Tutorial: Descriptive Analysis for Network Graphs - hints

MSc in Statistics for Smart Data – Introduction to graph analysis and modeling

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1 Packages requirements

```
library(tidygraph)
library(scholar)
library(igraph)
library(ggraph)
library(viridis)
```

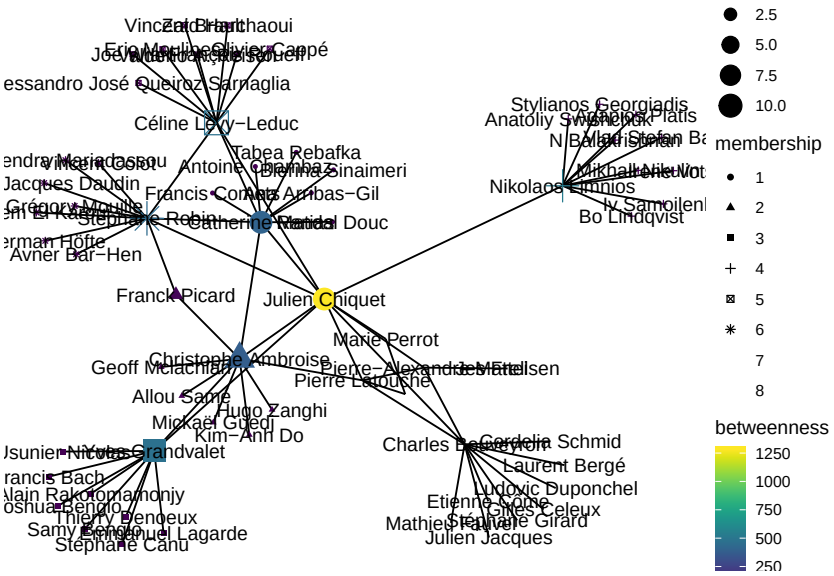
2 Network extraction

I found working with my co-authors' network was more fun: I use the **scholar** package to extract it.

```
chiquet <- "FM2gRsYAAAAJ"
my_coauthors_network <-
  scholar::get_coauthors(chiquet, n_coauthors = 10, n_deep = 1) %>%
  graph_from_data_frame(directed = FALSE) %>%
  igraph::simplify(remove.multiple = TRUE, remove.loops = TRUE)
```

Here is a fancy representation of this network with the **ggraph** package:

```
groups <- as.factor(as.numeric(membership(cluster_edge_betweenness(my_coauthors_networ
my_coauthors_network %>%
  tidygraph::as_tbl_graph() %>% activate(nodes) %>%
  mutate(degree = centrality_degree(),
         membership = groups,
         betweenness = centrality_betweenness()) %>%
  ggraph() + scale_color_viridis() +
    geom_edge_link() +
    geom_node_point(aes(size = degree, shape = membership, color = betweenness) ) +
    geom_node_text(aes(label = name)) +
    theme_void()
```

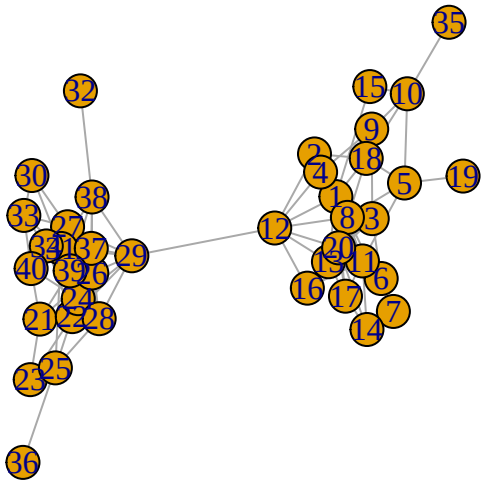


3 Spectral Analysis

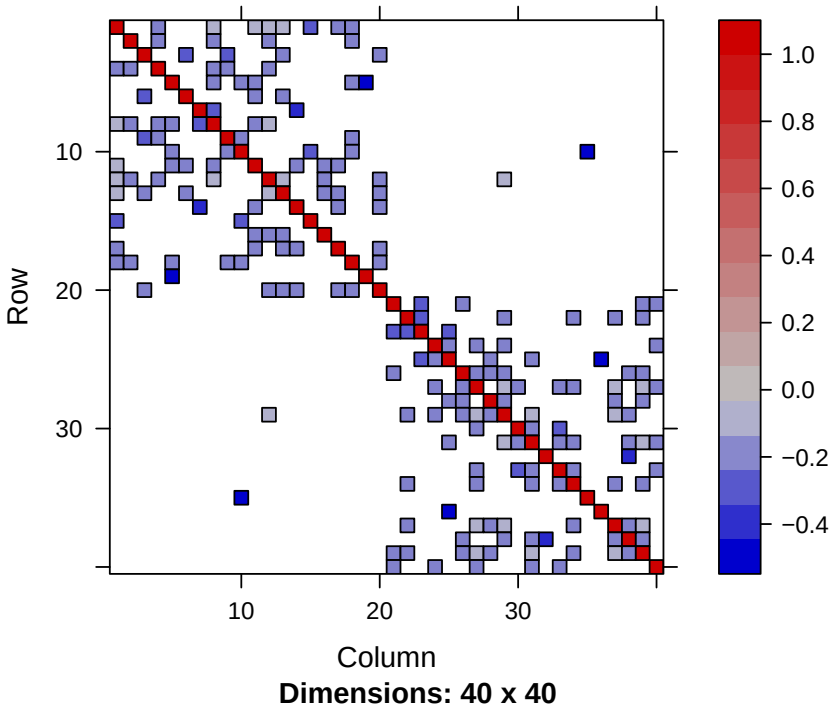
3.1 Simple community network

Let us star by studying toy examples to better understand th spectral graph theory:

```
community <- igraph::sample_sbm(40, matrix(c(.25, .01, .01, .25), 2, 2), c(20, 20))
plot(community)
```

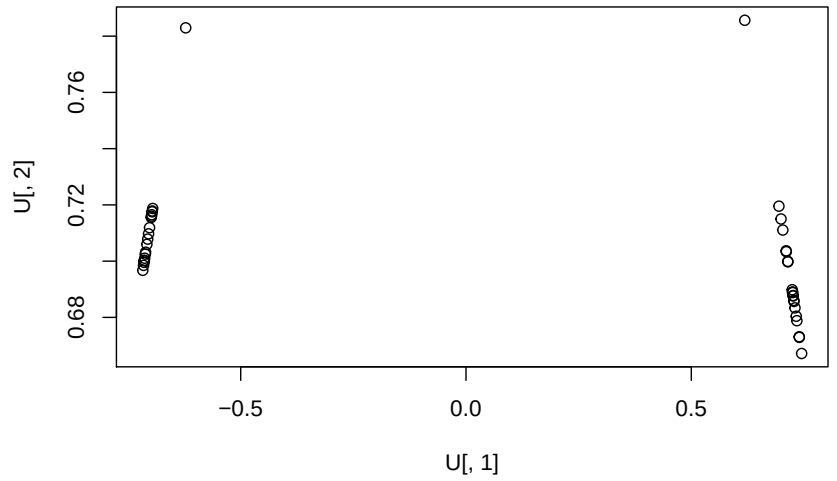


```
L <- graph.laplacian(community, normalized = TRUE)
Matrix::image(L)
```



By, looking at space spawned by the first two eigen vector of L, we see that the clustering problem is outrageously easy (all point from the same community are superimposed)

```
U <- eigen(L)$vectors
Q <- 2
U <- U[,c((ncol(U)-Q+1):ncol(U))]
U <- U / rowSums(U^2)^(1/2)
plot(U[, 1], U[, 2])
```



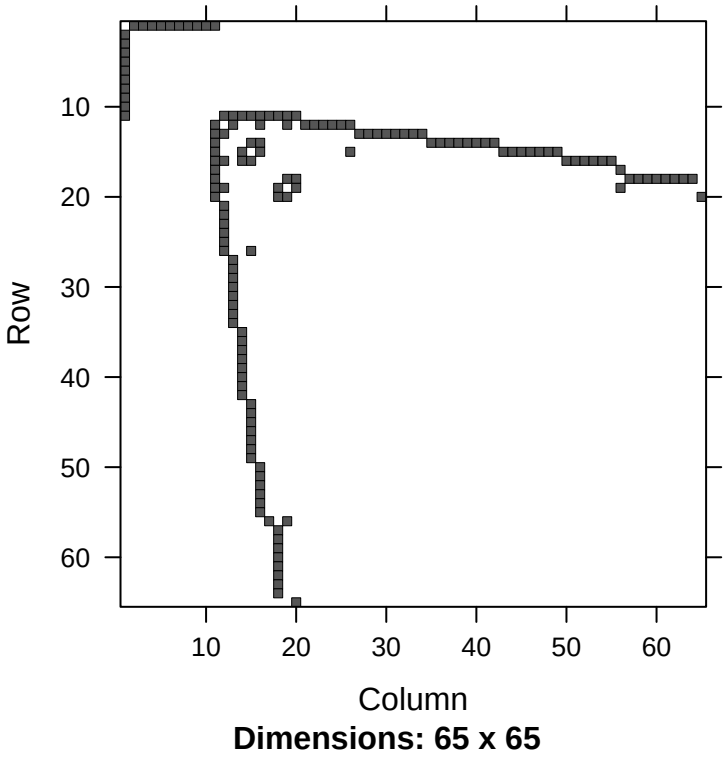
3.2 Spectral clustering of coauthorship network

Hereafter, an implementation of the spectral clustering algorithm studied during last session,

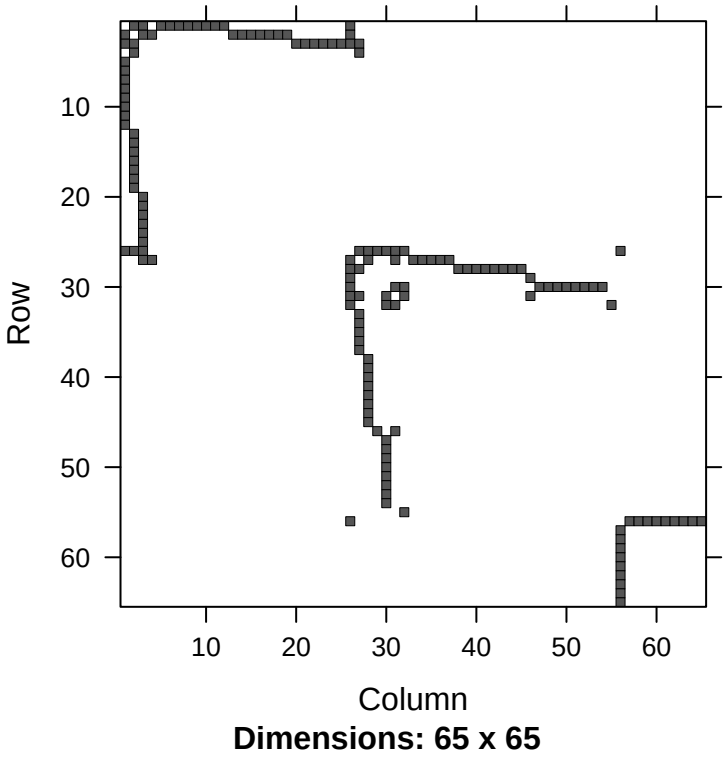
```
SpectralClustering <- function (A,Q) {

  p <- ncol(A)
  if (Q > 1) {

    ## Normalized Laplacian
    L <- graph.laplacian(A, normalized = TRUE)
    ## go into eigenspace
    U <- eigen(L)$vectors
    U <- U[,c((ncol(U)-Q+1):ncol(U))]
    U <- U / rowSums(U^2)^(1/2)

    ## Applying the K-means in the eigenspace
    cl <- kmeans(U, Q, nstart = 10, iter.max = 30)$cluster
  } else {
    cl <- as.factor(rep(1,ncol(A)))
  }
  cl
}
```

```
cl_list <- lapply(2:7, function(Q)
  SpectralClustering(my_coauthors_network, Q)
)
A <- as_adj(my_coauthors_network)
lapply(cl_list, function(cl)
  Matrix::image(
    A[order(cl), order(cl)],
    main = paste('number of cluster =',length(unique(cl)))
  )
)
```

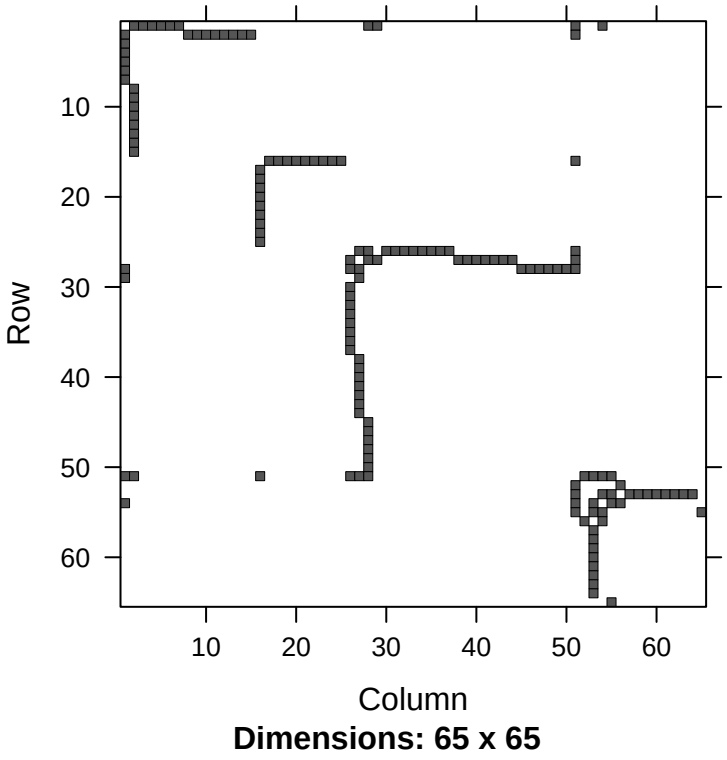
```
## [[1]]
```


number of cluster = 2
Row
10
20
30
40
50
60
Column
10
20
30
40
50
60
Dimensions: 65 x 65

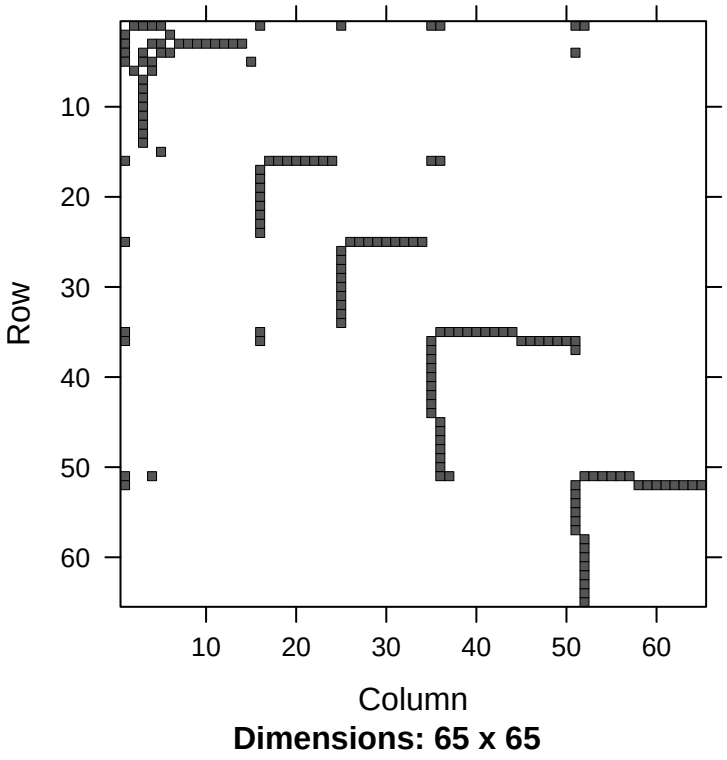
```
##
## [[2]]
```


number of cluster = 3
Row
10
20
30
40
50
60
10
20
30
40
50
60
Column
Dimensions: 65 x 65

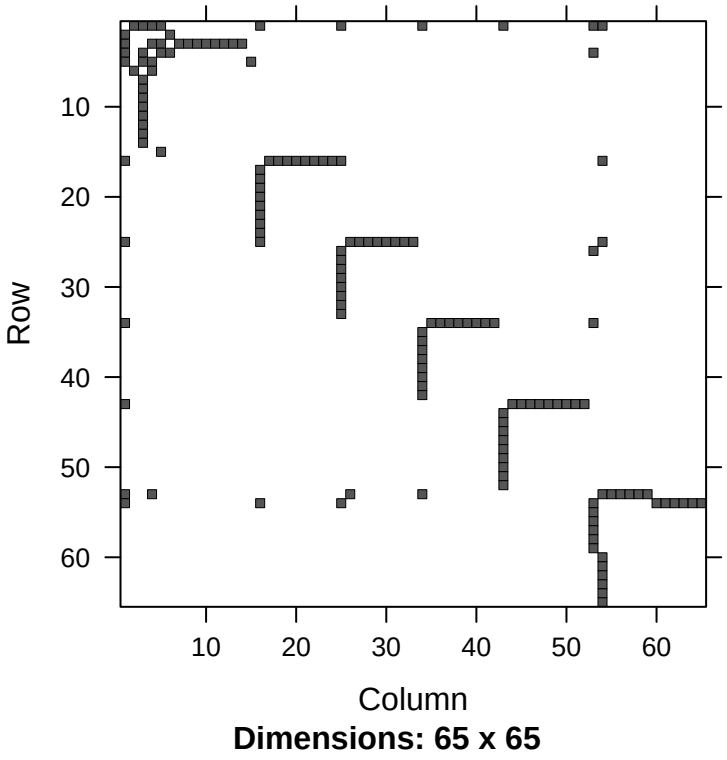
```
##
## [[3]]
```


number of cluster = 4
Row
10
20
30
40
50
60
10
20
30
40
50
60
Column
Dimensions: 65 x 65

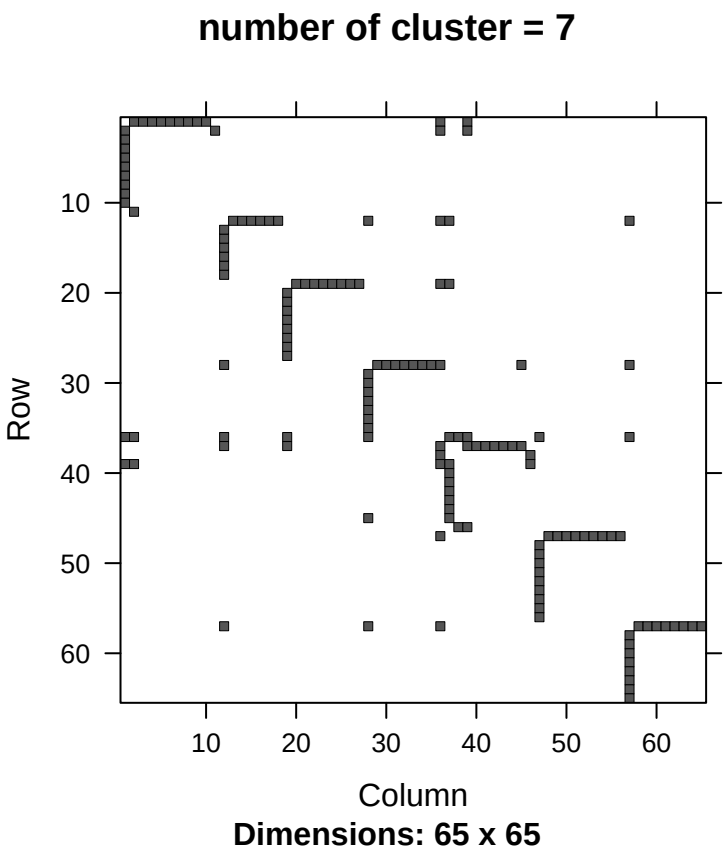
```
##
## [[4]]
```


number of cluster = 5
Row
10
20
30
40
50
60
10
20
30
40
50
60
Column
Dimensions: 65 x 65

```
##
## [[5]]
```


number of cluster = 6
Row
10
20
30
40
50
60
10
20
30
40
50
60
Column
Dimensions: 65 x 65

```
##
## [[6]]
```


number of cluster = 7
Row
10
20
30
40
50
60
10
20
30
40
50
60
Column
Dimensions: 65 x 65