C     10         10          10          10              1      1
##  4 D9     D     10         10          10          10              1      1
##  5 A3     A     11         11          11          11              1      1
##  6 D38    D     11         11          11          11              1      1
##  7 B12    B     12         12          12          12              1      1
##  8 D19    D     12         12          12          12              1      1
##  9 A1     A     13         13          13          13              1      1
## 10 D40    D     13         13          13          13              1      1
## # i 90 more rows
## # i 1 more variable: Strength <dbl>
## #
## # Edge Data: 50 x 4
##     from    to weight correlation
##    <int> <int>  <dbl>       <dbl>
## 1      9    10   45.2        45.2
```

```
## 2     15     16    50.6          50.6
## 3      5      6    37.8          37.8
## # i 47 more rows
```

```r
graph_obj_from_df2 <- build_graph_from_df(
  df = df,
  node_annotation = NULL,
  directed = F,
  module.method = "Fast_greedy",
  top_modules = 15,
  seed = 1115
)


graph_obj_from_df2
```

```
## # A tbl_graph: 100 nodes and 50 edges
## #
## # An unrooted forest with 50 trees
## #
## # Node Data: 100 x 8 (active)
##     name  modularity modularity2 modularity3 Modularity Degree Segree Strength
##     <chr> <fct>      <fct>       <chr>       <fct>      <dbl>  <dbl>  <dbl>
## 1 C13   1          1           1           1              1      1   26.7
## 2 C28   1          1           1           1              1      1   26.7
## 3 C2    10         10          10          10             1      1   37.4
## 4 D9    10         10          10          10             1      1   37.4
## 5 A3    11         11          11          11             1      1   37.8
## 6 D38   11         11          11          11             1      1   37.8
## 7 B12   12         12          12          12             1      1   41.3
## 8 D19   12         12          12          12             1      1   41.3
## 9 A1    13         13          13          13             1      1   45.2
## 10 D40   13         13          13          13             1      1   45.2
## # i 90 more rows
## #
## # Edge Data: 50 x 4
##    from    to weight correlation
##   <int> <int>  <dbl>       <dbl>
## 1     9    10   45.2        45.2
## 2    15    16   50.6        50.6
## 3     5     6   37.8        37.8
## # i 47 more rows
```

2.3 Build graph from data frame with module

Example data

```
# Access built-in example datasets in ggNetView
data("ppi_module")
df = ppi_module$ppi
head(df)
```

```
##   from  to    weight
## 1   A1 D40  9.306533
## 2   A2 D39 11.783920
## 3   A3 D38 23.005025
## 4   A4 D37  7.412060
## 5   A5 D36 18.778894
## 6   A6 D35 16.592965
```

```
node_annotation = ppi_module$annotation
head(node_annotation)
```

```
##   node Modularity
## 1   A1          A
## 2   A2          A
## 3   A3          A
## 4   A4          A
## 5   A5          A
## 6   A6          A
```

Build graph object

```
graph_obj_from_module <- build_graph_from_module(
  df = df,
  node_annotation = node_annotation,
  directed = F,
  top_modules = 15,
  seed = 1115
)

graph_obj_from_module
```

```
## # A tbl_graph: 100 nodes and 50 edges
## #
## # An unrooted forest with 50 trees
```

```
## #
## # Node Data: 100 x 7 (active)
##     name  Modularity modularity2 modularity3 Degree Segree Strength
##     <chr> <ord>      <ord>       <chr>        <dbl>  <dbl>    <dbl>
## 1  D1     D          D           D                1      1     37.1
## 2  D2     D          D           D                1      1     63.9
## 3  D3     D          D           D                1      1     54.6
## 4  D4     D          D           D                1      1     61.7
## 5  D5     D          D           D                1      1     36.1
## 6  D6     D          D           D                1      1     71.0
## 7  D7     D          D           D                1      1     27.9
## 8  D8     D          D           D                1      1     34.6
## 9  D9     D          D           D                1      1     37.4
## 10 D10    D          D           D                1      1     63.2
## # i 90 more rows
## #
## # Edge Data: 50 x 4
##     from     to weight correlation
##    <int> <int>  <dbl>       <dbl>
## 1     40    91   45.2        45.2
## 2     39    92   50.6        50.6
## 3     38    93   37.8        37.8
## # i 47 more rows
```

2.4   Build graph from adjacency matrix

Example data

```
data("adjacency_matrix_example")
dim(adjacency_matrix_example)
```

```
## [1] 2859 2859
```

```
adjacency_matrix_example[1:5, 1:5]
```

```
##         ASV_1      ASV_2 ASV_3 ASV_4      ASV_6
## ASV_1       0 0.0000000     0     0 0.0000000
## ASV_2       0 0.0000000     0     0 0.8947427
## ASV_3       0 0.0000000     0     0 0.0000000
## ASV_4       0 0.0000000     0     0 0.0000000
## ASV_6       0 0.8947427     0     0 0.0000000
```

```
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859    8
```

```
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##    OTUID  Kingdom  Phylum          Class          Order
##    <chr>  <chr>    <chr>           <chr>          <chr>
## 1 ASV_2   Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 2 ASV_3   Bacteria Verrucomicrobia Spartobacteria Unassigned
## 3 ASV_31  Bacteria Actinobacteria  Actinobacteria Actinomycetales
## 4 ASV_27  Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 5 ASV_9   Bacteria Unassigned      Unassigned     Unassigned
```

Build graph object

```
graph_obj_adj <- build_graph_from_adj_mat(
  adjacency_matrix = adjacency_matrix_example,
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj_adj
```

```
## # A tbl_graph: 2049 nodes and 9602 edges
## #
## # An undirected simple graph with 100 components
## #
## # Node Data: 2,049 x 14 (active)
##      name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##      <chr>   <fct>      <ord>       <chr>       <ord>      <dbl>   <dbl> <chr>
## 1 1 ASV_916 1          1           1           1             58    50.5 Bacter~
## 2 2 ASV_777 1          1           1           1             58    48.7 Bacter~
## 3 3 ASV_606 1          1           1           1             55    45.8 Bacter~
## 4 4 ASV_740 1          1           1           1             54    47.2 Bacter~
## 5 5 ASV_14~ 1          1           1           1             54    44.5 Bacter~
## 6 6 ASV_23~ 1          1           1           1             54    47.4 Bacter~
## 7 7 ASV_15~ 1          1           1           1             52    45.3 Bacter~
## 8 8 ASV_24~ 1          1           1           1             52    43.0 Bacter~
```

```
##  9 ASV_19~ 1           1           1           1              52       43.0 Bacter~
## 10 ASV_568 1           1           1           1              51       45.1 Bacter~
## # i 2,039 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 9,602 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1  1771  1825  0.793       0.793 Positive
## 2   594   597  0.895       0.895 Positive
## 3   588   597  0.864       0.864 Positive
## # i 9,599 more rows
```

2.5 Build graph from double matrix

Example data

```
data("BASV_tab")
dim(BASV_tab)
```

```
## [1] 50 10
```

```
BASV_tab[1:5, 1:5]
```

```
##           Sample1    Sample2    Sample3    Sample4    Sample5
## BASV1   7.769249 14.676091   6.822246 11.806957 12.086254
## BASV2 10.771846  7.749385 14.966987   7.486507 12.645461
## BASV3 11.746937 10.023547 10.025906 11.967562  8.748440
## BASV4  8.210859  4.408296 10.070862  8.954202 14.639298
## BASV5  9.833271  9.776280 10.465463  8.380012  8.905738
```

```
data("FASV_tab")
dim(FASV_tab)
```

```
## [1] 50 10
```

```
FASV_tab[1:5, 1:5]
```

```
##          Sample1    Sample2    Sample3    Sample4    Sample5
## FASV1  8.195641   7.715472  13.247401  10.419618  11.961410
## FASV2 10.032701  12.427388   7.693471  10.711077  12.157527
## FASV3 10.109549  11.891917   9.607849   8.256637   9.989264
## FASV4  9.817056   8.038730   5.519155   7.601228  12.688531
## FASV5 13.370263   9.795554  13.639041  11.071635   8.176218
```

```r
data("double_mat_node_df")
dim(double_mat_node_df)
```

```
## [1] 100    2
```

```r
head(double_mat_node_df)
```

```
##     name       type
## 1 BASV1 Bacterial
## 2 BASV2 Bacterial
## 3 BASV3 Bacterial
## 4 BASV4 Bacterial
## 5 BASV5 Bacterial
## 6 BASV6 Bacterial
```

Build graph object

```r
graph_obj_double_mat <- build_graph_from_double_mat(
  mat1 = BASV_tab,
  mat2 = FASV_tab,
   module.method = "Fast_greedy",
  node_annotation = double_mat_node_df,
  top_modules = 15,
  seed = 1115
)
```

```
## The max module in network is 4 we use the 4  modules for next analysis
```

```r
graph_obj_double_mat
```

```
## # A tbl_graph: 100 nodes and 2500 edges
## #
## # A bipartite simple graph with 1 component
## #
## # Node Data: 100 x 9 (active)
```

```
##     name    type     modularity modularity2 modularity3 Modularity Degree Segree
##     <chr>   <chr>    <fct>      <fct>        <chr>        <fct>      <dbl>  <dbl>
##  1 BASV3  Bacterial 1          1            1            1             50     50
##  2 BASV6  Bacterial 1          1            1            1             50     50
##  3 BASV8  Bacterial 1          1            1            1             50     50
##  4 BASV13 Bacterial 1          1            1            1             50     50
##  5 BASV17 Bacterial 1          1            1            1             50     50
##  6 BASV19 Bacterial 1          1            1            1             50     50
##  7 BASV25 Bacterial 1          1            1            1             50     50
##  8 BASV26 Bacterial 1          1            1            1             50     50
##  9 BASV27 Bacterial 1          1            1            1             50     50
## 10 BASV31 Bacterial 1          1            1            1             50     50
## # i 90 more rows
## # i 1 more variable: Strength <dbl>
## #
## # Edge Data: 2,500 x 4
##     from    to weight correlation
##    <int> <int>  <dbl>       <dbl>
## 1    15    57  0.338      -0.338
## 2    57    90  0.648       0.648
## 3    16    57  0.162       0.162
## # i 2,497 more rows
```

Chapter 3

Random Matrix Theory (RMT)–based random network

When a numerical matrix is used as input, it is necessary to filter and screen the resulting correlation matrix. Empirical thresholds are commonly adopted, usually between 0.6 to 0.85; however, these thresholds are largely subjective.

Compared with empirical thresholding, random matrix theory (RMT) provides a data-driven and objective approach for determining correlation thresholds, effectively separating true biological signals from random noise and improving the robustness and comparability of ecological networks.

3.1 Random Matrix Theory (RMT)

Load R Package

```
library(tidyverse)
library(ggNetView)
```

3.2   Example data

Example data

```
# Access built-in example datasets in ggNetView

# Relative abundance table of rarefied ASVs or OTUs
data("otu_rare_relative")
dim(otu_rare_relative)
```

```
## [1] 2859   18
```

```
otu_rare_relative[1:5, 1:5]
```

```
##               KO1        KO2        KO3        KO4        KO5
## ASV_1 0.03306667 0.05453333 0.02013333 0.03613333 0.02686667
## ASV_2 0.05750000 0.03393333 0.06046667 0.05810000 0.07320000
## ASV_3 0.01733333 0.01296667 0.02290000 0.02336667 0.03106667
## ASV_4 0.04266667 0.01093333 0.01416667 0.01933333 0.03346667
## ASV_6 0.02646667 0.01856667 0.02110000 0.02353333 0.03806667
```

```
# Taxonomic annotation table of ASVs or OTUs
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859    8
```

```
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##   OTUID  Kingdom  Phylum          Class          Order
##   <chr>  <chr>    <chr>           <chr>          <chr>
## 1 ASV_2  Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 2 ASV_3  Bacteria Verrucomicrobia Spartobacteria Unassigned
## 3 ASV_31 Bacteria Actinobacteria  Actinobacteria Actinomycetales
## 4 ASV_27 Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 5 ASV_9  Bacteria Unassigned      Unassigned     Unassigned
```

3.3   Compute RMT threshold

```
out <- ggNetView_RMT(mat = otu_rare_relative,
                     transfrom.method = "none",
                     method = "WGCNA",
                     cor.method = "pearson",
                     unfold.method = "gaussian",
                     bandwidth = "nrd0",
                     nr.fit.points = 20,
                     discard.outliers = TRUE,
                     discard.zeros = TRUE,
                     min.mat.dim = 40,
                     max.ev.spacing = 3,
                     save_plots = FALSE,
                     out_dir = "RMT_plots",
                     verbose = TRUE,
                     seed = 1115
                     )
```

```
## [Info] Matrix dimension: 2859 x 2859

## [Info] #non-zeros: 8173831 | Sparseness: 0.0000

##    [Scan]   1/51 | threshold = 0

##           Effective dimension: 2859

##    [Scan]   2/51 | threshold = 0.02

##           Effective dimension: 2859

##    [Scan]   3/51 | threshold = 0.04

##           Effective dimension: 2859

##    [Scan]   4/51 | threshold = 0.06

##           Effective dimension: 2859

##    [Scan]   5/51 | threshold = 0.08

##           Effective dimension: 2859
```

```
##   [Scan]   6/51 | threshold = 0.1

##          Effective dimension: 2859

##   [Scan]   7/51 | threshold = 0.12

##          Effective dimension: 2859

##   [Scan]   8/51 | threshold = 0.14

##          Effective dimension: 2859

##   [Scan]   9/51 | threshold = 0.16

##          Effective dimension: 2859

##   [Scan]  10/51 | threshold = 0.18

##          Effective dimension: 2859

##   [Scan]  11/51 | threshold = 0.2

##          Effective dimension: 2859

##   [Scan]  12/51 | threshold = 0.22

##          Effective dimension: 2859

##   [Scan]  13/51 | threshold = 0.24

##          Effective dimension: 2859

##   [Scan]  14/51 | threshold = 0.26

##          Effective dimension: 2859

##   [Scan]  15/51 | threshold = 0.28

##          Effective dimension: 2859

##   [Scan]  16/51 | threshold = 0.3
```

```
##          Effective dimension: 2859

##    [Scan]  17/51 | threshold = 0.32

##          Effective dimension: 2859

##    [Scan]  18/51 | threshold = 0.34

##          Effective dimension: 2859

##    [Scan]  19/51 | threshold = 0.36

##          Effective dimension: 2859

##    [Scan]  20/51 | threshold = 0.38

##          Effective dimension: 2859

##    [Scan]  21/51 | threshold = 0.4

##          Effective dimension: 2859

##    [Scan]  22/51 | threshold = 0.42

##          Effective dimension: 2859

##    [Scan]  23/51 | threshold = 0.44

##          Effective dimension: 2859

##    [Scan]  24/51 | threshold = 0.46

##          Effective dimension: 2859

##    [Scan]  25/51 | threshold = 0.48

##          Effective dimension: 2859

##    [Scan]  26/51 | threshold = 0.5

##          Effective dimension: 2859
```

```
##    [Scan]   27/51 | threshold = 0.52

##            Effective dimension: 2859

##    [Scan]   28/51 | threshold = 0.54

##            Effective dimension: 2859

##    [Scan]   29/51 | threshold = 0.56

##            Effective dimension: 2859

##    [Scan]   30/51 | threshold = 0.58

##            Effective dimension: 2859

##    [Scan]   31/51 | threshold = 0.6

##            Effective dimension: 2859

##    [Scan]   32/51 | threshold = 0.62

##            Effective dimension: 2859

##    [Scan]   33/51 | threshold = 0.64

##            Effective dimension: 2857

##    [Scan]   34/51 | threshold = 0.66

##            Effective dimension: 2855

##    [Scan]   35/51 | threshold = 0.68

##            Effective dimension: 2842

##    [Scan]   36/51 | threshold = 0.7

##            Effective dimension: 2800

##    [Scan]   37/51 | threshold = 0.72
```

```
##          Effective dimension: 2705

##   [Scan]  38/51 | threshold = 0.74

##          Effective dimension: 2546

##   [Scan]  39/51 | threshold = 0.76

##          Effective dimension: 2333

##   [Scan]  40/51 | threshold = 0.78

##          Effective dimension: 2049

##   [Scan]  41/51 | threshold = 0.8

##          Effective dimension: 1735

##   [Scan]  42/51 | threshold = 0.82

##          Effective dimension: 1396

##   [Scan]  43/51 | threshold = 0.84

##          Effective dimension: 1082

##   [Scan]  44/51 | threshold = 0.86

##          Effective dimension: 825

##   [Scan]  45/51 | threshold = 0.88

##          Effective dimension: 600

##   [Scan]  46/51 | threshold = 0.9

##          Effective dimension: 454

##   [Scan]  47/51 | threshold = 0.92

##          Effective dimension: 324
```

```
##    [Scan]   48/51 | threshold = 0.94

##             Effective dimension: 215

##    [Scan]   49/51 | threshold = 0.96

##             Effective dimension: 157

##    [Scan]   50/51 | threshold = 0.98

##             Effective dimension: 79

##    [Scan]   51/51 | threshold = 1

##             Effective dimension: 2

##             Too small. Stop scanning.
```

```
out$chosen_threshold
```

```
## [1] 0.82
```

```
out2 <- ggNetView_RMT(mat = otu_rare_relative,
                      transfrom.method = "none",
                      method = "cor",
                      cor.method = "pearson",
                      unfold.method = "gaussian",
                      bandwidth = "nrd0",
                      nr.fit.points = 20,
                      discard.outliers = TRUE,
                      discard.zeros = TRUE,
                      min.mat.dim = 40,
                      max.ev.spacing = 3,
                      save_plots = FALSE,
                      out_dir = "RMT_plots",
                      verbose = TRUE,
                      seed = 1115
                      )
```

```
## [Info] Matrix dimension: 2859 x 2859

## [Info] #non-zeros: 8173761 | Sparseness: 0.0000
```

```
## [Scan]   1/51 | threshold = 0

##          Effective dimension: 2859

## [Scan]   2/51 | threshold = 0.02

##          Effective dimension: 2859

## [Scan]   3/51 | threshold = 0.04

##          Effective dimension: 2859

## [Scan]   4/51 | threshold = 0.06

##          Effective dimension: 2859

## [Scan]   5/51 | threshold = 0.08

##          Effective dimension: 2859

## [Scan]   6/51 | threshold = 0.1

##          Effective dimension: 2859

## [Scan]   7/51 | threshold = 0.12

##          Effective dimension: 2859

## [Scan]   8/51 | threshold = 0.14

##          Effective dimension: 2859

## [Scan]   9/51 | threshold = 0.16

##          Effective dimension: 2859

## [Scan]  10/51 | threshold = 0.18

##          Effective dimension: 2859

## [Scan]  11/51 | threshold = 0.2
```

```
##          Effective dimension: 2859

##   [Scan]  12/51 | threshold = 0.22

##          Effective dimension: 2859

##   [Scan]  13/51 | threshold = 0.24

##          Effective dimension: 2859

##   [Scan]  14/51 | threshold = 0.26

##          Effective dimension: 2859

##   [Scan]  15/51 | threshold = 0.28

##          Effective dimension: 2859

##   [Scan]  16/51 | threshold = 0.3

##          Effective dimension: 2859

##   [Scan]  17/51 | threshold = 0.32

##          Effective dimension: 2859

##   [Scan]  18/51 | threshold = 0.34

##          Effective dimension: 2859

##   [Scan]  19/51 | threshold = 0.36

##          Effective dimension: 2859

##   [Scan]  20/51 | threshold = 0.38

##          Effective dimension: 2859

##   [Scan]  21/51 | threshold = 0.4

##          Effective dimension: 2859
```

```
##    [Scan]   22/51 | threshold = 0.42

##             Effective dimension: 2859

##    [Scan]   23/51 | threshold = 0.44

##             Effective dimension: 2859

##    [Scan]   24/51 | threshold = 0.46

##             Effective dimension: 2859

##    [Scan]   25/51 | threshold = 0.48

##             Effective dimension: 2859

##    [Scan]   26/51 | threshold = 0.5

##             Effective dimension: 2859

##    [Scan]   27/51 | threshold = 0.52

##             Effective dimension: 2859

##    [Scan]   28/51 | threshold = 0.54

##             Effective dimension: 2859

##    [Scan]   29/51 | threshold = 0.56

##             Effective dimension: 2859

##    [Scan]   30/51 | threshold = 0.58

##             Effective dimension: 2859

##    [Scan]   31/51 | threshold = 0.6

##             Effective dimension: 2859

##    [Scan]   32/51 | threshold = 0.62
```

```
##          Effective dimension: 2859

##   [Scan]  33/51 | threshold = 0.64

##          Effective dimension: 2857

##   [Scan]  34/51 | threshold = 0.66

##          Effective dimension: 2855

##   [Scan]  35/51 | threshold = 0.68

##          Effective dimension: 2842

##   [Scan]  36/51 | threshold = 0.7

##          Effective dimension: 2800

##   [Scan]  37/51 | threshold = 0.72

##          Effective dimension: 2705

##   [Scan]  38/51 | threshold = 0.74

##          Effective dimension: 2546

##   [Scan]  39/51 | threshold = 0.76

##          Effective dimension: 2333

##   [Scan]  40/51 | threshold = 0.78

##          Effective dimension: 2049

##   [Scan]  41/51 | threshold = 0.8

##          Effective dimension: 1735

##   [Scan]  42/51 | threshold = 0.82

##          Effective dimension: 1396
```

```
## [Scan] 43/51 | threshold = 0.84

## Effective dimension: 1082

## [Scan] 44/51 | threshold = 0.86

## Effective dimension: 825

## [Scan] 45/51 | threshold = 0.88

## Effective dimension: 600

## [Scan] 46/51 | threshold = 0.9

## Effective dimension: 454

## [Scan] 47/51 | threshold = 0.92

## Effective dimension: 324

## [Scan] 48/51 | threshold = 0.94

## Effective dimension: 215

## [Scan] 49/51 | threshold = 0.96

## Effective dimension: 157

## [Scan] 50/51 | threshold = 0.98

## Effective dimension: 79

## [Scan] 51/51 | threshold = 1

## Effective dimension: 10

## Too small. Stop scanning.
```

```
out2$chosen_threshold
```

```
## [1] 0.82
```

3.4 Build graph from matrix based on RMT-threshold

Build graph object

```
graph_obj <- build_graph_from_mat(
  mat = otu_rare_relative,
  transfrom.method = "none", #  based your input data
  r.threshold = out$chosen_threshold,
  p.threshold = 0.05,
  method = "WGCNA",
  cor.method = "pearson",
  proc = "Bonferroni",
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj
```

```
## # A tbl_graph: 213 nodes and 844 edges
## #
## # An undirected simple graph with 29 components
## #
## # Node Data: 213 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>        <chr>        <ord>       <dbl>  <dbl> <chr>
##  1 ASV_649 5          5            5            5              27   26.5 Bacter~
##  2 ASV_705 5          5            5            5              27   26.5 Bacter~
##  3 ASV_12~ 5          5            5            5              27   26.5 Bacter~
##  4 ASV_13~ 5          5            5            5              27   26.5 Bacter~
##  5 ASV_14~ 5          5            5            5              27   26.5 Bacter~
##  6 ASV_14~ 5          5            5            5              27   26.5 Bacter~
##  7 ASV_24~ 5          5            5            5              27   26.5 Bacter~
##  8 ASV_25~ 5          5            5            5              27   26.4 Bacter~
##  9 ASV_28~ 5          5            5            5              27   26.5 Bacter~
## 10 ASV_28~ 5          5            5            5              27   26.5 Bacter~
```

```
## # i 203 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 844 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1   194   195  0.959       0.959 Positive
## 2   185   208  0.954       0.954 Positive
## 3   185   213  0.957       0.957 Positive
## # i 841 more rows
```

Chapter 4

Get network information

Once the graph object is constructed, basic network information can be retrieved, and subnetworks can be extracted.

Load R Package

```
library(tidyverse)
library(ggNetView)
```

Example data

```
# Access built-in example datasets in ggNetView

# Relative abundance table of rarefied ASVs or OTUs
data("otu_rare_relative")
dim(otu_rare_relative)
```

```
## [1] 2859    18
```

```
otu_rare_relative[1:5, 1:5]
```

```
##              K01        K02        K03        K04        K05
## ASV_1 0.03306667 0.05453333 0.02013333 0.03613333 0.02686667
## ASV_2 0.05750000 0.03393333 0.06046667 0.05810000 0.07320000
## ASV_3 0.01733333 0.01296667 0.02290000 0.02336667 0.03106667
## ASV_4 0.04266667 0.01093333 0.01416667 0.01933333 0.03346667
## ASV_6 0.02646667 0.01856667 0.02110000 0.02353333 0.03806667
```

```r
# Taxonomic annotation table of ASVs or OTUs
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859    8
```

```r
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##   OTUID   Kingdom  Phylum          Class          Order
##   <chr>   <chr>    <chr>           <chr>          <chr>
## 1 ASV_2   Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 2 ASV_3   Bacteria Verrucomicrobia Spartobacteria Unassigned
## 3 ASV_31  Bacteria Actinobacteria  Actinobacteria Actinomycetales
## 4 ASV_27  Archaea  Thaumarchaeota  Unassigned     Nitrososphaerales
## 5 ASV_9   Bacteria Unassigned      Unassigned     Unassigned
```

Build graph object

```r
graph_obj <- build_graph_from_mat(
  mat = otu_rare_relative,
  transfrom.method = "none", #  based your input data
  r.threshold = 0.7,
  p.threshold = 0.05,
  method = "WGCNA",
  cor.method = "pearson",
  proc = "Bonferroni",
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj
```

```
## # A tbl_graph: 213 nodes and 844 edges
## #
## # An undirected simple graph with 29 components
## #
## # Node Data: 213 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1 ASV_649 5          5           5           5              27     26.5 Bacter~
```

```
##  2 ASV_705 5          5          5          5          27      26.5 Bacter~
##  3 ASV_12~ 5          5          5          5          27      26.5 Bacter~
##  4 ASV_13~ 5          5          5          5          27      26.5 Bacter~
##  5 ASV_14~ 5          5          5          5          27      26.5 Bacter~
##  6 ASV_14~ 5          5          5          5          27      26.5 Bacter~
##  7 ASV_24~ 5          5          5          5          27      26.5 Bacter~
##  8 ASV_25~ 5          5          5          5          27      26.4 Bacter~
##  9 ASV_28~ 5          5          5          5          27      26.5 Bacter~
## 10 ASV_28~ 5          5          5          5          27      26.5 Bacter~
## # i 203 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 844 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1    194   195  0.959       0.959 Positive
## 2    185   208  0.954       0.954 Positive
## 3    185   213  0.957       0.957 Positive
## # i 841 more rows
```

4.1 Full-network information

```
graph_obj_info <- get_info_from_graph(graph_obj = graph_obj)

# return a list
class(graph_obj_info)
```

```
## [1] "list"
```

```
names(graph_obj_info)
```

```
## [1] "node_info" "edge_info"
```

```
graph_obj_info$node_info
```

```
## # A tibble: 213 x 11
##    name    Modularity Degree Strength Kingdom  Phylum  Class Order Family Genus
##    <chr>   <ord>       <dbl>    <dbl> <chr>    <chr>   <chr> <chr> <chr>  <chr>
## 1 ASV_649 5              27     26.5 Bacteria Proteo~ Alph~ Rhiz~ Unass~ Unas~
## 2 ASV_705 5              27     26.5 Bacteria Actino~ Acti~ Acti~ Cellu~ Cell~
```

```
##  3 ASV_1234 5              27      26.5 Bacteria Gemmat~ Gemm~ Gemm~ Gemma~ Gemm~
##  4 ASV_1373 5              27      26.5 Bacteria Actino~ Acti~ Soli~ Solir~ Soli~
##  5 ASV_1479 5              27      26.5 Bacteria Verruc~ Spar~ Unas~ Unass~ Spar~
##  6 ASV_1481 5              27      26.5 Bacteria Proteo~ Gamm~ Unas~ Unass~ Unas~
##  7 ASV_2453 5              27      26.5 Bacteria Bacter~ Sphi~ Sphi~ Chiti~ Unas~
##  8 ASV_2562 5              27      26.4 Bacteria Bacter~ Sphi~ Sphi~ Chiti~ Unas~
##  9 ASV_2848 5              27      26.5 Bacteria Planct~ Plan~ Plan~ Planc~ Unas~
## 10 ASV_2844 5              27      26.5 Bacteria Proteo~ Unas~ Unas~ Unass~ Unas~
## # i 203 more rows
## # i 1 more variable: Species <chr>
```

```
graph_obj_info$edge_info
```

```
## # A tibble: 844 x 5
##    from     to       weight correlation corr_direction
##    <chr>    <chr>     <dbl>       <dbl> <chr>
##  1 ASV_6    ASV_39    0.959       0.959 Positive
##  2 ASV_20   ASV_1852  0.954       0.954 Positive
##  3 ASV_20   ASV_2911  0.957       0.957 Positive
##  4 ASV_172  ASV_43    0.969       0.969 Positive
##  5 ASV_614  ASV_65    0.943       0.943 Positive
##  6 ASV_69   ASV_173   0.995       0.995 Positive
##  7 ASV_69   ASV_206   0.994       0.994 Positive
##  8 ASV_69   ASV_744   0.976       0.976 Positive
##  9 ASV_945  ASV_69    0.985       0.985 Positive
## 10 ASV_69   ASV_1418  0.975       0.975 Positive
## # i 834 more rows
```

4.2 Sub-network (modularity) information

```
subgraph_info <- get_subgraph(graph_obj = graph_obj,
                              select_module = NULL)
```

```
##     Module Number
## 1        5     31
## 2        2     24
## 3        8     22
## 4       21     15
## 5        1     13
## 6        3     11
## 7        4     11
## 8        6     11
```

```
## 9       25      8
## 10       7      6
## 11      12      5
## 12      22      5
## 13      10      4
## 14      11      4
## 15      15      4
## 16 Others     39
```

```
# return a list
class(subgraph_info)
```

```
## [1] "list"
```

```
names(subgraph_info)
```

```
## [1] "sub_graph_all"    "stat_module"      "sub_graph_select"
```

```
subgraph_info$stat_module
```

```
##     Module Number
## 1        5     31
## 2        2     24
## 3        8     22
## 4       21     15
## 5        1     13
## 6        3     11
## 7        4     11
## 8        6     11
## 9       25      8
## 10       7      6
## 11      12      5
## 12      22      5
## 13      10      4
## 14      11      4
## 15      15      4
## 16 Others     39
```

```
subgraph_info$sub_graph_all
```

```
## $`5`
## # A tbl_graph: 31 nodes and 330 edges
```

```
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 31 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>        <chr>       <ord>      <dbl>    <dbl> <chr>
##  1 ASV_649 5          5            5           5             27     26.5 Bacter~
##  2 ASV_705 5          5            5           5             27     26.5 Bacter~
##  3 ASV_12~ 5          5            5           5             27     26.5 Bacter~
##  4 ASV_13~ 5          5            5           5             27     26.5 Bacter~
##  5 ASV_14~ 5          5            5           5             27     26.5 Bacter~
##  6 ASV_14~ 5          5            5           5             27     26.5 Bacter~
##  7 ASV_24~ 5          5            5           5             27     26.5 Bacter~
##  8 ASV_25~ 5          5            5           5             27     26.4 Bacter~
##  9 ASV_28~ 5          5            5           5             27     26.5 Bacter~
## 10 ASV_28~ 5          5            5           5             27     26.5 Bacter~
## # i 21 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 330 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.996       0.996 Positive
## 2     1     3  0.997       0.997 Positive
## 3     2     3  0.994       0.994 Positive
## # i 327 more rows
##
## $`2`
## # A tbl_graph: 24 nodes and 121 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 24 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>        <chr>       <ord>      <dbl>    <dbl> <chr>
##  1 ASV_671 2          2            2           2             18     17.5 Bacter~
##  2 ASV_18~ 2          2            2           2             17     16.6 Bacter~
##  3 ASV_29~ 2          2            2           2             17     16.6 Bacter~
##  4 ASV_568 2          2            2           2             16     15.6 Bacter~
##  5 ASV_10~ 2          2            2           2             16     15.6 Bacter~
##  6 ASV_11~ 2          2            2           2             16     15.6 Bacter~
##  7 ASV_24~ 2          2            2           2             15     14.5 Bacter~
##  8 ASV_28~ 2          2            2           2             14     13.5 Bacter~
##  9 ASV_15~ 2          2            2           2             13     12.6 Bacter~
## 10 ASV_24~ 2          2            2           2             13     12.5 Bacter~
```

```
## # i 14 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 121 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.991       0.991 Positive
## 2     1     3  0.992       0.992 Positive
## 3     2     3  0.996       0.996 Positive
## # i 118 more rows
##
## $`8`
## # A tbl_graph: 22 nodes and 131 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 22 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>       <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_802 8           8           8           8              18    17.5 Bacter~
## 2 ASV_723 8           8           8           8              18    17.5 Bacter~
## 3 ASV_11~ 8           8           8           8              18    17.6 Bacter~
## 4 ASV_29~ 8           8           8           8              18    17.6 Bacter~
## 5 ASV_927 8           8           8           8              16    15.6 Bacter~
## 6 ASV_13~ 8           8           8           8              16    15.5 Bacter~
## 7 ASV_29~ 8           8           8           8              16    15.5 Bacter~
## 8 ASV_10~ 8           8           8           8              15    14.4 Bacter~
## 9 ASV_13~ 8           8           8           8              15    14.6 Bacter~
## 10 ASV_14~ 8          8           8           8              15    14.7 Bacter~
## # i 12 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 131 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.990       0.990 Positive
## 2     1     3  0.993       0.993 Positive
## 3     2     3  0.997       0.997 Positive
## # i 128 more rows
##
## $`21`
## # A tbl_graph: 15 nodes and 42 edges
## #
## # An undirected simple graph with 1 component
```

```
## #
## # Node Data: 15 x 14 (active)
##     name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>    <fct>      <ord>       <chr>       <ord>         <dbl>    <dbl> <chr>
## 1 ASV_25~ 21         21          21          21               13     12.5  Bacter~
## 2 ASV_27~ 21         21          21          21               12     11.6  Bacter~
## 3 ASV_879 21         21          21          21                8      7.67 Bacter~
## 4 ASV_10~ 21         21          21          21                6      5.76 Bacter~
## 5 ASV_16~ 21         21          21          21                6      5.70 Bacter~
## 6 ASV_511 21         21          21          21                5      4.80 Bacter~
## 7 ASV_578 21         21          21          21                5      4.76 Bacter~
## 8 ASV_917 21         21          21          21                5      4.80 Bacter~
## 9 ASV_18~ 21         21          21          21                5      4.81 Bacter~
## 10 ASV_70  21         21          21          21                4      3.82 Bacter~
## 11 ASV_13~ 21         21          21          21                4      3.86 Bacter~
## 12 ASV_839 21         21          21          21                3      2.85 Bacter~
## 13 ASV_20~ 21         21          21          21                3      2.86 Bacter~
## 14 ASV_21~ 21         21          21          21                3      2.86 Bacter~
## 15 ASV_88  21         21          21          21                2      1.90 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 42 x 5
##     from   to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.986       0.986 Positive
## 2     1     3  0.973       0.973 Positive
## 3     2     3  0.976       0.976 Positive
## # i 39 more rows
##
## $`1`
## # A tbl_graph: 13 nodes and 43 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 13 x 14 (active)
##     name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>    <fct>      <ord>       <chr>       <ord>         <dbl>    <dbl> <chr>
## 1 ASV_19~ 1          1           1           1                 9     8.86  Bacter~
## 2 ASV_15~ 1          1           1           1                 9     8.86  Bacter~
## 3 ASV_24~ 1          1           1           1                 9     8.87  Bacter~
## 4 ASV_20~ 1          1           1           1                 9     8.79  Bacter~
## 5 ASV_20~ 1          1           1           1                 9     8.87  Bacter~
## 6 ASV_26~ 1          1           1           1                 9     8.87  Unassi~
## 7 ASV_968 1          1           1           1                 8     7.88  Bacter~
## 8 ASV_27~ 1          1           1           1                 8     7.73  Bacter~
```

```
##  9 ASV_161 1           1           1           1           7    6.80  Bacter~
## 10 ASV_25~ 1           1           1           1           5    4.72  Bacter~
## 11 ASV_534 1           1           1           1           2    1.90  Bacter~
## 12 ASV_26~ 1           1           1           1           1    0.944 Bacter~
## 13 ASV_29~ 1           1           1           1           1    0.963 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 43 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.998       0.998 Positive
## 2     1     3  0.999       0.999 Positive
## 3     2     3  1.000       1.000 Positive
## # i 40 more rows
##
## $`3`
## # A tbl_graph: 11 nodes and 38 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##     name   modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1  ASV_945 3          3           3           3               9   8.71  Bacter~
## 2  ASV_19~ 3          3           3           3               9   8.72  Bacter~
## 3  ASV_69  3          3           3           3               8   7.85  Bacter~
## 4  ASV_173 3          3           3           3               8   7.87  Bacter~
## 5  ASV_206 3          3           3           3               8   7.83  Bacter~
## 6  ASV_744 3          3           3           3               8   7.71  Bacter~
## 7  ASV_14~ 3          3           3           3               8   7.71  Bacter~
## 8  ASV_23~ 3          3           3           3               8   7.67  Bacter~
## 9  ASV_22~ 3          3           3           3               8   7.70  Bacter~
## 10 ASV_218 3          3           3           3               1   0.955 Bacter~
## 11 ASV_14~ 3          3           3           3               1   0.944 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 38 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.982       0.982 Positive
## 2     1     3  0.985       0.985 Positive
## 3     2     3  0.986       0.986 Positive
## # i 35 more rows
##
```

```
## $`4`
## # A tbl_graph: 11 nodes and 33 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##  1 ASV_459 4          4           4           4              8   7.87  Bacter~
##  2 ASV_533 4          4           4           4              8   7.85  Bacter~
##  3 ASV_10~ 4          4           4           4              8   7.87  Bacter~
##  4 ASV_13~ 4          4           4           4              8   7.81  Bacter~
##  5 ASV_23~ 4          4           4           4              8   7.87  Bacter~
##  6 ASV_24~ 4          4           4           4              7   6.88  Bacter~
##  7 ASV_22~ 4          4           4           4              7   6.81  Bacter~
##  8 ASV_29~ 4          4           4           4              6   5.77  Bacter~
##  9 ASV_29~ 4          4           4           4              4   3.79  Bacter~
## 10 ASV_746 4          4           4           4              1   0.945 Bacter~
## 11 ASV_19~ 4          4           4           4              1   0.953 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 33 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.997       0.997 Positive
## 2     1     3  1.000       1.000 Positive
## 3     2     3  0.998       0.998 Positive
## # i 30 more rows
##
## $`6`
## # A tbl_graph: 11 nodes and 24 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##  1 ASV_116 6          6           6           6              8   7.67  Bacter~
##  2 ASV_661 6          6           6           6              8   7.71  Bacter~
##  3 ASV_25~ 6          6           6           6              6   5.79  Bacter~
##  4 ASV_975 6          6           6           6              5   4.78  Bacter~
##  5 ASV_10~ 6          6           6           6              5   4.77  Bacter~
##  6 ASV_20~ 6          6           6           6              5   4.79  Bacter~
##  7 ASV_27~ 6          6           6           6              4   3.84  Bacter~
##  8 ASV_94  6          6           6           6              3   2.84  Bacter~
```

```
##  9 ASV_20~ 6         6         6         6          2    1.92 Bacter~
## 10 ASV_442 6         6         6         6          1    0.946 Bacter~
## 11 ASV_408 6         6         6         6          1    0.959 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 24 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.974       0.974 Positive
## 2     1     3  0.966       0.966 Positive
## 3     2     3  0.979       0.979 Positive
## # i 21 more rows
##
## $`25`
## # A tbl_graph: 8 nodes and 22 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 8 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>      <dbl>    <dbl> <chr>
## 1 ASV_1505 25         25          25          25             7     6.66 Bacter~
## 2 ASV_415  25         25          25          25             6     5.78 Bacter~
## 3 ASV_517  25         25          25          25             6     5.84 Bacter~
## 4 ASV_842  25         25          25          25             6     5.80 Bacter~
## 5 ASV_1719 25         25          25          25             6     5.85 Bacter~
## 6 ASV_2286 25         25          25          25             6     5.81 Bacter~
## 7 ASV_2637 25         25          25          25             5     4.78 Bacter~
## 8 ASV_1474 25         25          25          25             2     1.90 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 22 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.947       0.947 Positive
## 2     1     3  0.951       0.951 Positive
## 3     2     3  0.970       0.970 Positive
## # i 19 more rows
##
## $`7`
## # A tbl_graph: 6 nodes and 5 edges
## #
## # An unrooted tree
## #
```

```
## # Node Data: 6 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_1896 7          7           7           7               3    2.87 Bacter~
## 2 ASV_454  7          7           7           7               2    1.89 Bacter~
## 3 ASV_1090 7          7           7           7               2    1.89 Bacter~
## 4 ASV_231  7          7           7           7               1   0.968 Bacter~
## 5 ASV_1800 7          7           7           7               1   0.943 Bacter~
## 6 ASV_2038 7          7           7           7               1   0.956 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##    from   to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1    1    2  0.945       0.945 Positive
## 2    2    3  0.944       0.944 Positive
## 3    1    4  0.968       0.968 Positive
## # i 2 more rows
##
## $`12`
## # A tbl_graph: 5 nodes and 5 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_1148 12         12          12          12              4    3.85 Bacter~
## 2 ASV_1104 12         12          12          12              2    1.92 Bacter~
## 3 ASV_1854 12         12          12          12              2    1.95 Bacter~
## 4 ASV_115  12         12          12          12              1   0.955 Bacter~
## 5 ASV_2484 12         12          12          12              1   0.948 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##    from   to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1    1    2  0.959       0.959 Positive
## 2    1    3  0.990       0.990 Positive
## 3    2    3  0.957       0.957 Positive
## # i 2 more rows
##
## $`22`
## # A tbl_graph: 5 nodes and 7 edges
```

```
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_1931 22         22          22          22             4    3.88  Bacter~
## 2 ASV_1320 22         22          22          22             3    2.89  Bacter~
## 3 ASV_1906 22         22          22          22             3    2.91  Bacter~
## 4 ASV_2704 22         22          22          22             3    2.91  Bacter~
## 5 ASV_1495 22         22          22          22             1    0.970 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 7 x 5
##     from   to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1    2  0.971       0.971 Positive
## 2     1    3  0.969       0.969 Positive
## 3     2    3  0.959       0.959 Positive
## # i 4 more rows
##
## $`10`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_2059 10         10          10          10             2    1.89  Bacter~
## 2 ASV_1965 10         10          10          10             2    1.91  Bacter~
## 3 ASV_544  10         10          10          10             1    0.964 Bacter~
## 4 ASV_1607 10         10          10          10             1    0.946 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##     from   to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1    2  0.943       0.943 Positive
## 2     2    3  0.964       0.964 Positive
## 3     1    4  0.946       0.946 Positive
##
## $`11`
## # A tbl_graph: 4 nodes and 3 edges
```

```
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_614   11         11          11          11             2    1.91  Bacter~
## 2 ASV_2916  11         11          11          11             2    1.93  Bacter~
## 3 ASV_65    11         11          11          11             1    0.943 Archaea
## 4 ASV_2168  11         11          11          11             1    0.965 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from   to weight correlation corr_direction
##   <int> <int>  <dbl>        <dbl> <chr>
## 1     1    2  0.966        0.966 Positive
## 2     1    3  0.943        0.943 Positive
## 3     2    4  0.965        0.965 Positive
##
## $`15`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_172   15         15          15          15             2    1.92  Bacter~
## 2 ASV_246   15         15          15          15             2    1.91  Bacter~
## 3 ASV_43    15         15          15          15             1    0.969 Bacter~
## 4 ASV_2211  15         15          15          15             1    0.955 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from   to weight correlation corr_direction
##   <int> <int>  <dbl>        <dbl> <chr>
## 1     1    2  0.952        0.952 Positive
## 2     1    3  0.969        0.969 Positive
## 3     2    4  0.955        0.955 Positive
##
## $Others
## # A tbl_graph: 39 nodes and 34 edges
## #
## # An undirected simple graph with 14 components
```

```
## #
## # Node Data: 39 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>        <dbl>    <dbl> <chr>
## 1  ASV_316 28         Others      Others      Others           3     2.89 Bacter~
## 2  ASV_610 28         Others      Others      Others           3     2.94 Bacter~
## 3  ASV_11~ 29         Others      Others      Others           3     2.94 Bacter~
## 4  ASV_18~ 29         Others      Others      Others           3     2.95 Bacter~
## 5  ASV_11~ 27         Others      Others      Others           3     2.91 Bacter~
## 6  ASV_18~ 28         Others      Others      Others           3     2.91 Bacter~
## 7  ASV_20~ 29         Others      Others      Others           3     2.89 Bacter~
## 8  ASV_24~ 27         Others      Others      Others           3     2.89 Bacter~
## 9  ASV_27~ 29         Others      Others      Others           3     2.95 Bacter~
## 10 ASV_28~ 28         Others      Others      Others           3     2.90 Bacter~
## # i 29 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 34 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.971       0.971 Positive
## 2     3     4  0.987       0.987 Positive
## 3     1     6  0.958       0.958 Positive
## # i 31 more rows
```

```
subgraph_info$sub_graph_select
```

```
## NULL
```

4.3 Sub-network (sample) information

Chapter 5

Extract subgraph

Load R Package

```r
library(tidyverse)
library(ggNetView)
```

Example data

```r
# Access built-in example datasets in ggNetView

# Relative abundance table of rarefied ASVs or OTUs
data("otu_rare_relative")
dim(otu_rare_relative)
```

```
## [1] 2859    18
```

```r
otu_rare_relative[1:5, 1:5]
```

```
##                 KO1        KO2        KO3        KO4        KO5
## ASV_1 0.03306667 0.05453333 0.02013333 0.03613333 0.02686667
## ASV_2 0.05750000 0.03393333 0.06046667 0.05810000 0.07320000
## ASV_3 0.01733333 0.01296667 0.02290000 0.02336667 0.03106667
## ASV_4 0.04266667 0.01093333 0.01416667 0.01933333 0.03346667
## ASV_6 0.02646667 0.01856667 0.02110000 0.02353333 0.03806667
```

```r
# Taxonomic annotation table of ASVs or OTUs
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859     8
```

```
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##   OTUID   Kingdom  Phylum          Class           Order
##   <chr>   <chr>    <chr>           <chr>           <chr>
## 1 ASV_2   Archaea  Thaumarchaeota  Unassigned      Nitrososphaerales
## 2 ASV_3   Bacteria Verrucomicrobia Spartobacteria  Unassigned
## 3 ASV_31  Bacteria Actinobacteria  Actinobacteria  Actinomycetales
## 4 ASV_27  Archaea  Thaumarchaeota  Unassigned      Nitrososphaerales
## 5 ASV_9   Bacteria Unassigned      Unassigned      Unassigned
```

Build graph object

```
graph_obj <- build_graph_from_mat(
  mat = otu_rare_relative,
  transfrom.method = "none", #  based your input data
  r.threshold = 0.7,
  p.threshold = 0.05,
  method = "WGCNA",
  cor.method = "pearson",
  proc = "Bonferroni",
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj
```

```
## # A tbl_graph: 213 nodes and 844 edges
## #
## # An undirected simple graph with 29 components
## #
## # Node Data: 213 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>  <dbl>   <chr>
## 1 ASV_649 5          5           5           5              27   26.5   Bacter~
## 2 ASV_705 5          5           5           5              27   26.5   Bacter~
## 3 ASV_12~ 5          5           5           5              27   26.5   Bacter~
## 4 ASV_13~ 5          5           5           5              27   26.5   Bacter~
## 5 ASV_14~ 5          5           5           5              27   26.5   Bacter~
## 6 ASV_14~ 5          5           5           5              27   26.5   Bacter~
```

```
##  7 ASV_24~ 5          5          5          5          27      26.5 Bacter~
##  8 ASV_25~ 5          5          5          5          27      26.4 Bacter~
##  9 ASV_28~ 5          5          5          5          27      26.5 Bacter~
## 10 ASV_28~ 5          5          5          5          27      26.5 Bacter~
## # i 203 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 844 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1    194   195  0.959       0.959 Positive
## 2    185   208  0.954       0.954 Positive
## 3    185   213  0.957       0.957 Positive
## # i 841 more rows
```

5.1 Extract subgraph by module

5.1.1 select subgraph by modularity

Select one modularity

```
module5_subgraph_info <- get_subgraph(graph_obj = graph_obj,
                                      select_module = "5")
```

```
##     Module Number
## 1        5     31
## 2        2     24
## 3        8     22
## 4       21     15
## 5        1     13
## 6        3     11
## 7        4     11
## 8        6     11
## 9       25      8
## 10       7      6
## 11      12      5
## 12      22      5
## 13      10      4
## 14      11      4
## 15      15      4
## 16 Others     39
```

```r
class(module5_subgraph_info)
```

```
## [1] "list"
```

```r
names(module5_subgraph_info)
```

```
## [1] "sub_graph_all"    "stat_module"        "sub_graph_select"
```

```r
module5_subgraph_info$stat_module
```

```
##      Module Number
## 1         5     31
## 2         2     24
## 3         8     22
## 4        21     15
## 5         1     13
## 6         3     11
## 7         4     11
## 8         6     11
## 9        25      8
## 10        7      6
## 11       12      5
## 12       22      5
## 13       10      4
## 14       11      4
## 15       15      4
## 16 Others     39
```

```r
module5_subgraph_info$sub_graph_all
```

```
## $`5`
## # A tbl_graph: 31 nodes and 330 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 31 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_649 5           5           5           5              27    26.5 Bacter~
## 2 ASV_705 5           5           5           5              27    26.5 Bacter~
## 3 ASV_12~ 5           5           5           5              27    26.5 Bacter~
## 4 ASV_13~ 5           5           5           5              27    26.5 Bacter~
```

```
##  5 ASV_14~ 5           5           5           5           27      26.5 Bacter~
##  6 ASV_14~ 5           5           5           5           27      26.5 Bacter~
##  7 ASV_24~ 5           5           5           5           27      26.5 Bacter~
##  8 ASV_25~ 5           5           5           5           27      26.4 Bacter~
##  9 ASV_28~ 5           5           5           5           27      26.5 Bacter~
## 10 ASV_28~ 5           5           5           5           27      26.5 Bacter~
## # i 21 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 330 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1      1     2  0.996       0.996 Positive
## 2      1     3  0.997       0.997 Positive
## 3      2     3  0.994       0.994 Positive
## # i 327 more rows
##
## $`2`
## # A tbl_graph: 24 nodes and 121 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 24 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>       <ord>       <chr>       <ord>      <dbl>    <dbl> <chr>
## 1  ASV_671 2           2           2           2             18     17.5 Bacter~
## 2  ASV_18~ 2           2           2           2             17     16.6 Bacter~
## 3  ASV_29~ 2           2           2           2             17     16.6 Bacter~
## 4  ASV_568 2           2           2           2             16     15.6 Bacter~
## 5  ASV_10~ 2           2           2           2             16     15.6 Bacter~
## 6  ASV_11~ 2           2           2           2             16     15.6 Bacter~
## 7  ASV_24~ 2           2           2           2             15     14.5 Bacter~
## 8  ASV_28~ 2           2           2           2             14     13.5 Bacter~
## 9  ASV_15~ 2           2           2           2             13     12.6 Bacter~
## 10 ASV_24~ 2           2           2           2             13     12.5 Bacter~
## # i 14 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 121 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1      1     2  0.991       0.991 Positive
## 2      1     3  0.992       0.992 Positive
## 3      2     3  0.996       0.996 Positive
```

```
## # i 118 more rows
##
## $`8`
## # A tbl_graph: 22 nodes and 131 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 22 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1  ASV_802 8          8           8           8              18    17.5 Bacter~
## 2  ASV_723 8          8           8           8              18    17.5 Bacter~
## 3  ASV_11~ 8          8           8           8              18    17.6 Bacter~
## 4  ASV_29~ 8          8           8           8              18    17.6 Bacter~
## 5  ASV_927 8          8           8           8              16    15.6 Bacter~
## 6  ASV_13~ 8          8           8           8              16    15.5 Bacter~
## 7  ASV_29~ 8          8           8           8              16    15.5 Bacter~
## 8  ASV_10~ 8          8           8           8              15    14.4 Bacter~
## 9  ASV_13~ 8          8           8           8              15    14.6 Bacter~
## 10 ASV_14~ 8          8           8           8              15    14.7 Bacter~
## # i 12 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 131 x 5
##    from     to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.990       0.990 Positive
## 2     1     3  0.993       0.993 Positive
## 3     2     3  0.997       0.997 Positive
## # i 128 more rows
##
## $`21`
## # A tbl_graph: 15 nodes and 42 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 15 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1  ASV_25~ 21         21          21          21             13    12.5 Bacter~
## 2  ASV_27~ 21         21          21          21             12    11.6 Bacter~
## 3  ASV_879 21         21          21          21              8    7.67 Bacter~
## 4  ASV_10~ 21         21          21          21              6    5.76 Bacter~
## 5  ASV_16~ 21         21          21          21              6    5.70 Bacter~
## 6  ASV_511 21         21          21          21              5    4.80 Bacter~
```

```
## 7 ASV_578 21           21           21           21           5   4.76 Bacter~
## 8 ASV_917 21           21           21           21           5   4.80 Bacter~
## 9 ASV_18~ 21           21           21           21           5   4.81 Bacter~
## 10 ASV_70  21           21           21           21           4   3.82 Bacter~
## 11 ASV_13~ 21           21           21           21           4   3.86 Bacter~
## 12 ASV_839 21           21           21           21           3   2.85 Bacter~
## 13 ASV_20~ 21           21           21           21           3   2.86 Bacter~
## 14 ASV_21~ 21           21           21           21           3   2.86 Bacter~
## 15 ASV_88  21           21           21           21           2   1.90 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 42 x 5
##    from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1    1     2  0.986       0.986 Positive
## 2    1     3  0.973       0.973 Positive
## 3    2     3  0.976       0.976 Positive
## # i 39 more rows
##
## $`1`
## # A tbl_graph: 13 nodes and 43 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 13 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_19~ 1          1           1           1               9   8.86  Bacter~
## 2 ASV_15~ 1          1           1           1               9   8.86  Bacter~
## 3 ASV_24~ 1          1           1           1               9   8.87  Bacter~
## 4 ASV_20~ 1          1           1           1               9   8.79  Bacter~
## 5 ASV_20~ 1          1           1           1               9   8.87  Bacter~
## 6 ASV_26~ 1          1           1           1               9   8.87  Unassi~
## 7 ASV_968 1          1           1           1               8   7.88  Bacter~
## 8 ASV_27~ 1          1           1           1               8   7.73  Bacter~
## 9 ASV_161 1          1           1           1               7   6.80  Bacter~
## 10 ASV_25~ 1          1           1           1               5   4.72  Bacter~
## 11 ASV_534 1          1           1           1               2   1.90  Bacter~
## 12 ASV_26~ 1          1           1           1               1   0.944 Bacter~
## 13 ASV_29~ 1          1           1           1               1   0.963 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 43 x 5
##    from    to weight correlation corr_direction
```

```
##   <int> <int>  <dbl>        <dbl> <chr>
## 1    1    2  0.998       0.998 Positive
## 2    1    3  0.999       0.999 Positive
## 3    2    3  1.000       1.000 Positive
## # i 40 more rows
##
## $`3`
## # A tbl_graph: 11 nodes and 38 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
##  1 ASV_945 3          3           3           3               9     8.71 Bacter~
##  2 ASV_19~ 3          3           3           3               9     8.72 Bacter~
##  3 ASV_69  3          3           3           3               8     7.85 Bacter~
##  4 ASV_173 3          3           3           3               8     7.87 Bacter~
##  5 ASV_206 3          3           3           3               8     7.83 Bacter~
##  6 ASV_744 3          3           3           3               8     7.71 Bacter~
##  7 ASV_14~ 3          3           3           3               8     7.71 Bacter~
##  8 ASV_23~ 3          3           3           3               8     7.67 Bacter~
##  9 ASV_22~ 3          3           3           3               8     7.70 Bacter~
## 10 ASV_218 3          3           3           3               1    0.955 Bacter~
## 11 ASV_14~ 3          3           3           3               1    0.944 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 38 x 5
##    from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1    1    2  0.982       0.982 Positive
## 2    1    3  0.985       0.985 Positive
## 3    2    3  0.986       0.986 Positive
## # i 35 more rows
##
## $`4`
## # A tbl_graph: 11 nodes and 33 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
##  1 ASV_459 4          4           4           4               8     7.87 Bacter~
##  2 ASV_533 4          4           4           4               8     7.85 Bacter~
```

```
##  3 ASV_10~ 4            4            4           4                 8    7.87   Bacter~
##  4 ASV_13~ 4            4            4           4                 8    7.81   Bacter~
##  5 ASV_23~ 4            4            4           4                 8    7.87   Bacter~
##  6 ASV_24~ 4            4            4           4                 7    6.88   Bacter~
##  7 ASV_22~ 4            4            4           4                 7    6.81   Bacter~
##  8 ASV_29~ 4            4            4           4                 6    5.77   Bacter~
##  9 ASV_29~ 4            4            4           4                 4    3.79   Bacter~
## 10 ASV_746 4            4            4           4                 1    0.945  Bacter~
## 11 ASV_19~ 4            4            4           4                 1    0.953  Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 33 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.997       0.997 Positive
## 2     1     3  1.000       1.000 Positive
## 3     2     3  0.998       0.998 Positive
## # i 30 more rows
##
## $`6`
## # A tbl_graph: 11 nodes and 24 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
##  1 ASV_116 6           6           6           6               8    7.67  Bacter~
##  2 ASV_661 6           6           6           6               8    7.71  Bacter~
##  3 ASV_25~ 6           6           6           6               6    5.79  Bacter~
##  4 ASV_975 6           6           6           6               5    4.78  Bacter~
##  5 ASV_10~ 6           6           6           6               5    4.77  Bacter~
##  6 ASV_20~ 6           6           6           6               5    4.79  Bacter~
##  7 ASV_27~ 6           6           6           6               4    3.84  Bacter~
##  8 ASV_94  6           6           6           6               3    2.84  Bacter~
##  9 ASV_20~ 6           6           6           6               2    1.92  Bacter~
## 10 ASV_442 6           6           6           6               1    0.946 Bacter~
## 11 ASV_408 6           6           6           6               1    0.959 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 24 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.974       0.974 Positive
```

```
## 2     1    3  0.966        0.966 Positive
## 3     2    3  0.979        0.979 Positive
## # i 21 more rows
##
## $`25`
## # A tbl_graph: 8 nodes and 22 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 8 x 14 (active)
##   name       modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>      <fct>      <ord>       <chr>       <ord>         <dbl>   <dbl> <chr>
## 1 ASV_1505 25           25          25          25               7    6.66 Bacter~
## 2 ASV_415  25           25          25          25               6    5.78 Bacter~
## 3 ASV_517  25           25          25          25               6    5.84 Bacter~
## 4 ASV_842  25           25          25          25               6    5.80 Bacter~
## 5 ASV_1719 25           25          25          25               6    5.85 Bacter~
## 6 ASV_2286 25           25          25          25               6    5.81 Bacter~
## 7 ASV_2637 25           25          25          25               5    4.78 Bacter~
## 8 ASV_1474 25           25          25          25               2    1.90 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 22 x 5
##    from   to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1    1    2  0.947        0.947 Positive
## 2    1    3  0.951        0.951 Positive
## 3    2    3  0.970        0.970 Positive
## # i 19 more rows
##
## $`7`
## # A tbl_graph: 6 nodes and 5 edges
## #
## # An unrooted tree
## #
## # Node Data: 6 x 14 (active)
##   name       modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>      <fct>      <ord>       <chr>       <ord>         <dbl>   <dbl> <chr>
## 1 ASV_1896 7            7           7           7                3    2.87  Bacter~
## 2 ASV_454  7            7           7           7                2    1.89  Bacter~
## 3 ASV_1090 7            7           7           7                2    1.89  Bacter~
## 4 ASV_231  7            7           7           7                1    0.968 Bacter~
## 5 ASV_1800 7            7           7           7                1    0.943 Bacter~
## 6 ASV_2038 7            7           7           7                1    0.956 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
```

```
## #    Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.945       0.945 Positive
## 2     2     3  0.944       0.944 Positive
## 3     1     4  0.968       0.968 Positive
## # i 2 more rows
##
## $`12`
## # A tbl_graph: 5 nodes and 5 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_1148 12         12          12          12              4    3.85 Bacter~
## 2 ASV_1104 12         12          12          12              2    1.92 Bacter~
## 3 ASV_1854 12         12          12          12              2    1.95 Bacter~
## 4 ASV_115  12         12          12          12              1   0.955 Bacter~
## 5 ASV_2484 12         12          12          12              1   0.948 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #    Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.959       0.959 Positive
## 2     1     3  0.990       0.990 Positive
## 3     2     3  0.957       0.957 Positive
## # i 2 more rows
##
## $`22`
## # A tbl_graph: 5 nodes and 7 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_1931 22         22          22          22              4    3.88 Bacter~
## 2 ASV_1320 22         22          22          22              3    2.89 Bacter~
## 3 ASV_1906 22         22          22          22              3    2.91 Bacter~
## 4 ASV_2704 22         22          22          22              3    2.91 Bacter~
```

```
## 5 ASV_1495 22           22          22          22           1    0.970 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 7 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.971       0.971 Positive
## 2     1     3  0.969       0.969 Positive
## 3     2     3  0.959       0.959 Positive
## # i 4 more rows
##
## $`10`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>    <fct>       <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1 ASV_2059 10          10          10          10              2     1.89 Bacter~
## 2 ASV_1965 10          10          10          10              2     1.91 Bacter~
## 3 ASV_544  10          10          10          10              1    0.964 Bacter~
## 4 ASV_1607 10          10          10          10              1    0.946 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.943       0.943 Positive
## 2     2     3  0.964       0.964 Positive
## 3     1     4  0.946       0.946 Positive
##
## $`11`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>    <fct>       <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1 ASV_614  11          11          11          11              2     1.91 Bacter~
## 2 ASV_2916 11          11          11          11              2     1.93 Bacter~
## 3 ASV_65   11          11          11          11              1    0.943 Archaea
## 4 ASV_2168 11          11          11          11              1    0.965 Bacter~
```

```
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.966       0.966 Positive
## 2     1     3  0.943       0.943 Positive
## 3     2     4  0.965       0.965 Positive
##
## $`15`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>       <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_172   15          15          15          15              2    1.92 Bacter~
## 2 ASV_246   15          15          15          15              2    1.91 Bacter~
## 3 ASV_43    15          15          15          15              1   0.969 Bacter~
## 4 ASV_2211  15          15          15          15              1   0.955 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.952       0.952 Positive
## 2     1     3  0.969       0.969 Positive
## 3     2     4  0.955       0.955 Positive
##
## $Others
## # A tbl_graph: 39 nodes and 34 edges
## #
## # An undirected simple graph with 14 components
## #
## # Node Data: 39 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>       <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_316  28          Others      Others      Others          3    2.89 Bacter~
## 2 ASV_610  28          Others      Others      Others          3    2.94 Bacter~
## 3 ASV_11~  29          Others      Others      Others          3    2.94 Bacter~
## 4 ASV_18~  29          Others      Others      Others          3    2.95 Bacter~
## 5 ASV_11~  27          Others      Others      Others          3    2.91 Bacter~
## 6 ASV_18~  28          Others      Others      Others          3    2.91 Bacter~
```

```
##  7 ASV_20~ 29           Others        Others        Others            3     2.89 Bacter~
##  8 ASV_24~ 27           Others        Others        Others            3     2.89 Bacter~
##  9 ASV_27~ 29           Others        Others        Others            3     2.95 Bacter~
## 10 ASV_28~ 28           Others        Others        Others            3     2.90 Bacter~
## # i 29 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 34 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.971       0.971 Positive
## 2     3     4  0.987       0.987 Positive
## 3     1     6  0.958       0.958 Positive
## # i 31 more rows
```

```
module5_subgraph_info$sub_graph_select
```

```
## # A tbl_graph: 31 nodes and 330 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 31 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>       <ord>       <chr>       <ord>        <dbl>    <dbl> <chr>
## 1  ASV_649 5           5           5           5               27     26.5 Bacter~
## 2  ASV_705 5           5           5           5               27     26.5 Bacter~
## 3  ASV_12~ 5           5           5           5               27     26.5 Bacter~
## 4  ASV_13~ 5           5           5           5               27     26.5 Bacter~
## 5  ASV_14~ 5           5           5           5               27     26.5 Bacter~
## 6  ASV_14~ 5           5           5           5               27     26.5 Bacter~
## 7  ASV_24~ 5           5           5           5               27     26.5 Bacter~
## 8  ASV_25~ 5           5           5           5               27     26.4 Bacter~
## 9  ASV_28~ 5           5           5           5               27     26.5 Bacter~
## 10 ASV_28~ 5           5           5           5               27     26.5 Bacter~
## # i 21 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 330 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1    29    30  0.949       0.949 Positive
## 2    21    29  0.952       0.952 Positive
## 3    25    29  0.965       0.965 Positive
```

```
## # i 327 more rows
```

Select multi-modularity

```
module5_2_8_subgraph_info <- get_subgraph(graph_obj = graph_obj,
                                          select_module = c("5","2","8"))
```

```
##      Module Number
## 1         5     31
## 2         2     24
## 3         8     22
## 4        21     15
## 5         1     13
## 6         3     11
## 7         4     11
## 8         6     11
## 9        25      8
## 10        7      6
## 11       12      5
## 12       22      5
## 13       10      4
## 14       11      4
## 15       15      4
## 16 Others     39
```

```
class(module5_2_8_subgraph_info)
```

```
## [1] "list"
```

```
names(module5_2_8_subgraph_info)
```

```
## [1] "sub_graph_all"    "stat_module"       "sub_graph_select"
```

```
module5_2_8_subgraph_info$stat_module
```

```
##      Module Number
## 1         5     31
## 2         2     24
## 3         8     22
## 4        21     15
## 5         1     13
## 6         3     11
```

```
## 7          4      11
## 8          6      11
## 9         25       8
## 10         7       6
## 11        12       5
## 12        22       5
## 13        10       4
## 14        11       4
## 15        15       4
## 16 Others         39
```

```
module5_2_8_subgraph_info$sub_graph_all
```

```
## $`5`
## # A tbl_graph: 31 nodes and 330 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 31 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_649 5          5           5           5              27    26.5 Bacter~
## 2 ASV_705 5          5           5           5              27    26.5 Bacter~
## 3 ASV_12~ 5          5           5           5              27    26.5 Bacter~
## 4 ASV_13~ 5          5           5           5              27    26.5 Bacter~
## 5 ASV_14~ 5          5           5           5              27    26.5 Bacter~
## 6 ASV_14~ 5          5           5           5              27    26.5 Bacter~
## 7 ASV_24~ 5          5           5           5              27    26.5 Bacter~
## 8 ASV_25~ 5          5           5           5              27    26.4 Bacter~
## 9 ASV_28~ 5          5           5           5              27    26.5 Bacter~
## 10 ASV_28~ 5          5           5           5              27    26.5 Bacter~
## # i 21 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 330 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.996       0.996 Positive
## 2     1     3  0.997       0.997 Positive
## 3     2     3  0.994       0.994 Positive
## # i 327 more rows
##
## $`2`
## # A tbl_graph: 24 nodes and 121 edges
```

```
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 24 x 14 (active)
##      name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##      <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##   1 ASV_671 2          2           2           2              18    17.5 Bacter~
##   2 ASV_18~ 2          2           2           2              17    16.6 Bacter~
##   3 ASV_29~ 2          2           2           2              17    16.6 Bacter~
##   4 ASV_568 2          2           2           2              16    15.6 Bacter~
##   5 ASV_10~ 2          2           2           2              16    15.6 Bacter~
##   6 ASV_11~ 2          2           2           2              16    15.6 Bacter~
##   7 ASV_24~ 2          2           2           2              15    14.5 Bacter~
##   8 ASV_28~ 2          2           2           2              14    13.5 Bacter~
##   9 ASV_15~ 2          2           2           2              13    12.6 Bacter~
## 10 ASV_24~ 2          2           2           2              13    12.5 Bacter~
## # i 14 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 121 x 5
##      from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.991       0.991 Positive
## 2     1     3  0.992       0.992 Positive
## 3     2     3  0.996       0.996 Positive
## # i 118 more rows
##
## $`8`
## # A tbl_graph: 22 nodes and 131 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 22 x 14 (active)
##      name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##      <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##   1 ASV_802 8          8           8           8              18    17.5 Bacter~
##   2 ASV_723 8          8           8           8              18    17.5 Bacter~
##   3 ASV_11~ 8          8           8           8              18    17.6 Bacter~
##   4 ASV_29~ 8          8           8           8              18    17.6 Bacter~
##   5 ASV_927 8          8           8           8              16    15.6 Bacter~
##   6 ASV_13~ 8          8           8           8              16    15.5 Bacter~
##   7 ASV_29~ 8          8           8           8              16    15.5 Bacter~
##   8 ASV_10~ 8          8           8           8              15    14.4 Bacter~
##   9 ASV_13~ 8          8           8           8              15    14.6 Bacter~
## 10 ASV_14~ 8          8           8           8              15    14.7 Bacter~
```

```
## # i 12 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 131 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.990       0.990 Positive
## 2     1     3  0.993       0.993 Positive
## 3     2     3  0.997       0.997 Positive
## # i 128 more rows
##
## $`21`
## # A tbl_graph: 15 nodes and 42 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 15 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##  1 ASV_25~  21         21          21          21             13   12.5  Bacter~
##  2 ASV_27~  21         21          21          21             12   11.6  Bacter~
##  3 ASV_879  21         21          21          21              8    7.67 Bacter~
##  4 ASV_10~  21         21          21          21              6    5.76 Bacter~
##  5 ASV_16~  21         21          21          21              6    5.70 Bacter~
##  6 ASV_511  21         21          21          21              5    4.80 Bacter~
##  7 ASV_578  21         21          21          21              5    4.76 Bacter~
##  8 ASV_917  21         21          21          21              5    4.80 Bacter~
##  9 ASV_18~  21         21          21          21              5    4.81 Bacter~
## 10 ASV_70   21         21          21          21              4    3.82 Bacter~
## 11 ASV_13~  21         21          21          21              4    3.86 Bacter~
## 12 ASV_839  21         21          21          21              3    2.85 Bacter~
## 13 ASV_20~  21         21          21          21              3    2.86 Bacter~
## 14 ASV_21~  21         21          21          21              3    2.86 Bacter~
## 15 ASV_88   21         21          21          21              2    1.90 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 42 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.986       0.986 Positive
## 2     1     3  0.973       0.973 Positive
## 3     2     3  0.976       0.976 Positive
## # i 39 more rows
##
```

```
## $`1`
## # A tbl_graph: 13 nodes and 43 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 13 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_19~ 1          1           1           1               9    8.86 Bacter~
## 2 ASV_15~ 1          1           1           1               9    8.86 Bacter~
## 3 ASV_24~ 1          1           1           1               9    8.87 Bacter~
## 4 ASV_20~ 1          1           1           1               9    8.79 Bacter~
## 5 ASV_20~ 1          1           1           1               9    8.87 Bacter~
## 6 ASV_26~ 1          1           1           1               9    8.87 Unassi~
## 7 ASV_968 1          1           1           1               8    7.88 Bacter~
## 8 ASV_27~ 1          1           1           1               8    7.73 Bacter~
## 9 ASV_161 1          1           1           1               7    6.80 Bacter~
## 10 ASV_25~ 1          1           1           1               5    4.72 Bacter~
## 11 ASV_534 1          1           1           1               2    1.90 Bacter~
## 12 ASV_26~ 1          1           1           1               1   0.944 Bacter~
## 13 ASV_29~ 1          1           1           1               1   0.963 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 43 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.998       0.998 Positive
## 2     1     3  0.999       0.999 Positive
## 3     2     3  1.000       1.000 Positive
## # i 40 more rows
##
## $`3`
## # A tbl_graph: 11 nodes and 38 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_945 3          3           3           3               9    8.71 Bacter~
## 2 ASV_19~ 3          3           3           3               9    8.72 Bacter~
## 3 ASV_69  3          3           3           3               8    7.85 Bacter~
## 4 ASV_173 3          3           3           3               8    7.87 Bacter~
## 5 ASV_206 3          3           3           3               8    7.83 Bacter~
## 6 ASV_744 3          3           3           3               8    7.71 Bacter~
```

```
##  7 ASV_14~ 3            3            3            3            8    7.71   Bacter~
##  8 ASV_23~ 3            3            3            3            8    7.67   Bacter~
##  9 ASV_22~ 3            3            3            3            8    7.70   Bacter~
## 10 ASV_218 3            3            3            3            1    0.955  Bacter~
## 11 ASV_14~ 3            3            3            3            1    0.944  Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 38 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.982       0.982 Positive
## 2     1     3  0.985       0.985 Positive
## 3     2     3  0.986       0.986 Positive
## # i 35 more rows
##
## $`4`
## # A tbl_graph: 11 nodes and 33 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##     name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1  ASV_459 4           4           4           4               8    7.87  Bacter~
## 2  ASV_533 4           4           4           4               8    7.85  Bacter~
## 3  ASV_10~ 4           4           4           4               8    7.87  Bacter~
## 4  ASV_13~ 4           4           4           4               8    7.81  Bacter~
## 5  ASV_23~ 4           4           4           4               8    7.87  Bacter~
## 6  ASV_24~ 4           4           4           4               7    6.88  Bacter~
## 7  ASV_22~ 4           4           4           4               7    6.81  Bacter~
## 8  ASV_29~ 4           4           4           4               6    5.77  Bacter~
## 9  ASV_29~ 4           4           4           4               4    3.79  Bacter~
## 10 ASV_746 4           4           4           4               1    0.945 Bacter~
## 11 ASV_19~ 4           4           4           4               1    0.953 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 33 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.997       0.997 Positive
## 2     1     3  1.000       1.000 Positive
## 3     2     3  0.998       0.998 Positive
## # i 30 more rows
##
```

```
## $`6`
## # A tbl_graph: 11 nodes and 24 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 11 x 14 (active)
##      name   modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##      <chr>  <fct>      <ord>       <chr>       <ord>      <dbl>    <dbl> <chr>
##  1 ASV_116 6          6           6           6              8     7.67  Bacter~
##  2 ASV_661 6          6           6           6              8     7.71  Bacter~
##  3 ASV_25~ 6          6           6           6              6     5.79  Bacter~
##  4 ASV_975 6          6           6           6              5     4.78  Bacter~
##  5 ASV_10~ 6          6           6           6              5     4.77  Bacter~
##  6 ASV_20~ 6          6           6           6              5     4.79  Bacter~
##  7 ASV_27~ 6          6           6           6              4     3.84  Bacter~
##  8 ASV_94  6          6           6           6              3     2.84  Bacter~
##  9 ASV_20~ 6          6           6           6              2     1.92  Bacter~
## 10 ASV_442 6          6           6           6              1    0.946  Bacter~
## 11 ASV_408 6          6           6           6              1    0.959  Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 24 x 5
##     from    to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.974       0.974 Positive
## 2     1     3  0.966       0.966 Positive
## 3     2     3  0.979       0.979 Positive
## # i 21 more rows
##
## $`25`
## # A tbl_graph: 8 nodes and 22 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 8 x 14 (active)
##      name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##      <chr>   <fct>      <ord>       <chr>       <ord>      <dbl>    <dbl> <chr>
## 1 ASV_1505 25         25          25          25             7     6.66 Bacter~
## 2 ASV_415  25         25          25          25             6     5.78 Bacter~
## 3 ASV_517  25         25          25          25             6     5.84 Bacter~
## 4 ASV_842  25         25          25          25             6     5.80 Bacter~
## 5 ASV_1719 25         25          25          25             6     5.85 Bacter~
## 6 ASV_2286 25         25          25          25             6     5.81 Bacter~
## 7 ASV_2637 25         25          25          25             5     4.78 Bacter~
## 8 ASV_1474 25         25          25          25             2     1.90 Bacter~
```

```
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 22 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.947       0.947 Positive
## 2     1     3  0.951       0.951 Positive
## 3     2     3  0.970       0.970 Positive
## # i 19 more rows
##
## $`7`
## # A tbl_graph: 6 nodes and 5 edges
## #
## # An unrooted tree
## #
## # Node Data: 6 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1 ASV_1896  7          7           7           7               3     2.87 Bacter~
## 2 ASV_454   7          7           7           7               2     1.89 Bacter~
## 3 ASV_1090  7          7           7           7               2     1.89 Bacter~
## 4 ASV_231   7          7           7           7               1    0.968 Bacter~
## 5 ASV_1800  7          7           7           7               1    0.943 Bacter~
## 6 ASV_2038  7          7           7           7               1    0.956 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.945       0.945 Positive
## 2     2     3  0.944       0.944 Positive
## 3     1     4  0.968       0.968 Positive
## # i 2 more rows
##
## $`12`
## # A tbl_graph: 5 nodes and 5 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##   name      modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>     <fct>      <ord>       <chr>       <ord>       <dbl>    <dbl> <chr>
## 1 ASV_1148  12         12          12          12              4     3.85 Bacter~
## 2 ASV_1104  12         12          12          12              2     1.92 Bacter~
```

```
## 3 ASV_1854 12           12           12           12                   2    1.95  Bacter~
## 4 ASV_115  12           12           12           12                   1    0.955 Bacter~
## 5 ASV_2484 12           12           12           12                   1    0.948 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 5 x 5
##     from   to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1    2  0.959       0.959 Positive
## 2     1    3  0.990       0.990 Positive
## 3     2    3  0.957       0.957 Positive
## # i 2 more rows
##
## $`22`
## # A tbl_graph: 5 nodes and 7 edges
## #
## # An undirected simple graph with 1 component
## #
## # Node Data: 5 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>         <dbl>    <dbl> <chr>
## 1 ASV_1931 22         22          22          22                4    3.88  Bacter~
## 2 ASV_1320 22         22          22          22                3    2.89  Bacter~
## 3 ASV_1906 22         22          22          22                3    2.91  Bacter~
## 4 ASV_2704 22         22          22          22                3    2.91  Bacter~
## 5 ASV_1495 22         22          22          22                1    0.970 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 7 x 5
##     from   to weight correlation corr_direction
##    <int> <int>  <dbl>       <dbl> <chr>
## 1     1    2  0.971       0.971 Positive
## 2     1    3  0.969       0.969 Positive
## 3     2    3  0.959       0.959 Positive
## # i 4 more rows
##
## $`10`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##    name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>    <fct>      <ord>       <chr>       <ord>         <dbl>    <dbl> <chr>
```

```
## 1 ASV_2059 10          10          10          10               2   1.89  Bacter~
## 2 ASV_1965 10          10          10          10               2   1.91  Bacter~
## 3 ASV_544  10          10          10          10               1   0.964 Bacter~
## 4 ASV_1607 10          10          10          10               1   0.946 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.943       0.943 Positive
## 2     2     3  0.964       0.964 Positive
## 3     1     4  0.946       0.946 Positive
##
## $`11`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_614  11         11          11          11              2   1.91  Bacter~
## 2 ASV_2916 11         11          11          11              2   1.93  Bacter~
## 3 ASV_65   11         11          11          11              1   0.943 Archaea
## 4 ASV_2168 11         11          11          11              1   0.965 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.966       0.966 Positive
## 2     1     3  0.943       0.943 Positive
## 3     2     4  0.965       0.965 Positive
##
## $`15`
## # A tbl_graph: 4 nodes and 3 edges
## #
## # An unrooted tree
## #
## # Node Data: 4 x 14 (active)
##   name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##   <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_172  15         15          15          15              2   1.92  Bacter~
## 2 ASV_246  15         15          15          15              2   1.91  Bacter~
```

```
## 3 ASV_43   15          15          15          15           1    0.969 Bacter~
## 4 ASV_2211 15          15          15          15           1    0.955 Bacter~
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 3 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.952       0.952 Positive
## 2     1     3  0.969       0.969 Positive
## 3     2     4  0.955       0.955 Positive
##
## $Others
## # A tbl_graph: 39 nodes and 34 edges
## #
## # An undirected simple graph with 14 components
## #
## # Node Data: 39 x 14 (active)
##     name     modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##     <chr>    <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1 ASV_316  28         Others      Others      Others          3    2.89 Bacter~
## 2 ASV_610  28         Others      Others      Others          3    2.94 Bacter~
## 3 ASV_11~  29         Others      Others      Others          3    2.94 Bacter~
## 4 ASV_18~  29         Others      Others      Others          3    2.95 Bacter~
## 5 ASV_11~  27         Others      Others      Others          3    2.91 Bacter~
## 6 ASV_18~  28         Others      Others      Others          3    2.91 Bacter~
## 7 ASV_20~  29         Others      Others      Others          3    2.89 Bacter~
## 8 ASV_24~  27         Others      Others      Others          3    2.89 Bacter~
## 9 ASV_27~  29         Others      Others      Others          3    2.95 Bacter~
## 10 ASV_28~ 28         Others      Others      Others          3    2.90 Bacter~
## # i 29 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 34 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1     1     2  0.971       0.971 Positive
## 2     3     4  0.987       0.987 Positive
## 3     1     6  0.958       0.958 Positive
## # i 31 more rows
```

```
module5_2_8_subgraph_info$sub_graph_select
```

```
## # A tbl_graph: 77 nodes and 582 edges
```

```
## #
## # An undirected simple graph with 3 components
## #
## # Node Data: 77 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
##  1 ASV_649 5          5           5           5              27    26.5 Bacter~
##  2 ASV_705 5          5           5           5              27    26.5 Bacter~
##  3 ASV_12~ 5          5           5           5              27    26.5 Bacter~
##  4 ASV_13~ 5          5           5           5              27    26.5 Bacter~
##  5 ASV_14~ 5          5           5           5              27    26.5 Bacter~
##  6 ASV_14~ 5          5           5           5              27    26.5 Bacter~
##  7 ASV_24~ 5          5           5           5              27    26.5 Bacter~
##  8 ASV_25~ 5          5           5           5              27    26.4 Bacter~
##  9 ASV_28~ 5          5           5           5              27    26.5 Bacter~
## 10 ASV_28~ 5          5           5           5              27    26.5 Bacter~
## # i 67 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 582 x 5
##     from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1    56    74  0.952       0.952 Positive
## 2    57    74  0.954       0.954 Positive
## 3    58    74  0.947       0.947 Positive
## # i 579 more rows
```

5.2   Extract subgraph by sample

Chapter 6

Network layout

Load R Package

```
library(tidyverse)
library(ggNetView)
```

Example data

```
# Access built-in example datasets in ggNetView

# Relative abundance table of rarefied ASVs or OTUs
data("otu_rare_relative")
dim(otu_rare_relative)
```

```
## [1] 2859    18
```

```
otu_rare_relative[1:5, 1:5]
```

```
##                 KO1        KO2        KO3        KO4        KO5
## ASV_1 0.03306667 0.05453333 0.02013333 0.03613333 0.02686667
## ASV_2 0.05750000 0.03393333 0.06046667 0.05810000 0.07320000
## ASV_3 0.01733333 0.01296667 0.02290000 0.02336667 0.03106667
## ASV_4 0.04266667 0.01093333 0.01416667 0.01933333 0.03346667
## ASV_6 0.02646667 0.01856667 0.02110000 0.02353333 0.03806667
```

```
# Taxonomic annotation table of ASVs or OTUs
data("tax_tab")
dim(tax_tab)
```

```
## [1] 2859    8
```

```
tax_tab[1:5, 1:5]
```

```
## # A tibble: 5 x 5
##   OTUID  Kingdom  Phylum          Class         Order
##   <chr>  <chr>    <chr>           <chr>         <chr>
## 1 ASV_2  Archaea  Thaumarchaeota  Unassigned    Nitrososphaerales
## 2 ASV_3  Bacteria Verrucomicrobia Spartobacteria Unassigned
## 3 ASV_31 Bacteria Actinobacteria  Actinobacteria Actinomycetales
## 4 ASV_27 Archaea  Thaumarchaeota  Unassigned    Nitrososphaerales
## 5 ASV_9  Bacteria Unassigned      Unassigned    Unassigned
```

Build graph object

```
graph_obj <- build_graph_from_mat(
  mat = otu_rare_relative,
  transfrom.method = "none", #  based your input data
  r.threshold = 0.7,
  p.threshold = 0.05,
  method = "WGCNA",
  cor.method = "pearson",
  proc = "BH",
  module.method = "Fast_greedy",
  node_annotation = tax_tab,
  top_modules = 15,
  seed = 1115
)

graph_obj
```

```
## # A tbl_graph: 2049 nodes and 9602 edges
## #
## # An undirected simple graph with 100 components
## #
## # Node Data: 2,049 x 14 (active)
##    name    modularity modularity2 modularity3 Modularity Degree Strength Kingdom
##    <chr>   <fct>      <ord>       <chr>       <ord>       <dbl>   <dbl> <chr>
## 1  ASV_916 1          1           1           1              58    50.5 Bacter~
## 2  ASV_777 1          1           1           1              58    48.7 Bacter~
## 3  ASV_606 1          1           1           1              55    45.8 Bacter~
## 4  ASV_740 1          1           1           1              54    47.2 Bacter~
## 5  ASV_14~ 1          1           1           1              54    44.5 Bacter~
## 6  ASV_23~ 1          1           1           1              54    47.4 Bacter~
```
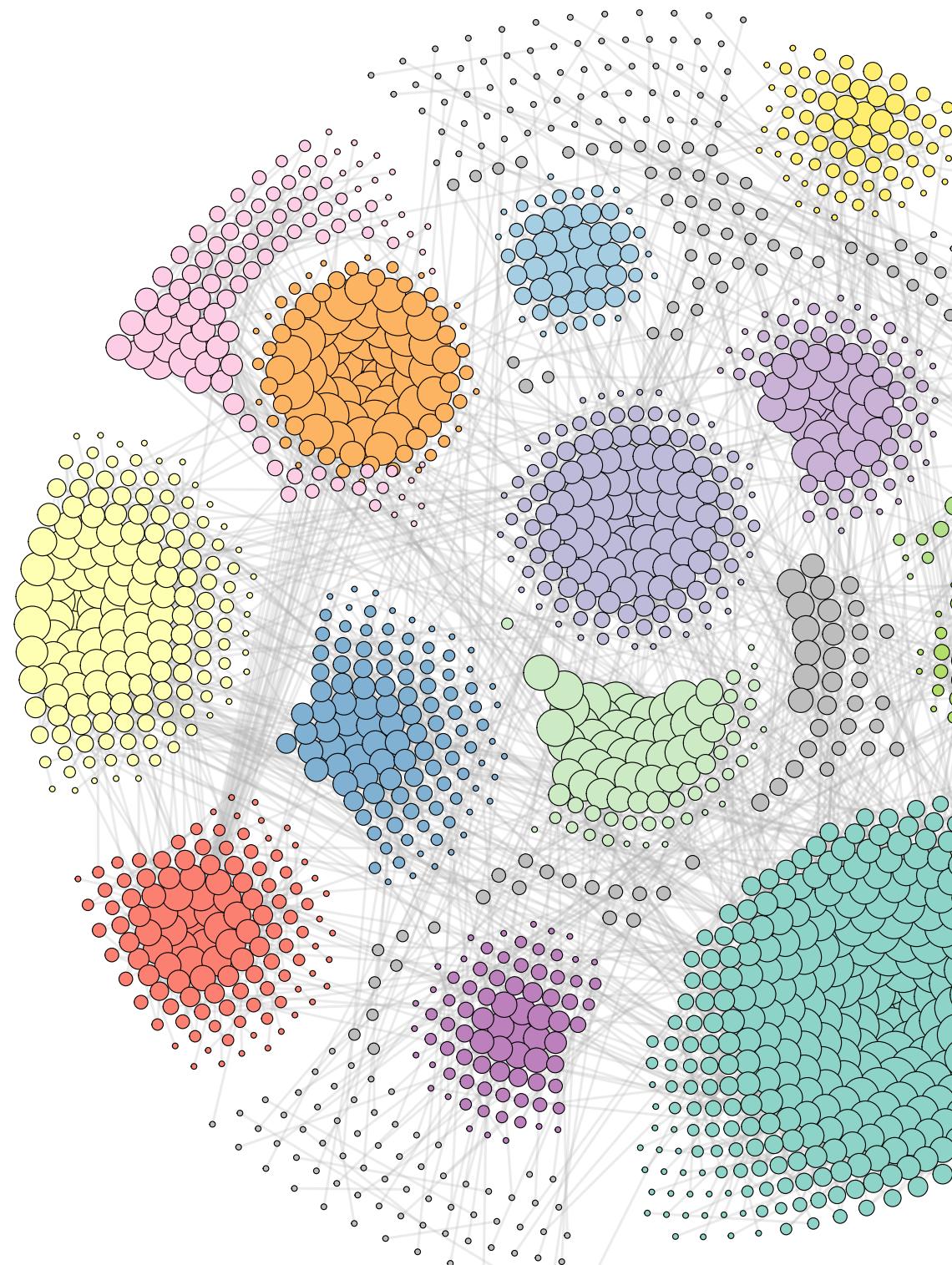
```
##  7 ASV_15~ 1          1          1          1          52     45.3 Bacter~
##  8 ASV_24~ 1          1          1          1          52     43.0 Bacter~
##  9 ASV_19~ 1          1          1          1          52     43.0 Bacter~
## 10 ASV_568 1          1          1          1          51     45.1 Bacter~
## # i 2,039 more rows
## # i 6 more variables: Phylum <chr>, Class <chr>, Order <chr>, Family <chr>,
## #   Genus <chr>, Species <chr>
## #
## # Edge Data: 9,602 x 5
##    from    to weight correlation corr_direction
##   <int> <int>  <dbl>       <dbl> <chr>
## 1  1771  1825  0.793       0.793 Positive
## 2   594   597  0.895       0.895 Positive
## 3   588   597  0.864       0.864 Positive
## # i 9,599 more rows
```

6.1   Gephi layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "gephi",
  center = F,
  shrink = 0.8,
  layout.module = "random",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
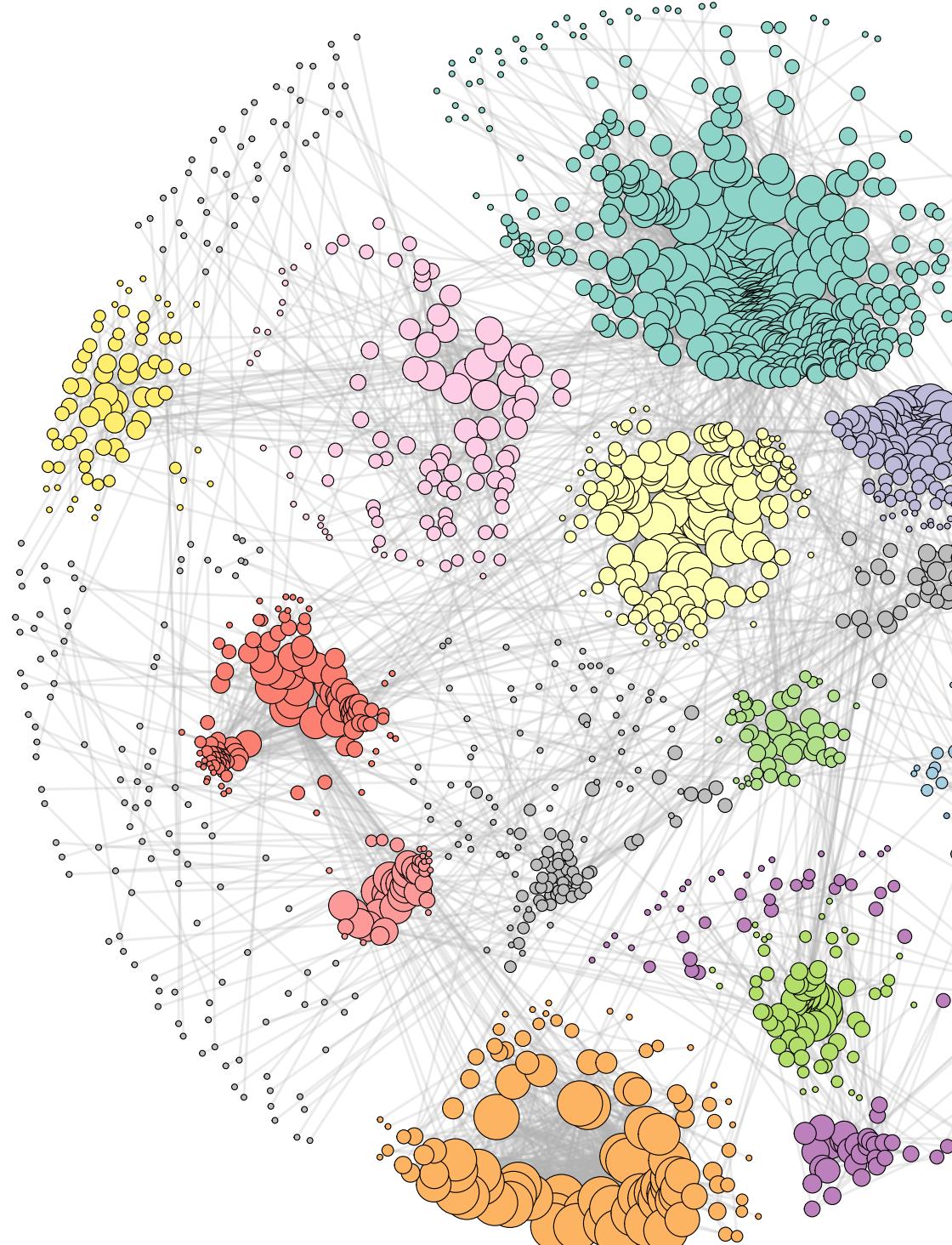
Node = 2049
Edge = 9602

6.2 Fruchterman–Reingold force-directed layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "fr2",
  center = F,
  shrink = 0.8,
  layout.module = "random",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
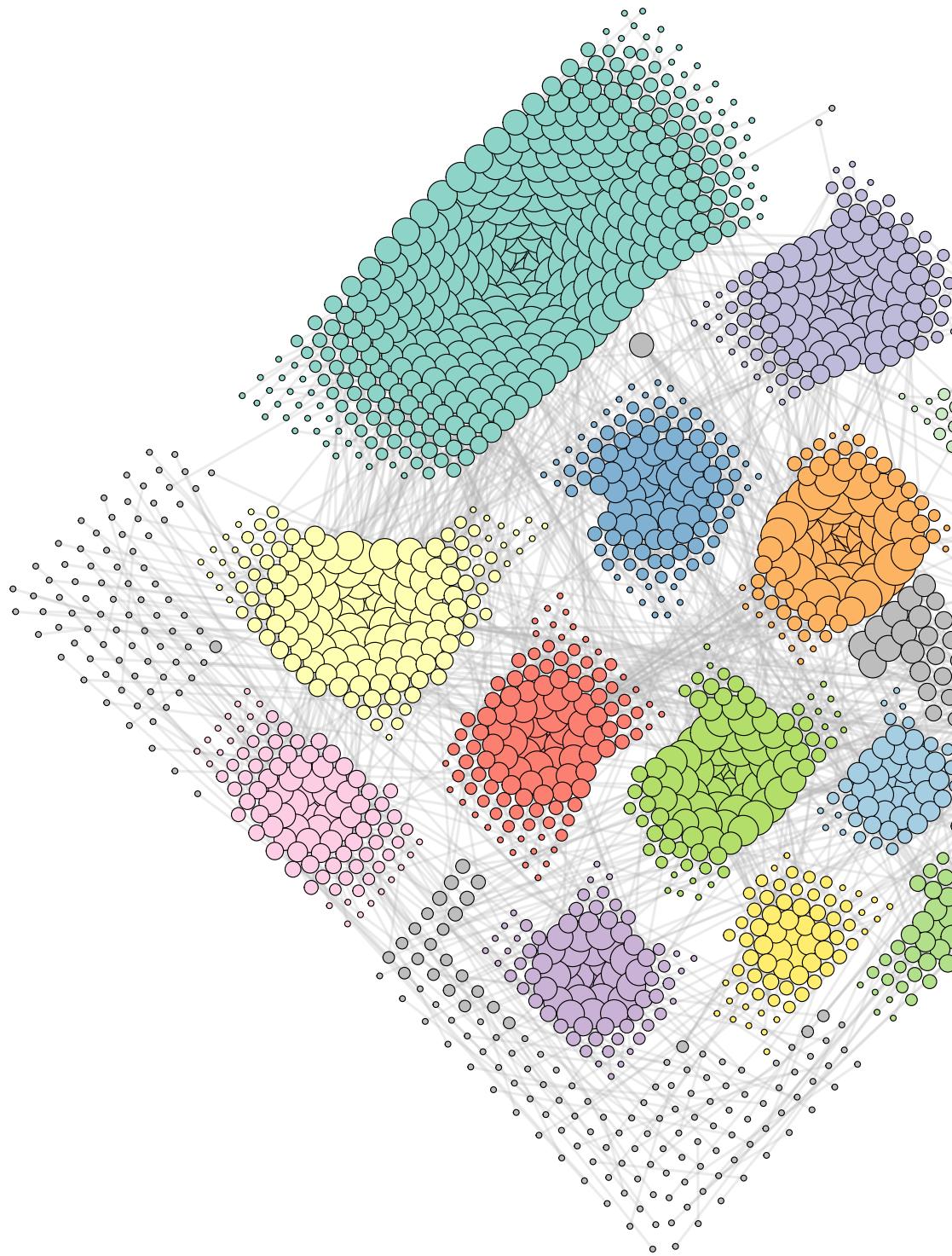
Node = 2049
Edge = 9602

6.3 Diamond layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "diamond",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
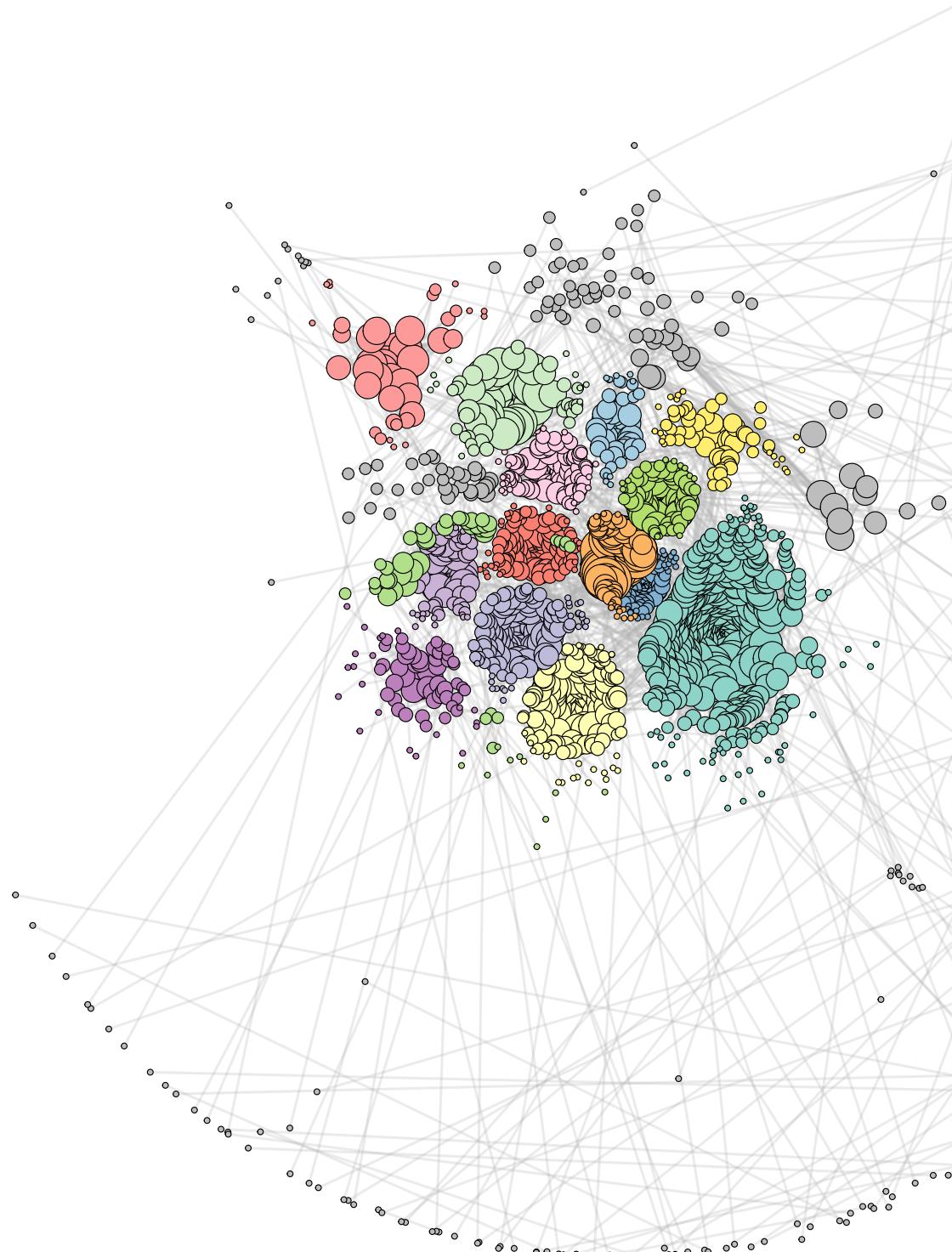
Node = 2049
Edge = 9602

6.4   Kk layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "kk",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
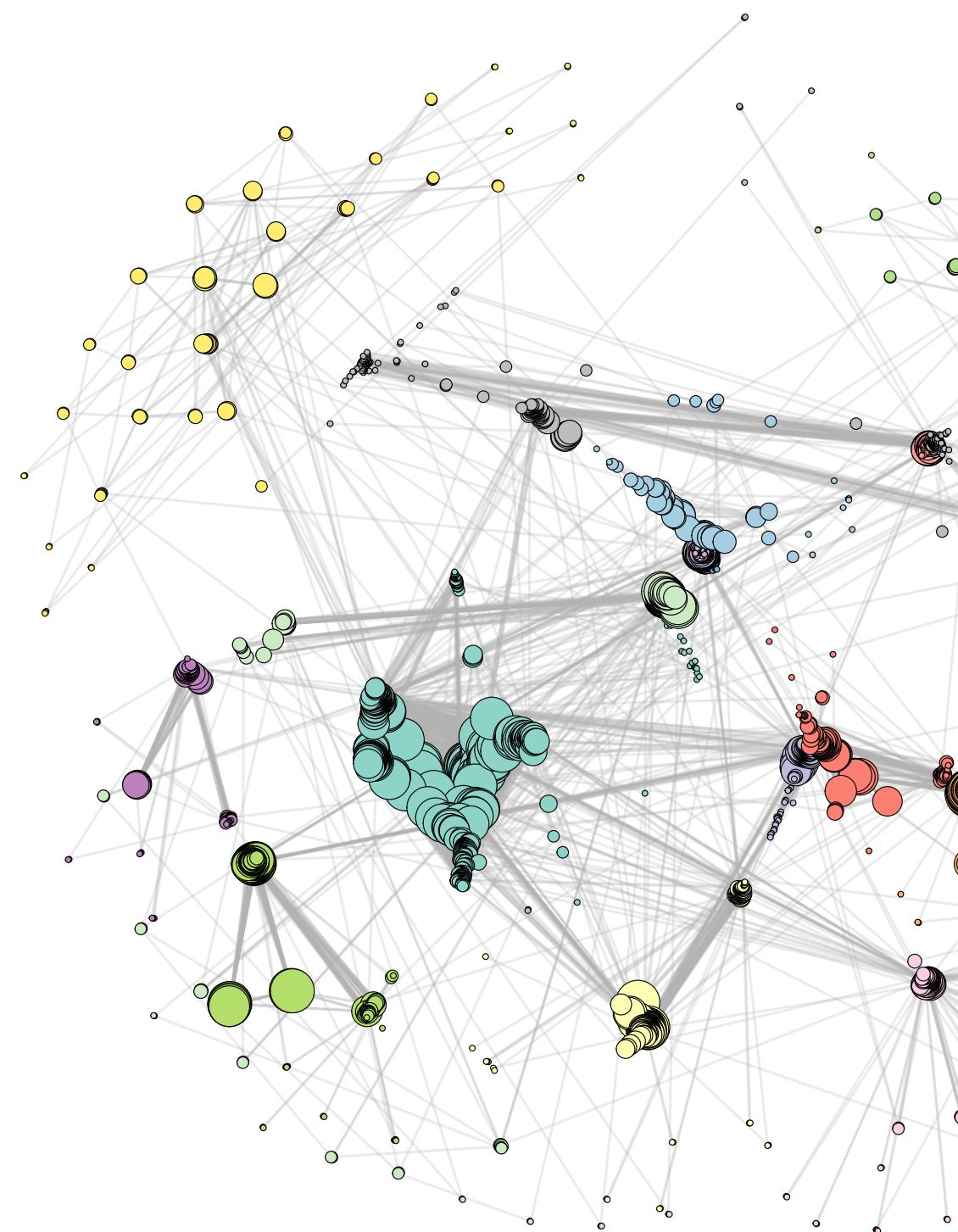
**Node = 2049**
**Edge = 9602**

## 6.5 Nicley layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "nicely",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
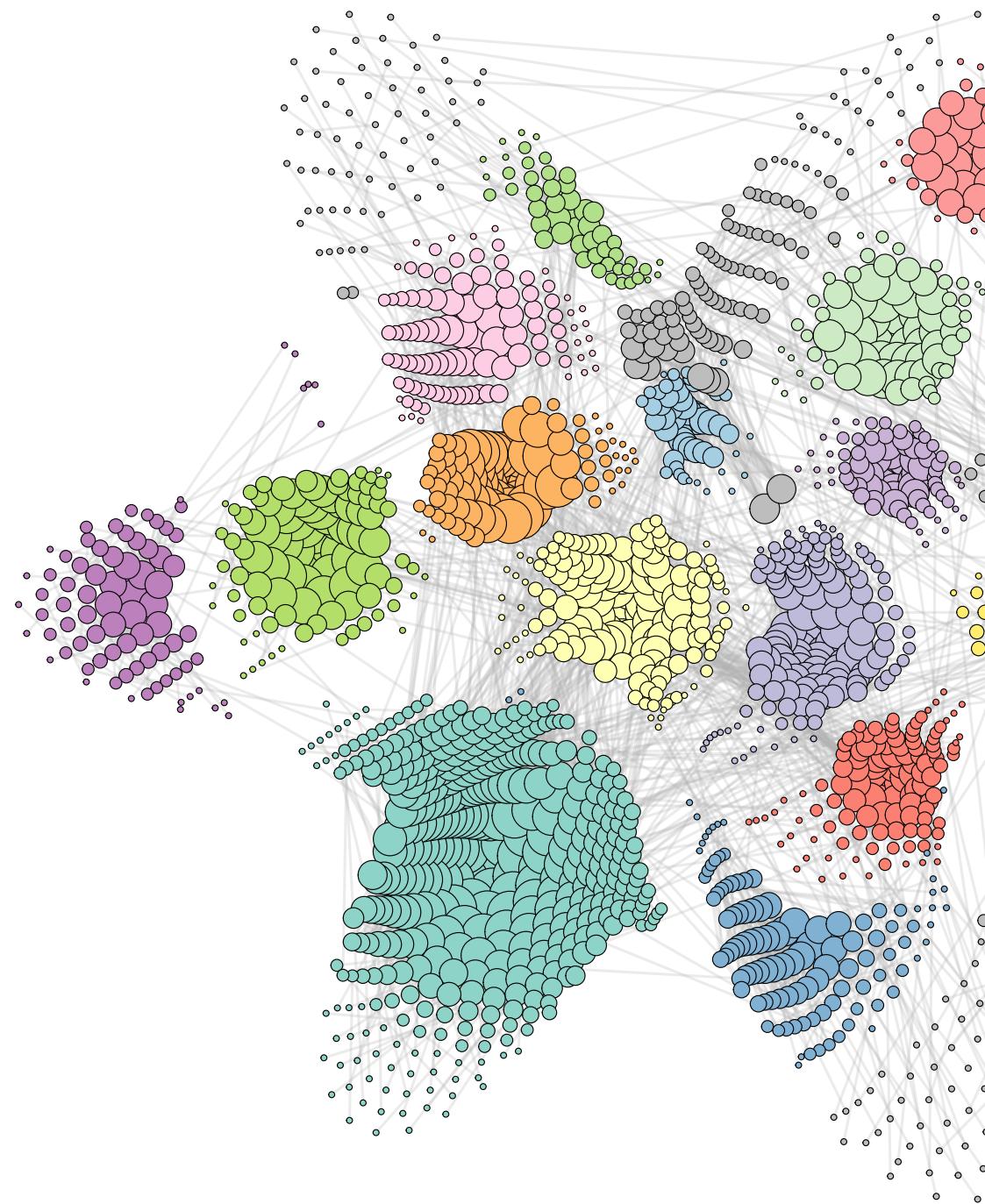
Node = 2049
Edge = 9602

6.6 Petal layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "petal",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
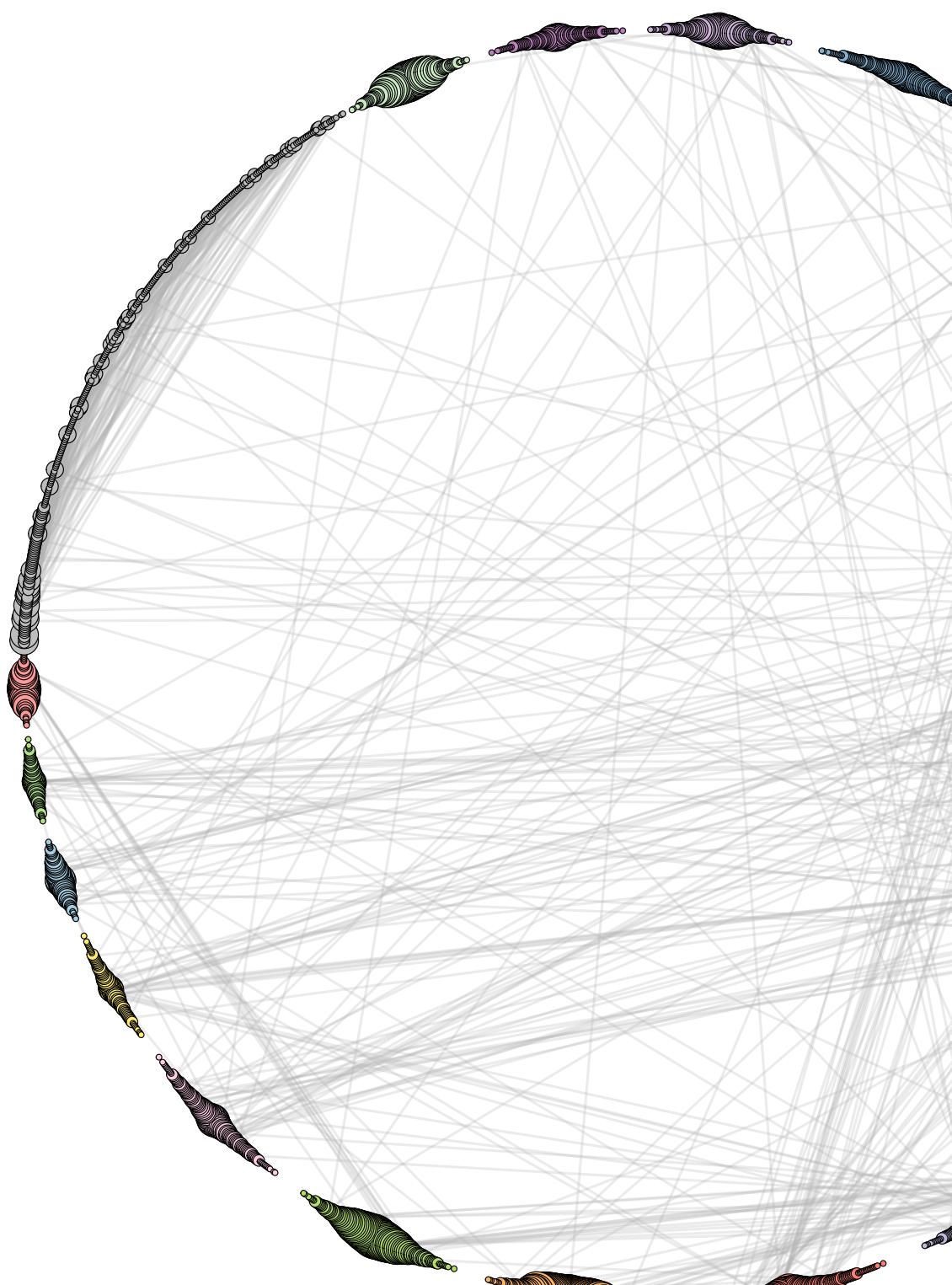
Node = 2049
Edge = 9602

6.7 Circle layout

6.8 Petal layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "circle",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
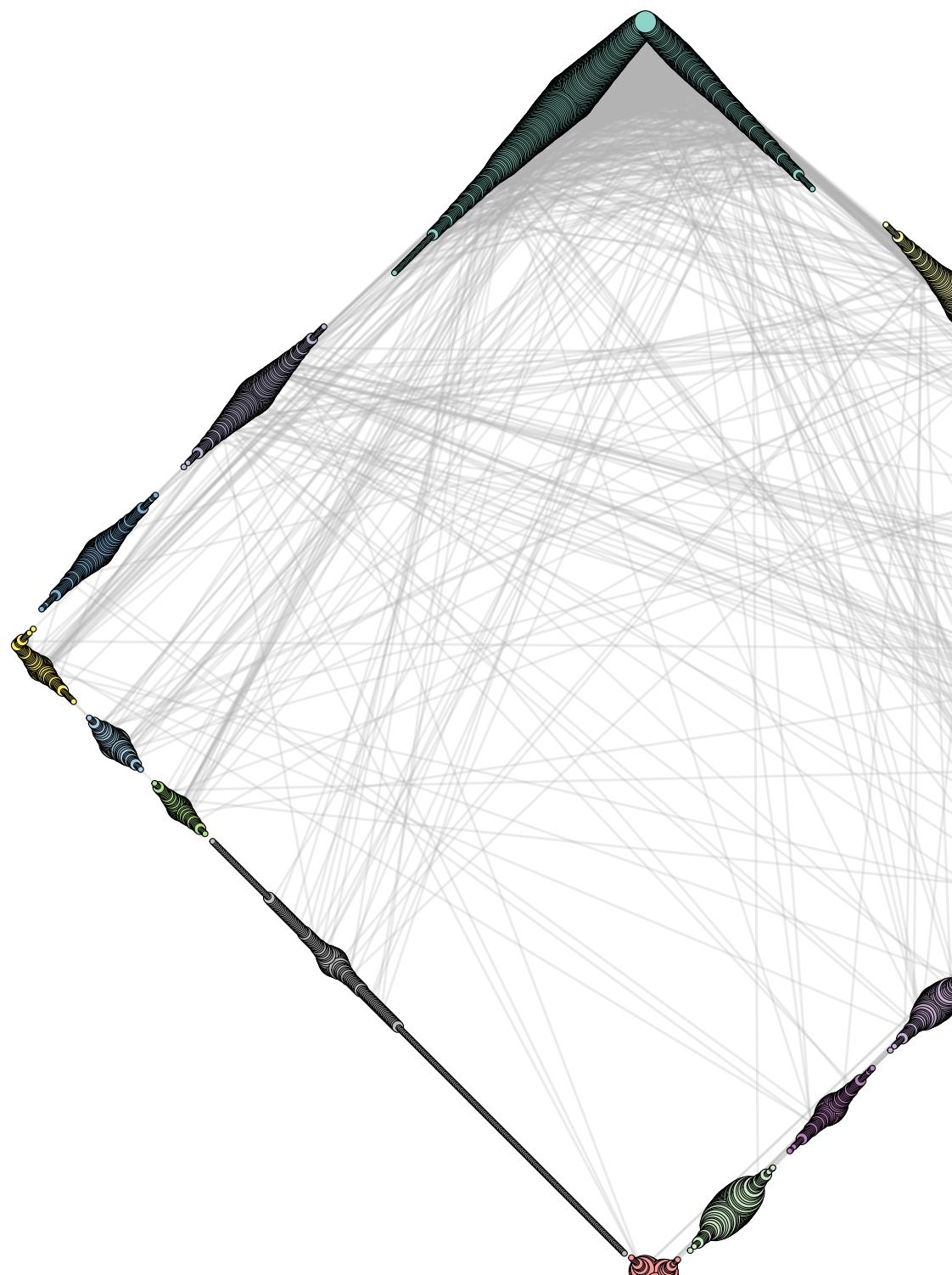
Node = 2049
Edge = 9602

6.9 Diamond outline layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "diamond_outline",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
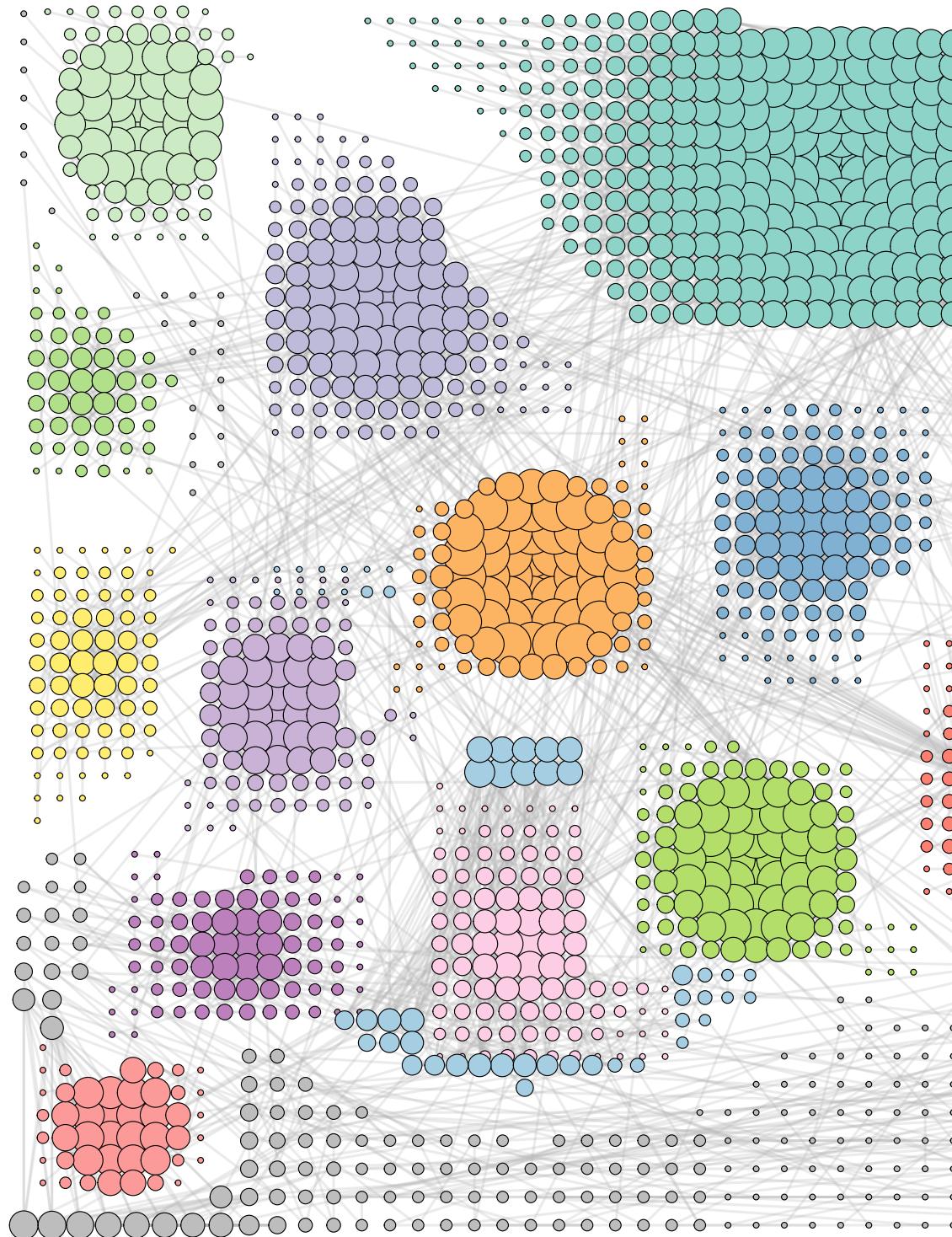
Node = 2049
Edge = 9602

6.10 Grid layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "grid",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
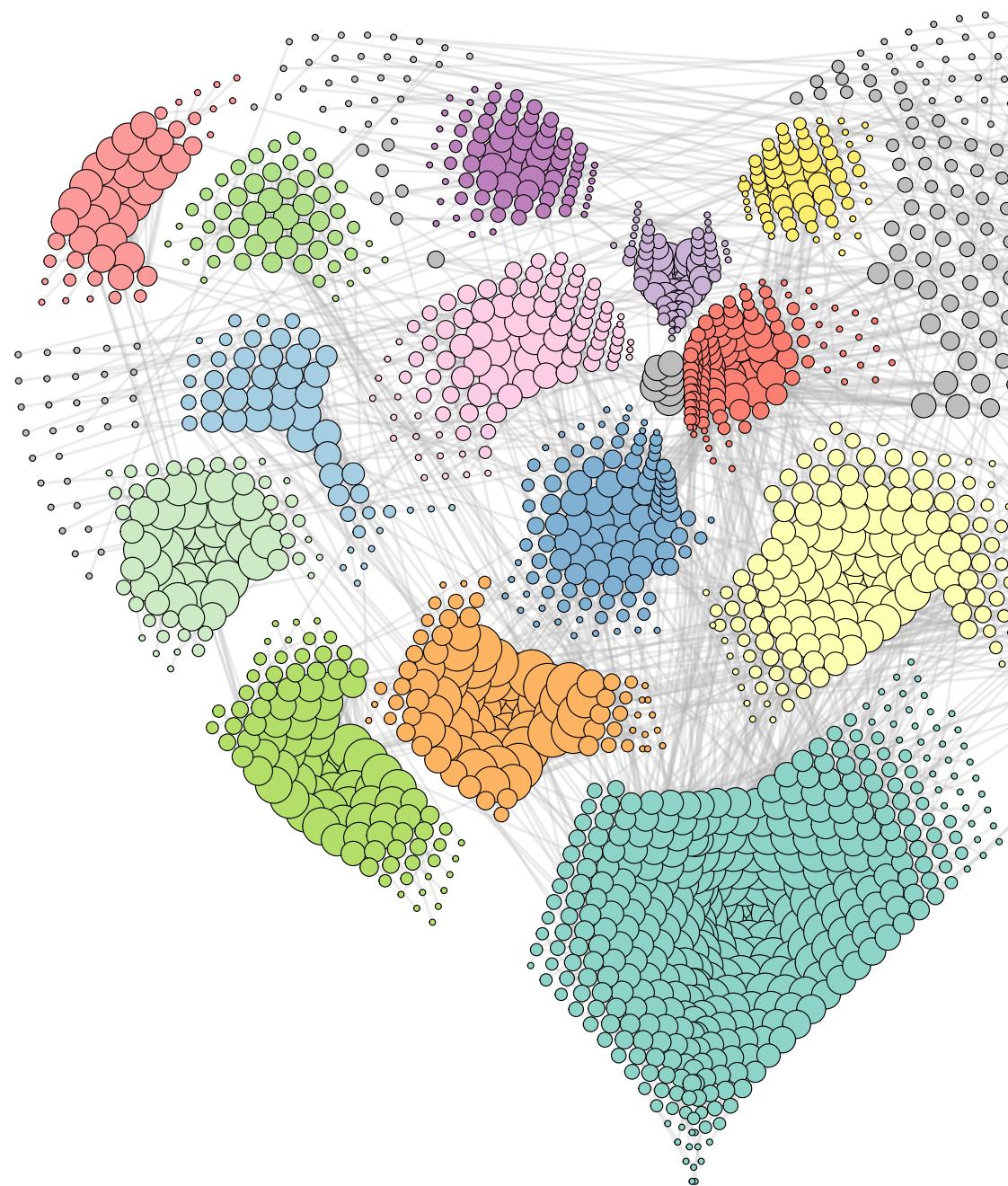
Node = 2049
Edge = 9602

6.11   Heart_centered layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "heart_centered",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```

Node = 2049
Edge = 9602
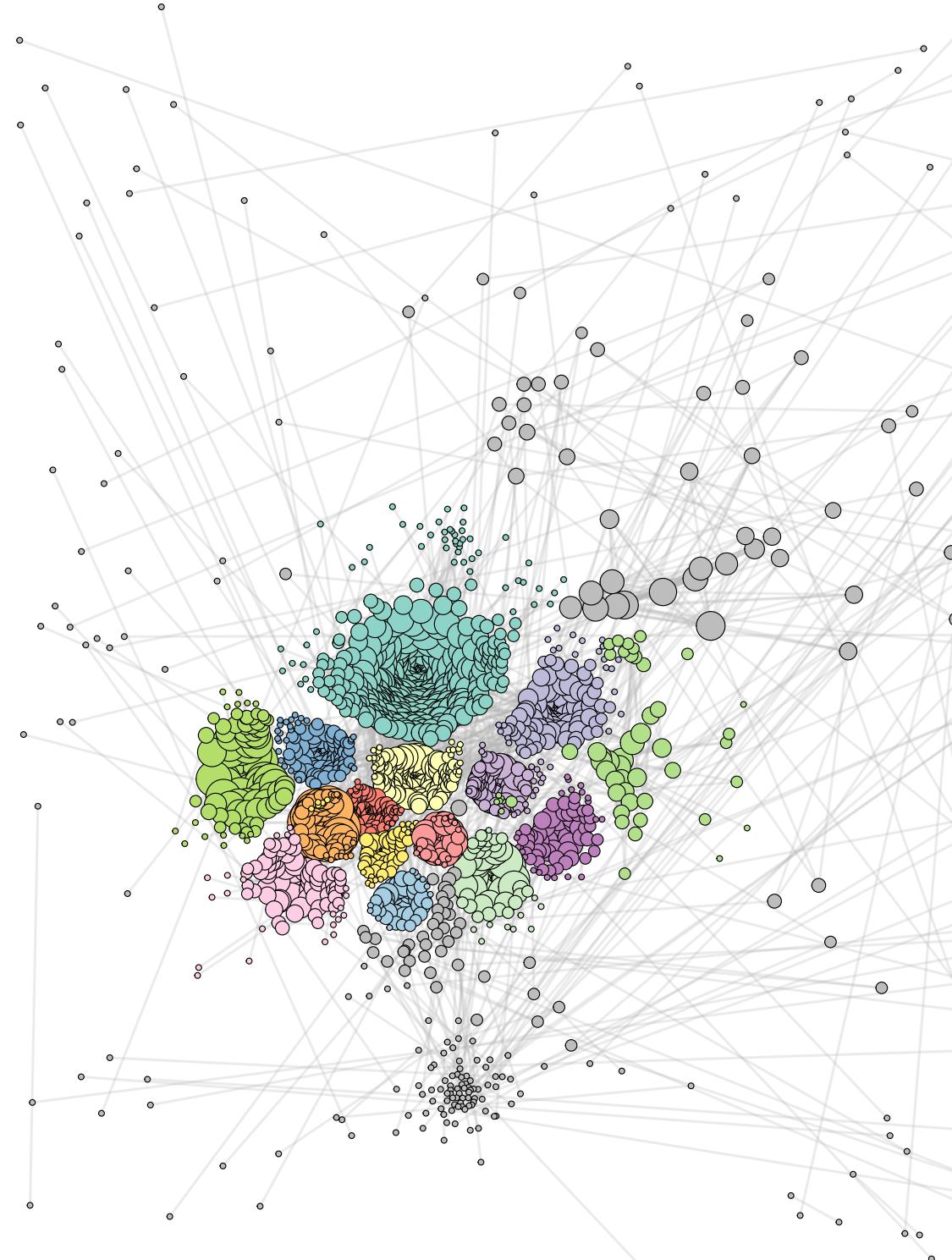
6.12 Lgl layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "lgl",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)
```

```
## Warning in alg_fun(graph): At vendor/cigraph/src/layout/large_graph.c:179 : LGL
## layout does not support disconnected graphs yet.
```

```
p
```
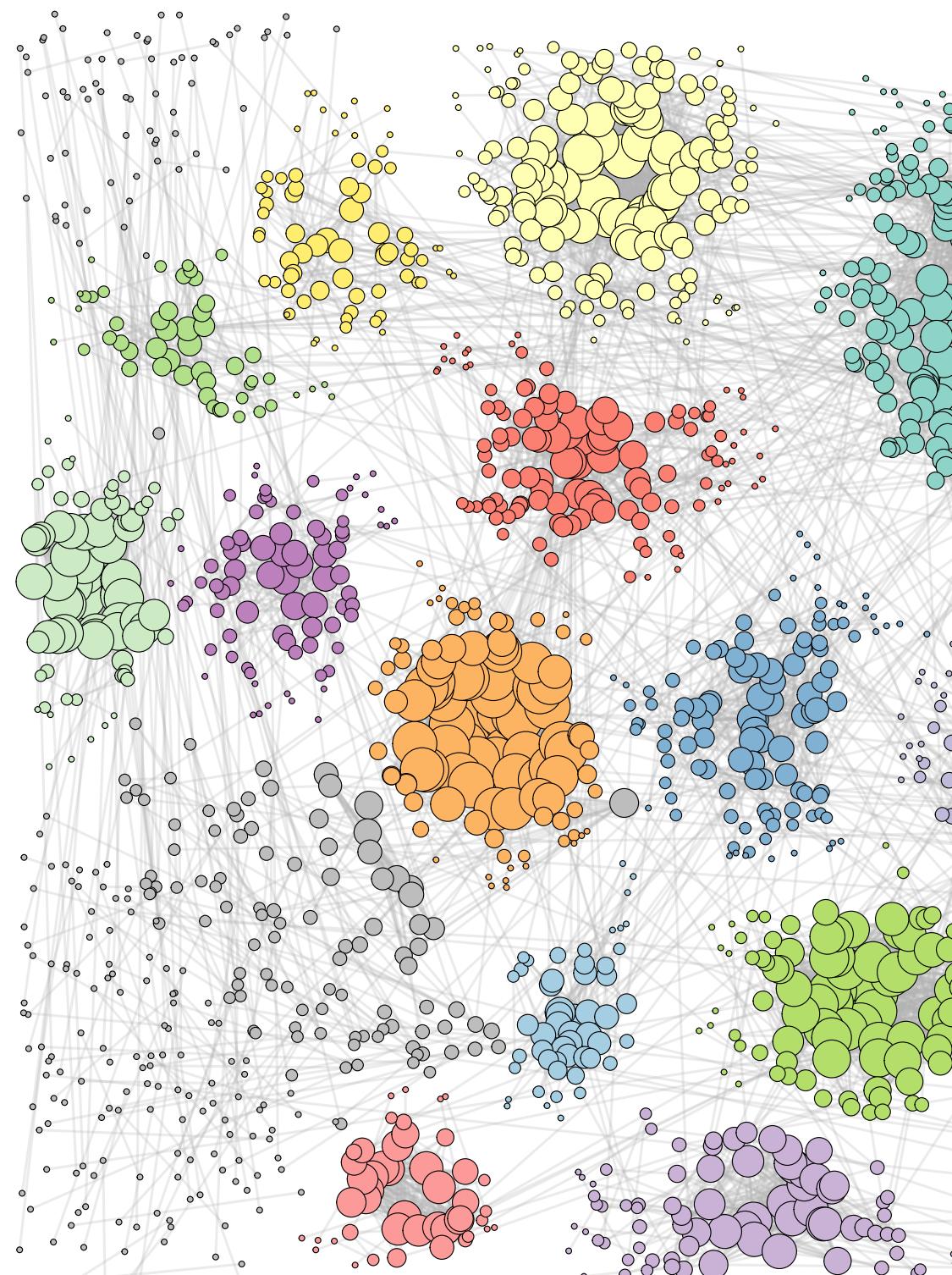
Node = 2049
Edge = 9602

6.13 Randomly layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "randomly",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
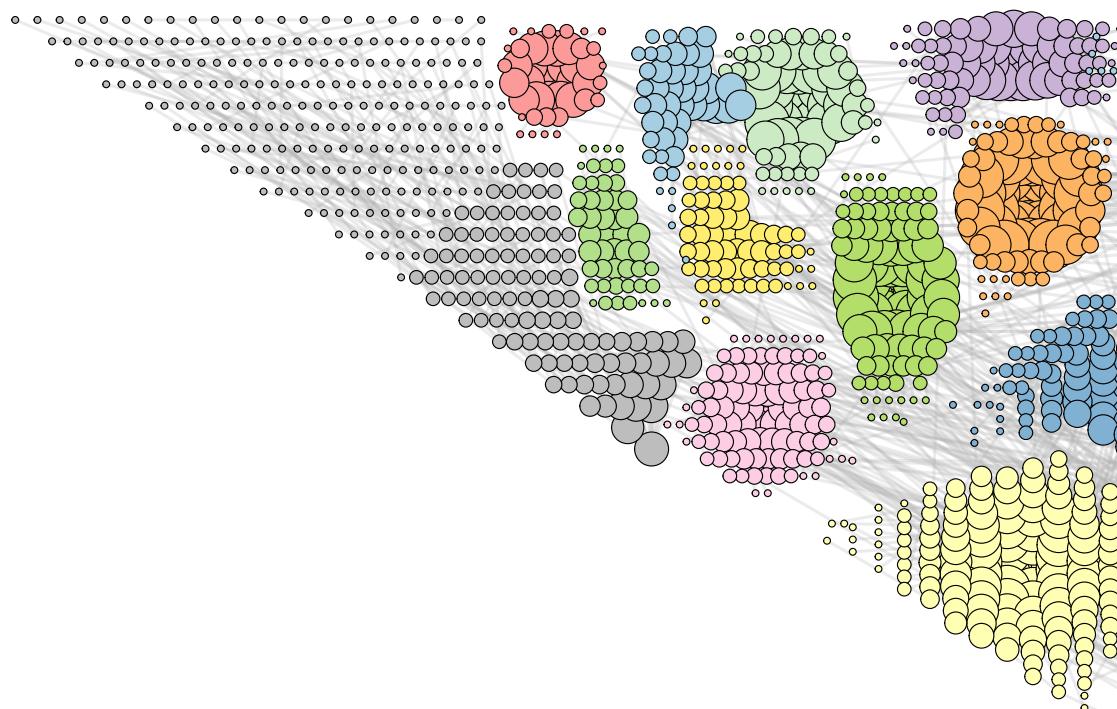
Node = 2049
Edge = 9602

6.14   Rectangle layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "rectangle",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
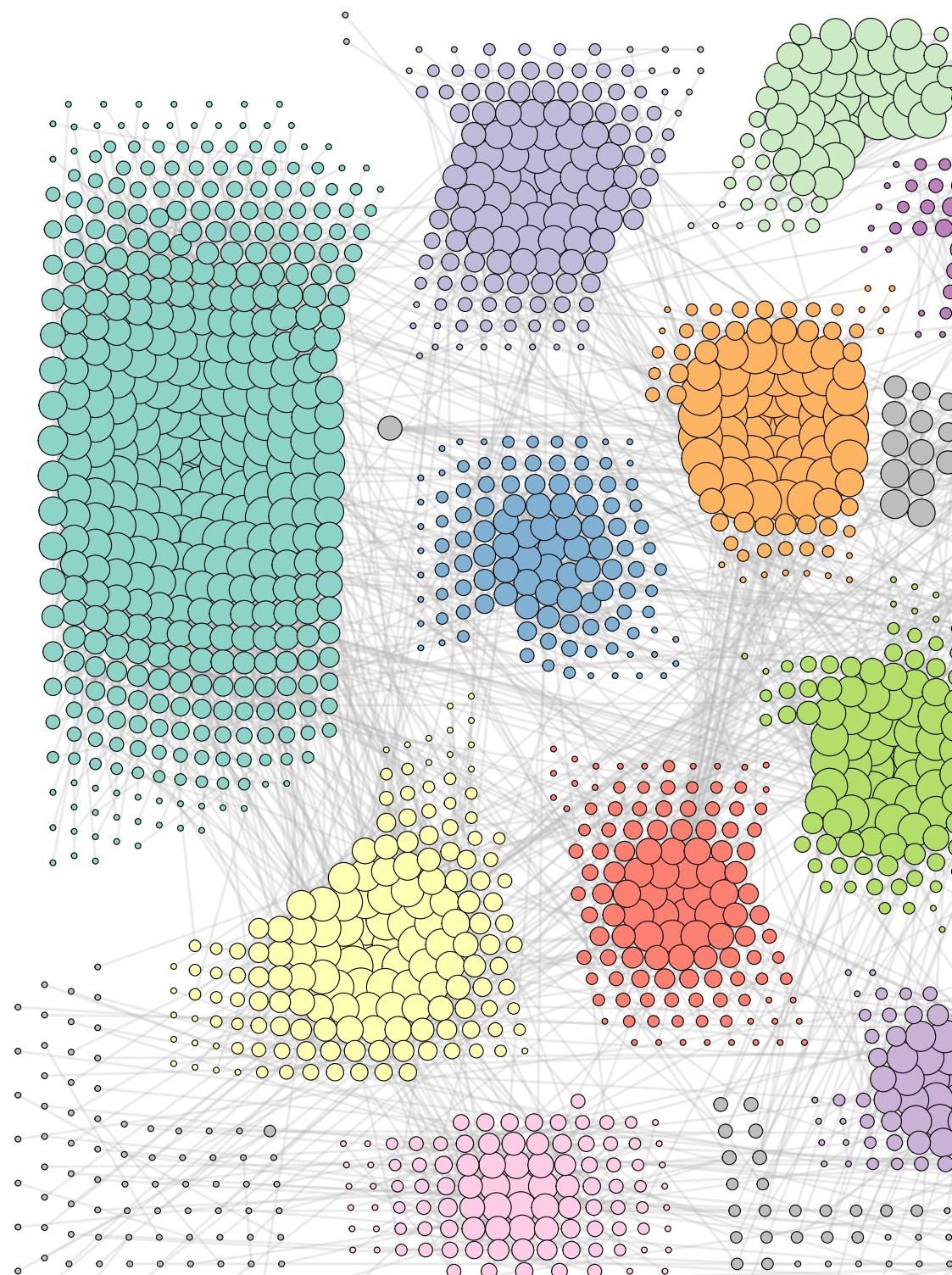
Node = 2049
Edge = 9602

6.15   Square layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "square",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
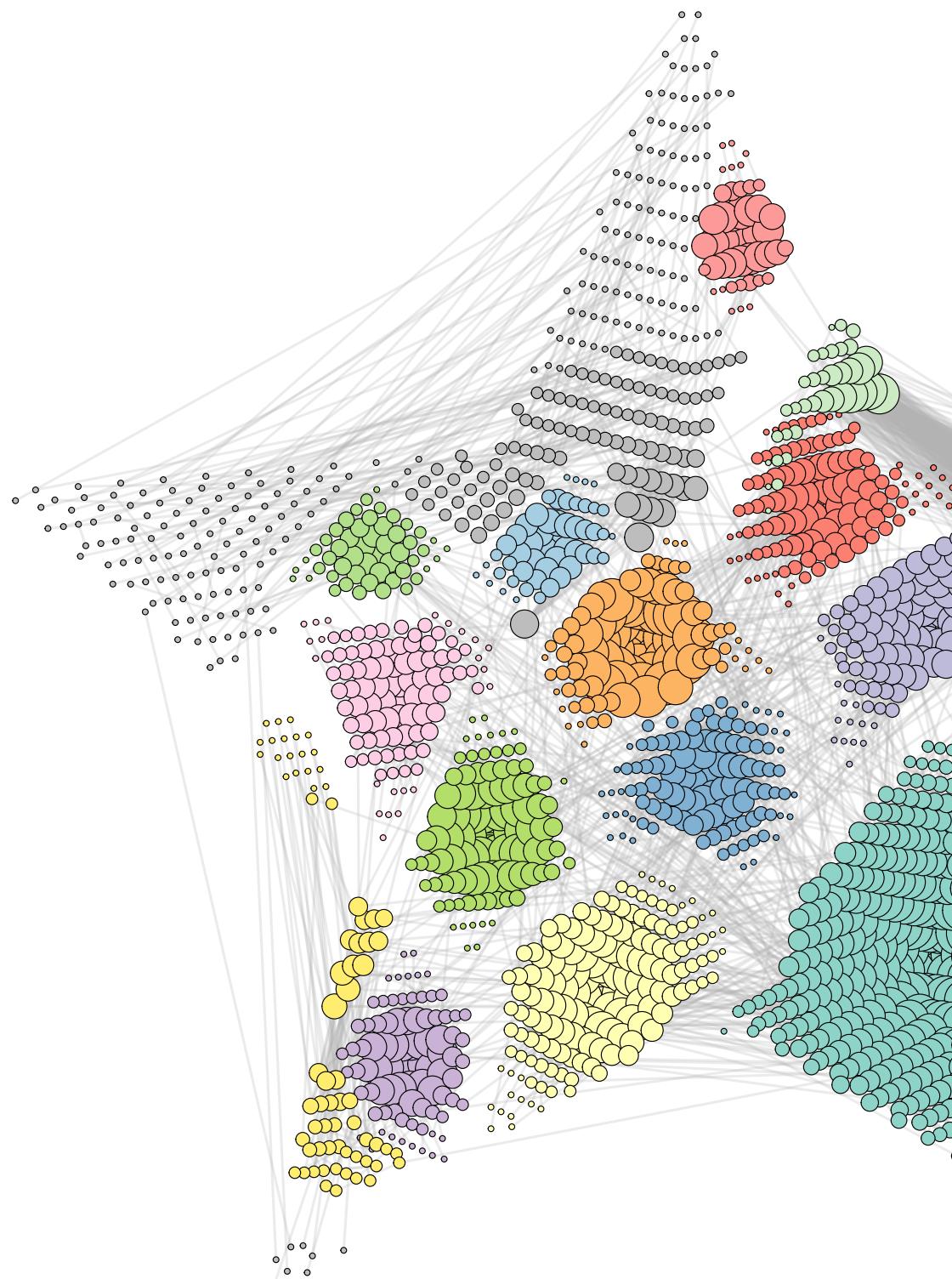
Node = 2049
Edge = 9602

6.16 Star layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "star",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
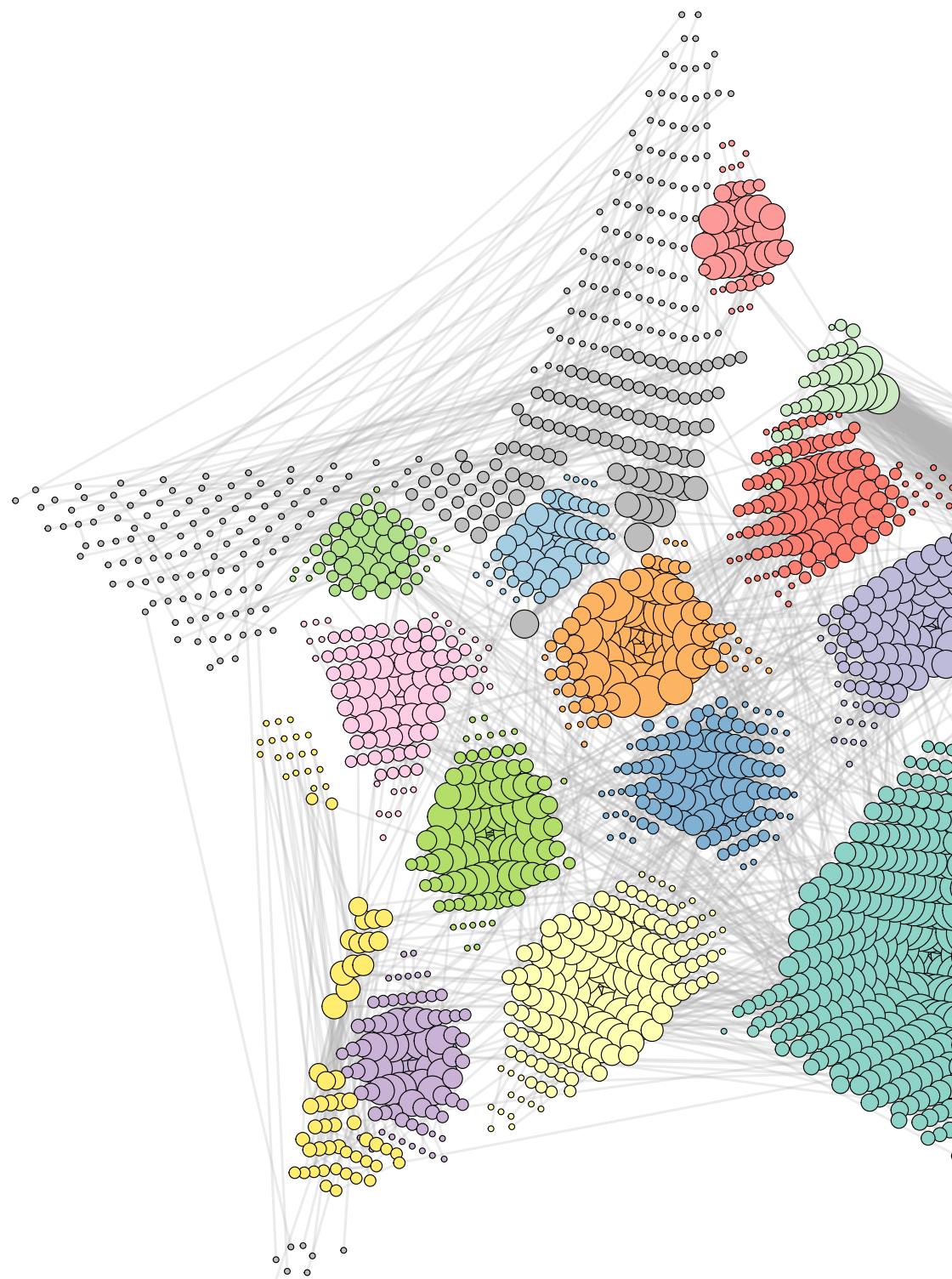
Node = 2049
Edge = 9602

6.17 Star_concentric layout

```
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "star_concentric",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```
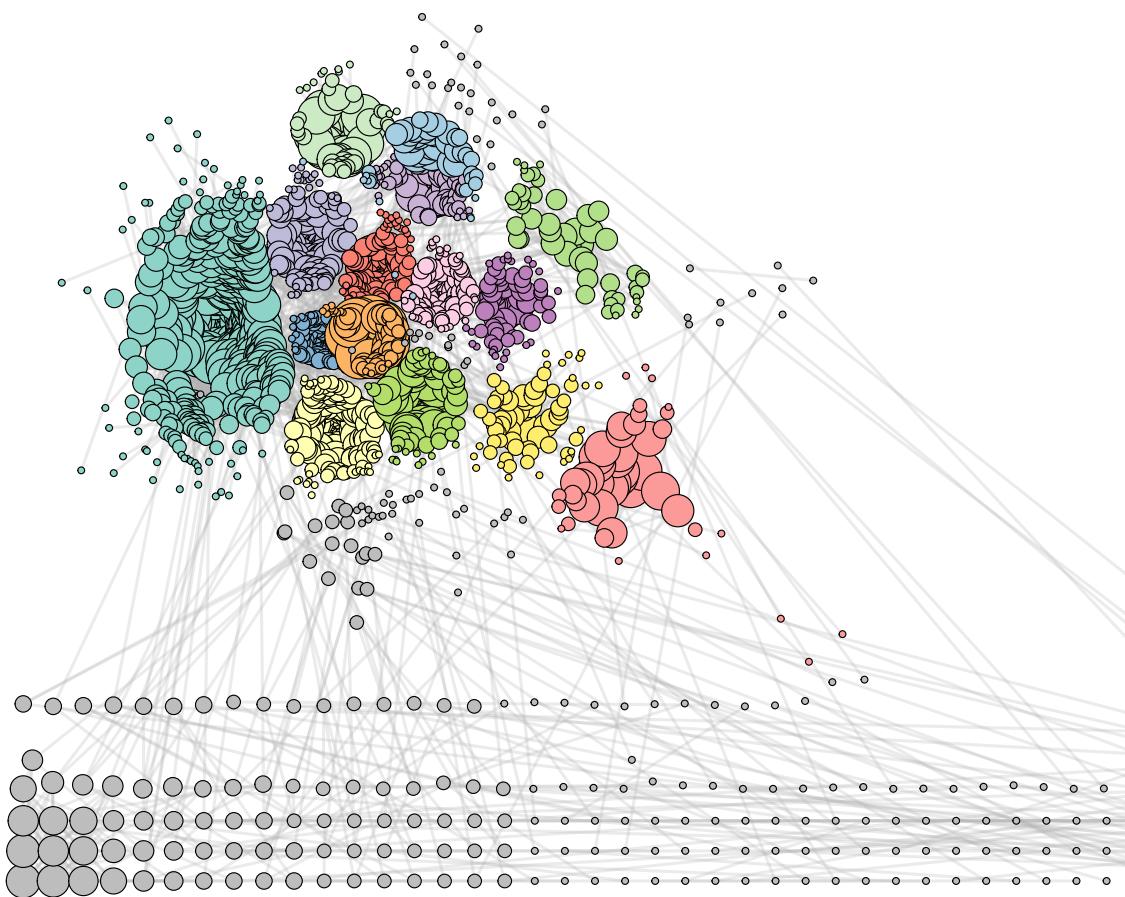
Node = 2049
Edge = 9602

6.18 Stress layout

```r
p <- ggNetView(
  graph_obj = graph_obj,
  layout = "stress",
  center = F,
  shrink = 0.8,
  layout.module = "adjacent",
  group.by = "Modularity",
  fill.by = "Modularity"
)


p
```

Node = 2049
Edge = 9602

Chapter 7

Network topology information

Chapter 8

Network comparison

8.1 Subgraph comparisopn

8.2 Comparison of multi-sample networks

Chapter 9

Network & Environment

9.1 Network Environment

Chapter 10

Multi-omics network analysis

10.1 Multi-omics