Community Detection

Load libraries

```
library(dplyr)
library(igraph)
library(ggplot2)
library(tidygraph)
library(networkD3)
library(visNetwork)
library(knitr) # For table rendering
```

Graph object

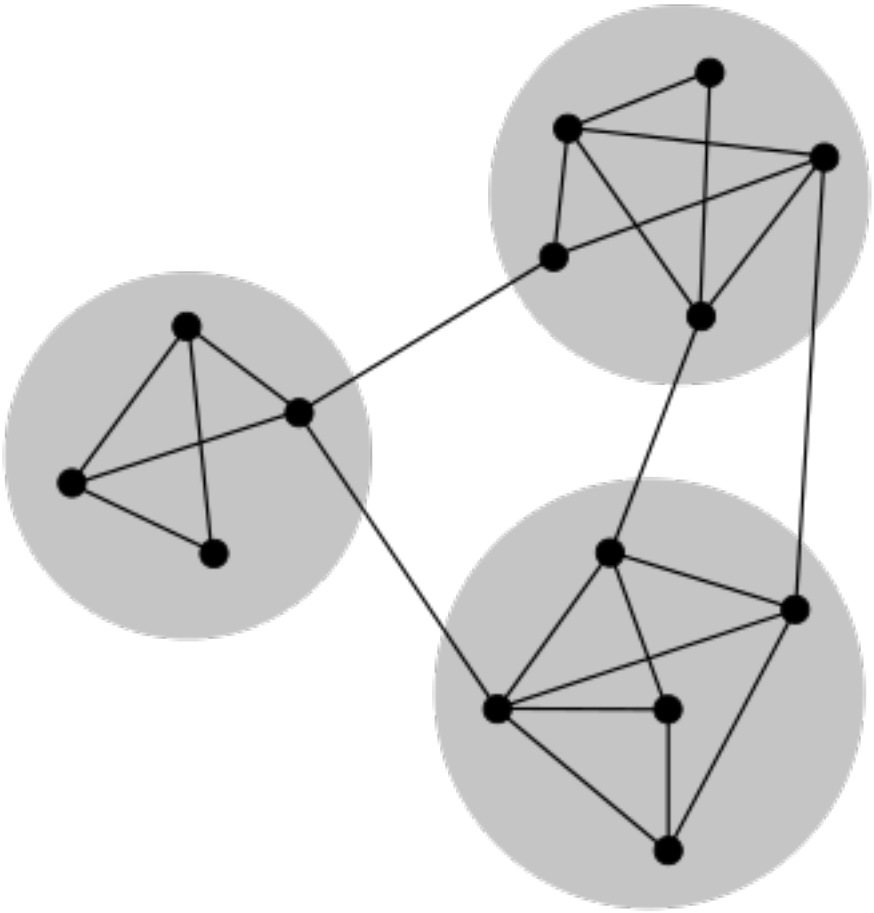
```
df = read.table("./data/data.tsv", header = T)
veccol = c(rep("pink",5), rep("light blue",6))
g = graph_from_data_frame(df)
net = g
```

Community detection

A number of algorithms aim to detect groups that consist of densely connected nodes with fewer connections across groups.

In the study of complex networks, a network is said to have community structure if the nodes of the network can be easily grouped into (potentially overlapping) sets of nodes such that each set of nodes is densely connected internally. In the particular case of non-overlapping community finding, this implies that the network divides naturally into groups of nodes with dense connections internally and sparser connections between groups. But overlapping communities are also allowed. The more general definition is based on the principle that pairs of nodes are more likely to be connected if they are both members of the same community(ies), and less likely to be connected if they do not share communities [3].

A sketch of a small network displaying community structure, with three groups of nodes with dense internal connections and sparser connections between groups [3].



Summary of community detection algorithms in igraph 0.6: https://www.r-bloggers.com/summary-of-community-detection-algorithms-in-igraph-0-6/

Cliques

Cliques are subgraphs in which every node is connected to every other node in the clique i.e. complete subgraphs of an undirected graph [3].

As nodes can not be more tightly connected than this, it is not surprising that there are many approaches to community detection in networks based on the detection of cliques in a graph and the analysis of how these overlap.

Note that as a node can be a member of more than one clique, a node can be a member of more than one community in these methods giving an "overlapping community structure". One approach is to find the **"maximal cliques"**, that is find the cliques which are not the subgraph of any other clique.

```
# Find cliques
net.sym <- as.undirected(net, mode= "collapse")
head(cliques(net.sym)) # list of cliques
```

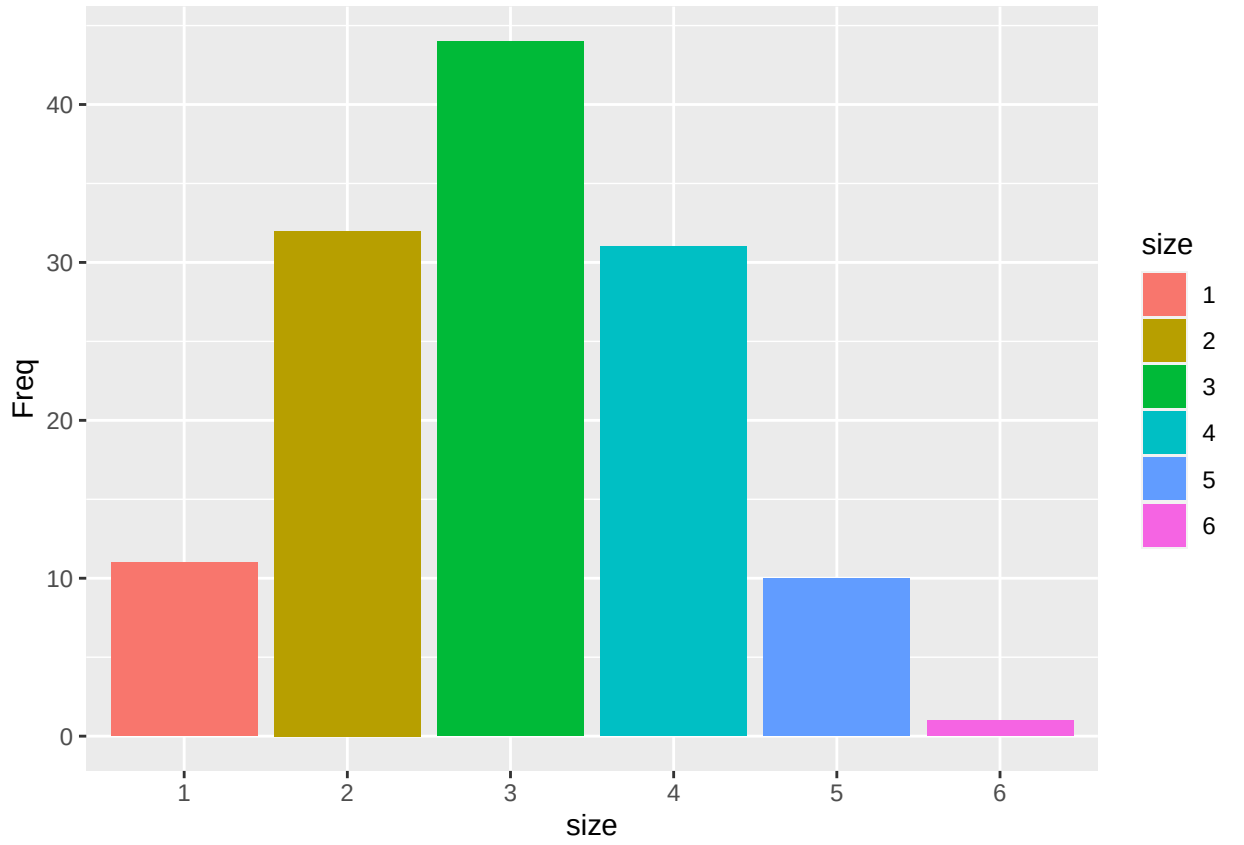
```
## [[1]]
## + 1/11 vertex, named, from 071d013:
## [1] FAA4
##
```

```
## [[2]]
## + 1/11 vertex, named, from 071d013:
## [1] FAA2
##
## [[3]]
## + 2/11 vertices, named, from 071d013:
## [1] FAA4 FAA2
##
## [[4]]
## + 1/11 vertex, named, from 071d013:
## [1] INA1
##
## [[5]]
## + 2/11 vertices, named, from 071d013:
## [1] FAA4 INA1
##
## [[6]]
## + 1/11 vertex, named, from 071d013:
## [1] FAA1
```

```
sapply(cliques(net.sym), length) # clique sizes
```

```
##   [1] 1 1 2 1 2 1 2 3 2 1 2 3 4 3 2 3 2 1 2 3 4 3 2 3 2 1 2 3 4 5 4 3 4 3 2 3 4
##  [38] 3 2 3 2 1 2 3 4 5 4 3 4 3 2 3 4 3 2 3 2 1 2 3 4 5 4 3 4 3 2 3 4 3 2 3 2 1
##  [75] 2 3 4 5 6 5 4 5 4 3 4 5 4 3 4 3 2 3 4 5 4 3 4 3 2 3 4 3 2 3 2 1 2 3 4 5 4
## [112] 3 4 3 2 3 4 5 4 3 4 3 2 3 4 3 2 3 2
```

```
sapply(cliques(net.sym), length) %>% table() %>% as.data.frame() %>% {colnames(.)[1]="size"; .} %>% ggpl
```



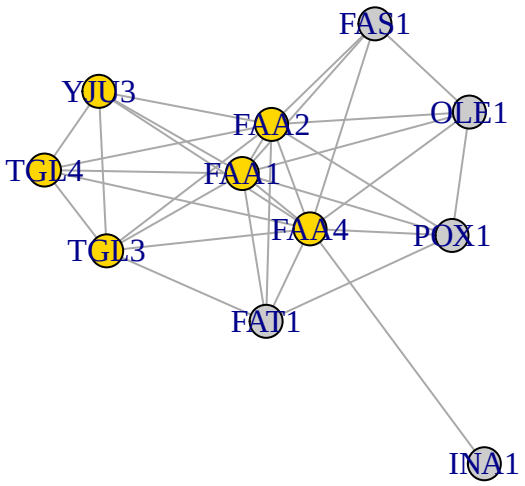

```
largest_cliques(net.sym) # cliques with max number of nodes
```

```
## [[1]]
## + 6/11 vertices, named, from 071d013:
## [1] FAA4 FAA1 FAA2 TGL3 TGL4 YJU3
```

```
# clique.number calculates the size of the largest clique(s).
clique.number(net.sym)
```

```
## [1] 6
```

```
# plot
vcol <- rep("grey80", vcount(net.sym))
vcol[unlist(largest_cliques(net.sym))] <- "gold"
plot(as.undirected(net.sym), vertex.label=V(net.sym)$name, vertex.color=vcol)
```




```
# cliques with minimum 6 nodes
cliques(net.sym, min=6)
```

```
## [[1]]
## + 6/11 vertices, named, from 071d013:
## [1] FAA1 TGL3 TGL4 FAA4 FAA2 YJU3
```

```
# calculate all the maximal cliques in an undirected graph
# maximal cliques: cliques which are not the subgraph of any other clique.
max_cliques(net.sym)
```

```
## [[1]]
## + 2/11 vertices, named, from 071d013:
## [1] INA1 FAA4
##
## [[2]]
## + 5/11 vertices, named, from 071d013:
## [1] FAS1 FAA1 OLE1 FAA2 FAA4
##
## [[3]]
## + 5/11 vertices, named, from 071d013:
## [1] POX1 FAA1 FAA2 FAA4 OLE1
##
## [[4]]
## + 5/11 vertices, named, from 071d013:
```

```
## [1] POX1 FAA1 FAA2 FAA4 FAT1
##
## [[5]]
## + 5/11 vertices, named, from 071d013:
## [1] FAT1 FAA1 FAA2 FAA4 TGL3
##
## [[6]]
## + 6/11 vertices, named, from 071d013:
## [1] FAA1 TGL3 YJU3 FAA2 FAA4 TGL4
```

Key functions to deal with the result of network community detection

Key functions to deal with the result of network community detection

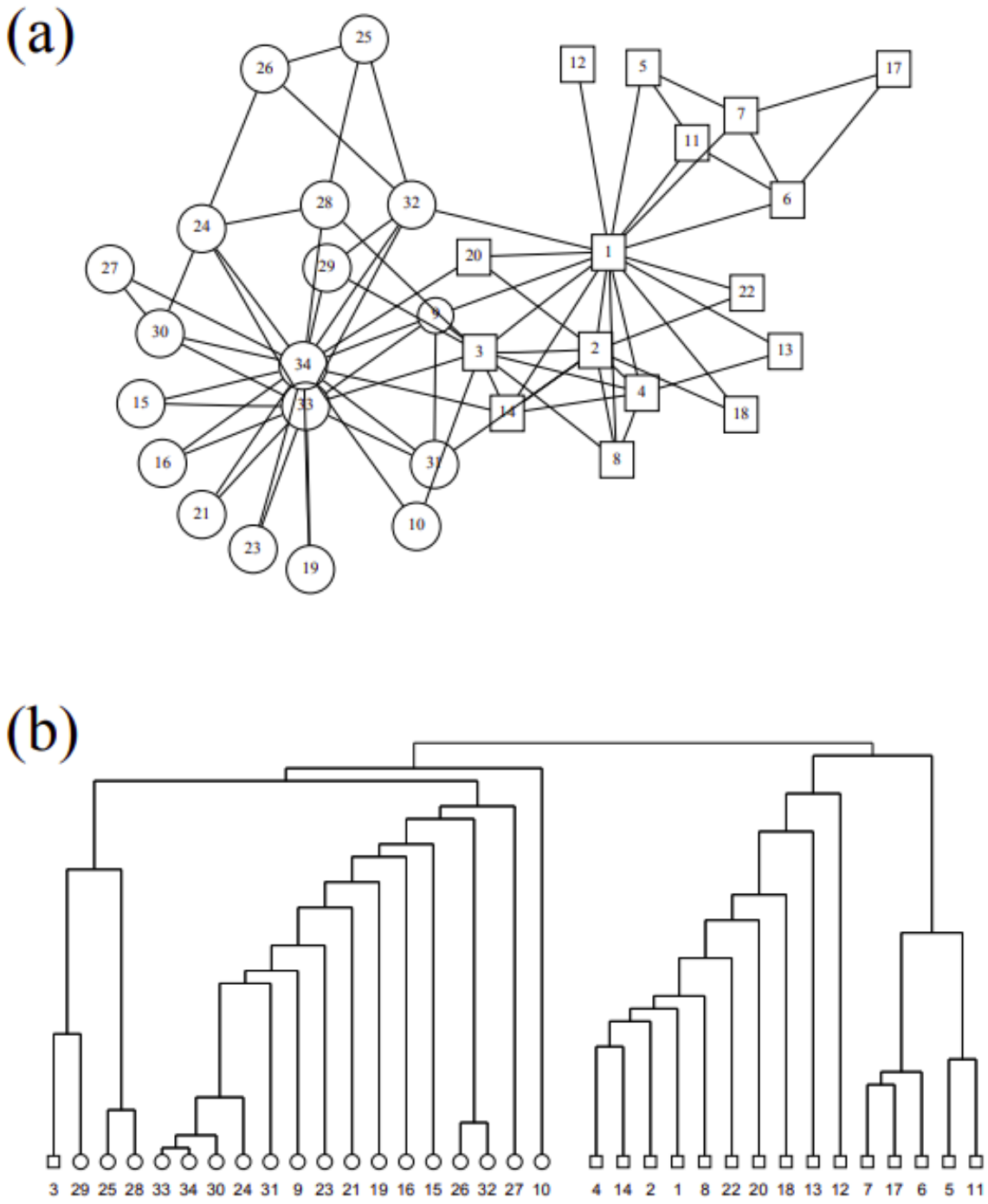
- membership: For each node, returns id of its community
- modularity: modularity gives the modularity score of the partitioning.
- length: returns the number of communities.
- sizes: The sizes function returns the community sizes, in the order of their ids.
- algorithm: algorithm gives the name of the algorithm that was used to calculate the community structure.
- crossing: crossing returns a logical vector, with one value for each edge, ordered according to the edge ids. The value is TRUE iff the edge connects two different communities, according to the (best) membership vector, as returned by membership()
- code_len

Based on edge betweenness (Newman-Girvan)

The edge betweenness score of an edge measures the number of shortest paths through it. The idea of the edge betweenness based community structure detection is that it is likely that edges connecting separate modules have high edge betweenness as all the shortest paths from one module to another must traverse through them. So if we gradually remove the edge with the highest edge betweenness score we will get a hierarchical map, a rooted tree, called a dendrogram of the graph. The leafs of the tree are the individual vertices and the root of the tree represents the whole graph.

High-betweenness edges are removed sequentially (recalculating at each step) and the best partitioning of the network is selected i.e. cluster_edge_betweenness performs this algorithm by calculating the edge betweenness of the graph, removing the edge with the highest edge betweenness score, then recalculating edge betweenness of the edges and again removing the one with the highest score, etc.

Further reading: https://arxiv.org/pdf/cond-mat/0112110.pdf



The hierarchical tree showing the complete community structure for the network.

```
ceb <- cluster_edge_betweenness(net)
length(ceb)     # number of communities
```

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

```
ceb
```

```
## IGRAPH clustering edge betweenness, groups: 1, mod: 0
## + groups:
##   $`1`
##    [1] "POX1" "FAA1" "TGL3" "TGL4" "FAA4" "FAS1" "FAA2" "YJU3" "OLE1" "FAT1"
##   [11] "INA1"
##
```

```
sizes(ceb) # sizes of communities
```

```
## Community sizes
##  1
## 11
```

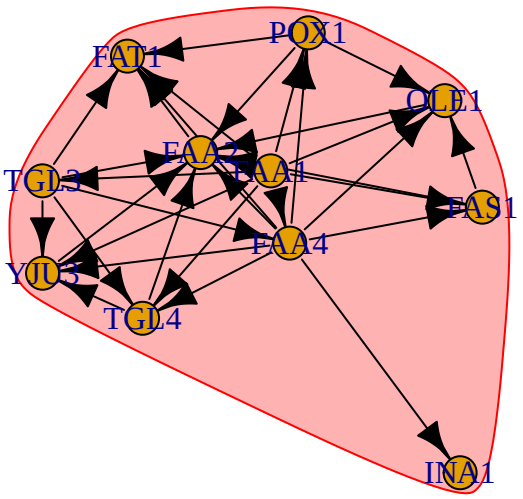
```
membership(ceb) # community membership for each node
```

```
## POX1 FAA1 TGL3 TGL4 FAA4 FAS1 FAA2 YJU3 OLE1 FAT1 INA1
##    1    1    1    1    1    1    1    1    1    1    1
```

```
modularity(ceb) # how modular the graph partitioning is
```

```
## [1] 0
```

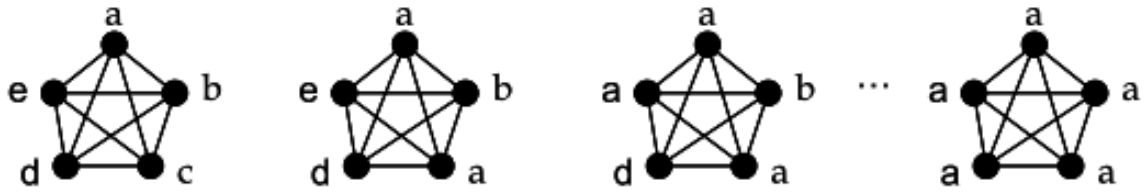
```
plot(ceb, net)
```



Community detection based on based on propagating labels

Assigns node labels, randomizes, than replaces each vertex's label with the label that appears most frequently among neighbors. Those steps are repeated until each vertex has the most common label of its neighbors. In other words

From the abstract of the paper https://arxiv.org/abs/0709.2938: "In our algorithm every node is initialized with a unique label and at every step each node adopts the label that most of its neighbors currently have. In this iterative process densely connected groups of nodes form a consensus on a unique label to form communities."



Nodes are updated one by one as we move from left to right. Due to a high density of edges (highest possible in this case), all nodes acquire the same label.

```
clp <- cluster_label_prop(net)
length(clp)     # number of communities
```

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

```
clp
```

```
## IGRAPH clustering label propagation, groups: 1, mod: 0
## + groups:
##   $`1`
##    [1] "POX1" "FAA1" "TGL3" "TGL4" "FAA4" "FAS1" "FAA2" "YJU3" "OLE1" "FAT1"
##   [11] "INA1"
##
```

```
sizes(clp) # sizes of communities
```

```
## Community sizes
##  1
## 11
```

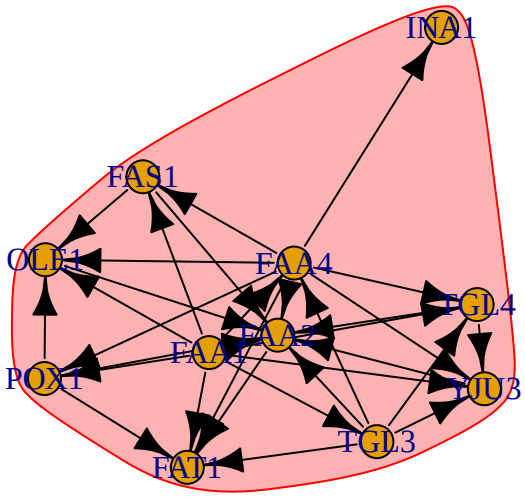
```
membership(clp) # community membership for each node
```

```
## POX1 FAA1 TGL3 TGL4 FAA4 FAS1 FAA2 YJU3 OLE1 FAT1 INA1
##    1    1    1    1    1    1    1    1    1    1    1
```

```
modularity(clp) # how modular the graph partitioning is
```

```
## [1] 0
```

```
plot(clp, net)
```



Community detection based on greedy optimization of modularity

This function tries to find dense subgraph, also called communities in graphs via directly optimizing a modularity score.

Modularity [21] is a property of a network and a specific proposed division of that network into communities. It measures when the division is a good one, in the sense that there are many edges within communities and only a few between them. https://arxiv.org/pdf/cond-mat/0408187.pdf

Modularity is one measure of the structure of networks or graphs. It was designed to measure the strength of division of a network into modules (also called groups, clusters or communities). Networks with high modularity have dense connections between the nodes within modules but sparse connections between nodes in different modules. https://en.wikipedia.org/wiki/Modularity_(networks)

```
cfg <- cluster_fast_greedy(as.undirected(net))
length(cfg)     # number of communities
```

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

```
cfg
```

```
## IGRAPH clustering fast greedy, groups: 2, mod: 0.07
```

```
## + groups:
##   $`1`
##   [1] "POX1" "FAA1" "FAA4" "FAS1" "OLE1" "FAT1" "INA1"
##
##   $`2`
##   [1] "TGL3" "TGL4" "FAA2" "YJU3"
##
```

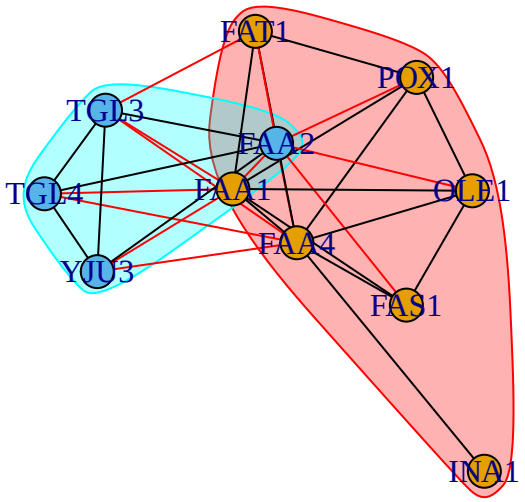
```
membership(cfg) # community membership for each node
```

```
## POX1 FAA1 TGL3 TGL4 FAA4 FAS1 FAA2 YJU3 OLE1 FAT1 INA1
##    1    1    2    2    1    1    2    2    1    1    1
```

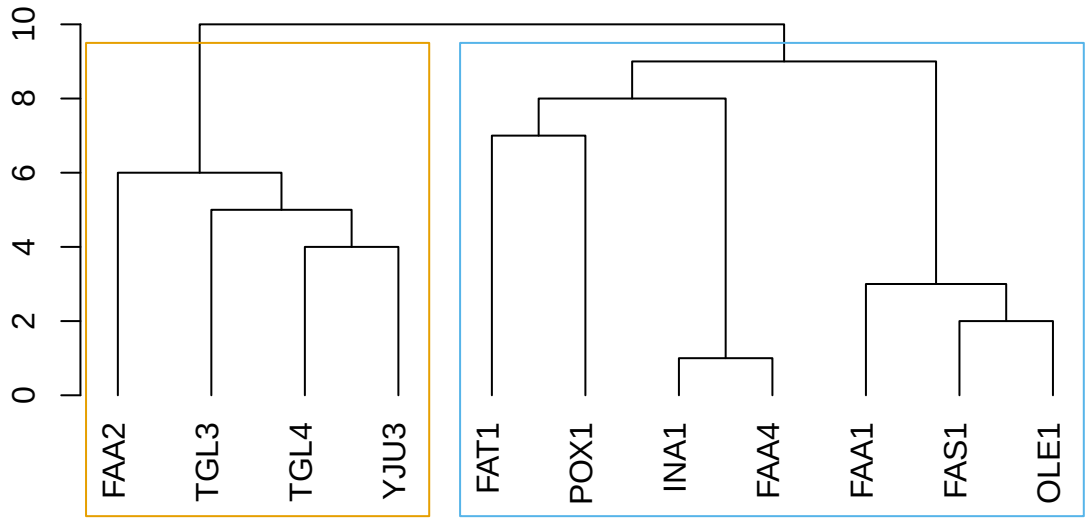
```
sizes(cfg) # sizes of communities
```

```
## Community sizes
## 1 2
## 7 4
```

```
plot(cfg, as.undirected(net))
```




```
plot_dendrogram(cfg)
```




```
modularity(cfg) # how modular the graph partitioning is i.e more modular a graph is more easy would be
```

```
## [1] 0.06982422
```

```
crossing(cfg, net)
```

```
## POX1|FAA2 FAA1|POX1 TGL3|YJU3 TGL4|YJU3 TGL3|TGL4 FAA4|POX1 POX1|FAT1 FAA1|FAT1
##      TRUE     FALSE     FALSE     FALSE     FALSE     FALSE     FALSE     FALSE
## FAA4|FAS1 FAA1|FAS1 FAA4|FAT1 FAS1|FAA2 FAA4|OLE1 FAA1|FAA4 FAA1|OLE1 FAA2|FAT1
##     FALSE     FALSE     FALSE      TRUE     FALSE     FALSE     FALSE      TRUE
## FAA1|TGL4 TGL3|FAA4 FAA1|TGL3 FAS1|OLE1 FAA1|YJU3 YJU3|FAA2 FAA4|YJU3 POX1|OLE1
##      TRUE      TRUE      TRUE     FALSE      TRUE     FALSE      TRUE     FALSE
## FAA4|INA1 FAA1|FAA2 FAA4|FAA2 FAA4|TGL4 OLE1|FAA2 TGL3|FAT1 TGL4|FAA2 TGL3|FAA2
##     FALSE      TRUE      TRUE      TRUE      TRUE      TRUE     FALSE     FALSE
```

Optimal community detection

Group nodes by optimising the moldularity score. This function calculates the optimal community structure of a graph, by maximizing the modularity measure over all possible partitions.

Note that modularity optimization is an NP-complete problem, and all known algorithms for it have exponential time complexity. This means that you probably don't want to run this function on larger graphs. Graphs with up to fifty vertices should be fine, graphs with a couple of hundred vertices might be possible.

```
# GLPK needs to be installed
# The calculation is done by transforming the modularity maximization into an integer programming probl

oc <- cluster_optimal(g)
plot(c4, g)
```

Community strucure via short random walks

This function tries to find densely connected subgraphs, also called communities in a graph via random walks. The idea is that short random walks tend to stay in the same community.

https://arxiv.org/abs/physics/0512106

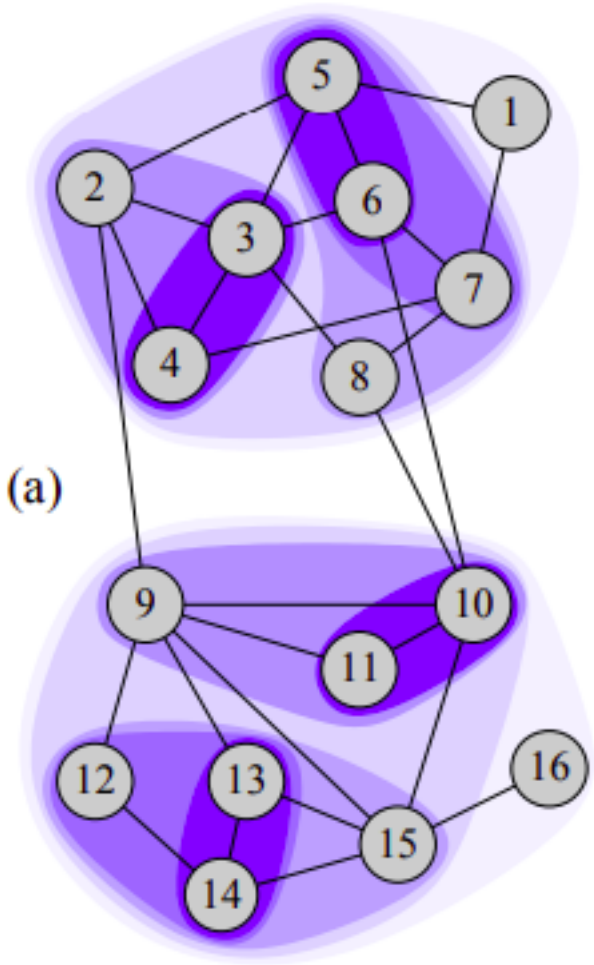
Steps parameter decides: The length of the random walks to perform.

2 Preliminaries on random walks

The graph G is associated to its *adjacency matrix* A: $A_{ij} = 1$ if vertices i and j are connected and $A_{ij} = 0$ otherwise. The degree $d(i) = \sum_j A_{ij}$ of vertex i is the number of its neighbors (including itself). As we discussed in the introduction, the graph is assumed to be connected. To simplify the notations, we only consider unweighted graphs in this paper. It is however trivial to extend our results to weighted graphs ($A_{ij} \in \mathbb{R}^+$ instead of $A_{ij} \in \{0, 1\}$), which is an advantage of this approach.

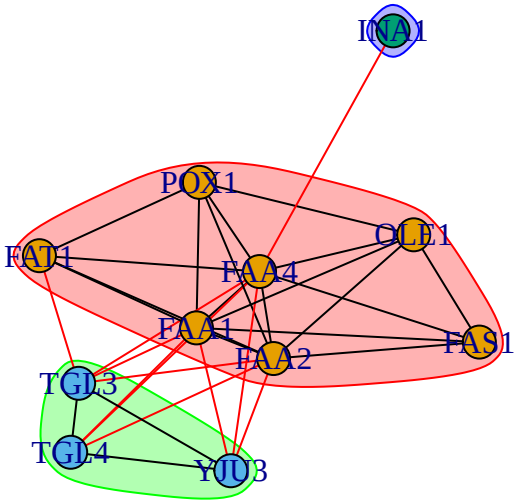
Let us consider a discrete *random walk process* (or diffusion process) on the graph G (see [30, 4] for a complete presentation of the topic). At each time step a walker is on a vertex and moves to a vertex chosen randomly and uniformly among its neighbors. The sequence of visited vertices is a *Markov chain*, the states of which are the vertices of the graph. At each step, the transition probability from vertex i to vertex j is $P_{ij} = \frac{A_{ij}}{d(i)}$. This defines the *transition matrix* P of random walk processes. One can also write $P = D^{-1}A$ where D is the diagonal matrix of the degrees ($\forall i, D_{ii} = d(i)$ and $D_{ij} = 0$ for $i \neq j$).

The process is driven by the powers of the matrix P: the probability of going from i to j through a random walk of length t is $(P^t)_{ij}$. In the following, we will denote this probability by P^t_{ij}. It satisfies two well known properties of the random walk process which we will use in the sequel:

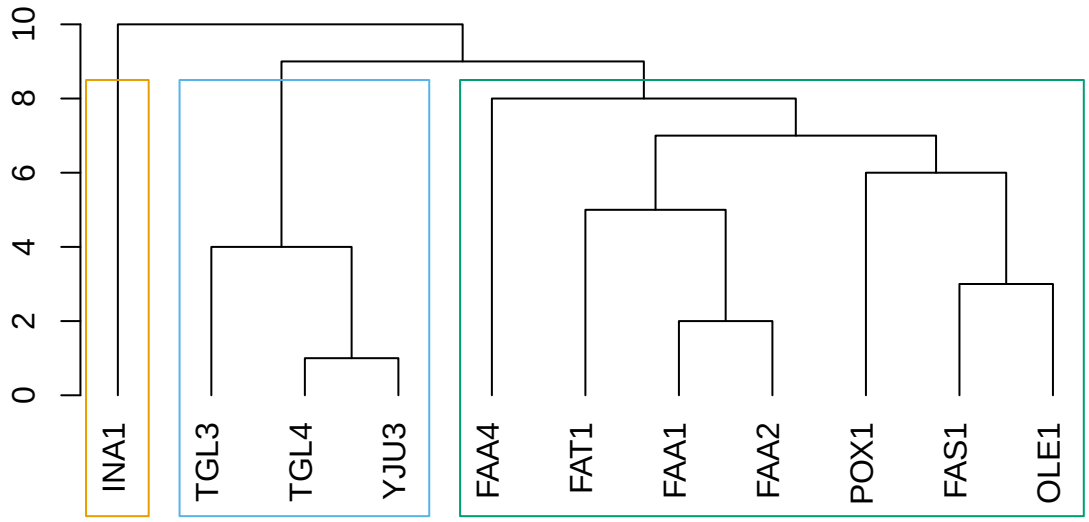


An example of community structure found by our algorithm using random walks of length t = 3.

```
cwt = cluster_walktrap(net)
plot(cwt, as.undirected(net))
```




```
plot_dendrogram(cwt)
```




```
print(cwt)
```

```
## IGRAPH clustering walktrap, groups: 3, mod: 0.054
## + groups:
##   $`1`
##   [1] "POX1" "FAA1" "FAA4" "FAS1" "FAA2" "OLE1" "FAT1"
##
##   $`2`
##   [1] "TGL3" "TGL4" "YJU3"
##
##   $`3`
##   [1] "INA1"
##
```

```
modularity(cwt)
```

```
## [1] 0.05419922
```

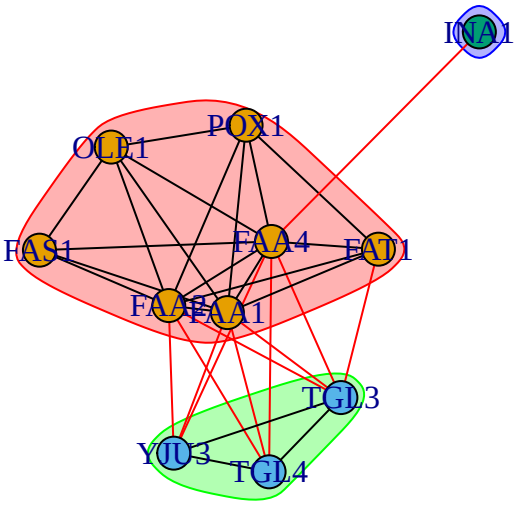
```
sizes(cwt)
```

```
## Community sizes
## 1 2 3
## 7 3 1
```

```
membership(cwt)
```

```
## POX1 FAA1 TGL3 TGL4 FAA4 FAS1 FAA2 YJU3 OLE1 FAT1 INA1
##    1    1    2    2    1    1    1    2    1    1    3
```

```
# tune stepsize
cwt = cluster_walktrap(net, steps = 4)
plot(cwt, as.undirected(net))
```



Infomap community finding

Find community structure that minimizes the expected description length of a random walker trajectory.

Information flow-based and information-theoretic method to detect community. Maps of information flow reveal community structure in complex networks. [https://arxiv.org/abs/0906.1405]

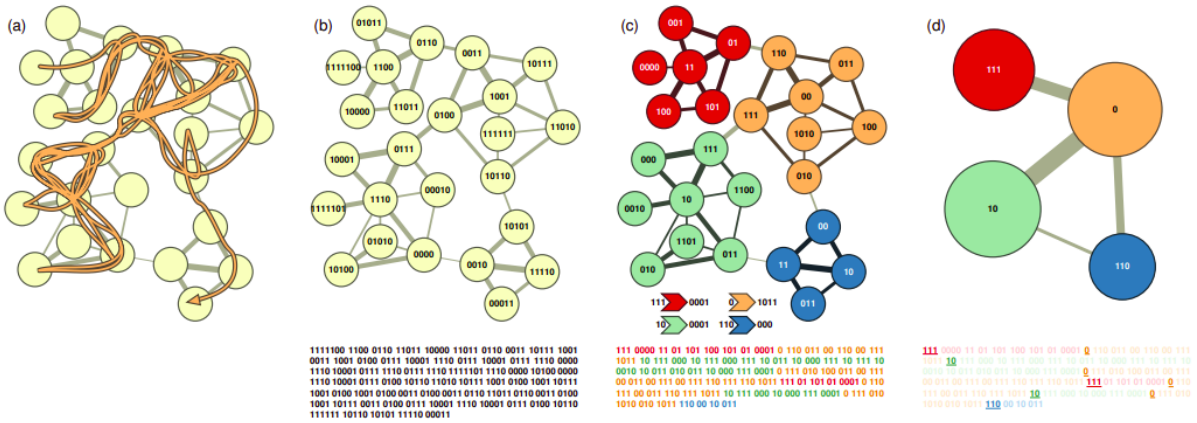
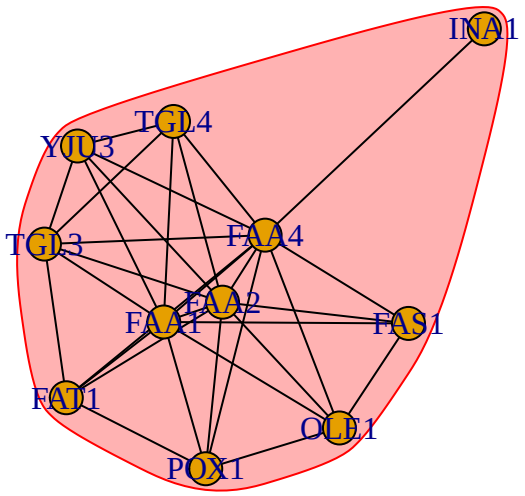


FIG. 1 Detecting regularities in patterns of movement on a network (derived from (14) and also available in a dynamic version (18)). (a) We want to effectively and concisely describe the trace of a random walker on a network. The orange line shows one sample trajectory. For an optimally efficient one-level description, we can use the codewords of the Huffman codebook depicted in (b). The 314 bits shown under the network describes the sample trajectory in (a), starting with 1111100 for the first node on the walk in the upper left corner, 1100 for the second node, etc., and ending with 00011 for the last node on the walk in the lower right corner. (c) A two-level description of the random walk, in which an index codebook is used to switch between module codebooks, yields on average a 32% shorter description for this network. The codes of the index codebook for switching module codebooks and the codes used to indicate an exit from each module are shown to the left and the right of the arrows under the network, respectively. Using this code, we capitalize on structures with long persistence times, and we can use fewer bits than we could do with a one-level description. For the walk in (a), we only need the 243 bits shown under the the network in (c). The first three bits 111 indicate that the walk begins in the red module, the code 0000 specifies the first node on the walk, and so forth. (d) Reporting only the module names, and not the locations within the modules, provides an efficient coarse-graining of the network.

Many real-world networks are structured into a set of regions such that once the random walker enters a region, it tends to stay there for a long time, and movements between regions are relatively rare.

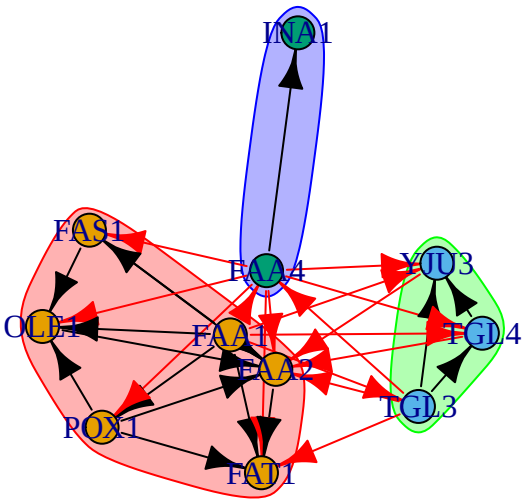
```
plot(cluster_infomap(net), as.undirected(g))
```



Spectral community detection

Group nodes based on the leading eigenvector of the modularity matrix. This function tries to find densely connected subgraphs in a graph by calculating the leading non-negative eigenvector of the modularity matrix of the graph.

```
c2 = cluster_leading_eigen(as.undirected(g))
plot(c2, g)
```

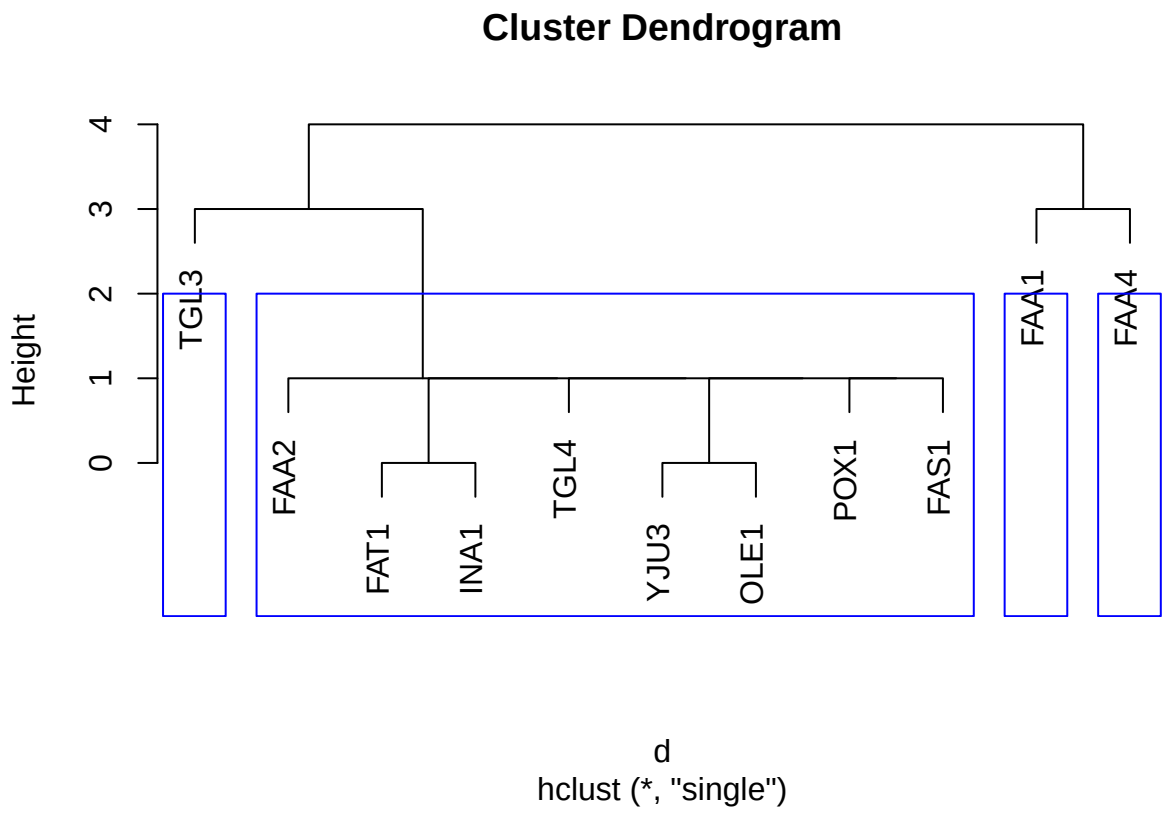


Hiearchical clustering based

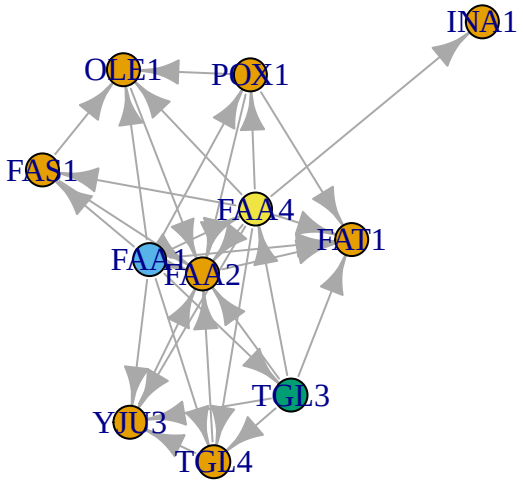
Another method for finding community structures in networks is hierarchical clustering. In this method one defines a similarity measure quantifying some (usually topological) type of similarity between node pairs. Commonly used measures include the cosine similarity, the Jaccard index, and the Hamming distance between rows of the adjacency matrix. Then one groups similar nodes into communities according to this measure. There are several common schemes for performing the grouping, the two simplest being single-linkage clustering, in which two groups are considered separate communities if and only if all pairs of nodes in different groups have similarity lower than a given threshold, and complete linkage clustering, in which all nodes within every group have similarity greater than a threshold. https://en.wikipedia.org/wiki/Community_structure#Hierarchical_clustering

```
# Obtain adjancy matrix
A = get.adjacency(g, sparse=FALSE)

# Calculate cosine similarity from Latent Semantic Analysis package
# library(lsa)
# S = cosine(A)
# D = 1-S # Convert similarity to distance
# d = as.dist(D) # Convert distance matrix to dist() object
# Error if NA/NaN/Inf is found in d

# Pearson similarity based
# S = cor(A, method="pearson")
# d = as.dist(1-S)
```

```
# Error if NA/NaN/Inf is found in d

# Hamming distance based measurement
library(e1071)
d = hamming.distance(A) %>% as.dist()

# Perform average-linkage hierarchical clustering method
cc = hclust(d, method = "single")

# plot dendrogram
plot(cc)

# draw blue borders around clusters
clusters.list = rect.hclust(cc, k = 4, border="blue")
```

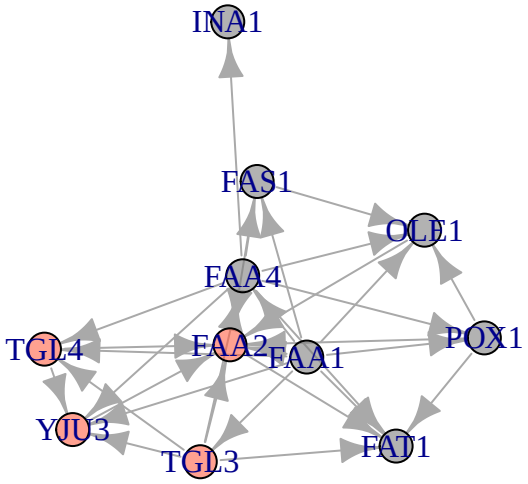



```
# cut dendrogram at 4 clusters
clusters = cutree(cc, k = 4)

# plot graph with clusters
plot(g, vertex.color=clusters)
```



We can also plot the communities without relying on their built-in plot:

```
V(net)$community <- cfg$membership
colrs <- adjustcolor( c("gray50", "tomato", "gold", "yellowgreen"), alpha=.6)
plot(net, vertex.color=colrs[V(net)$community])
```



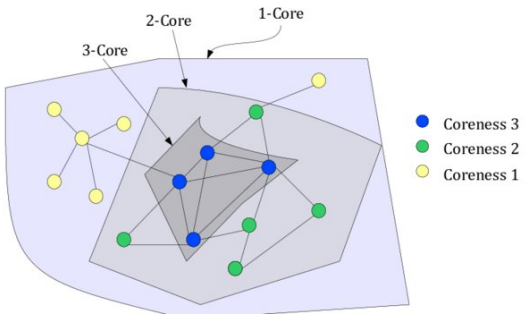
K-core decomposition

Coreness is a measure that can help identify **tightly interlinked groups** within a network.

A k-core is a maximal group of entities, all of which are connected to at least k other entities in the group. The k-core is the maximal subgraph in which every node has degree of at least k.

e.g. in a 5-core subgraph, every node has degree of at least 5. For example, a group is the two-core if it contains all entities that are connected to at least two other entities within the group. Similarly, a group is the three-core if it contains all entities that are linked to at least three other entities within the group.

The result here gives the coreness of each vertex in the network. A node has coreness D if it belongs to a D-core but not to (D+1)-core.



Refer: https://www.ibm.com/support/knowledgecenter/en/SSXVXZ_2.2.0/com.ibm.i2.anb.doc/about_k_core.html

Any entity in the three-core must have at least three links to all other members of the three-core. Clearly any such entity must necessarily have at least two links to every other member of the three-core. Put another way, the three-core is a subset (is contained within) the two-core. More generally, the K-Core form a nested hierarchy of entity groupings on the chart. The zero-core (entire chart) contains the one-core, which contains the two-core, which contains the three-core, and so on. As k increases, the core sizes decrease, but the cores become more interlinked. The K-Cores with the biggest coreness values (k-values) represent the most cohesive regions of the chart.

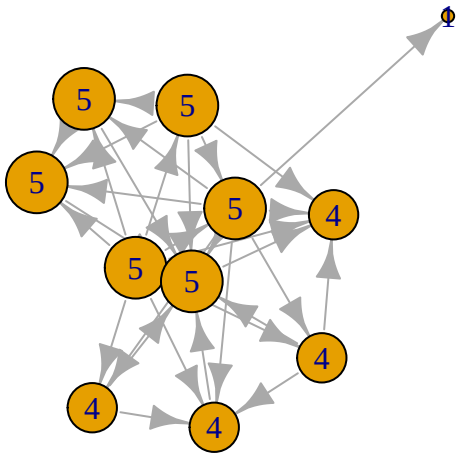
The following diagram illustrates the K-Core decomposition of a simple network, and shows a nested collection of zero, one, two and three-cores. Notice that the three-core actually consists of two separate groupings on the chart. Technically these groupings are regarded as a single three-core with two components.

Diagram indicating a K-Core structure.

```
# mode: The type of the core in directed graphs. Character constant, possible values: in: in-cores are
kc <- coreness(net, mode="all")
print(kc)
```

```
## POX1 FAA1 TGL3 TGL4 FAA4 FAS1 FAA2 YJU3 OLE1 FAT1 INA1
##    4    5    5    5    5    4    5    5    4    4    1
```

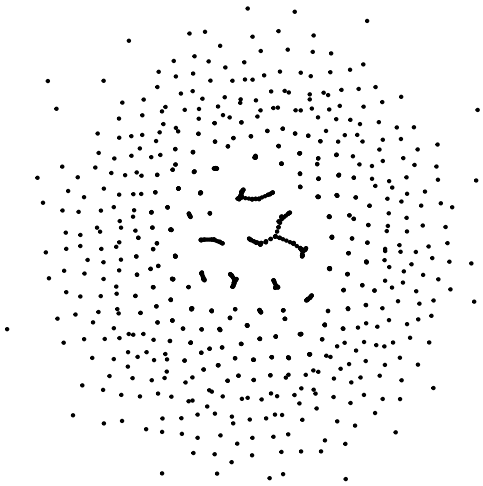
```
plot(net, vertex.size=kc*6, vertex.label=kc)
```



Decompose

Creates a separate graph for each component of a graph.

```r
# the diameter of each component in a random graph
g1 <- sample_gnp(1000, 1/1000)
plot(g1, vertex.size = 1, vertex.label = NA)
```



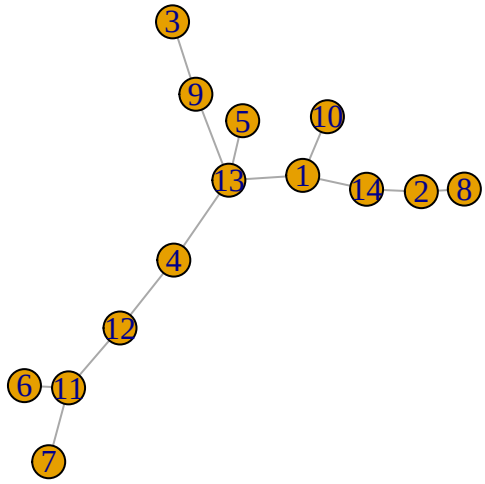
```r
components <- decompose(g1, min.vertices=8)
sapply(components, diameter)
```

```
##  [1]  8  9 25 15 10 22  8  5 10  8 11  6  7  5
```

```r
print(components[[1]])
```

```
## IGRAPH 0cfe9e3 U--- 14 13 -- Erdos renyi (gnp) graph
## + attr: name (g/c), type (g/c), loops (g/l), p (g/n)
## + edges from 0cfe9e3:
##  [1]  2-- 8  3-- 9  1--10  6--11  7--11  4--12 11--12  1--13  4--13  5--13
## [11]  9--13  1--14  2--14
```

```r
plot(components[[1]])
```


3
9
5
10
13
1
14
2
8
4
12
6
11
7