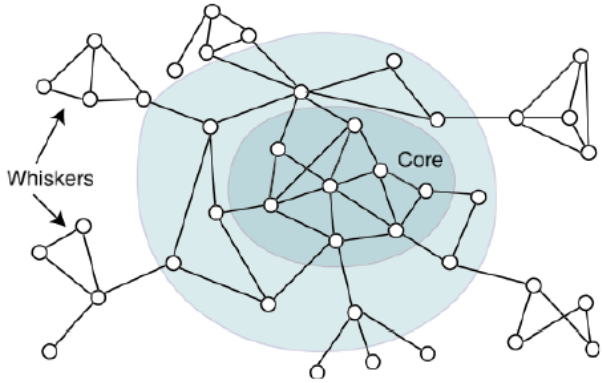
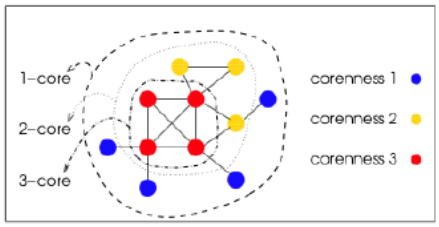
Graph Patterns and Visualization

Contents

Graph cores

A *k-core* is the largest subgraph such that each vertex is connected to at least k others in subset. Every vertex in k-core has a degree $k_i \geq k$. (k + 1)-core is always subgraph of k-core. The *core number* of a vertex is the highest order of a core that contains this vertex.



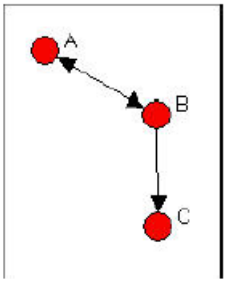


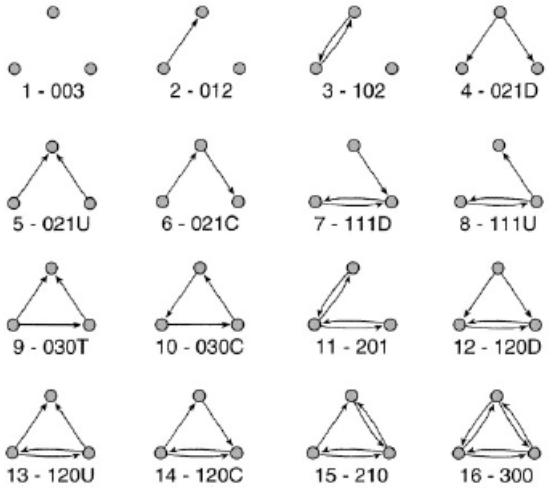
Dyads and triads

Dyad is a pair of vertices and possible relational ties between them: * mutual

- asymmetric
- null (non-existent)

Triad is a subgraph of three vertices and possible ties between them. Triad census :16 isomorphism classes. D - down, U - up, T - transitive, C - cyclic. Mutual dyads | assymetric dyads | null dyads.





Motifs

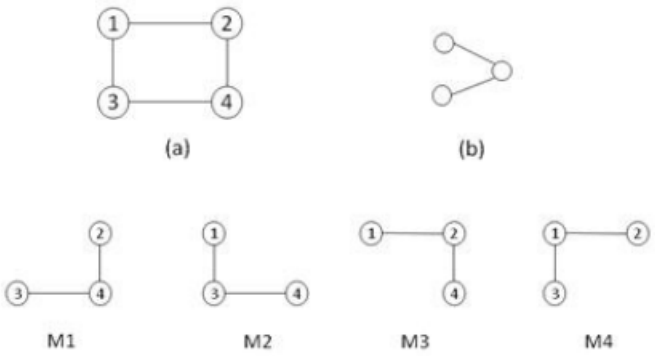
Motifs are often defined as recurrent and statistically significant sub-graphs or patterns. Here, we consider motifs as sub-graphs of a given graph, which are isomorphic to defined sample. Motifs are not induced subgraphs, i.e. they do not contain all the graph edges between selected vertices. Motifs appear in a network more frequently than in a comparable random network

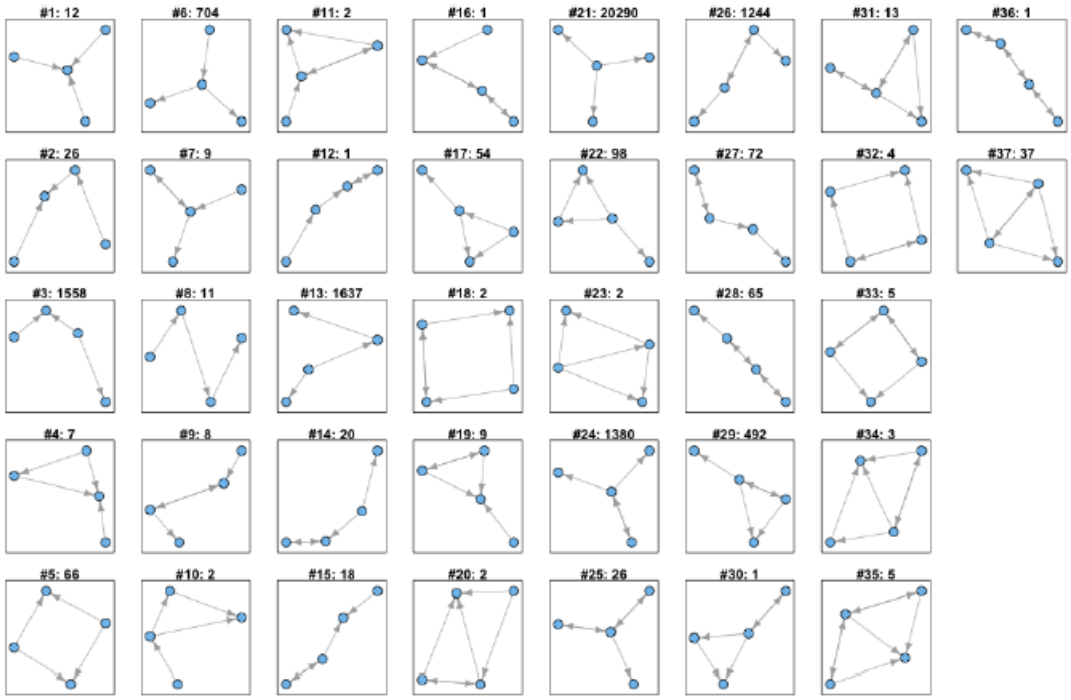
- calculate the number of occurrences of a sub graph
- evaluate the significance

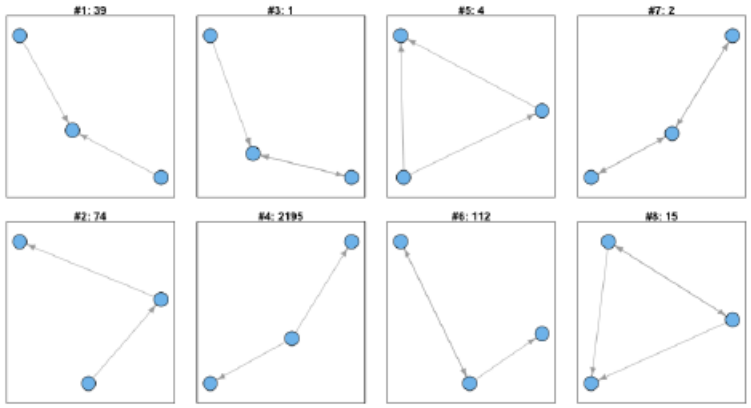
For G' subgraph (motif candidate) of G,

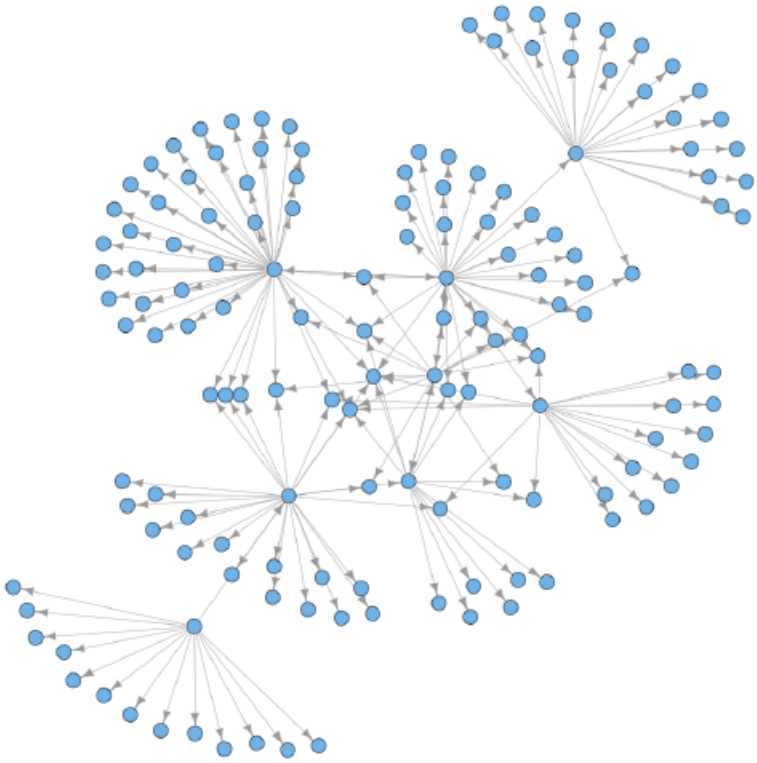
$$Z_{score}(G') = \frac{F_G(G') - \mu_R(G')}{\sigma_R(G')}$$

R - random graph, μ - mean frequency, σ -standard deviation.

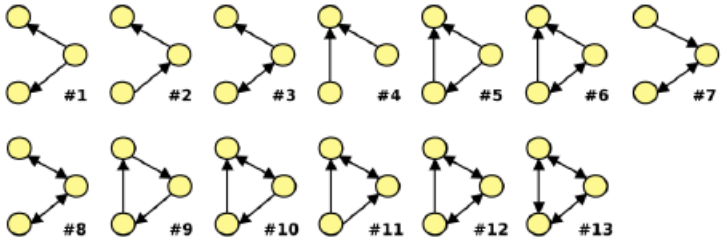



#1: 12
#6: 704
#11: 2
#16: 1
#21: 20290
#26: 1244
#31: 13
#36: 1
#2: 26
#7: 9
#12: 1
#17: 54
#22: 98
#27: 72
#32: 4
#37: 37
#3: 1558
#8: 11
#13: 1637
#18: 2
#23: 2
#28: 65
#33: 5
#4: 7
#9: 8
#14: 20
#19: 9
#24: 1380
#29: 492
#34: 3
#5: 66
#10: 2
#15: 18
#20: 2
#25: 26
#30: 1
#35: 5

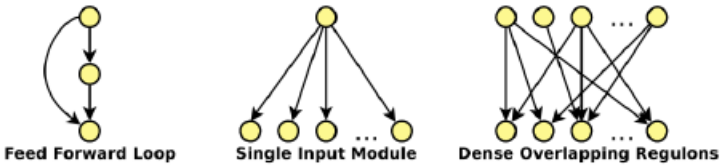

#1: 39
#3: 1
#5: 4
#7: 2
#2: 74
#4: 2195
#6: 112
#8: 15

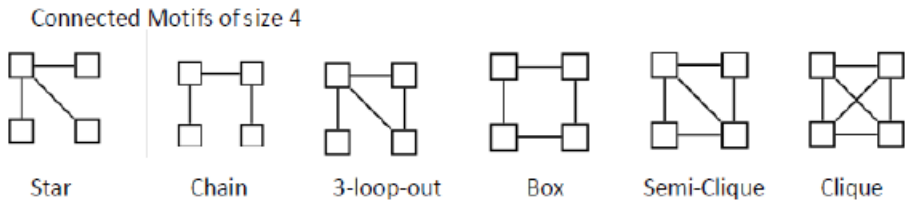


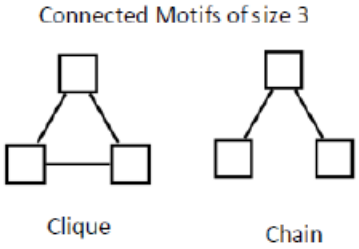
Connected triads - motifs of size 3



More complicated motifs:







Let's define a simple sample motif and calculate, if it is often in our graph:

```
#install.packages("rgl")
library('igraph')
sample1 = graph(c(c(1,2), c(2,3)))
plot(sample1)
isoclass_num = graph.isoclass(sample1) # defining number of corresponding isoclass
motifs3[isoclass_num] # returns number of motifs
#Here is our old friend:
g = graph.famous("Zachary")
motifs3 = graph.motifs(g, size = 3)
#Due to high computational time (isomorphism checks), `graph.motifs` are
#implemented for graps of sizes 3 and 4 only. However, we can easy check numbers
#for all motifs of size 4 to find more frequent patterns:
motifs4 = graph.motifs(g, size = 4)
#The most frequent pattern is fifth. Let's draw it.
plot(graph.isocreate(g,size=4, number=5))
#Not what we're looking for.. Second most frequent (seventh):
plot(graph.isocreate(g,size=3, number=7))
```

That is certainly better.

Visualisation

There are currently three different functions in the igraph package which can draw graph in various ways:

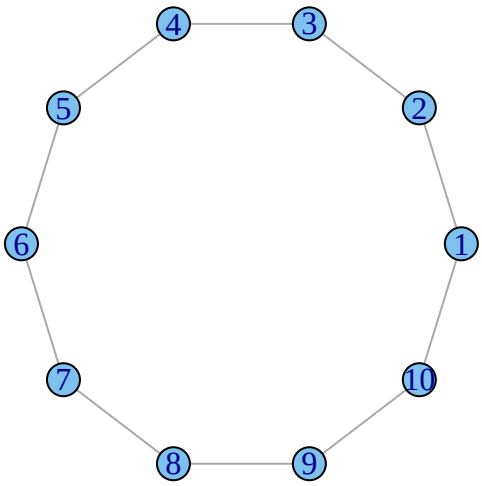
- `plot.igraph` does simple non-interactive 2D plotting to R devices. Actually it is an implementation of the plot generic function, so you can write plot(graph) instead of plot.igraph(graph). As it used the standard R devices it supports every output format for which R has an output device. The list is quite impressing: PostScript, PDF files, XFig files, SVG files, JPG, PNG and of course you can plot to the screen as well using the default devices, or the good-looking anti-aliased Cairo device. See plot.igraph for some more information.
- `tkplot` does interactive 2D plotting using the tcltk package. It can only handle graphs of moderate size, a thousend vertices is probably already too many. Some parameters of the plotted graph can be

changed interactively after issuing the tkplot command: the position, color and size of the vertices and the color and width of the edges. See tkplot for details.

- `rglplot` is an experimental function to draw graphs in 3D using OpenGL. See rglplot for some more information.

Let's draw a graph-ring using different three methods.

```
library(igraph)
library(rgl)

g <- graph.ring(10)
g$layout <- layout.circle
plot(g)
```




```
#doesn't work in R Markdown
tkplot(g)
```

```
## Loading required package: tcltk
```

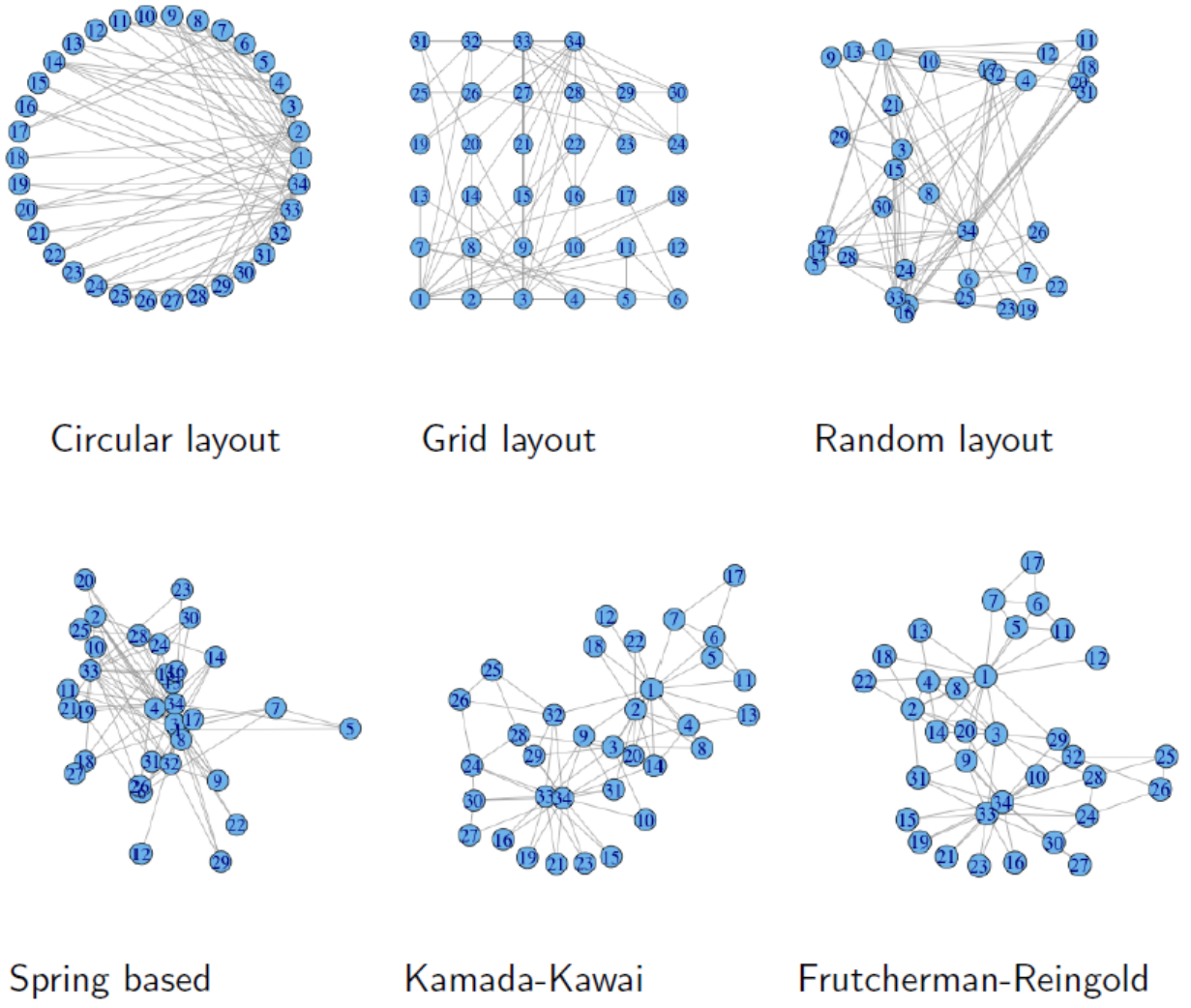
```
## [1] 1
```

```
rglplot(g)
```

Layout

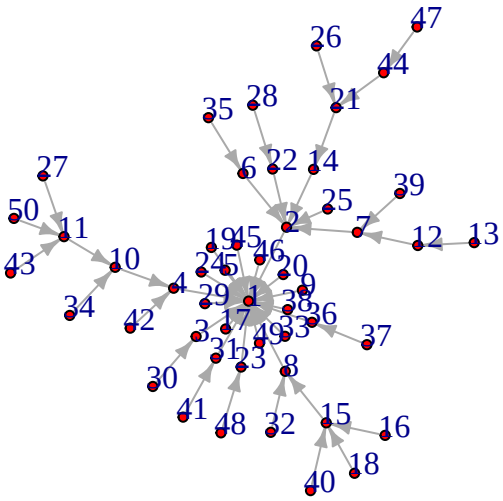
Either a function or a numeric matrix. It specifies how the vertices will be placed on the plot.
Let's demonstrate how it works on some graph. For example graph which based on barabashi model.

```
g <- barabasi.game(50)
```



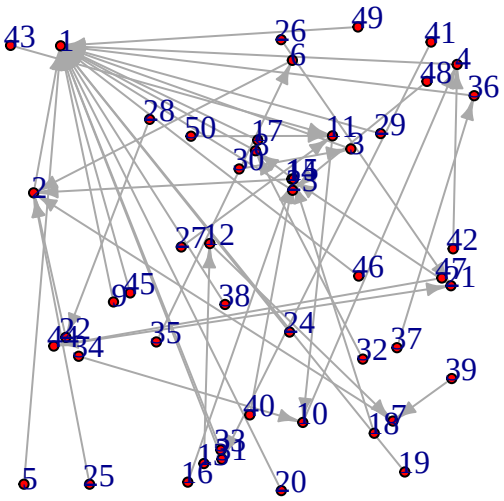
- `layout.auto` - tries to choose an appropriate layout function for the supplied graph, and uses that to generate the layout.

```
plot(g, layout=layout.auto, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



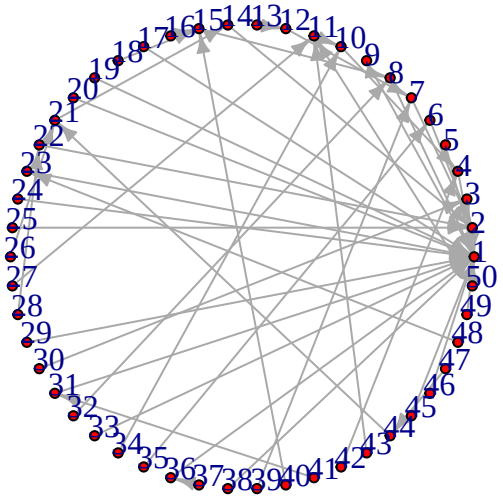
- `layout.random` - simply places the vertices randomly on a square.

```
plot(g, layout=layout.random, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



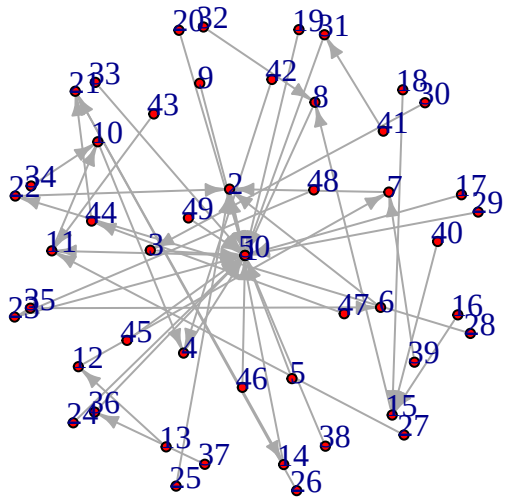
- `layout.circle` - places the vertices on a unit circle equidistantly.

```
plot(g, layout=layout.circle, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



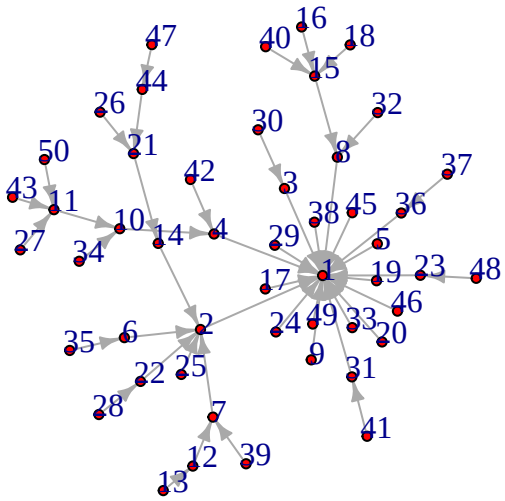
- `layout.sphere` - places the vertices (approximately) uniformly on the surface of a sphere, this is thus a 3d layout.

```
plot(g, layout=layout.sphere, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



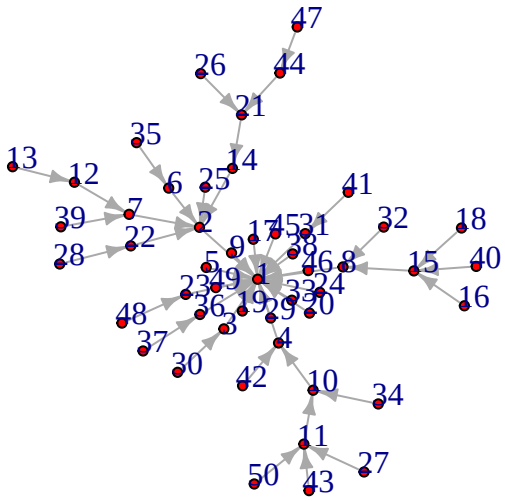
- `layout.fruchterman.reingold` uses a force-based algorithm proposed by Fruchterman and Reingold.

```
plot(g, layout=layout.fruchterman.reingold, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



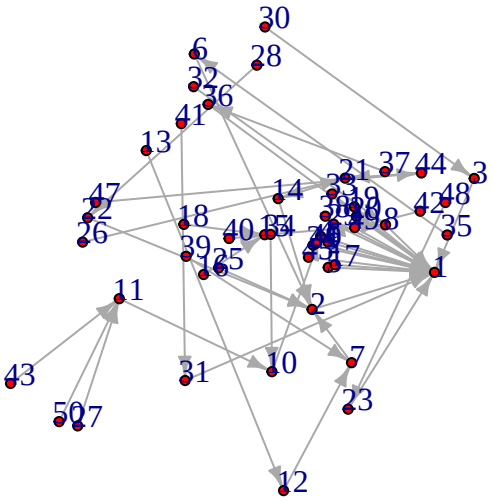
- `layout.kamada.kawai` is another force based algorithm.

```
plot(g, layout=layout.kamada.kawai, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



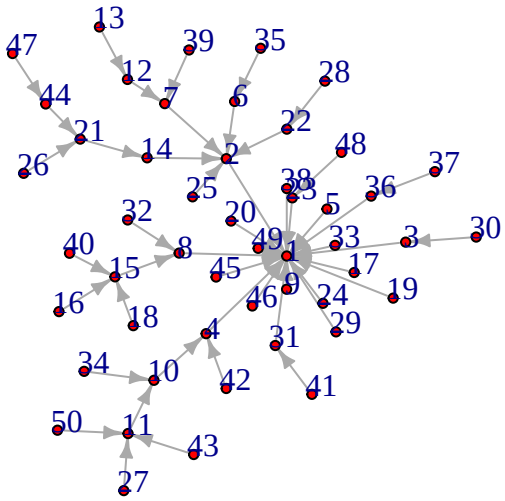
- `layout.spring` is a spring embedder algorithm.

```
plot(g, layout=layout.spring, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



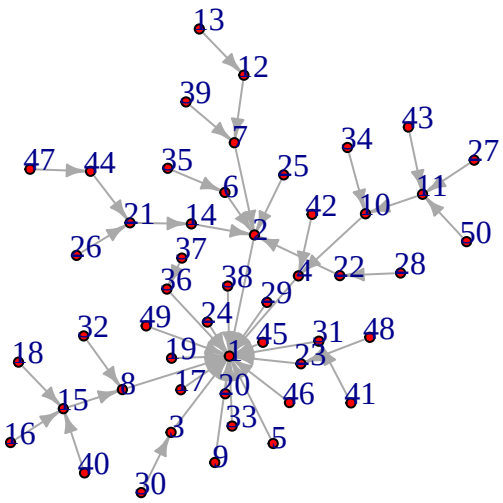
- `layout.fruchterman.reingold.grid` is similar to layout.fruchterman.reingold but repelling force is calculated only between vertices that are closer to each other than a limit, so it is faster.

```
plot(g, layout=layout.fruchterman.reingold.grid, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



- `layout.lgl` is for large connected graphs, it is similar to the layout generator of the Large Graph Layout software http://lgl.sourceforge.net/.

```
plot(g, layout=layout.lgl, vertex.size=4,
     vertex.label.dist=0.5, vertex.color="red", edge.arrow.size=0.5)
```



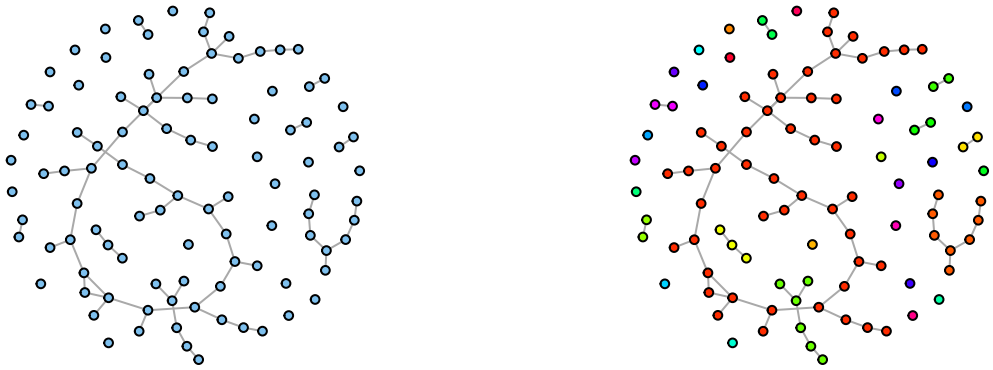
- `layout.graphopt` is a port of the graphopt layout algorithm by Michael Schmuhl. graphopt version 0.4.1 was rewritten in C and the support for layers was removed (might be added later) and a code was a bit reorganized to avoid some unneccessary steps is the node charge (see below) is zero.
- `layout.svd` is a currently experimental layout function based on singular value decomposition.
- `layout.norm` normalizes a layout, it linearly transforms each coordinate separately to fit into the given limits.
- `layout.drl` is another force-driven layout generator, it is suitable for quite large graphs.
- `layout.reingold.tilford` generates a tree-like layout, so it is mainly for tree.

Highlight components

Let's make different color for each graph component

```
g <- erdos.renyi.game(100, 1/100)

l <- layout.fruchterman.reingold(g)

op = par(mfrow = c(1,2))
plot(g, layout=l, vertex.size=5, vertex.label=NA)

comps <- clusters(g)$membership
colbar <- rainbow(max(comps)+1)
```

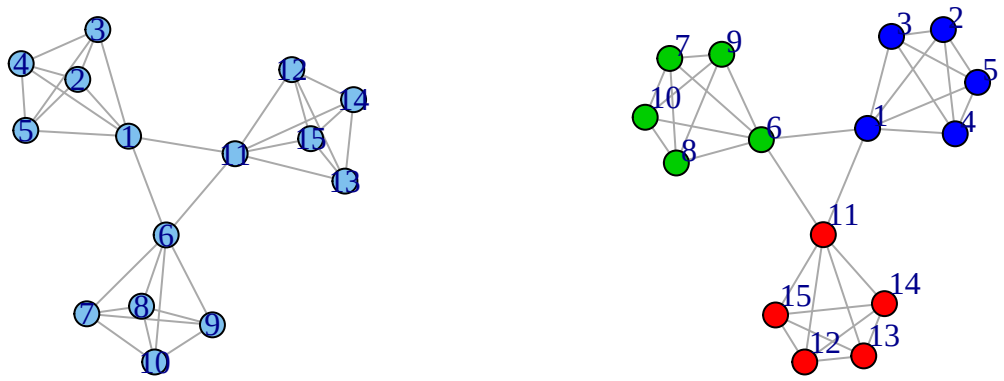
```
V(g)$color <- colbar[comps+1]

plot(g, layout=l, vertex.size=5, vertex.label=NA)
```



Highlight communities in graph

Let's make different color for each community

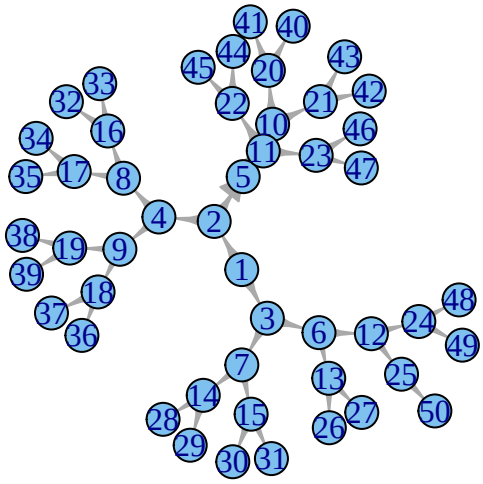
```
g <- graph.full(5) %du% graph.full(5) %du% graph.full(5)
g <- add.edges(g, c(1,6, 1,11, 6,11))

op = par(mfrow = c(1,2))
plot(g, layout = layout.kamada.kawai)

com <- spinglass.community(g, spins=5)
V(g)$color <- com$membership+1
g <- set.graph.attribute(g, "layout", layout.kamada.kawai(g))
plot(g, vertex.label.dist=1.5)
```




```
par(op)
```

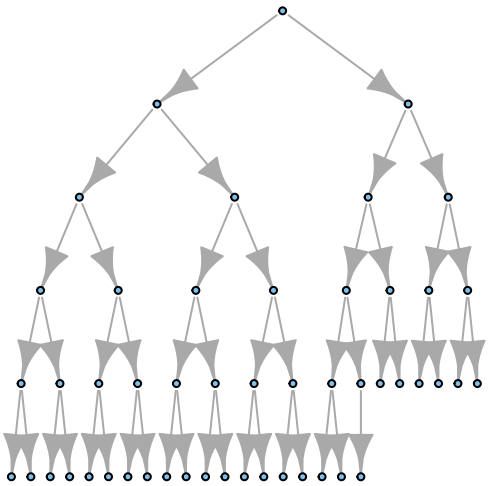
Trees Visualization

```
plot(graph.tree(50, 2))
```



We can use `layout = layout.reingold.tilford` to draw tree

```
plot(graph.tree(50, 2), vertex.size=3, vertex.label=NA, layout=layout.reingold.tilford)
```



```
tkplot(graph.tree(50, 2, mode="undirected"), vertex.size=10,
       vertex.color="green")
```

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

Mixing patterns

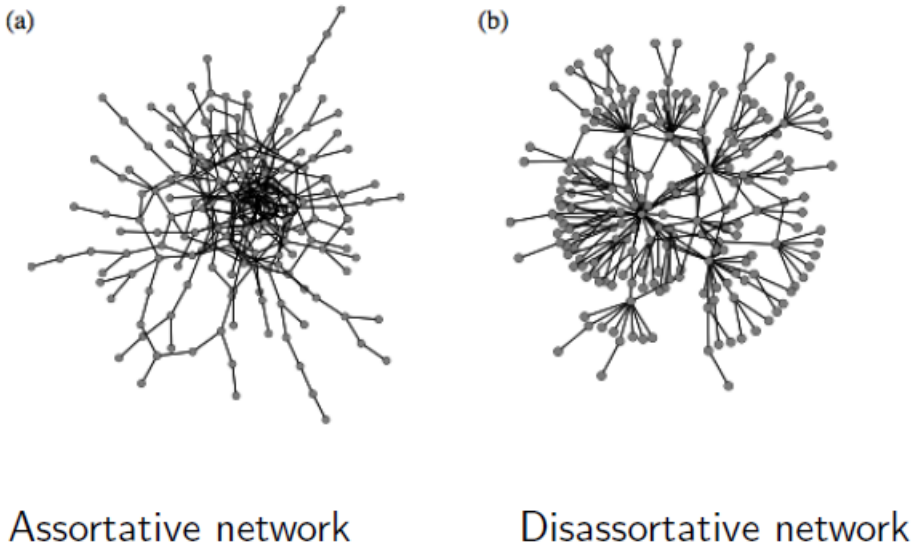
- Assortative mixing, "like links with like", attributed of connected nodes tend to be more similar than if there were no such edge
- Disassortative mixing, "like links with dislike", attributed of connected nodes tend to be less similar than if there were no such edge Examples:
- assortative mixing - in social networks political beliefs, obesity, race
- disassortative mixing - dating network, food web (predator/prey), economic networks (producers/consumers)

Assortative Mixing

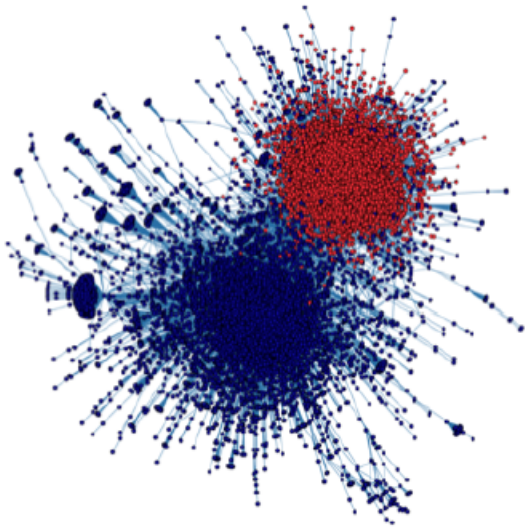
Assortative Mixing coefficient shows whether nodes with the same attribute values tend to form connections. Download Caltech friendship network. Inspect nodes attributes and compute assortativity coefficients with `assortativity` function

Assortative mixing by node degree, $x_i \leftarrow k_i - 1$:

$$r = \frac{\sum_{ij}\left(A_{ij} - \frac{k_i k_j}{2m}\right) k_i k_j}{\sum_{ij}\left(k_i \delta_{ij} - \frac{k_i k_j}{2m}\right) k_i k_j}$$



Political polarization on Twitter: political retweet network, red color - "right-learning" users, blue color - "left learning" users.



Assortativity measures

Discrete mixing by categorical attribute (ci -label: color, gender, ethnicity). How much more often do attributes match across edges than expected at random? Assortativity coefficient:

$$C = \frac{Q}{Q_{max}} = \frac{\sum_{ij}\left(A_{ij} - \frac{k_i k_j}{2m}\right) \delta(c_i, c_j)}{2m - \sum_{ij} \frac{k_i k_j}{2m} \delta(c_i, c_j)}$$

Mixing by scalar properties, scalar value attribute (age, income, number of friends). Correlation of values across edges. Assortativity coefficient:

$$r = \frac{cov}{var} = \frac{\sum_{ij}\left(A_{ij} - \frac{k_i k_j}{2m}x_i x_j\right)}{\sum_{ij}(k_i\delta_{ij} - \frac{k_i k_j}{2m})x_i x_j}$$

```
# Your code here
g <- read.graph(file = 'Caltech.gml', format = 'gml')
assortativity.nominal(graph = g, types = V(g)$dorm+1, directed = F)
```

```
## [1] 0.3491531
```

Basic network analysis pipeline

The basic pipeline for exploratory graph analysis consists of:

Loading

See Class 1.

Cleaning

After loading graph with all necessary attributes, it is often recommended to:

- delete empty nodes:

```
g = delete.vertices(g, degree(g) == 0)
```

- delete self-cycles and multiple edges - to make graph simple. `simplify` does all the work; some parameters could be tuned:

```
simplify(g)
```

```
## IGRAPH U--- 769 16656 --
## + attr: id (v/n), status (v/n), gender (v/n), magor (v/n),
##   sndmagor (v/n), dorm (v/n), year (v/n), school (v/n)
```

```
# is.simple(simplify(g, remove.multiple=FALSE))
```

Obtaining main characteristics

See Classes 2-4.

Clustering

See Class 5.

Visualization

See previous section + Classes 1, 4.