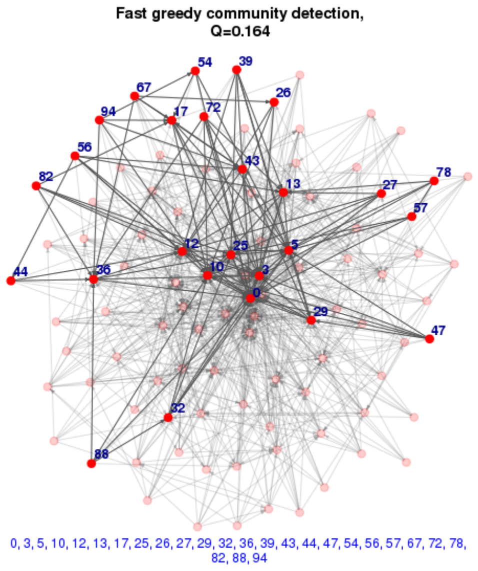
# Complex Networks
# tools for analyzing networks (igraph)

2018.11.29(Thu)

# igraph

- igraph is a free software package for creating and manipulating undirected and directed graphs. It includes implementations for classic graph theory problems like minimum spanning trees and network flow, and also implements algorithms for some recent network analysis methods, like community structure search.
- The following three are available:
  - igraph R package
  - python-igraph
  - igraph C library

http://igraph.org



## tutorials

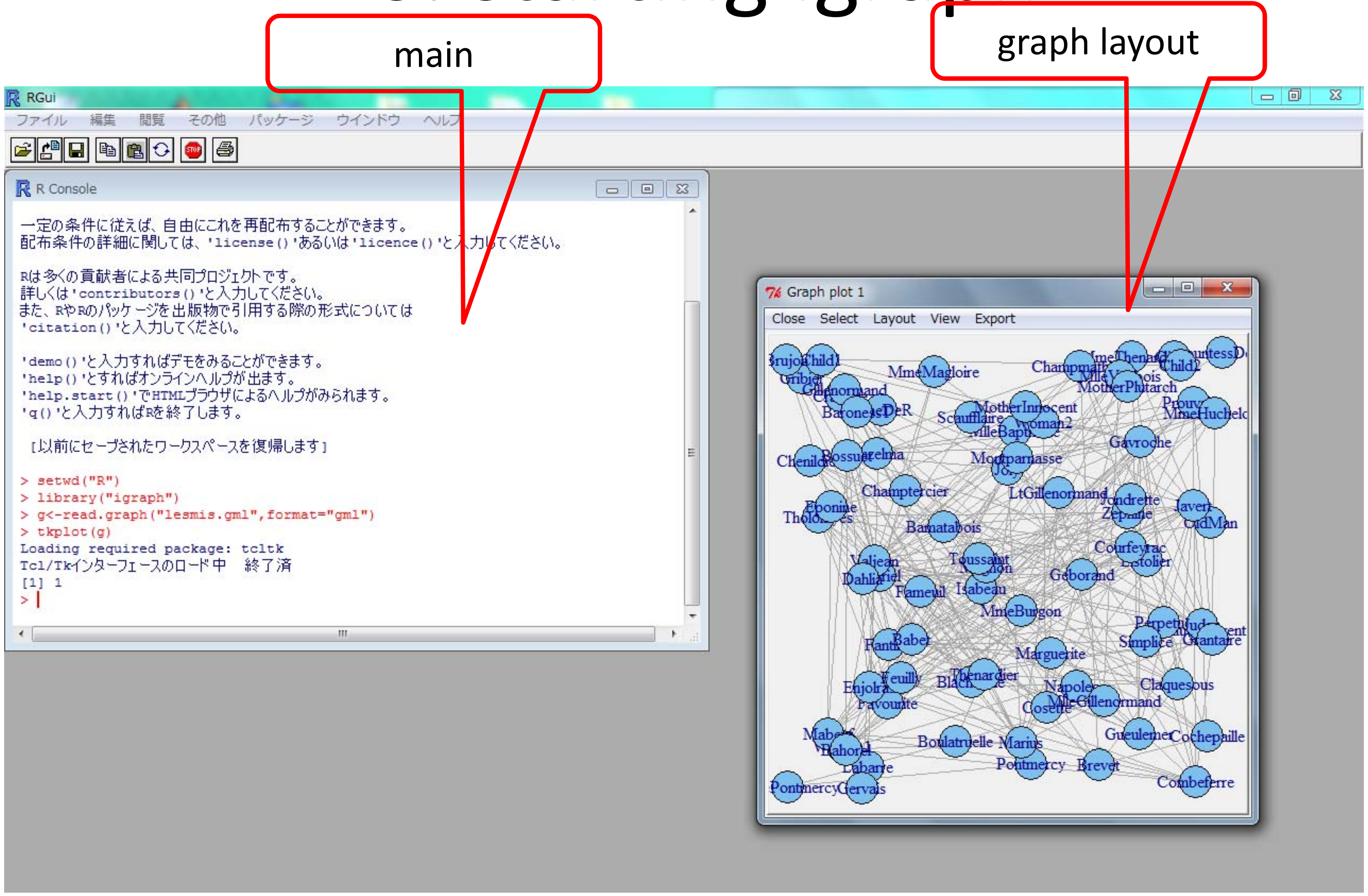
- tutorial of python-igraph
  - http://igraph.org/python/doc/tutorial/tutorial.html
- tutorials of R
  - http://cran.r-project.org/other-docs.html (many tutorials in English and other languages)

# procedure for analyzing network

1. create graph object
2. layout the network
3. ranking 找到重要的node
4. metrics

   social networks-> group of friends -> community
5. community detection
6. export

# 0. starting igraph


main
graph layout
RGui
ファイル　編集　閲覧　その他　パッケージ　ウインドウ　ヘルプ
R Console
Graph plot 1
Close　Select　Layout　View　Export

```
一定の条件に従えば、自由にこれを再配布することができます。
配布条件の詳細に関しては、'license()'あるいは'licence()'と入力してください。

Rは多くの貢献者による共同プロジェクトです。
詳しくは'contributors()'と入力してください。
また、RやRのパッケージを出版物で引用する際の形式については
'citation()'と入力してください。

'demo()'と入力すればデモをみることができます。
'help()'とすればオンラインヘルプが出ます。
'help.start()'でHTMLブラウザによるヘルプがみられます。
'q()'と入力すればRを終了します。

 [以前にセーブされたワークスペースを復帰します]

> setwd("R")
> library("igraph")
> g<-read.graph("lesmis.gml",format="gml")
> tkplot(g)
Loading required package: tcltk
Tcl/Tkインターフェースのロード中　終了済
[1] 1
> 
```

# 1. create graph object

- library(“igraph”)
- setwd(“R”)
- g<-read.graph(“lesmis.gml”, format=“gml”)
- tkplot(g)

start igraph

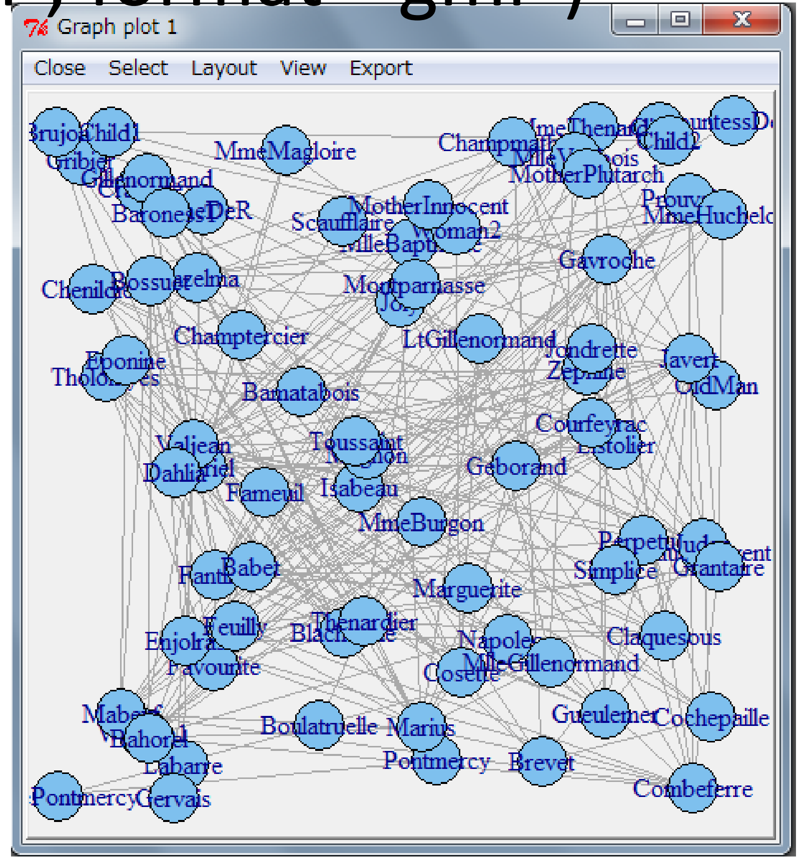
set directory

create graph

open graph window

lesmis.gml is available at

Mark Newman’s Website

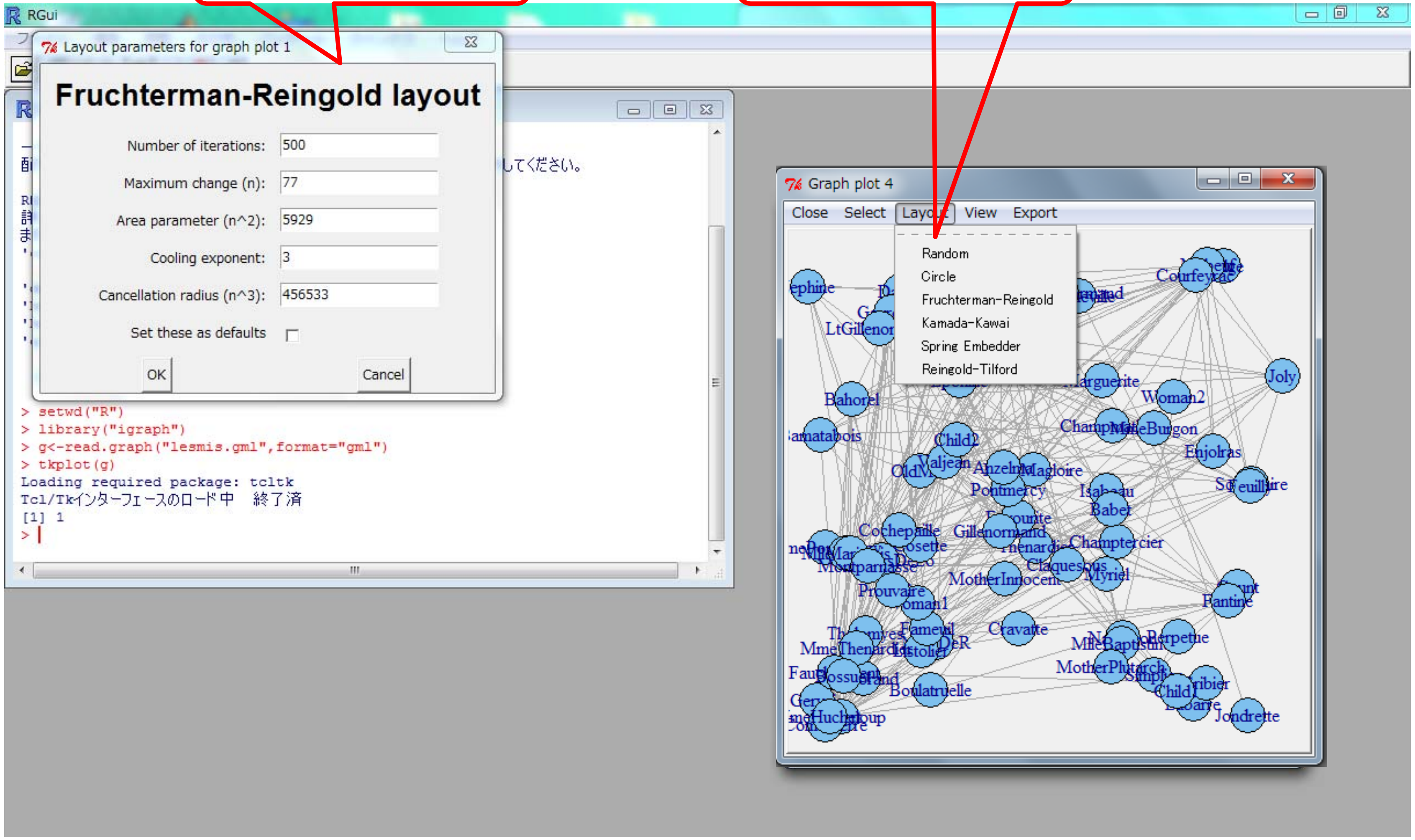


# 2. layout the network

set parameters

排版

choose layout

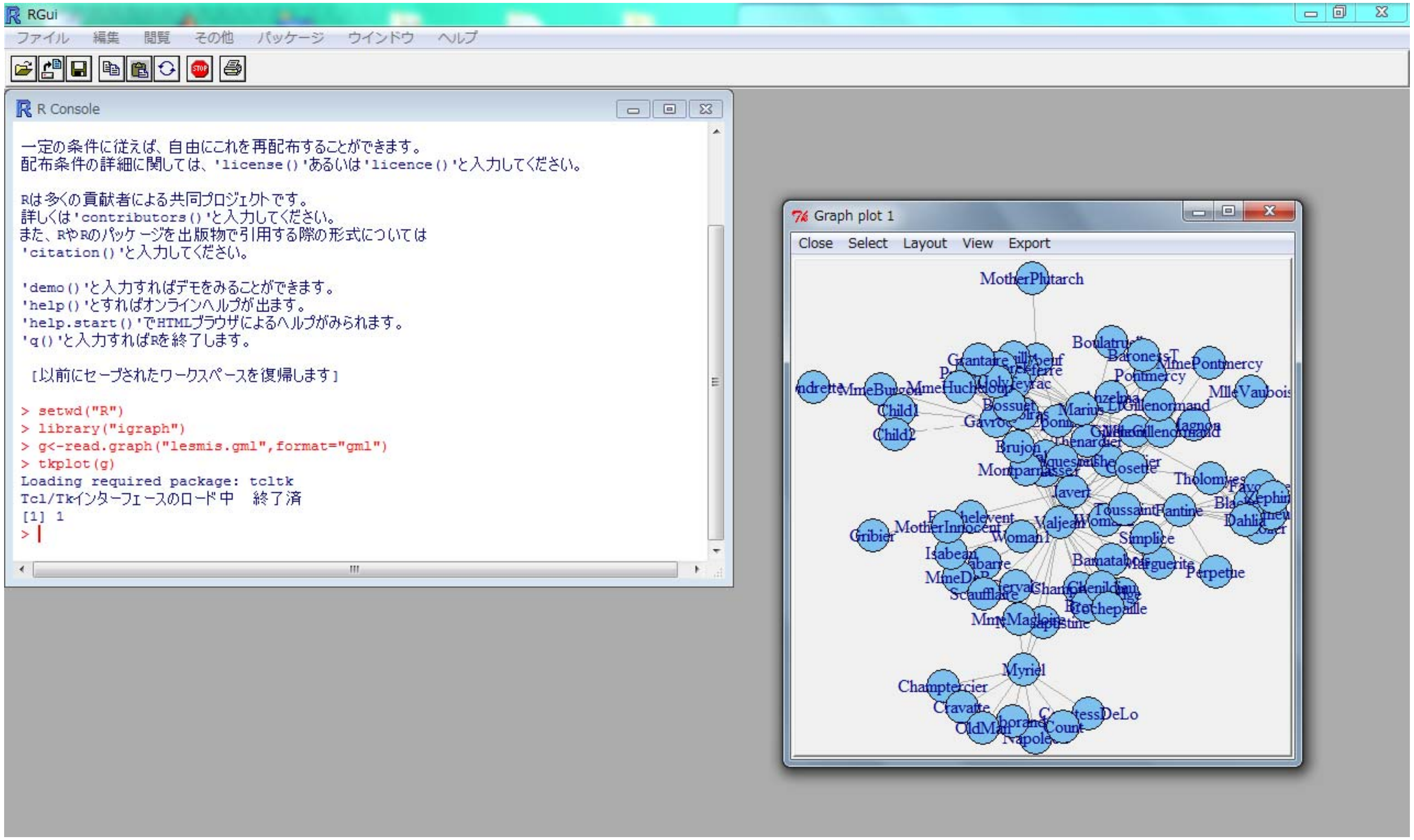


**Fruchterman-Reingold layout**

| | |
|---|---|
| Number of iterations: | 500 |
| Maximum change (n): | 77 |
| Area parameter (n^2): | 5929 |
| Cooling exponent: | 3 |
| Cancellation radius (n^3): | 456533 |
| Set these as defaults | ☐ |

```
> setwd("R")
> library("igraph")
> g<-read.graph("lesmis.gml",format="gml")
> tkplot(g)
Loading required package: tcltk
Tcl/Tkインターフェースのロード中　終了済
[1] 1
>
```

# 2. layout the network


RGui
ファイル 編集 閲覧 その他 パッケージ ウインドウ ヘルプ
R Console
Graph plot 1
Close Select Layout View Export

```
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> setwd("R")
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Loading required package: tcltk
Tcl/Tkインターフェースのロード中   終了済
[1] 1
> 
```
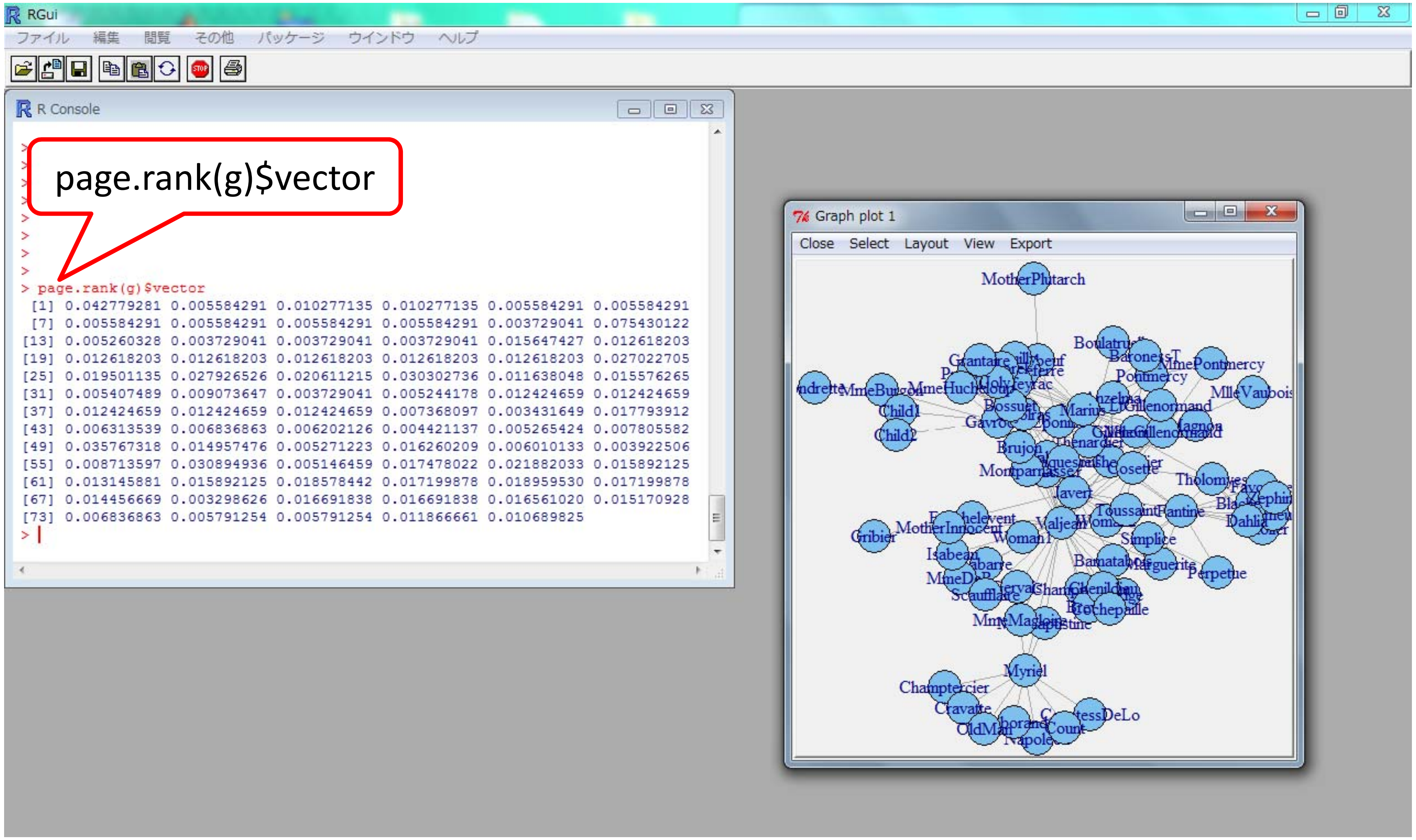
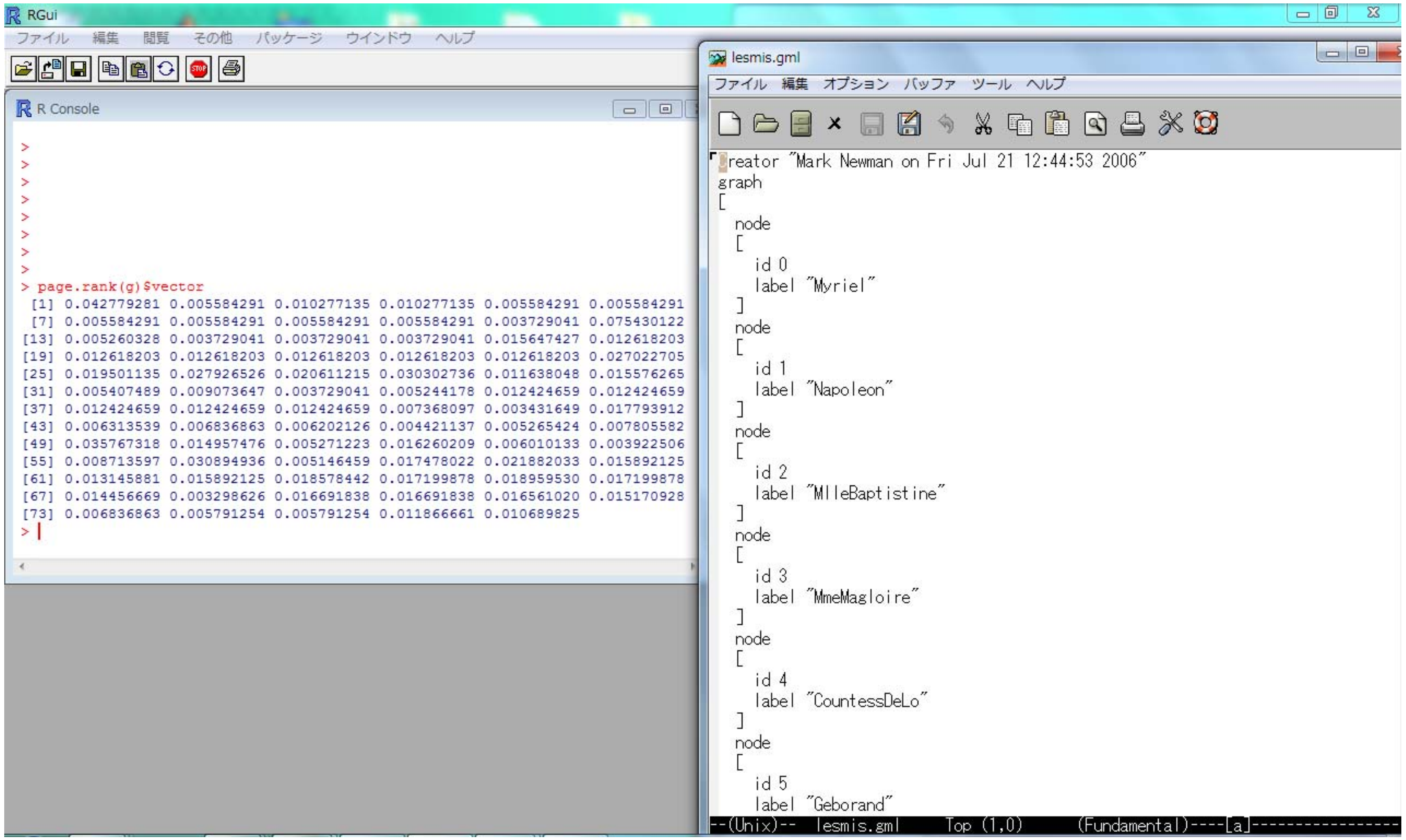

# 3. ranking



```
> page.rank(g)$vector
 [1] 0.042779281 0.005584291 0.010277135 0.010277135 0.005584291 0.005584291
 [7] 0.005584291 0.005584291 0.005584291 0.005584291 0.003729041 0.075430122
[13] 0.005260328 0.003729041 0.003729041 0.003729041 0.015647427 0.012618203
[19] 0.012618203 0.012618203 0.012618203 0.012618203 0.012618203 0.027022705
[25] 0.019501135 0.027926526 0.020611215 0.030302736 0.011638048 0.015576265
[31] 0.005407489 0.009073647 0.003729041 0.005244178 0.012424659 0.012424659
[37] 0.012424659 0.012424659 0.012424659 0.007368097 0.003431649 0.017793912
[43] 0.006313539 0.006836863 0.006202126 0.004421137 0.005265424 0.007805582
[49] 0.035767318 0.014957476 0.005271223 0.016260209 0.006010133 0.003922506
[55] 0.008713597 0.030894936 0.005146459 0.017478022 0.021882033 0.015892125
[61] 0.013145881 0.015892125 0.018578442 0.017199878 0.018959530 0.017199878
[67] 0.014456669 0.003298626 0.016691838 0.016691838 0.016561020 0.015170928
[73] 0.006836863 0.005791254 0.005791254 0.011866661 0.010689825
> 
```

# 3.ranking

- original gml file contain labels


RGui
ファイル 編集 閲覧 その他 パッケージ ウインドウ ヘルプ
R Console
lesmis.gml
ファイル 編集 オプション バッファ ツール ヘルプ

```
>
>
>
>
>
>
>
>
> page.rank(g)$vector
 [1] 0.042779281 0.005584291 0.010277135 0.010277135 0.005584291 0.005584291
 [7] 0.005584291 0.005584291 0.005584291 0.005584291 0.003729041 0.075430122
[13] 0.005260328 0.003729041 0.003729041 0.003729041 0.015647427 0.012618203
[19] 0.012618203 0.012618203 0.012618203 0.012618203 0.012618203 0.027022705
[25] 0.019501135 0.027926526 0.020611215 0.030302736 0.011638048 0.015576265
[31] 0.005407489 0.009073647 0.003729041 0.005244178 0.012424659 0.012424659
[37] 0.012424659 0.012424659 0.012424659 0.007368097 0.003431649 0.017793912
[43] 0.006313539 0.006836863 0.006202126 0.004421137 0.005265424 0.007805582
[49] 0.035767318 0.014957476 0.005271223 0.016260209 0.006010133 0.003922506
[55] 0.008713597 0.030894936 0.005146459 0.017478022 0.021882033 0.015892125
[61] 0.013145881 0.015892125 0.018578442 0.017199878 0.018959530 0.017199878
[67] 0.014456669 0.003298626 0.016691838 0.016691838 0.016561020 0.015170928
[73] 0.006836863 0.005791254 0.005791254 0.011866661 0.010689825
>
```

```
Creator "Mark Newman on Fri Jul 21 12:44:53 2006"
graph
[
  node
  [
    id 0
    label "Myriel"
  ]
  node
  [
    id 1
    label "Napoleon"
  ]
  node
  [
    id 2
    label "MlleBaptistine"
  ]
  node
  [
    id 3
    label "MmeMagloire"
  ]
  node
  [
    id 4
    label "CountessDeLo"
  ]
  node
  [
    id 5
    label "Geborand"
--(Unix)--  lesmis.gml      Top (1,0)      (Fundamental)----[a]----------------
```

# 4. metrics

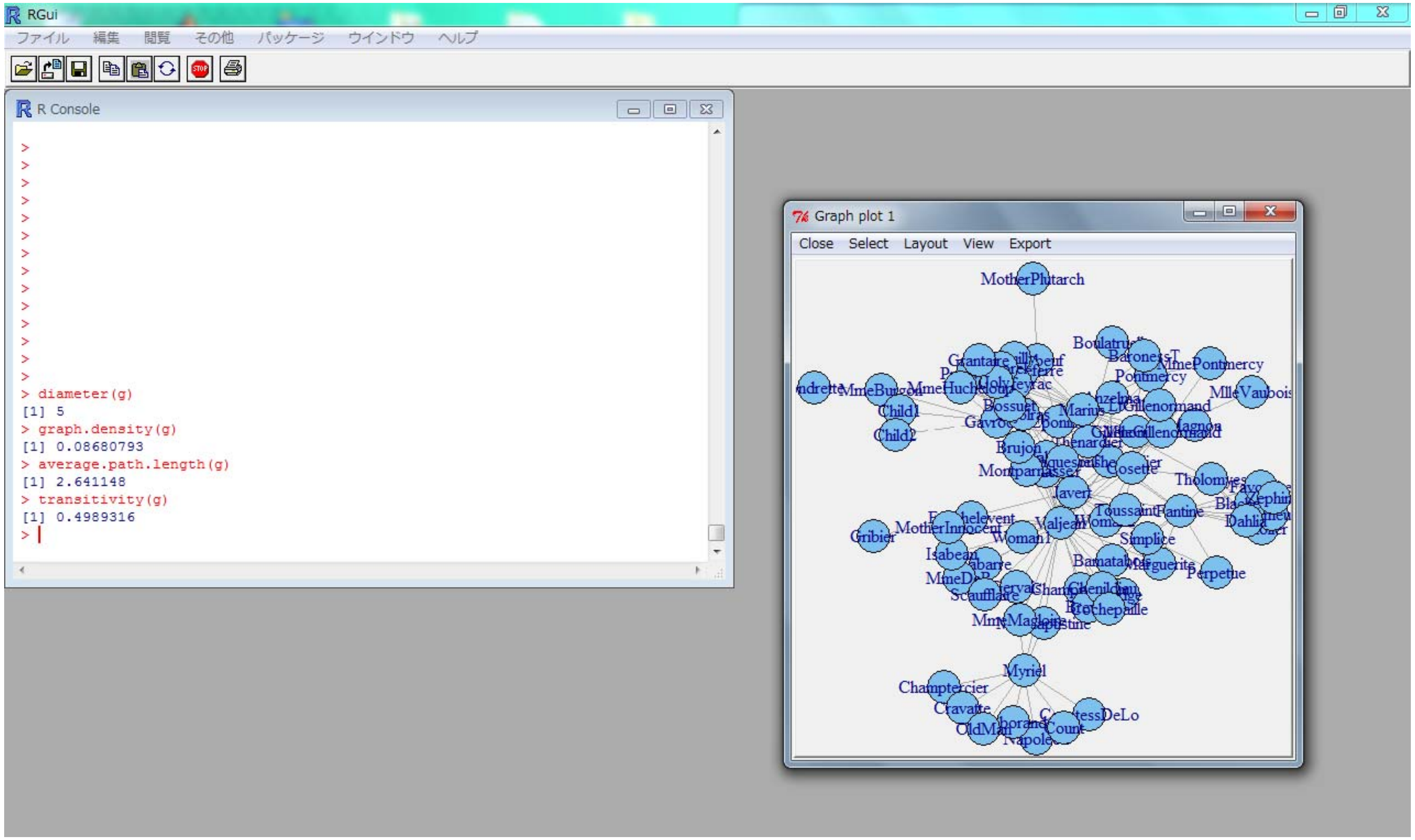
- diameter(g)
- graph.density(g)
- average.path.length(g)
- transitivity(g)

percentage two are friends,然后我们三个就是个三角

clustering coefficient

- help
  - ??rank
  - help(“page.rank”)

# 4. metrics



```
>
>
>
>
>
>
>
>
>
>
>
>
>
>
> diameter(g)
[1] 5
> graph.density(g)
[1] 0.08680793
> average.path.length(g)
[1] 2.641148
> transitivity(g)
[1] 0.4989316
>
```

# 5. community detection

modularity optimization

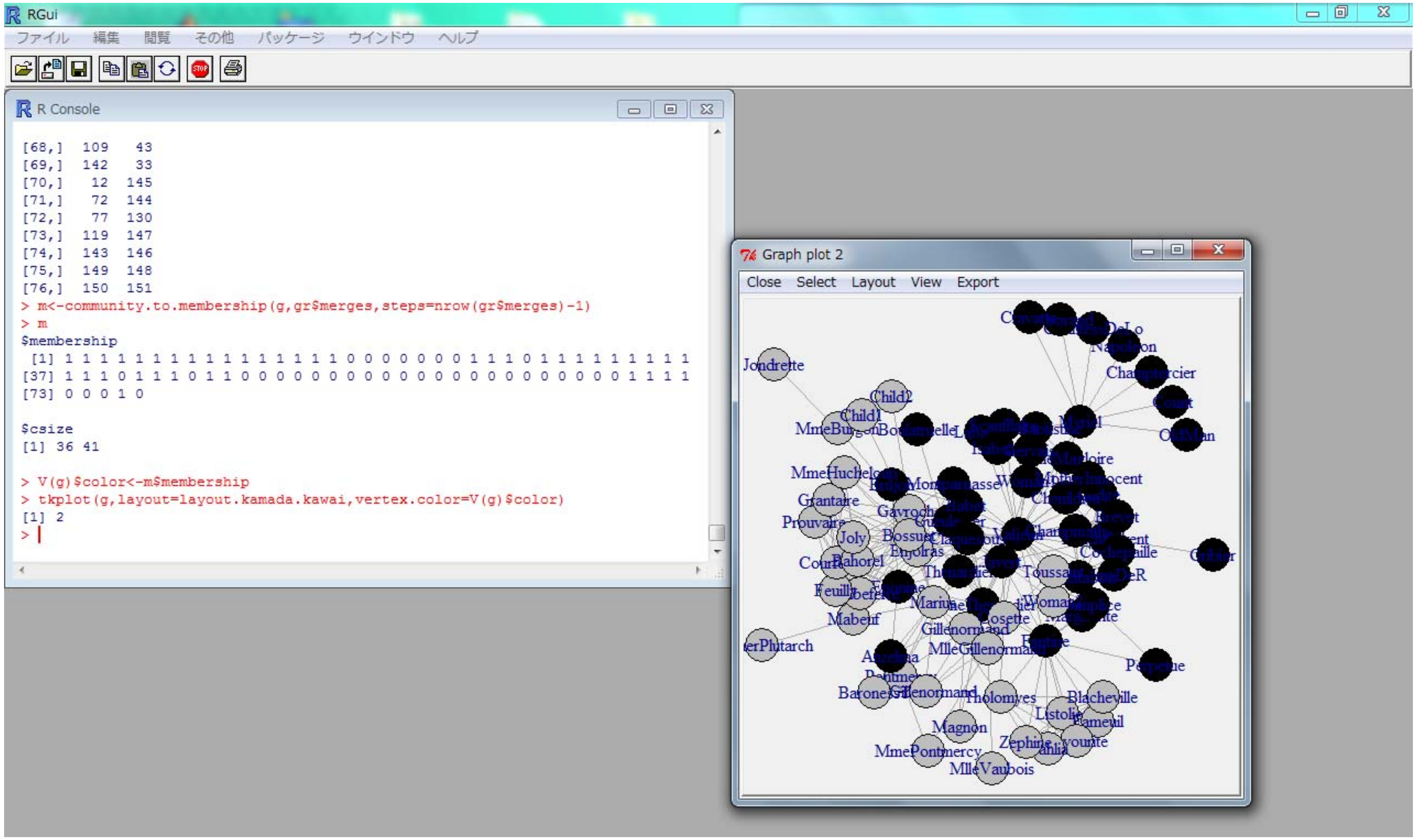
store membership and size

```
> gr<-fastgreedy.community(g)
> m<-community.to.membership(g,gr$merges,steps=nrow(gr$merges)-1)
> m
$membership
 [1] 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 1 0 0 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1
$csize
[1] 17 17
> V(g)$color<-m$membership
> V(g)$color
 [1] 0 0 0 0 0 0 0 0 1 0 0 0 0 0 1 1 0 0 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1
> tkplot(g,layout=layout.kamada.kawai,vertex.color=V(g)$color)
[1] 2
>
```

store membership

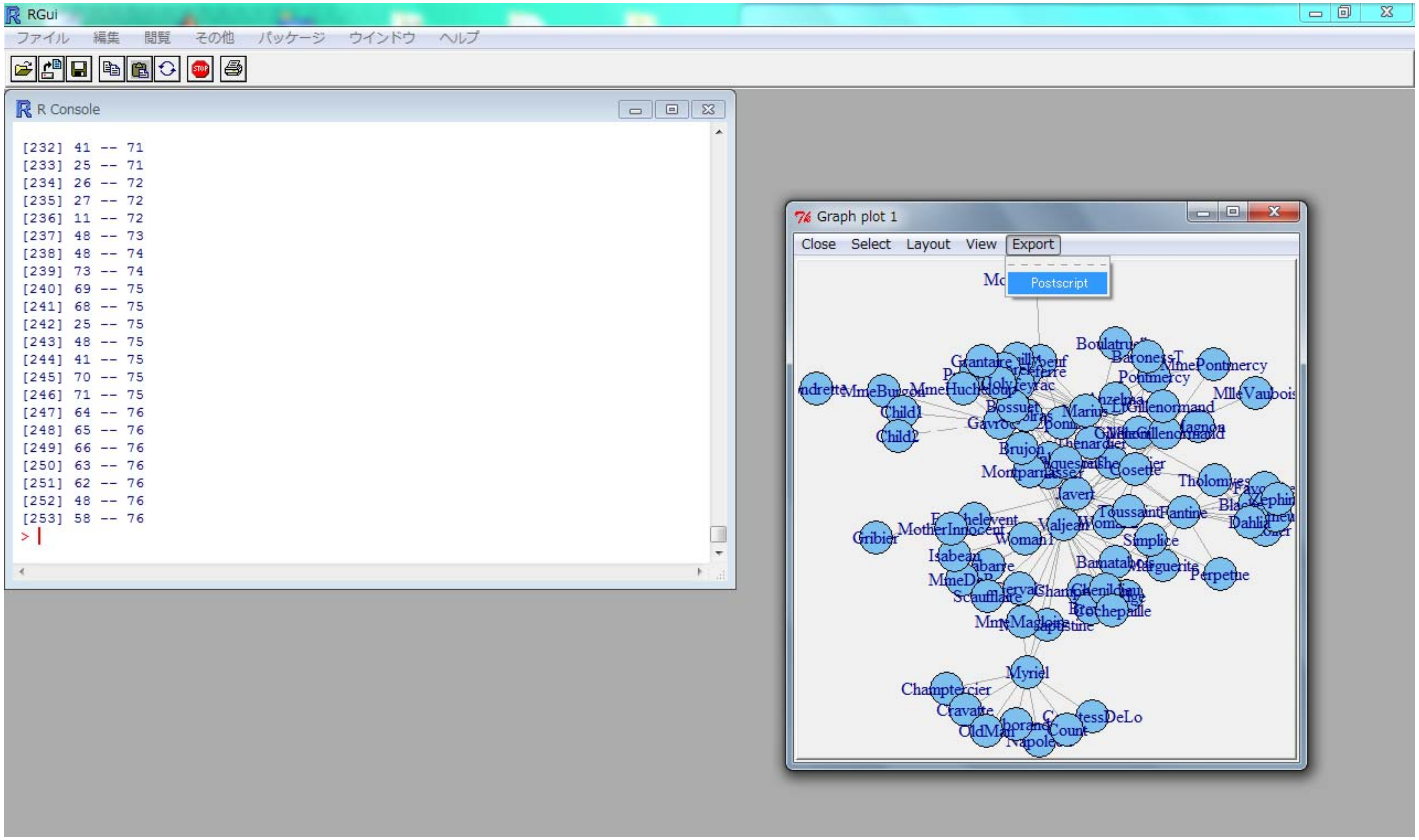
visualize network

# 5. community detection


RGui
ファイル 編集 閲覧 その他 パッケージ ウインドウ ヘルプ
R Console
Graph plot 2
Close Select Layout View Export

```
[68,]  109   43
[69,]  142   33
[70,]   12  145
[71,]   72  144
[72,]   77  130
[73,]  119  147
[74,]  143  146
[75,]  149  148
[76,]  150  151
> m<-community.to.membership(g,gr$merges,steps=nrow(gr$merges)-1)
> m
$membership
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 1 1 1 0 1 1 1 1 1 1 1 1 1
[37] 1 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1
[73] 0 0 0 1 0

$csize
[1] 36 41

> V(g)$color<-m$membership
> tkplot(g,layout=layout.kamada.kawai,vertex.color=V(g)$color)
[1] 2
> 
```

# 6. export


RGui
ファイル 編集 閲覧 その他 パッケージ ウインドウ ヘルプ
R Console
Graph plot 1
Close Select Layout View Export
Postscript

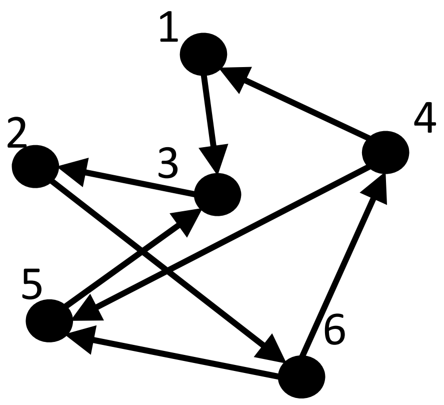
```
[232] 41 -- 71
[233] 25 -- 71
[234] 26 -- 72
[235] 27 -- 72
[236] 11 -- 72
[237] 48 -- 73
[238] 48 -- 74
[239] 73 -- 74
[240] 69 -- 75
[241] 68 -- 75
[242] 25 -- 75
[243] 48 -- 75
[244] 41 -- 75
[245] 70 -- 75
[246] 71 -- 75
[247] 64 -- 76
[248] 65 -- 76
[249] 66 -- 76
[250] 63 -- 76
[251] 62 -- 76
[252] 48 -- 76
[253] 58 -- 76
> 
```

# create from adjacency matrix(1)

- from adjacency matrix

```
> a <- matrix(c(0,0,0,1,0,0,
                0,0,1,0,0,0,
                1,0,0,0,1,0,
                0,0,0,0,0,1,
                0,0,0,1,0,1,
                0,1,0,0,0,0),nrow=6,byrow=TRUE)
```

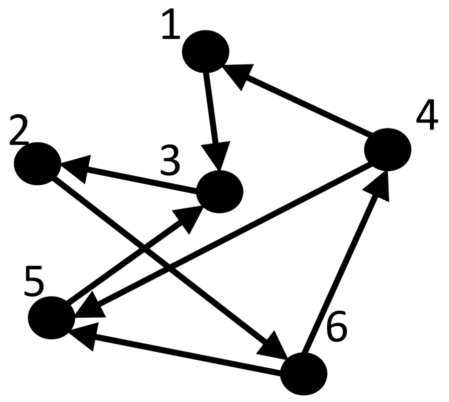
$$
\begin{array}{ccccccc}
 & & & & j & & \\
 & 0 & 0 & 0 & 1 & 0 & 0 \\
 & 0 & 0 & 1 & 0 & 0 & 0 \\
1\text{->}3 \quad i & \boxed{1} & 0 & 0 & 0 & 1 & 0 \\
A = & 0 & 0 & 0 & 0 & 0 & 1 \\
 & 0 & 0 & 0 & 1 & 0 & 1 \\
 & 0 & 1 & 0 & 0 & 0 & 0
\end{array}
$$



# create from adjacency matrix(2)

```
> ga <- graph.adjacency(t(a))
> ga
Vertices: 6
Edges: 8
Directed: TRUE
Edges:
[0] 0 -> 2
[1] 1 -> 5
[2] 2 -> 1
[3] 3 -> 0
[4] 3 -> 4
[5] 4 -> 2
[6] 5 -> 3
[7] 5 -> 4
```

transposition



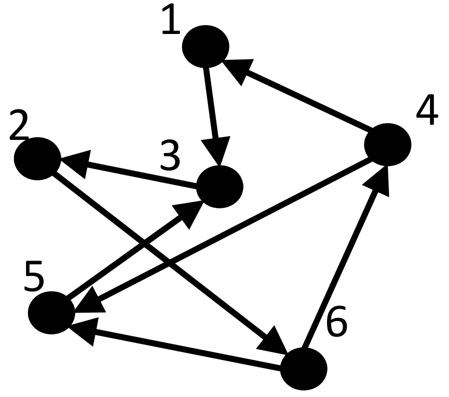
In igraph,

ID starts from 0 &

direction is from i to j

# create from edge list

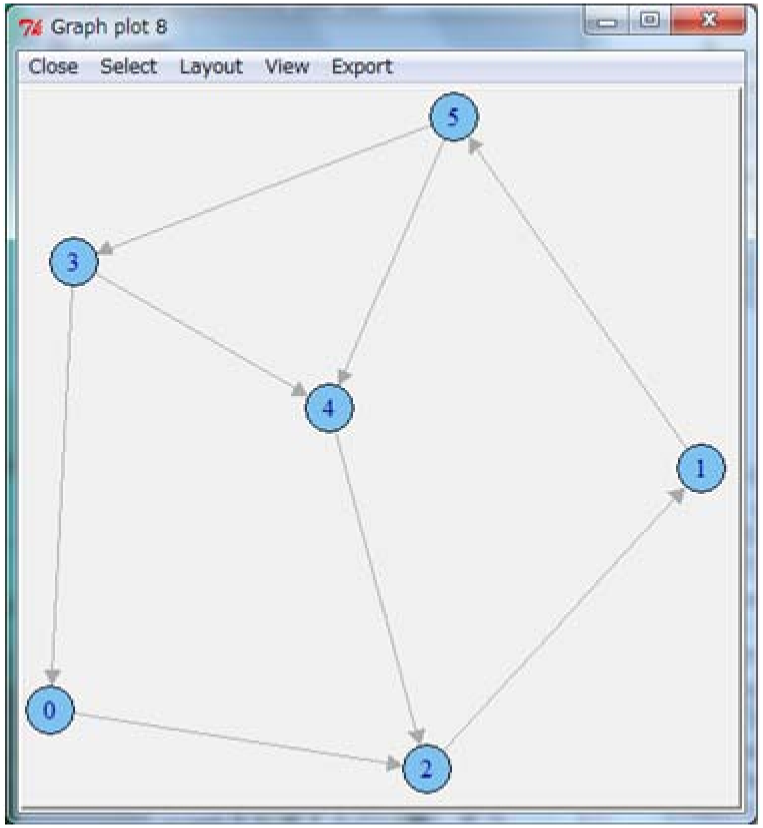
```
> el <-
    matrix(c(0,2,1,5,2,1,3,0,3,4,4,2,5,
    3,5,4),nc=2,byrow=TRUE)
> el
     [,1] [,2]
[1,]    0    2
[2,]    1    5
[3,]    2    1
[4,]    3    0
[5,]    4    2
[6,]    5    3
[7,]    5    4
```



```
> gb<-graph.edgelist(el)
> gb
Vertices: 6
Edges: 8
Directed: TRUE
Edges:
[0] 0 -> 2
[1] 1 -> 5
[2] 2 -> 1
[3] 3 -> 0
[4] 3 -> 4
[5] 4 -> 2
[6] 5 -> 3
[7] 5 -> 4
```

## layout the network

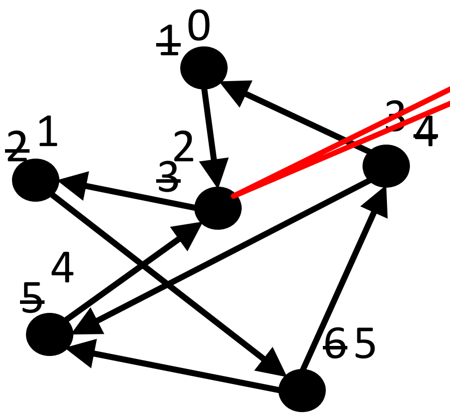
- > tkplot(ga,layout=layout.kamada.kawai)
  - choose layout (random, circle, Fruchterman-Reingold, Kamada-Kawai)
  - deform graph
  - export (Postscript)



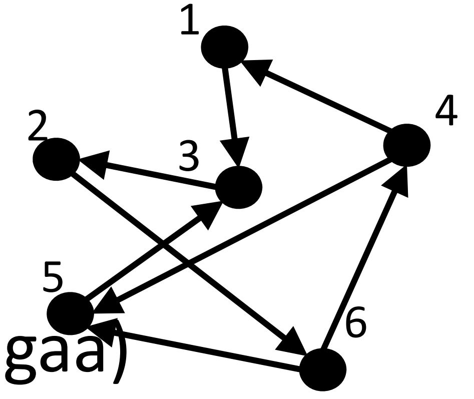
# ranking

- PageRank: importance of vertices
  - the probability that a random walker will visit

```
> page.rank(ga)$vector
[1] 0.07337065 0.21643820 0.22522142
   0.11381330 0.16218395 0.20897247
```



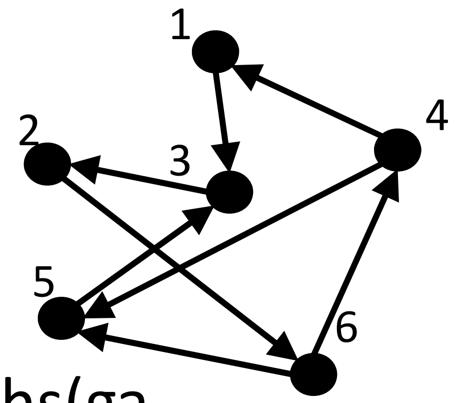
# metrics (1)



```
> cocitation(gaa)
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    0    0    0    0    1    0
[2,]    0    0    0    0    0    0
[3,]    0    0    0    0    0    0
[4,]    0    0    0    0    1    0
[5,]    1    0    0    1    0    0
[6,]    0    0    0    0    0    0
```

```
> bibcoupling(gaa)
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    0    0    0    0    1    0
[2,]    0    0    0    0    0    0
[3,]    0    0    0    0    0    0
[4,]    0    0    0    0    0    1
[5,]    1    0    0    0    0    0
[6,]    0    0    0    1    0    0
```

# metrics (2)



- undirected

```
> shortest.paths(ga)
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    0    2    1    1    2    2
[2,]    2    0    1    2    2    1
[3,]    1    1    0    2    1    2
[4,]    1    2    2    0    1    1
[5,]    2    2    1    1    0    1
[6,]    2    1    2    1    1    0
```

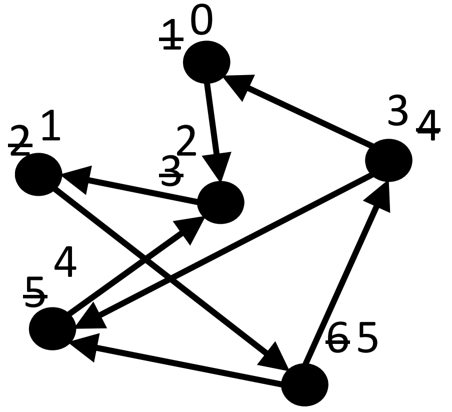
- directed

```
> shortest.paths(ga,
  mode="out")
                  to
         [,1] [,2] [,3] [,4] [,5] [,6]
    [1,]    0    2    1    4    4    3
from[2,]    3    0    3    2    2    1
    [3,]    4    1    0    3    3    2
    [4,]    1    3    2    0    1    4
    [5,]    5    2    1    4    0    3
    [6,]    2    3    2    1    1    0
```

# metrics (3)

```
> average.path.length(ga)
[1] 2.433333
> average.path.length(ga,directed=FALSE)
[1] 1.466667
```

directed

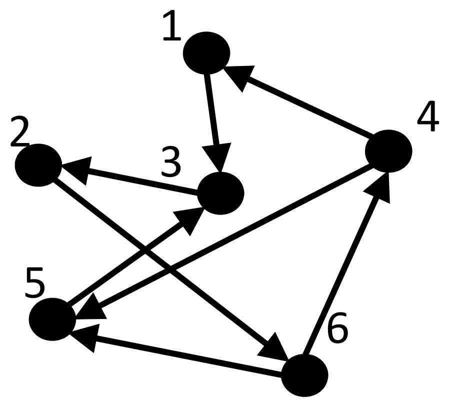


```
> get.all.shortest.paths(ga,0)
[[1]]
[1] 0
[[2]]
[1] 0 2 1
[[3]]
[1] 0 2
[[4]]
[1] 0 3
[[5]]
[1] 0 3 4
[[6]]
[1] 0 2 4
[[7]]
[1] 0 3 5
```

shortest paths from 0

# metrics (4)

```
> is.connected(ga)
[1] TRUE

> no.clusters(ga)
[1] 1

> clusters(ga)
$membership
[1] 0 0 0 0 0 0
$csize
[1] 6
$no
[1] 1
```



# metrics (5)

```
> graph.density(ga)
[1] 0.2666667
```

$$\rho = \frac{m}{n(n-1)} = \frac{8}{6 \cdot 5}$$