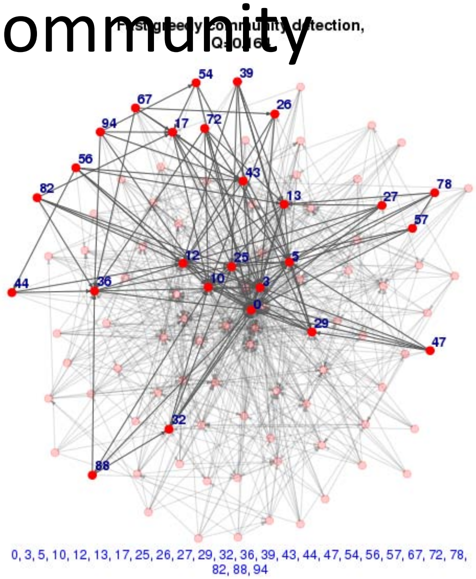
Complex Networks
tools for analyzing networks
(R+igraph)

2011.10.17

igraph

http://cneurocvs.rmki.kfki.hu/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.



tutorials

- tutorials of R
  - http://cran.r-project.org/other-docs.html (many tutorials in English and other languages)
- tutorial of igraph
  - http://igraph.sourceforge.net/igraphbook/ (English, under development)

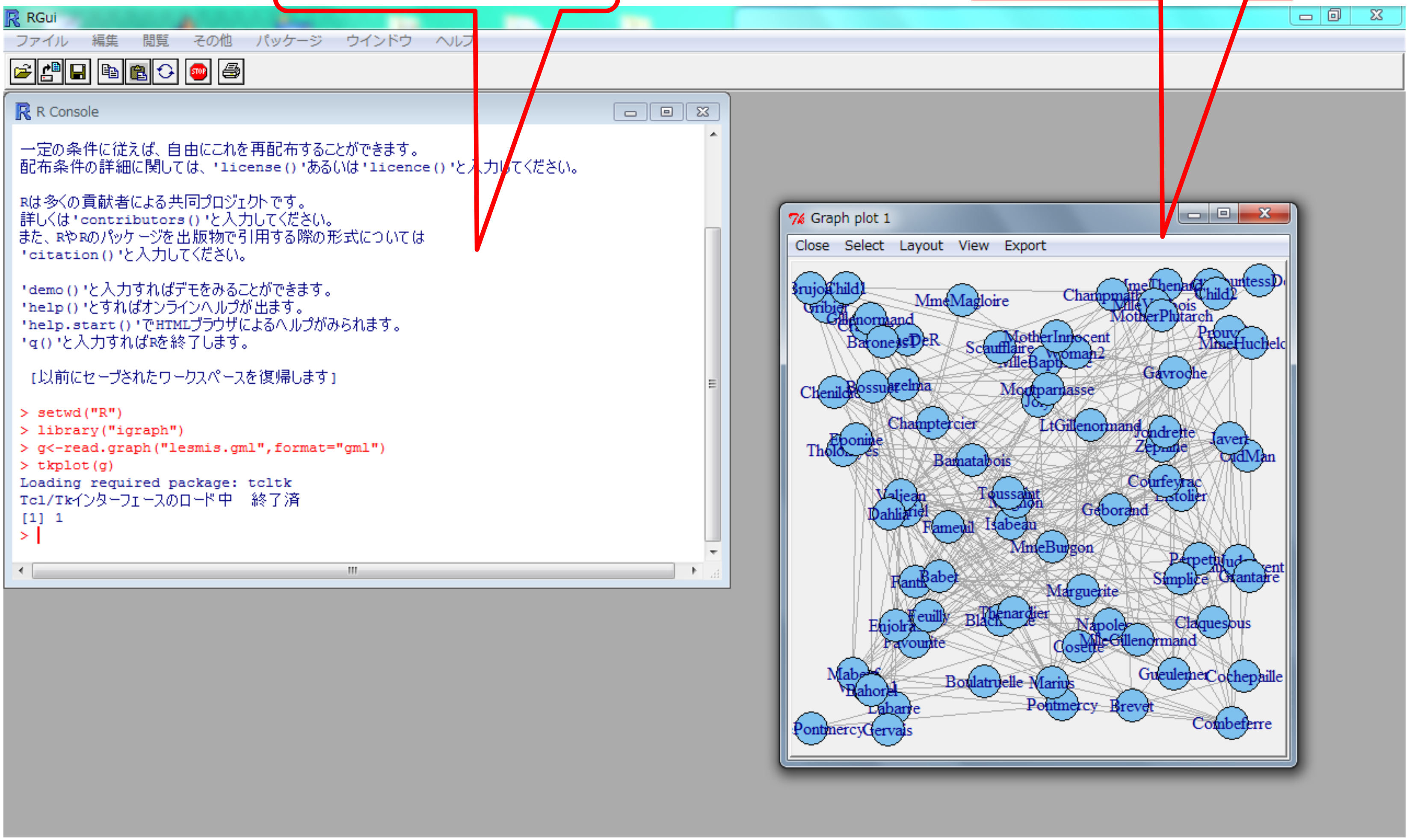
procedure for analyzing network

1. create graph object
2. layout the network
3. ranking
4. metrics
5. community detection
6. export

0. starting igraph

main

graph layout



```
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
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'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”)

start igraph

- setwd(“R”)

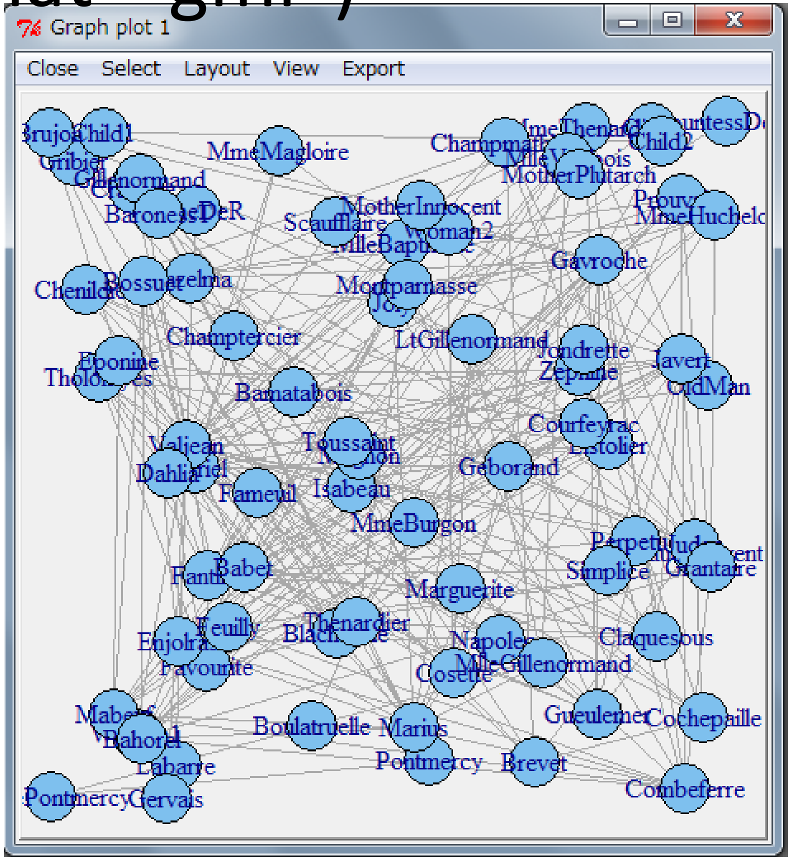
set directory

- g<-read(“lesmis.gml”, format=“gml”)

create graph

- tkplot(g)

open graph window



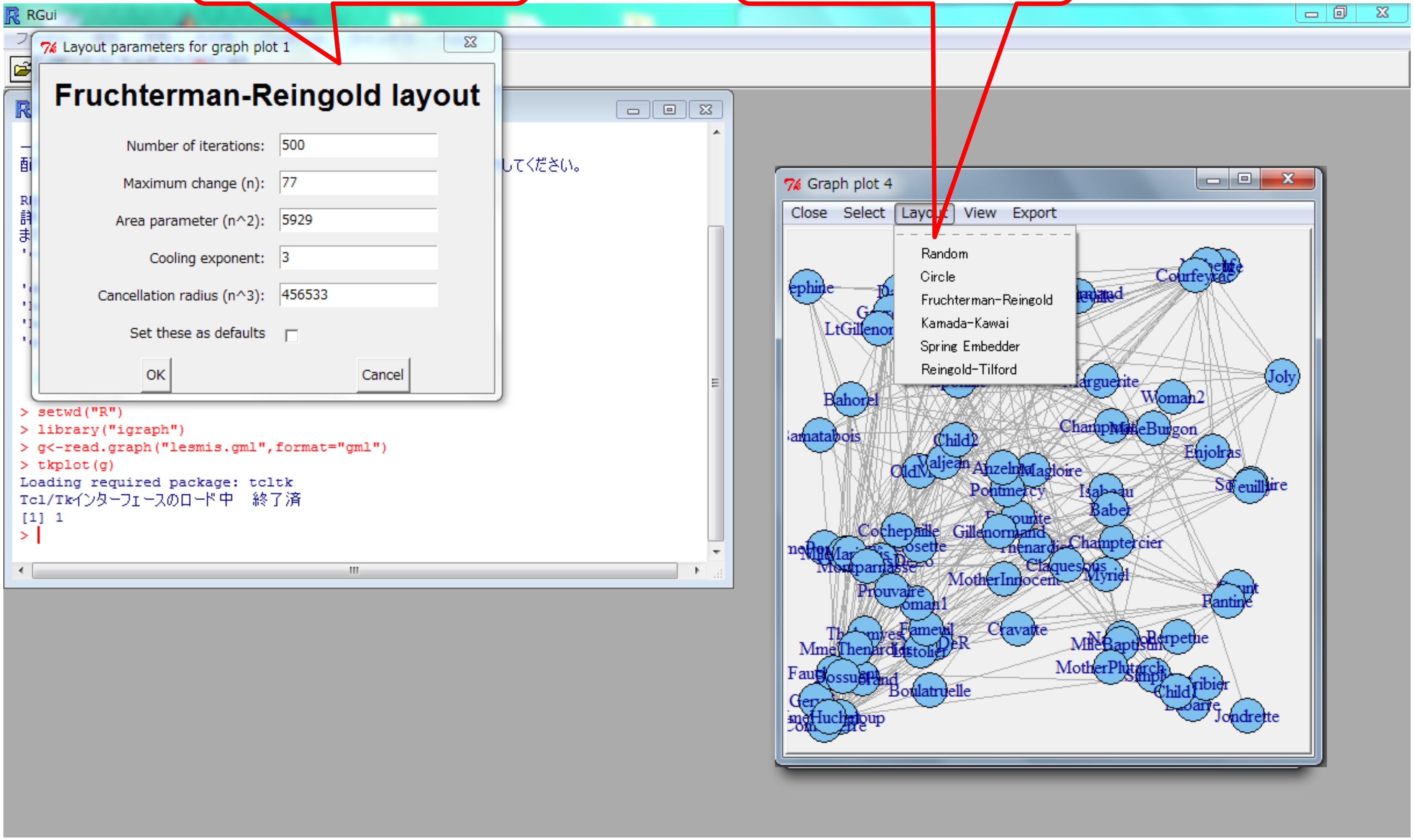
lesmis.gml is available at

Mark Newman’s Website

2. layout the network

set parameters

choose layout



Fruchterman-Reingold layout

Number of iterations: 500

Maximum change (n): 77

Area parameter (n^2): 5929

Cooling exponent: 3

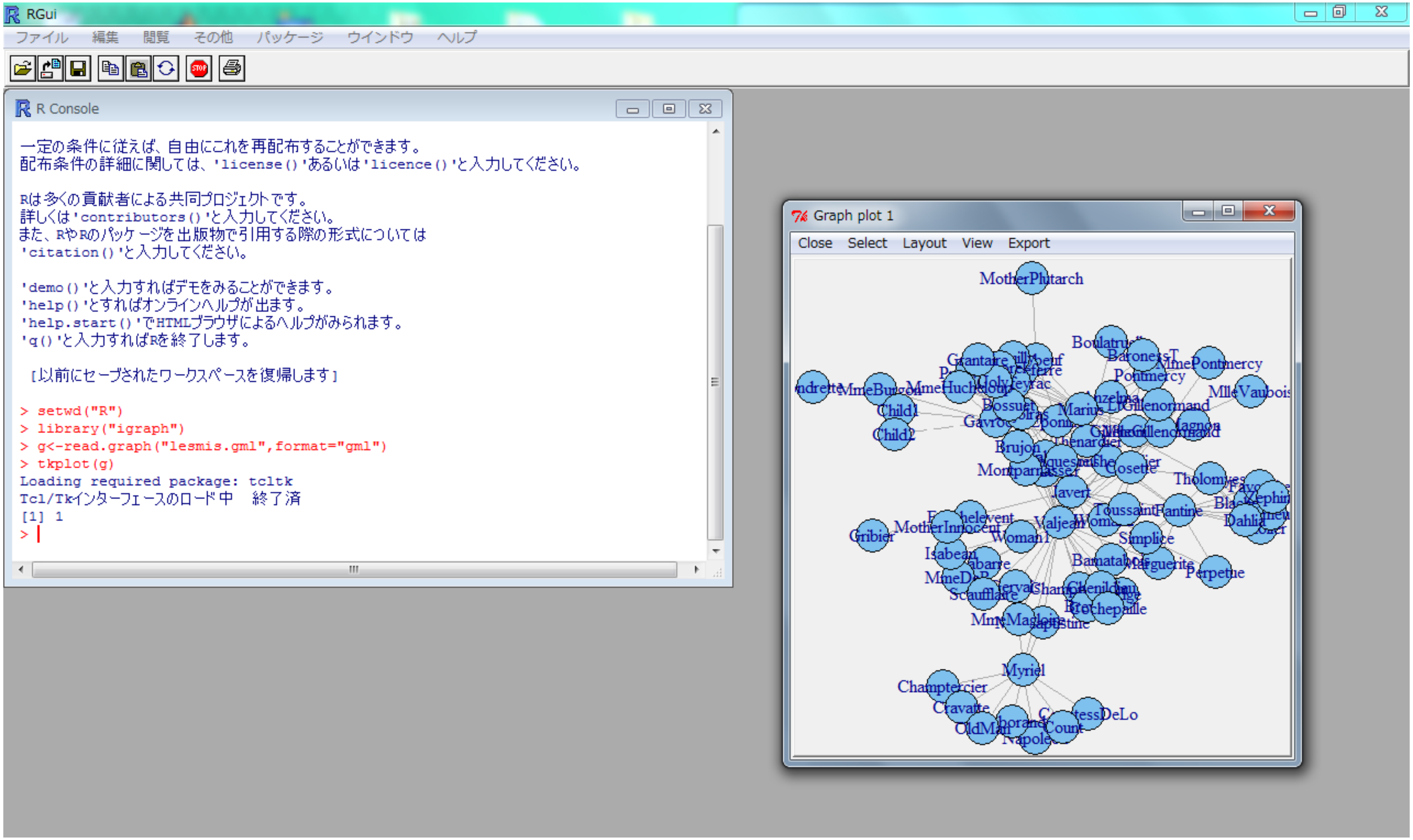
Cancellation radius (n^3): 456533

Set these as defaults □

OK Cancel

```
> 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



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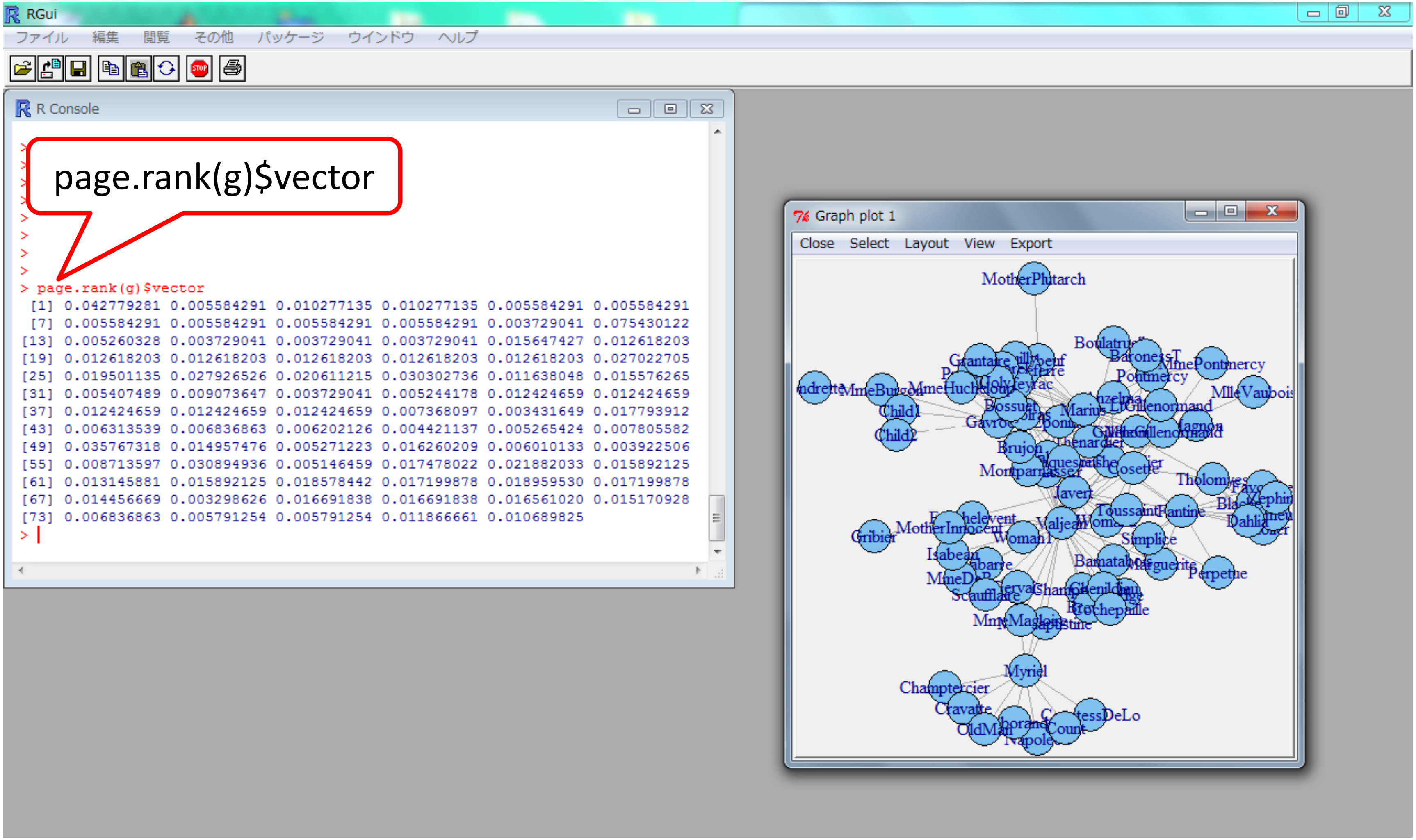
Loading required package: tcltk
Tcl/Tkインターフェースのロード中   終了済
[1] 1
> 
```

3. ranking

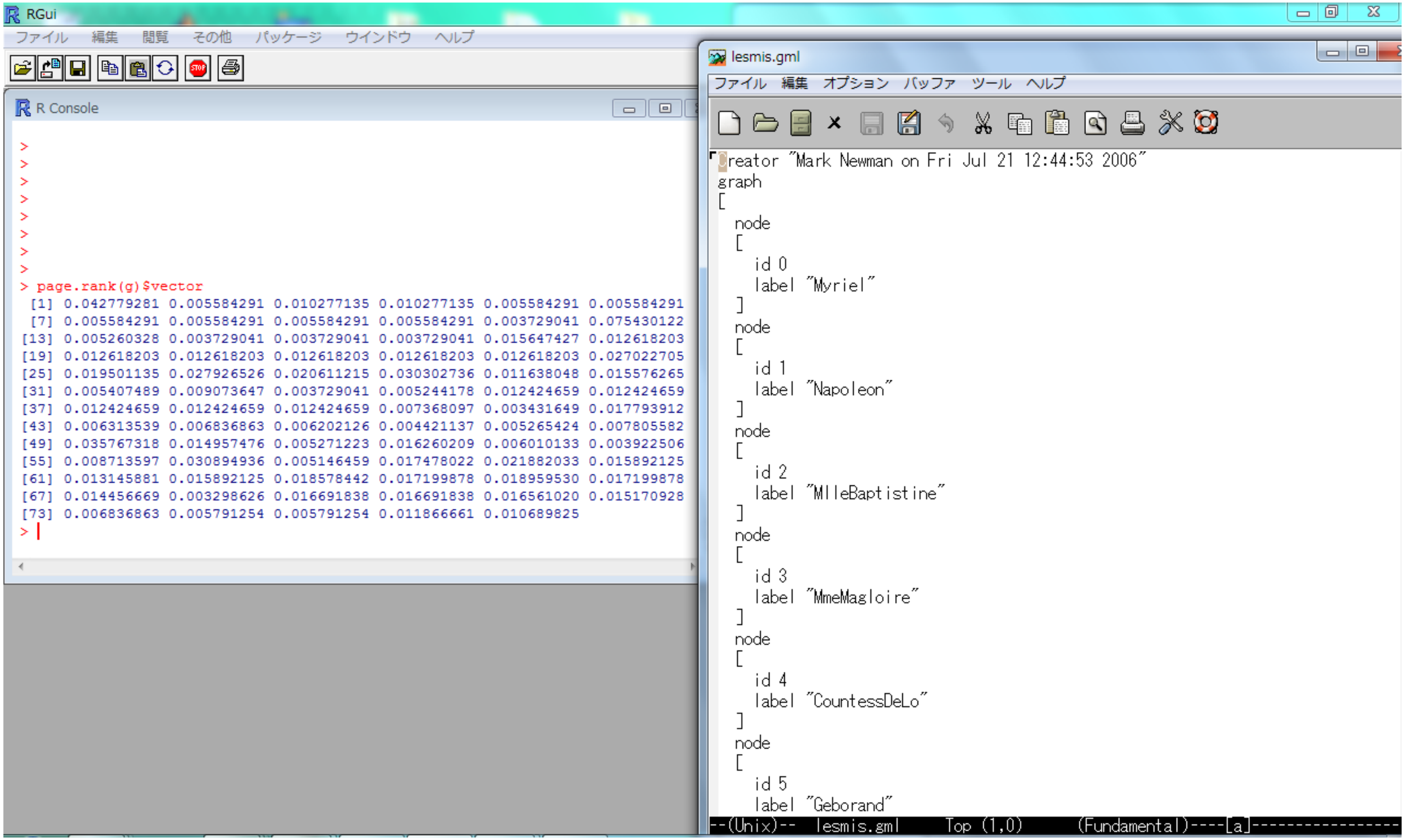


page.rank(g)$vector

```
>
>
>
>
>
>
>
>
> 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]----------------
```

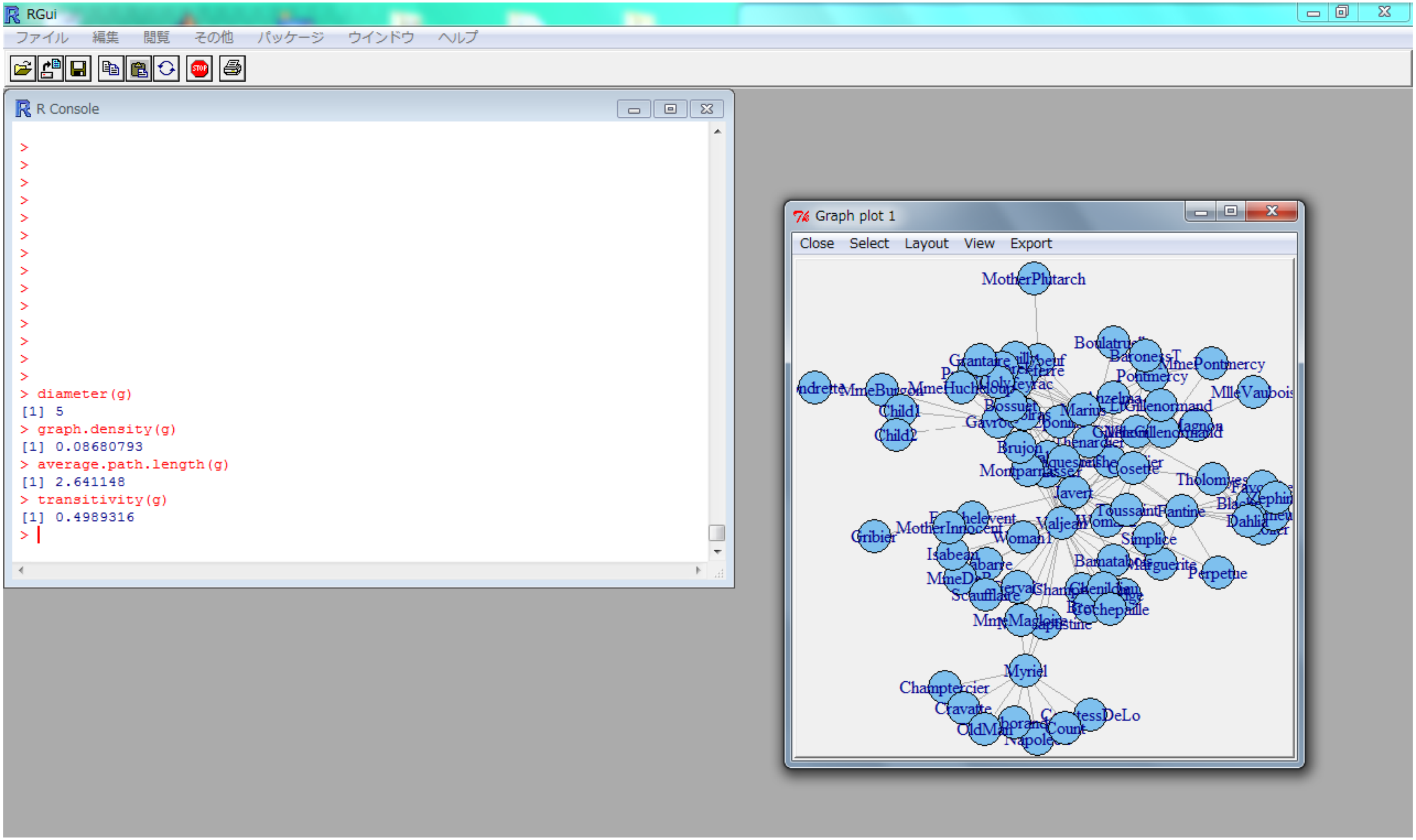
4. metrics

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

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

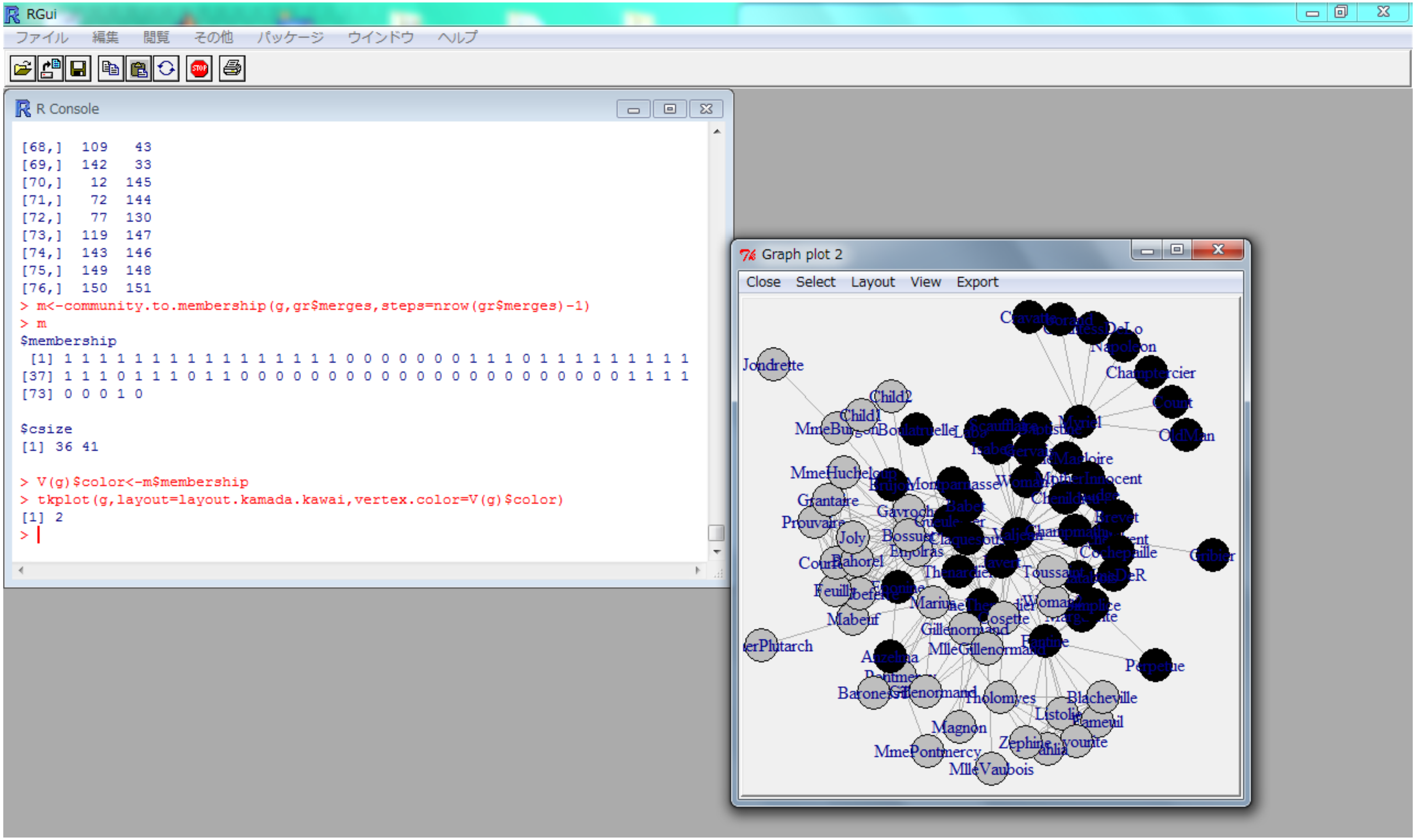
store membership and size

```
> 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

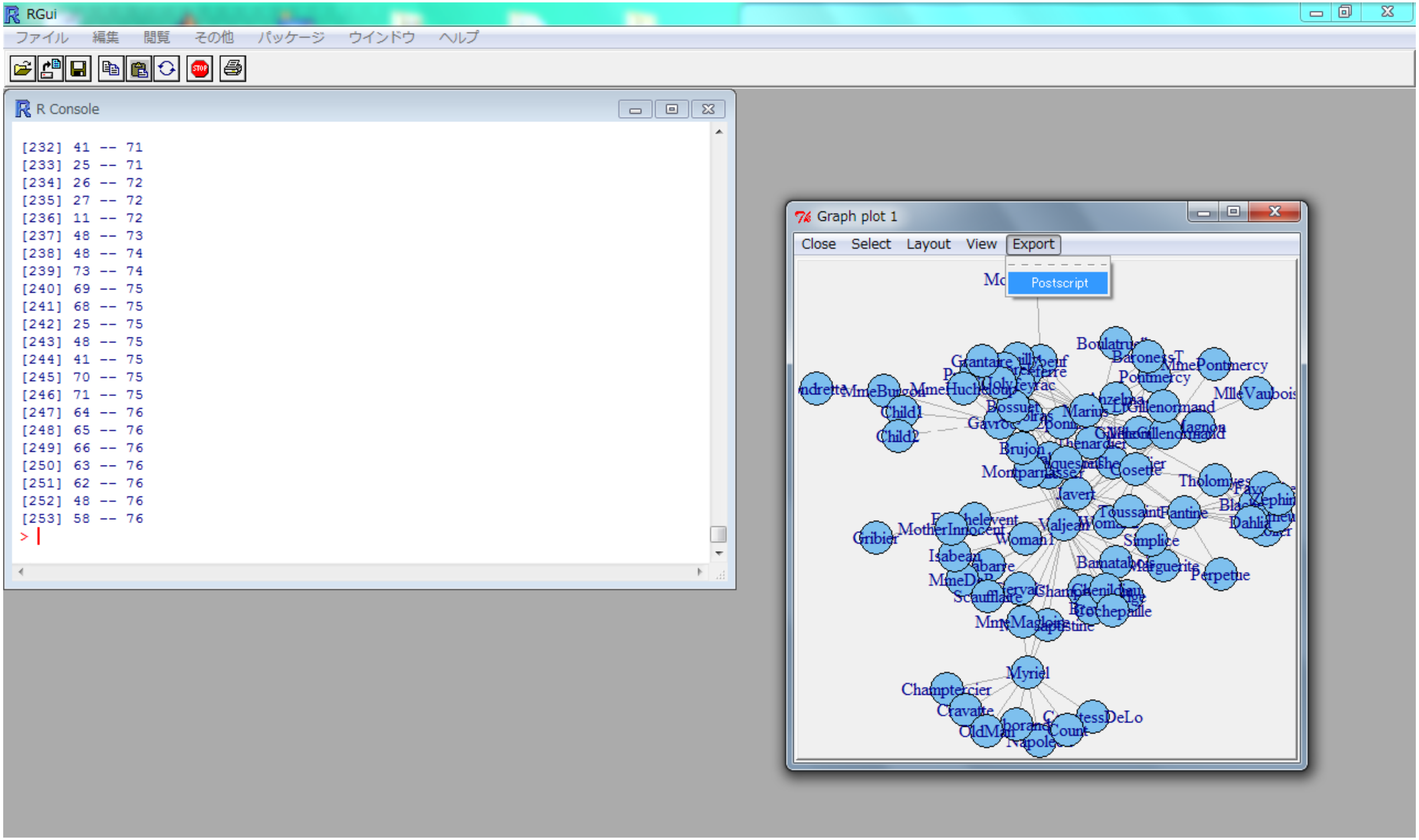


```
[68,]  109   43
[69,]  142   33
[70,]   12  145
[71,]   72  144
[72,]   77  130
[73,]  119  147
[74,]  143  146
[75,]  149  148
[76,]  150  151
> m<-community.to.membership(g,gr$merges,steps=nrow(gr$merges)-1)
> m
$membership
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 0 0 0 0 0 0 1 1 1 0 1 1 1 1 1 1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



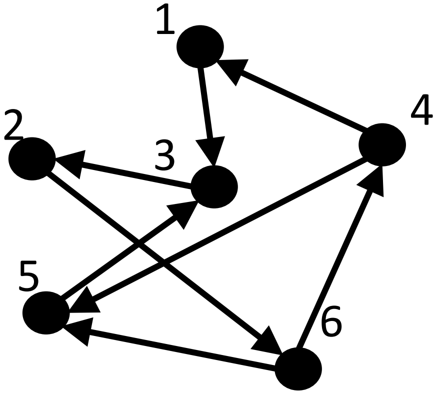
```
[232] 41 -- 71
[233] 25 -- 71
[234] 26 -- 72
[235] 27 -- 72
[236] 11 -- 72
[237] 48 -- 73
[238] 48 -- 74
[239] 73 -- 74
[240] 69 -- 75
[241] 68 -- 75
[242] 25 -- 75
[243] 48 -- 75
[244] 41 -- 75
[245] 70 -- 75
[246] 71 -- 75
[247] 64 -- 76
[248] 65 -- 76
[249] 66 -- 76
[250] 63 -- 76
[251] 62 --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

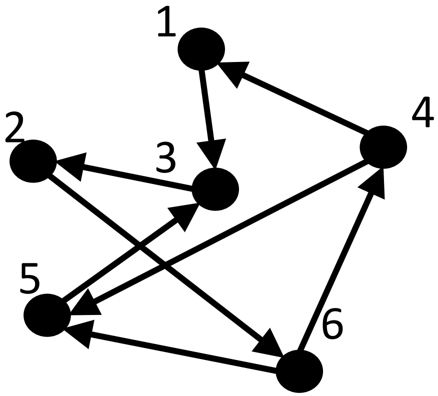
$$A=\left(\begin{array}{ccccccc} & & & & j & & \\ & 0&0&0&1&0&0 \\ & 0&0&1&0&0&0 \\ i & 1&0&0&0&1&0 \\ & 0&0&0&0&0&1 \\ & 0&0&0&1&0&1 \\ & 0&1&0&0&0&0 \end{array}\right)$$



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



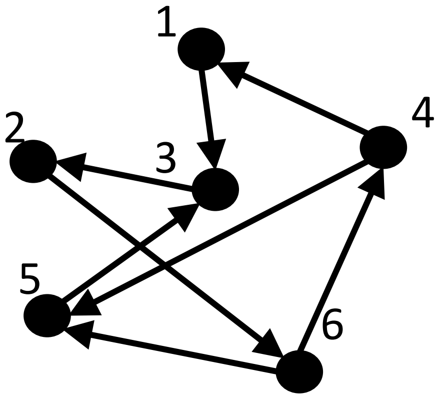
In igraph,

ID starts from 0 &

direction is from i to j

create from edge list

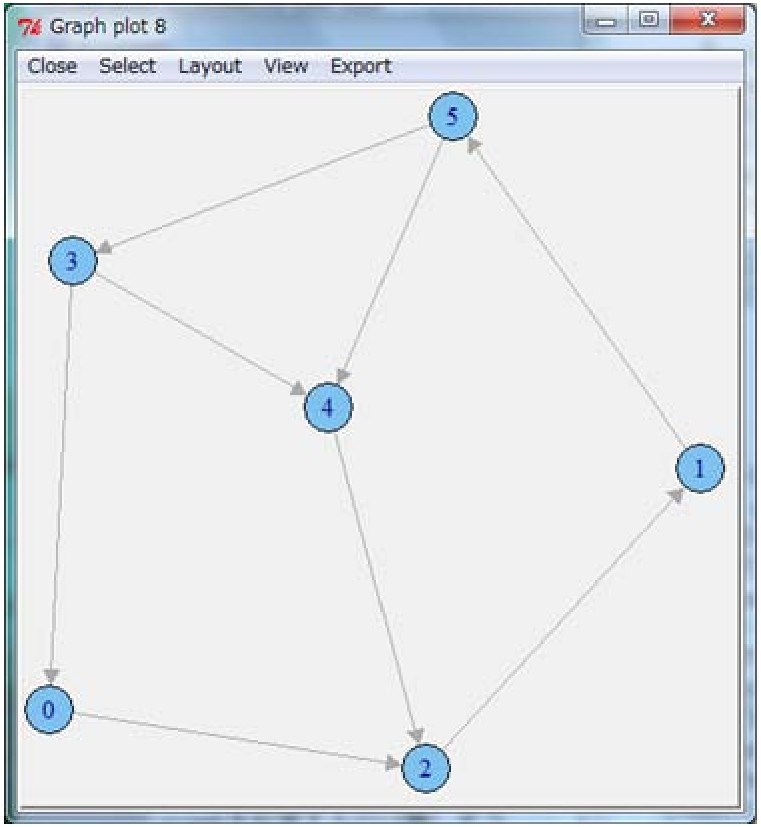
```
> el <-
    matrix(c(0,2,1,5,2,1,3,0,3,4,4,2,5,
    3,5,4),nc=2,byrow=TRUE)
> el
     [,1] [,2]
[1,]    0    2
[2,]    1    5
[3,]    2    1
[4,]    3    0
[5,]    4    2
[6,]    5    3
[7,]    5    4
```



```
> 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

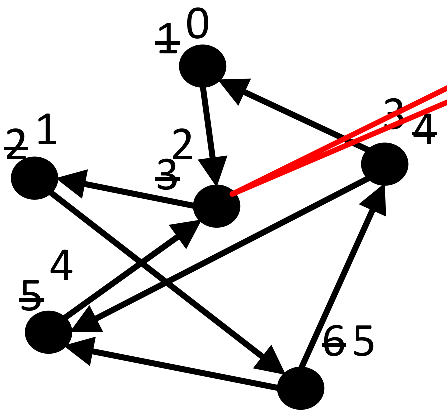
- > tkplot(ga,layout=layout.kamada.kawai)
  - choose layout (random, circle, Fruchterman-Reingold, Kamada-Kawai)
  - deform graph
  - export (Postscript)



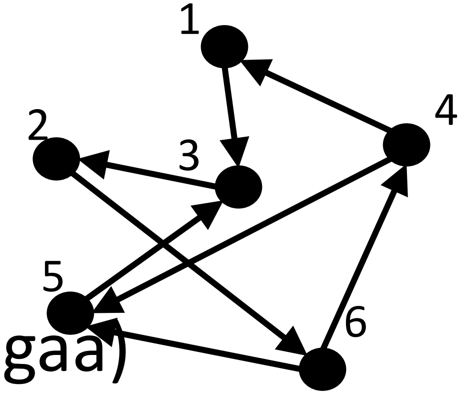
ranking

- 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
```



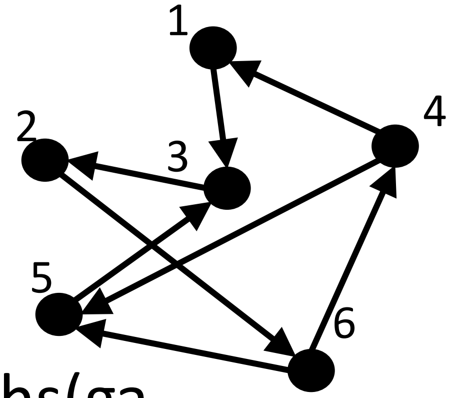
metrics (1)



```
> 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
```

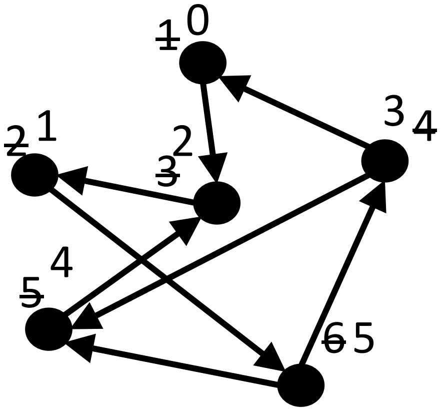
- directed

```
> 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
```

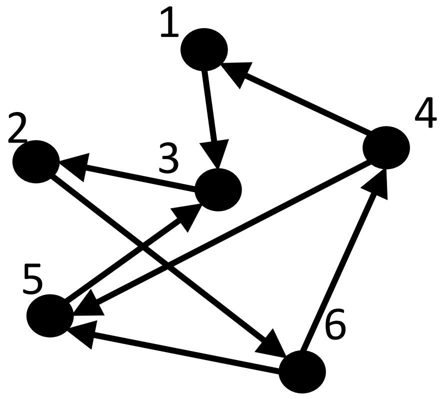
shortest paths from 0

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
```

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