

Network Science

Communities Part 1

Sean P. Cornelius
With
**Emma K. Towlson and Albert-László
Barabási**

Introduction

Section 1

Introduction: Belgium



Section 1

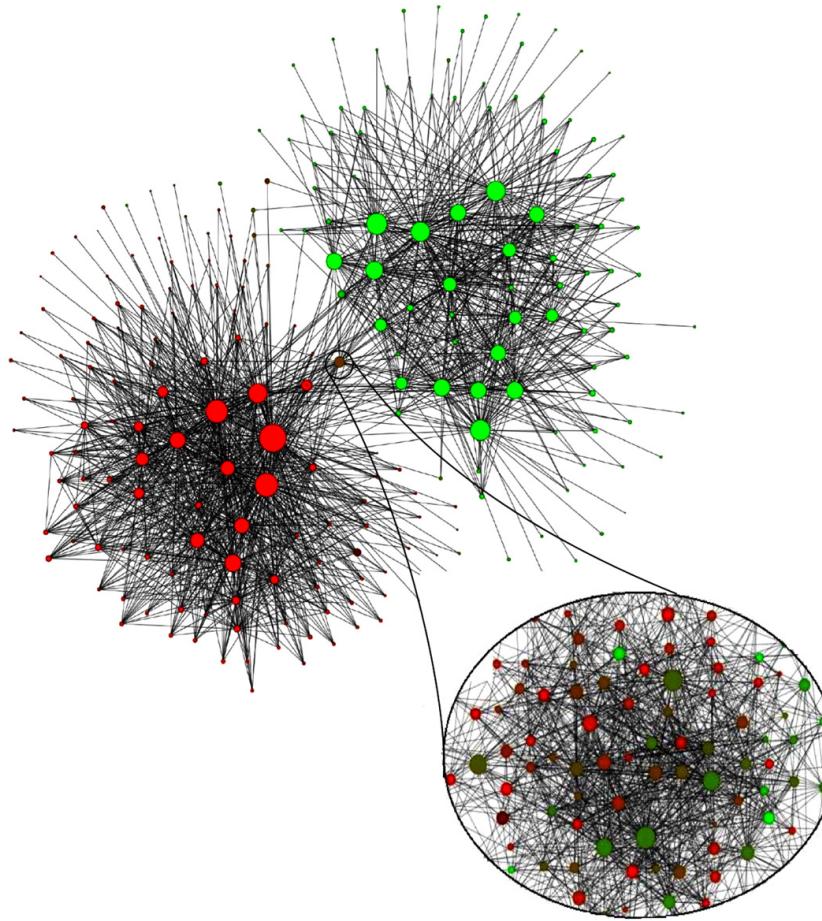
Introduction: Belgium



Same area as Massachusetts (~12,000 sq miles)
Same population as Ohio (~11.5 millions)

Section 1

Introduction: Belgium



V.D. Blondel et al, *J. Stat. Mech.* P10008 (2008).

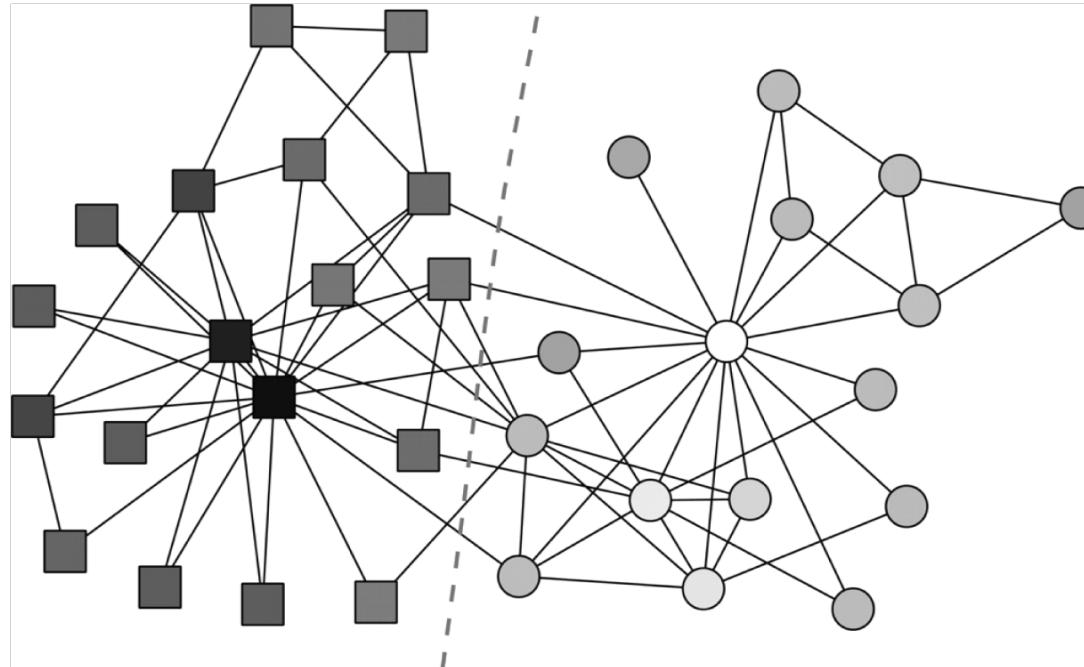
A.-L. Barabási, *Network Science: Communities*.

Section 2

Examples of communities

Section 2

Zachary's Karate Club



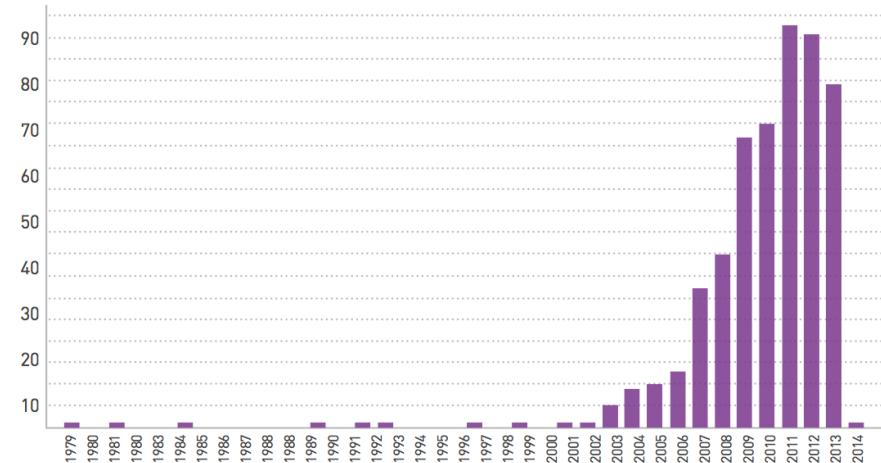
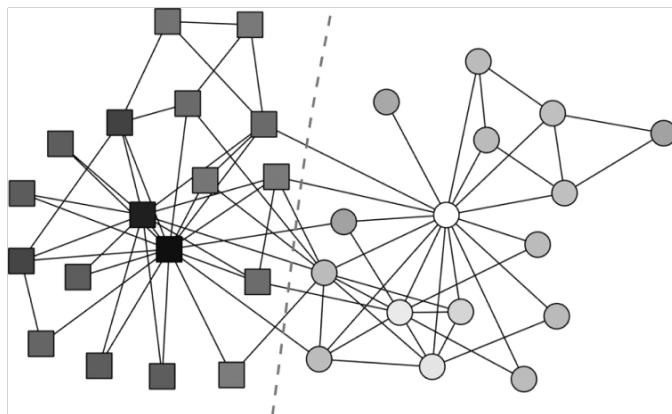
W.W. Zachary, *J. Anthropol. Res.* 33:452-473 (1977).

A.-L. Barabási, *Network Science: Communities*.

Section 2

Zachary's Karate Club

Citation history
of the Zachary's Karate club paper



W.W. Zachary, *J. Anthropol. Res.* 33:452-473 (1977).

A.-L. Barabási, *Network Science: Communities*.

Section 2

Zachary Karate Club Club

The first scientist at any conference on networks who uses Zachary's karate club as an example is inducted into the Zachary Karate Club Club, and awarded a prize.

Chris Moore (9 May 2013).

Mason Porter (NetSci, June 2013).

Yong-Year Ahn (Oxford University, July 2013)

Marián Boguñá (ECCS, September 2013).

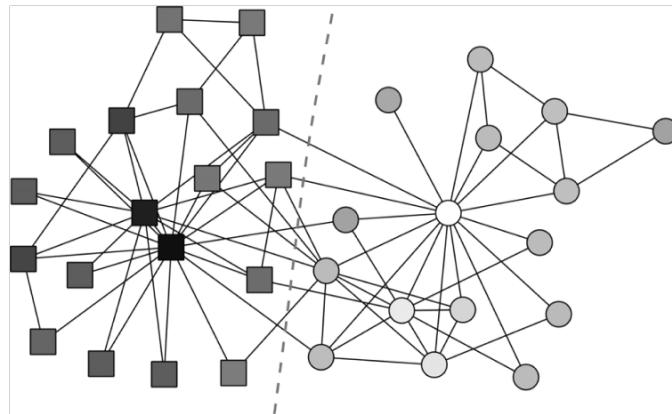
Mark Newman (Netsci, June 2014)



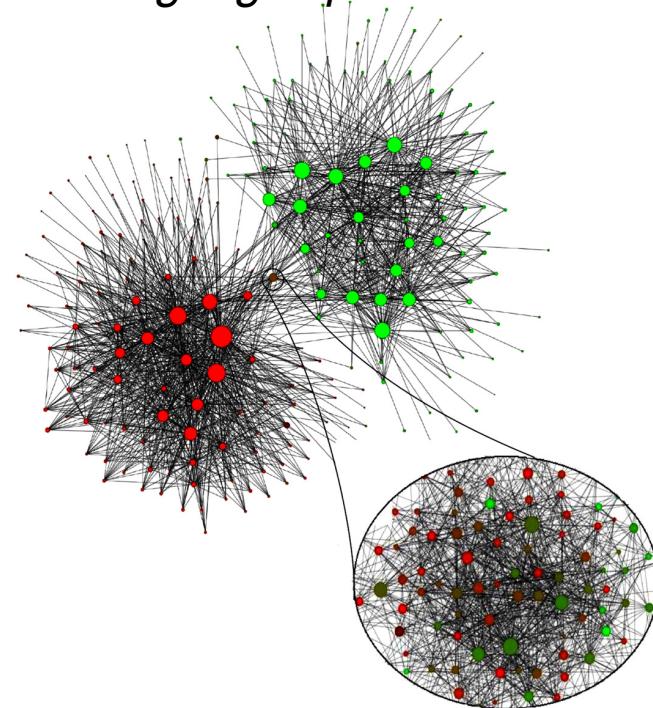
Section 2

Auxiliary information

→ Karate Club:
Breakup of the club

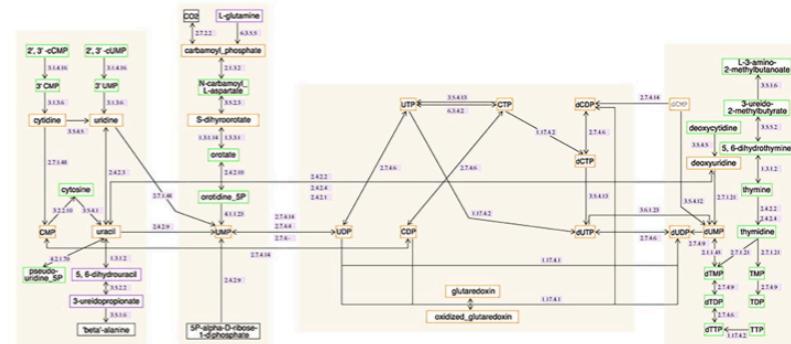
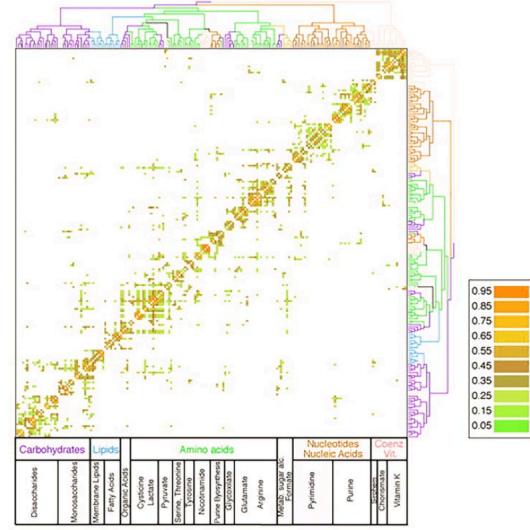
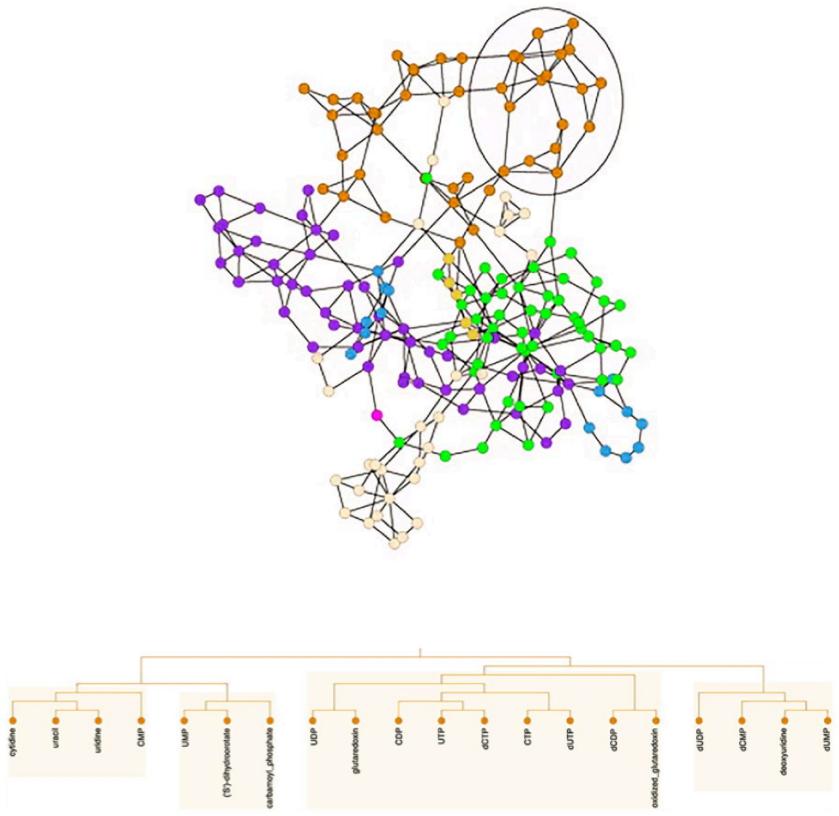


→ Belgian Phone Data:
Language spoken



Section 2

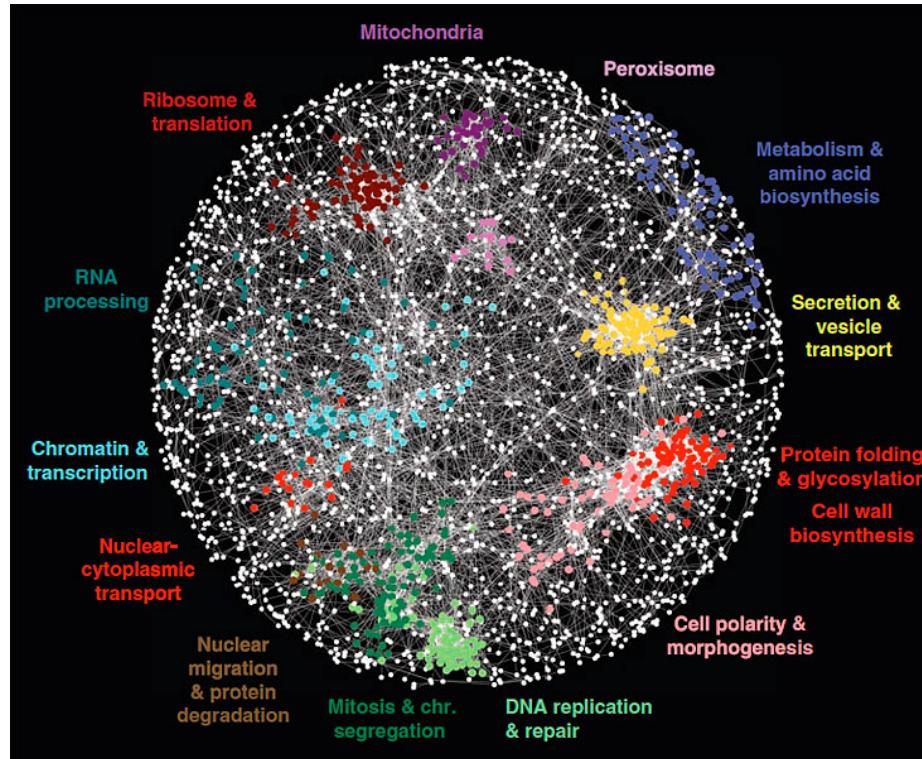
Biological Modules



E. Ravasz et al., *Science* 297 (2002).
 A.-L. Barabási, *Network Science: Communities*.

Section 2

Biological Modules

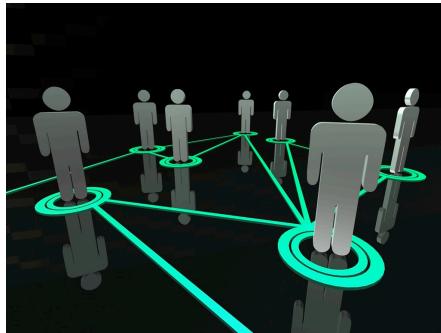


M. Costanzo et al, *Science*, 22 (2010).

A.-L. Barabási, *Network Science: Communities*.

Basics of communities

We focus on the **mesoscopic** scale of the network



Microscopic



Mesoscopic

Macroscopic



H1: A network's community structure is uniquely encoded in its wiring diagram

H2: Connectedness Hypothesis

A community corresponds to a connected subgraph.

H3: Density Hypothesis

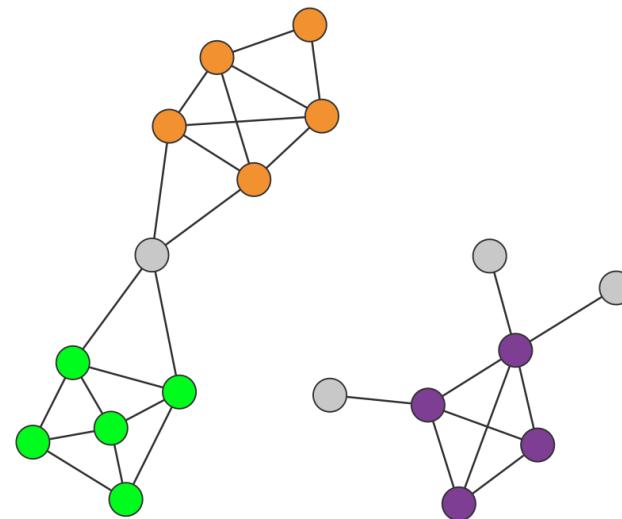
Communities correspond to locally dense neighborhoods of a network.

H2: Connectedness Hypothesis

A community corresponds to a connected subgraph.

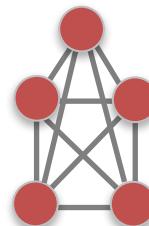
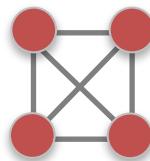
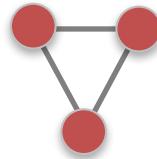
H3: Density Hypothesis

Communities correspond to locally dense neighborhoods of a network.



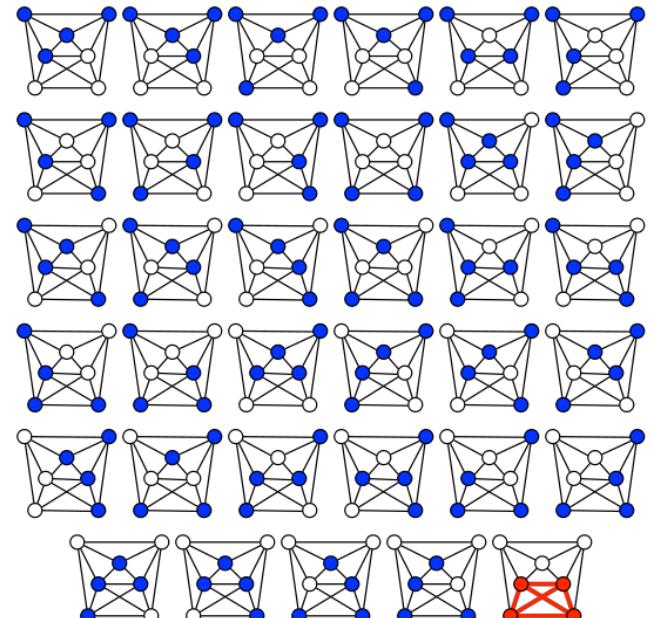
Cliques as communities

A clique is a complete subgraph of k -nodes



Cliques as communities

- Triangles are frequent; larger cliques are rare.
- Communities do not necessarily correspond to complete subgraphs, as many of their nodes do not link directly to each other.
- Finding the cliques of a network is computationally rather demanding, being a so-called NP-complete problem.



Strong and weak communities

Consider a connected subgraph C of N_c nodes

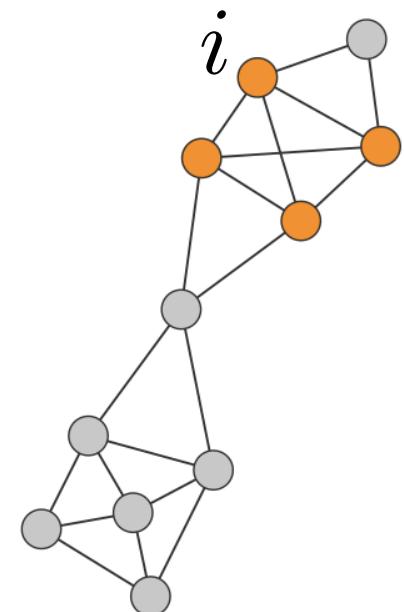
Internal degree, k_i^{int} : set of links of node i that connects to other nodes of the same community C .

External degree k_i^{ext} : the set of links of node i that connects to the rest of the network.

If $k_i^{ext}=0$: all neighbors of i belong to C , and C is a good community for i .

If $k_i^{int}=0$, all neighbors of i belong to other communities, then i should be assigned to a different community.

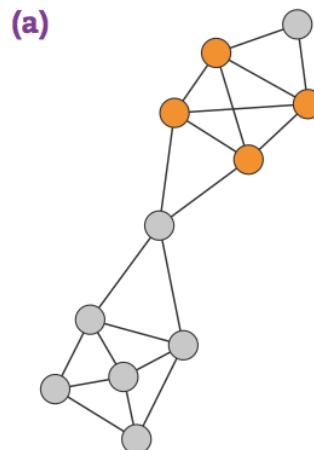
$$\begin{aligned}k_i^{int} &= 3 \\k_i^{ext} &= 1\end{aligned}$$



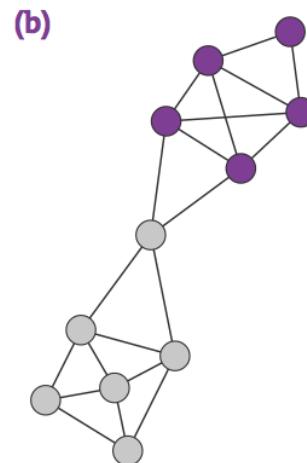
Strong community:

Each node of C has more links within the community than with the rest of the graph.

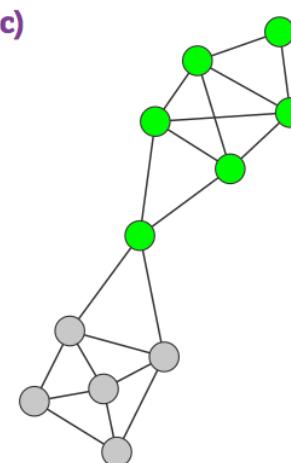
$$k_i^{\text{int}}(C) > k_i^{\text{ext}}(C)$$



Clique



Strong



Weak

Weak community:

The total internal degree of C exceeds its total external degree,

$$\sum_{i \in C} k_i^{\text{in}}(C) > \sum_{i \in C} k_i^{\text{out}}(C)$$

How many ways can we partition a network into 2 communities?

Graph bisection

Divide a network into two equal non-overlapping subgraphs, such that the number of links between the nodes in the two groups is minimized.

Two subgroups of size n_1 and n_2 . Total number of combinations: $\frac{N!}{n_1!n_2!}$

$$n! \simeq \sqrt{2\pi n} (n/e)^n$$

$$\frac{N!}{n_1!n_2!} \simeq \frac{\sqrt{2\pi N} (N/e)^n}{\sqrt{2\pi n_1} (n_1/e)^{n_1} \sqrt{2\pi n_2} (n_2/e)^{n_2}} \simeq \frac{N^{N+1/2}}{n_1^{n_1+1/2} n_2^{n_2+1/2}}$$

$$n_1 = n_2 = N/2$$

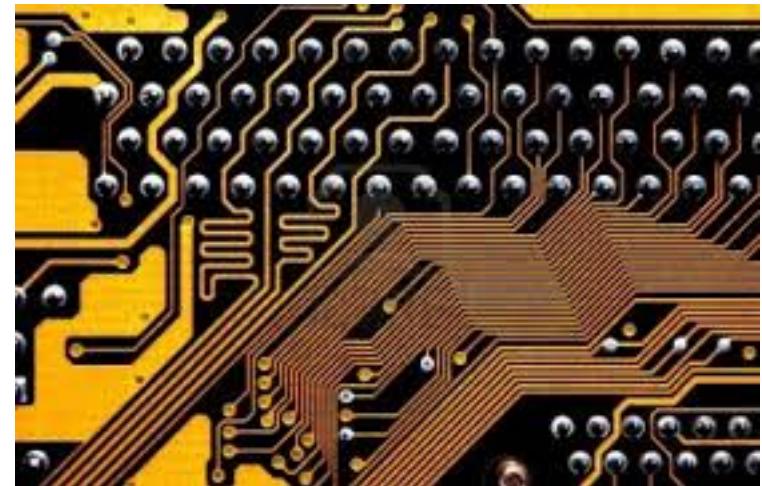
N=10 → 256 partitions (1 ms)

$$\frac{2^{N+1}}{\sqrt{N}} = e^{(N+1)\ln 2/\sqrt{N}}$$

N=100 → 10²⁶ partitions (10²¹ years)

Graph Partitioning

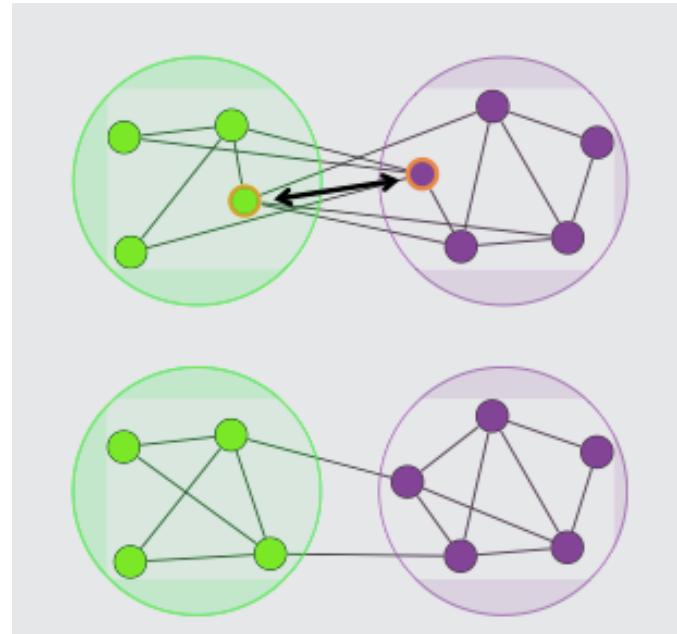
partition the full wiring diagram of an integrated circuit into smaller subgraphs, so that they minimize the number of connections between them.



2.5 billion transistors

Kernighan-Lin Algorithm for graph bisection

- Partition a network into two groups of predefined size. This partition is called **cut**.
- Inspect each a pair of nodes, one from each group. Identify the pair that results in the largest reduction of the cut size (links between the two groups) if we swap them
- Swap them.
- If no pair deduces the cut size, we swap the pair that increases the cut size the least.
- The process is repeated until each node is moved once.



Community detection

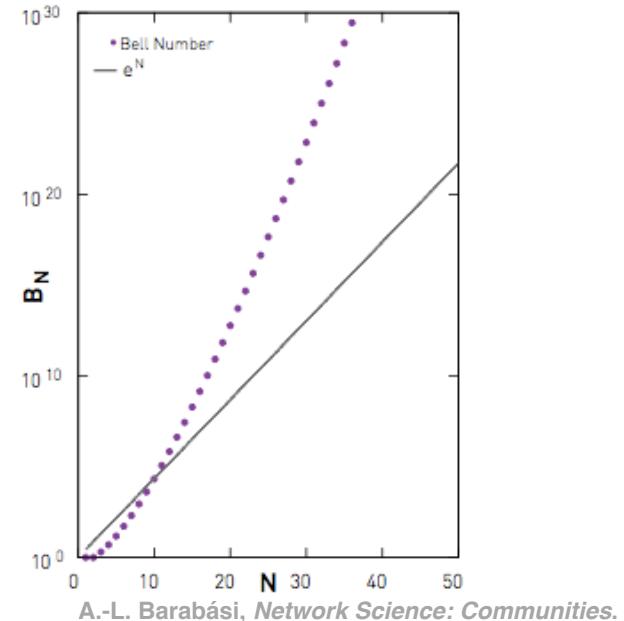
The *number* and *size* of the communities are unknown at the beginning.

Partition

Division of a network into groups of nodes, so that each node belongs to one group.

$$B_N = \frac{1}{e} \sum_{j=0}^{\infty} \frac{j^N}{j!} .$$

Bell Number: number of possible partitions of N nodes



Hierarchical Clustering

1. Build a similarity matrix for the network
2. *Similarity matrix*: how similar two nodes are to each other → we need to determine from the adjacency matrix
3. Hierarchical clustering iteratively identifies groups of nodes with high similarity, following one of two distinct strategies:
 - Agglomerative algorithms* merge nodes and communities with high similarity.
 - Divisive algorithms* split communities by removing links that connect nodes with low similarity.
4. *Hierarchical tree or dendrogram*: visualize the history of the merging or splitting process the algorithm follows. Horizontal cuts of this tree offer various community partitions.

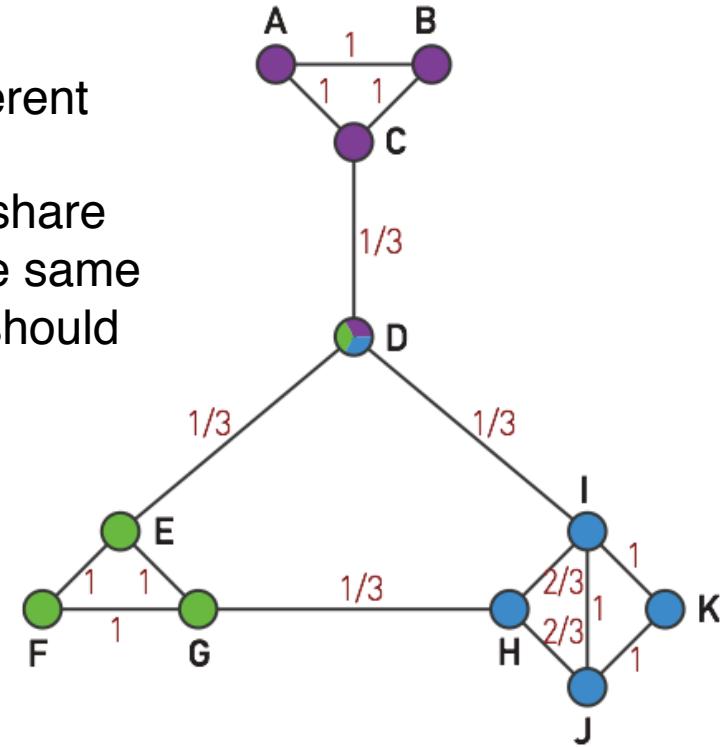
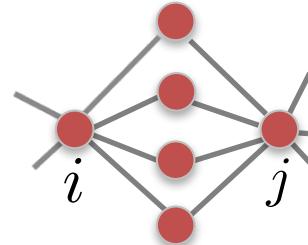
Agglomerative algorithms merge nodes and communities with high similarity.

Step 1: Define the Similarity Matrix (Ravasz algorithm)

- High for node pairs that likely belong to the same community, low for those that likely belong to different communities.
- Nodes that connect directly to each other and/or share multiple neighbors are more likely to belong to the same dense local neighborhood, hence their similarity should be large.

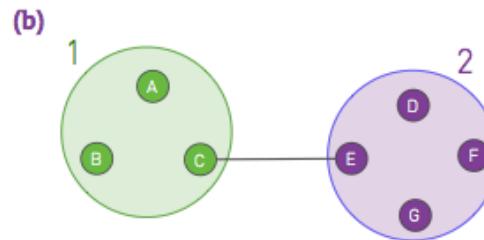
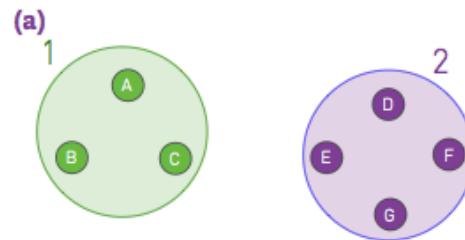
Topological overlap matrix: $x_{ij}^o = \frac{J_N(i, j)}{\min(k_i, k_j)}$

$J_N(i, j)$: number of common neighbors of node i and j ;
 $(+1)$ if there is a direct link between i and j ;



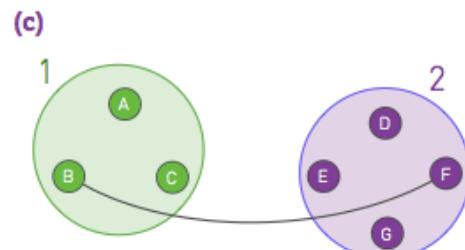
Step 2: Decide Group Similarity

- Groups are merged based on their mutual similarity through *single*, *complete* or *average cluster linkage*

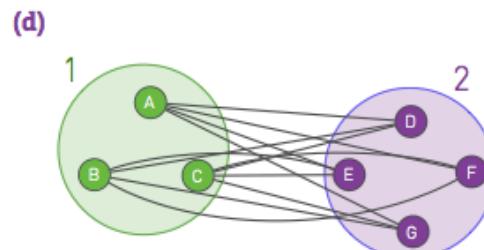


$$\frac{1}{x_{ij}} = r_{ij} = \begin{array}{c|cccc} & D & E & F & G \\ \hline A & 2.75 & 2.22 & 3.46 & 3.08 \\ B & 3.38 & 2.68 & 3.97 & 3.40 \\ C & 2.31 & 1.59 & 2.88 & 2.34 \end{array}$$

Single Linkage: $r_{12} = 1.59$



Complete Linkage: $r_{12} = 3.97$



Average Linkage: $r_{12} = 2.84$

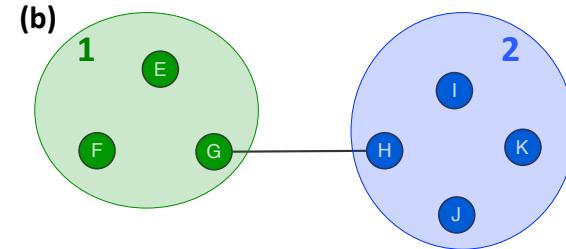
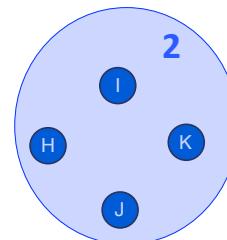
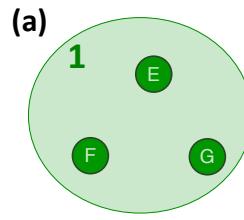
E. Ravasz et al., *Science* 297 (2002).

A.-L. Barabási, *Network Science: Communities*.

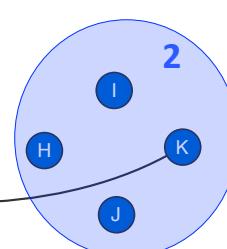
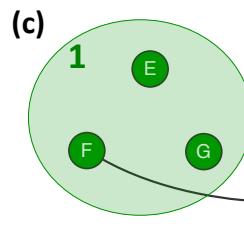
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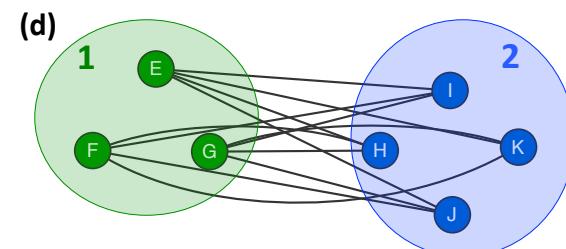
single, complete and average cluster similarity



Single Linkage: $x_{12} = 1.59$



Complete Linkage: $x_{12} = 3.97$



Average Linkage: $x_{12} = 2.84$

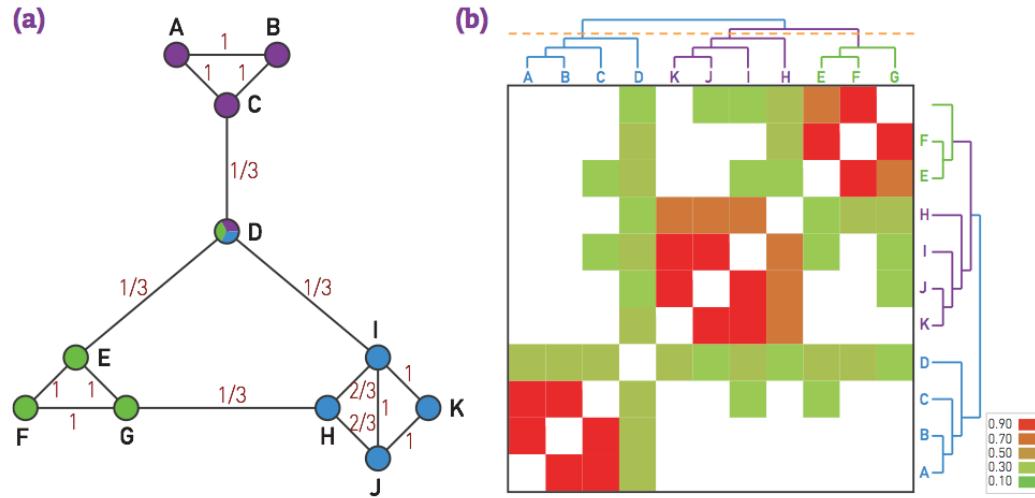
$$x_{ij} = \begin{array}{c|cccc} & H & I & J & K \\ \hline E & 2.22 & 2.75 & 3.08 & 3.46 \\ F & 2.68 & 3.38 & 3.40 & 3.97 \\ G & 1.59 & 2.31 & 2.34 & 2.88 \end{array}$$

Step 3: Apply Hierarchical Clustering

- Assign each node to a community of its own and evaluate the similarity for all node pairs. The initial similarities between these “communities” are simply the node similarities.
- Find the community pair with the highest similarity and merge them to form a single community.
- Calculate the similarity between the new community and all other communities.
- Repeat from Step 2 until all nodes are merged into a single community.

Step 4: Build Dendrogram

- Describes the precise order in which the nodes are assigned to communities.



Computational complexity:

- Step 1 (calculation similarity matrix): $O(N^2)$
 - Step 2-3 (group similarity): $O(N^2)$
 - Step 4 (dendrogram): $O(N \log N)$
- $\rightarrow O(N^2)$

E. Ravasz et al., *Science* 297 (2002).

A.-L. Barabási, *Network Science: Communities*.

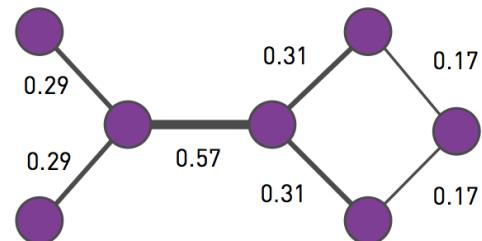
Divisive algorithms split communities by removing links that connect nodes with low similarity.

Step 1: Define a Centrality Measure (Girvan-Newman algorithm)

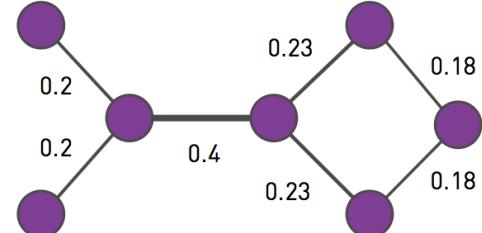
- *Link betweenness* is the number of shortest paths between all node pairs that run along a link.
- *Random-walk betweenness*. A pair of nodes m and n are chosen at random. A walker starts at m , following each adjacent link with equal probability until it reaches n . Random walk betweenness x_{ij} is the probability that the link $i \rightarrow j$ was crossed by the walker after averaging over all possible choices for the starting nodes m and n



(a)



(b)

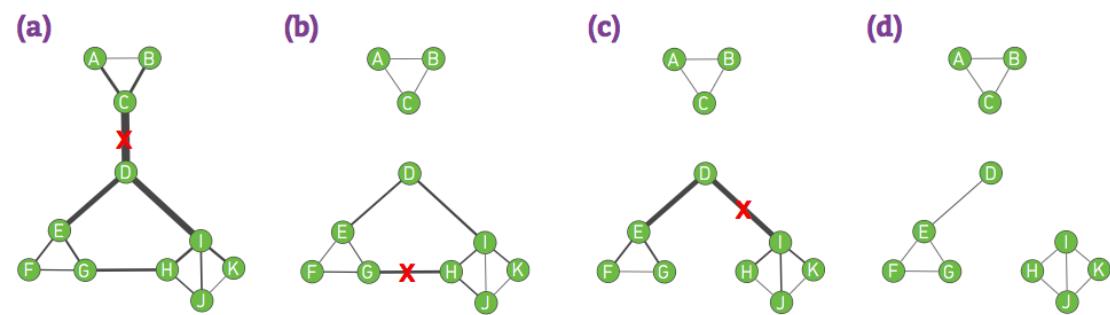


M. Girvan & M.E.J. Newman, PNAS 99 (2002).

A.-L. Barabási, *Network Science: Communities*.

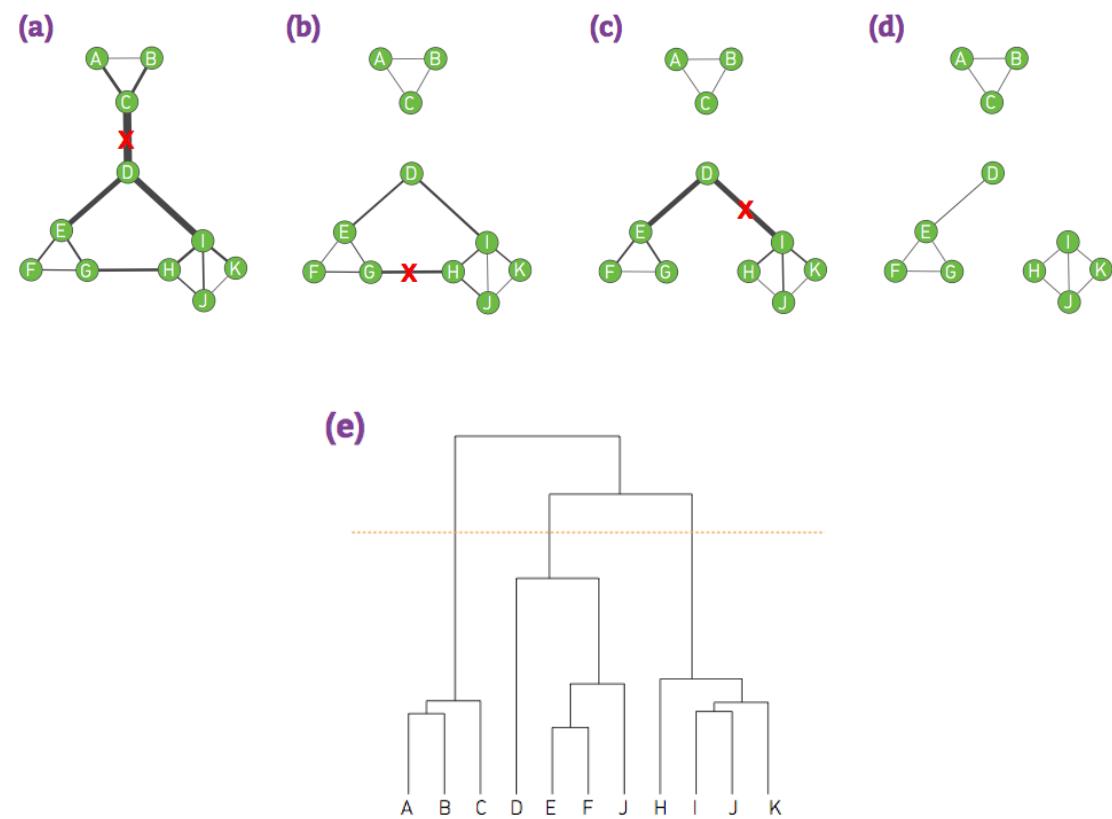
Step 2: Hierarchical Clustering

- Compute of the centrality of each link.
- Remove the link with the largest centrality; in case of a tie, choose one randomly.
- Recalculate the centrality of each link for the altered network.
- Repeat until all links are removed (yields a dendrogram).



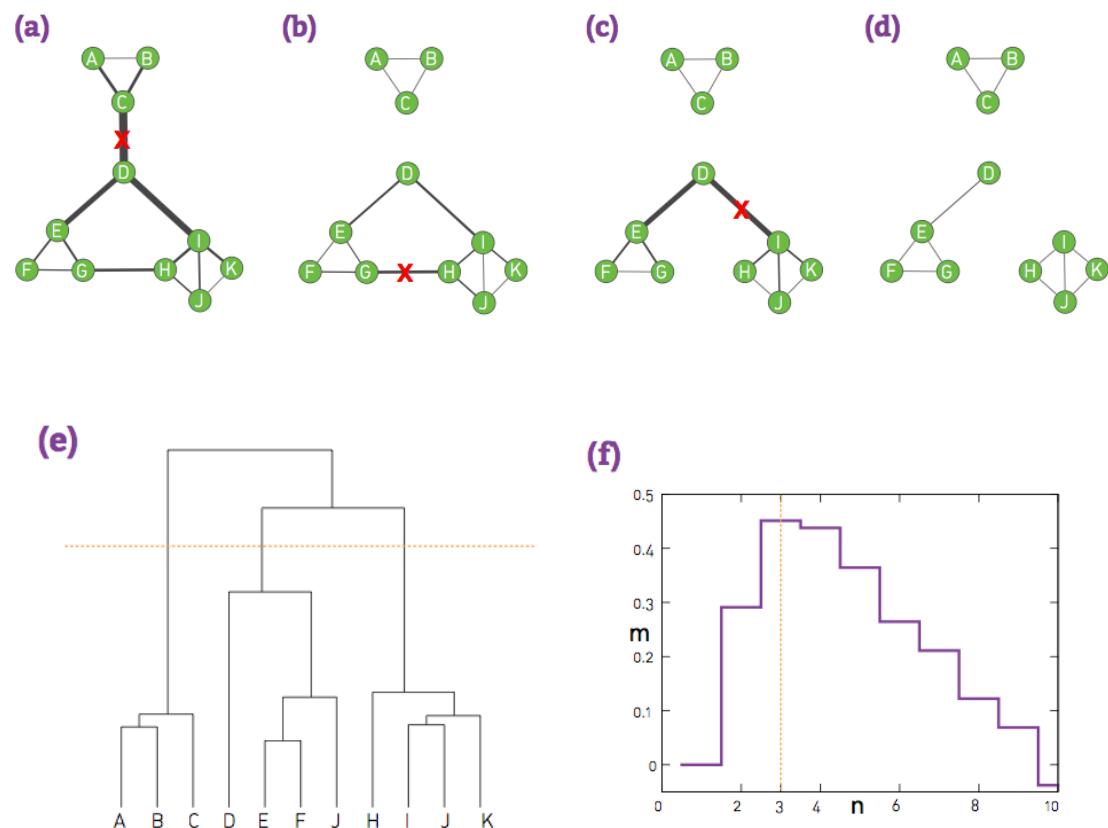
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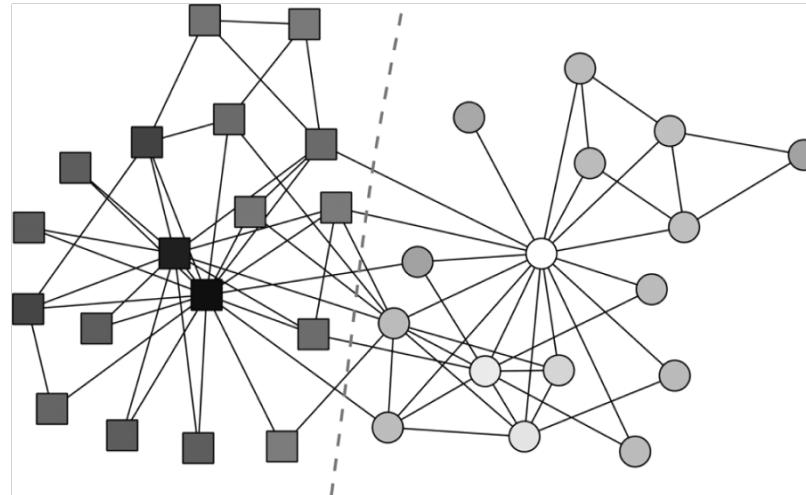
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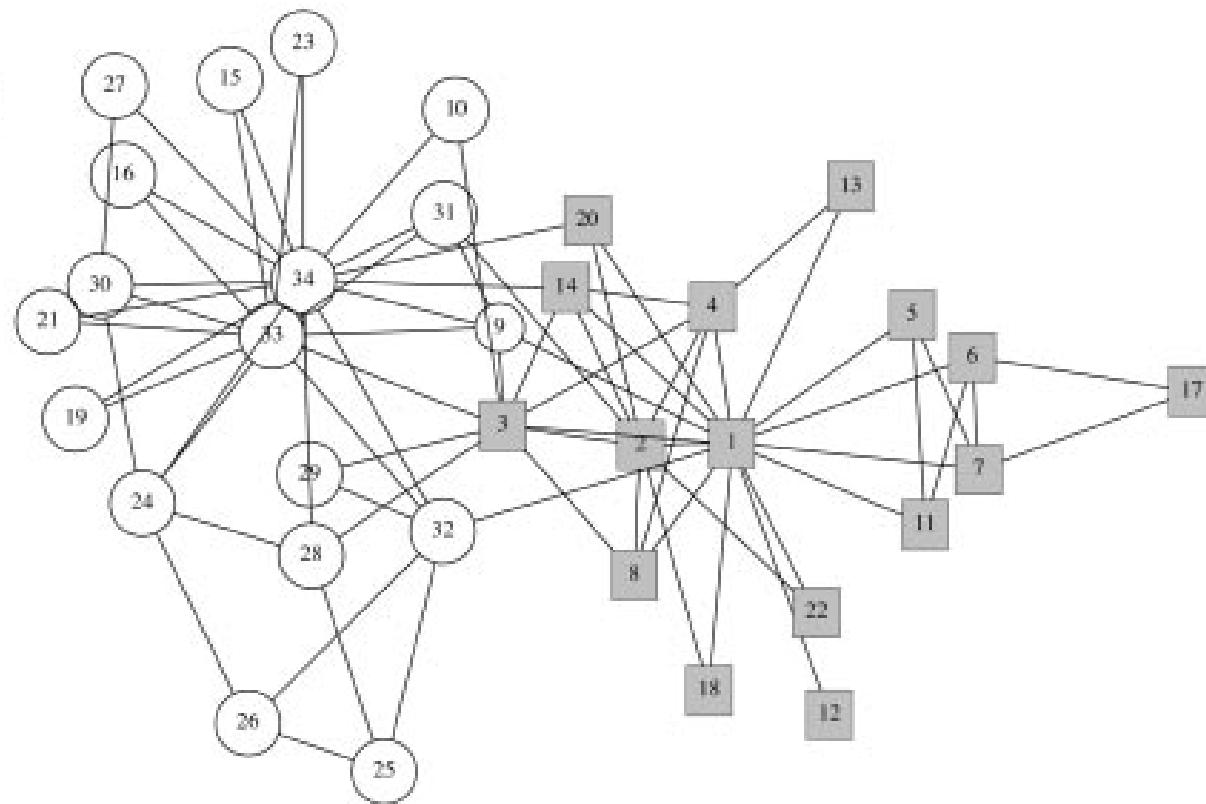
Computational complexity:

- Step 1a (calculation betweenness centrality): $O(N^2)$
- Step 1b (Recalculation of betweenness centrality for all links): $O(LN^2)$

for sparse networks  $O(N^3)$

Section 4

Divisive Algorithm

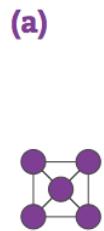


i. Nested Communities

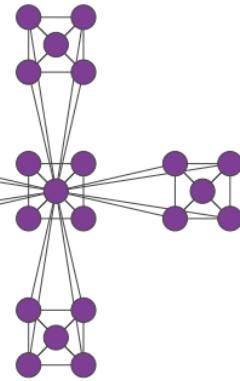
It assumes that communities are organized in a hierarchical fashion, i.e. small modules are nested into larger ones. This hierarchical nesting is captured by the dendrogram ([Figures 9.12a](#) and [9.15e](#)). How do we know, however, if such hierarchy is indeed present in a network? Could this hierarchy be imposed by the algorithm, whether or not the underlying network has a nested community structure?

ii. Communities and the Scale-Free Property

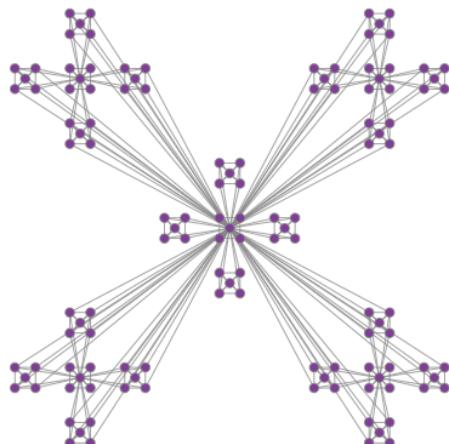
The density hypothesis states that a network can be partitioned into a collection of subgraphs that are only weakly linked to other subgraphs. How can we have somewhat isolated communities in a scale-free network, whose hubs inevitably connect to nodes that can belong to different communities?



(b)



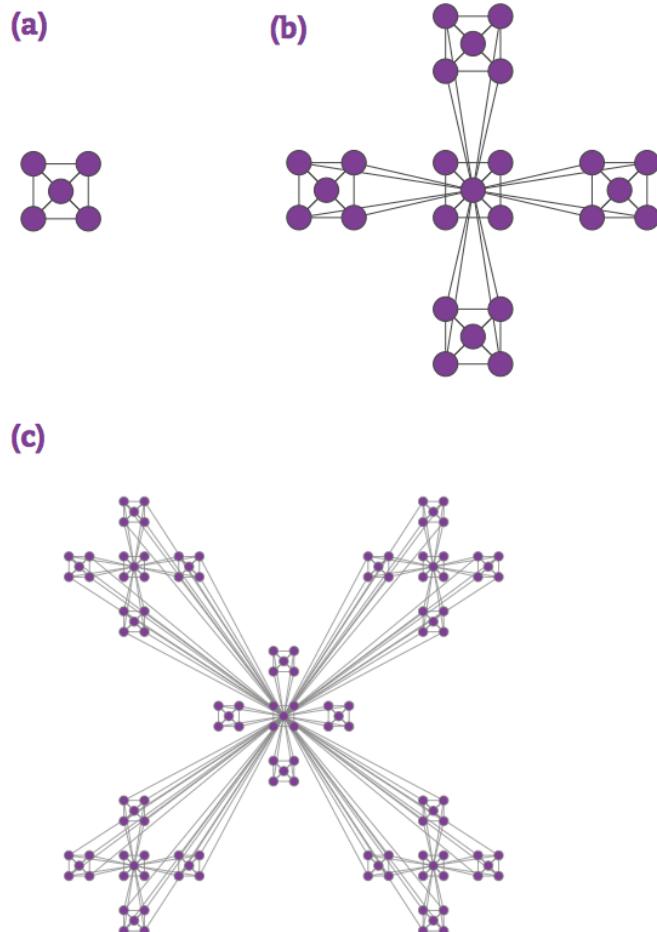
(c)



(1) Scale-free property

The obtained network is scale-free, its degree distribution following a power-law with

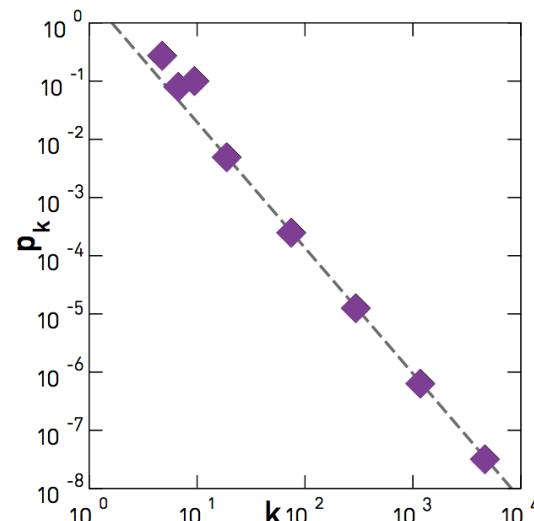
$$\gamma = 1 + \frac{\ln 5}{\ln 4} \simeq 2.16$$

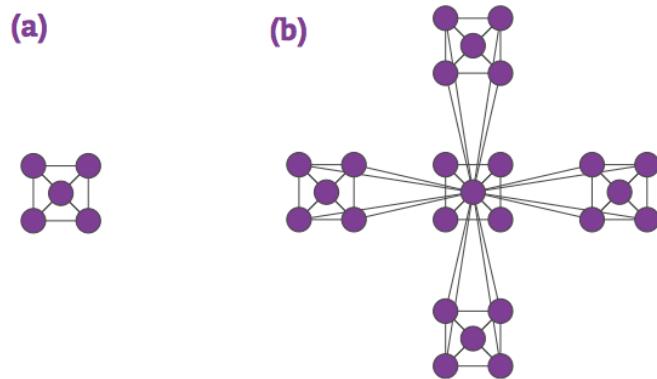


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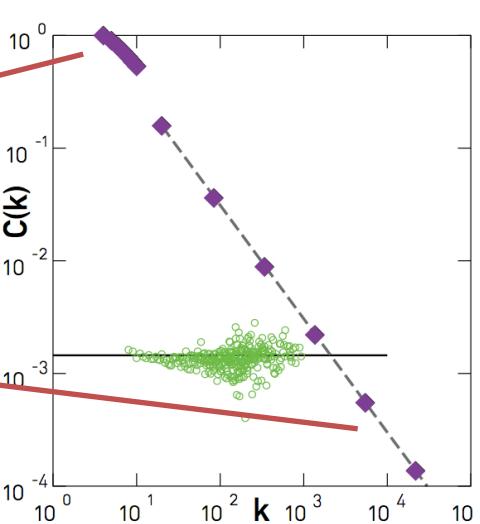
$$\gamma = 1 + \frac{\ln 5}{\ln 4} \simeq 2.16$$





(2) Clustering coefficient scaling with k

$$C(k) = \frac{\# \text{ between } k \text{ neighbors}}{k(k-1)/2} = C(k) \sim k^{-1}$$



Small k nodes:
 *high clustering coefficient;
 *their neighbors tend to link to each other in highly interlinked, compact communities.

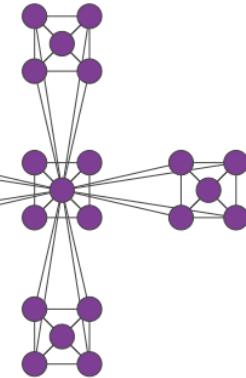
High k nodes (hubs):
 *small clustering coefficient;
 *connect independent communities.

Section 4

Hierarchy in networks



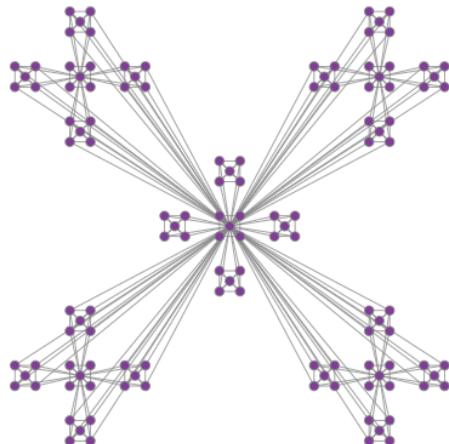
(b)



(3) Clustering coefficient independent of N

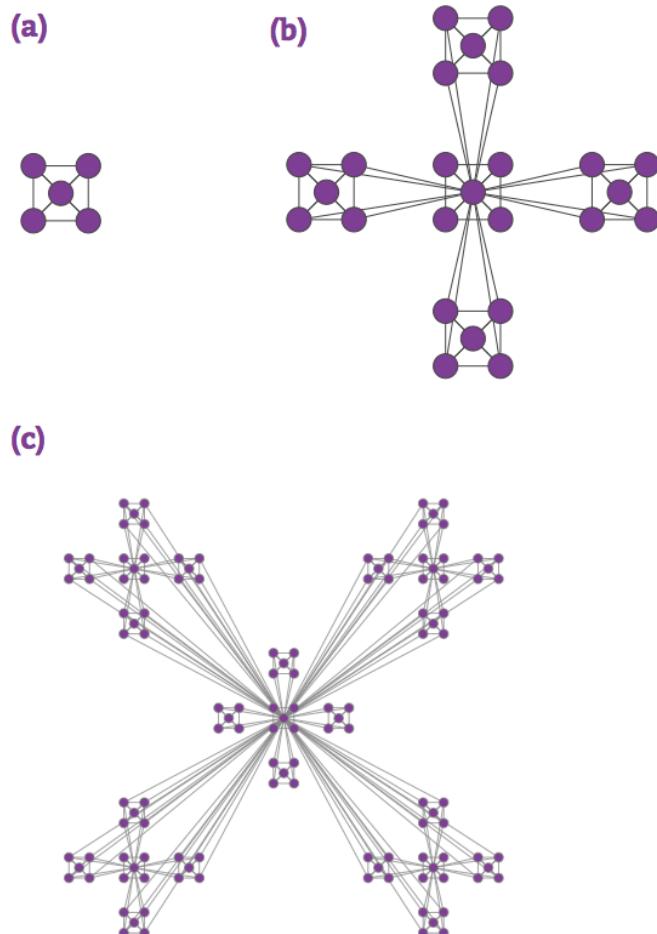
$$C = 0.743$$

(c)



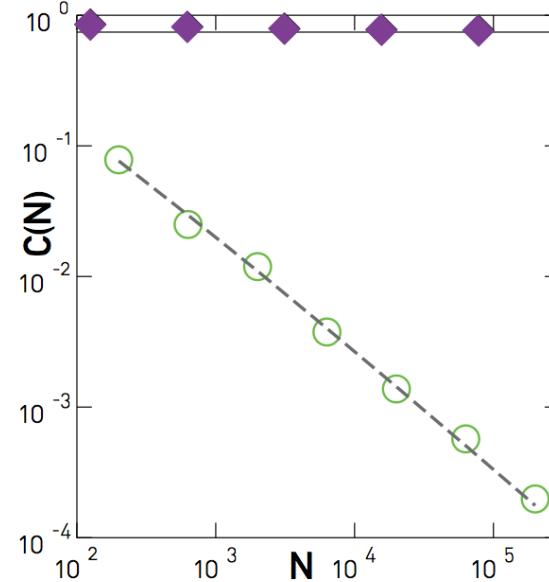
Section 4

Hierarchy in networks



(3) Clustering coefficient independent of N

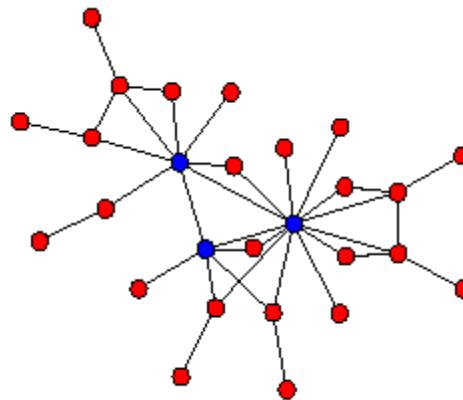
$$C = 0.743$$



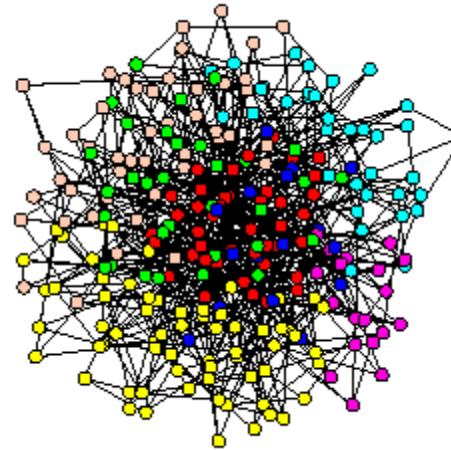
Section 4

Hierarchy in networks

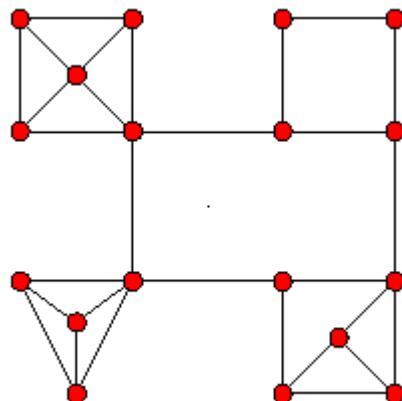
(a)



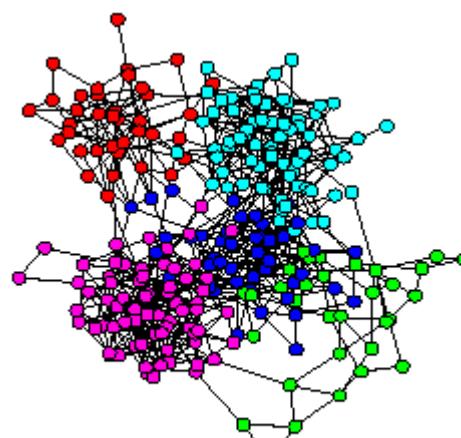
Scale-free



(b)

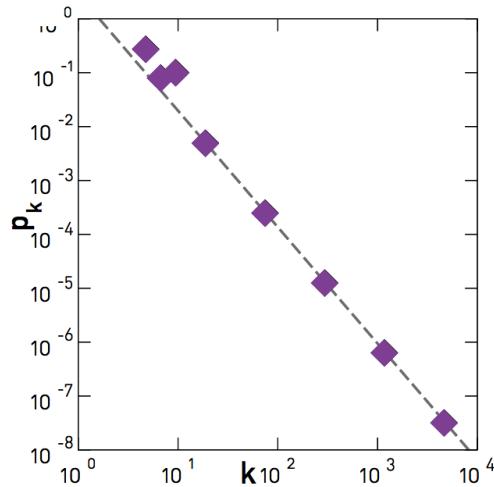


Modular

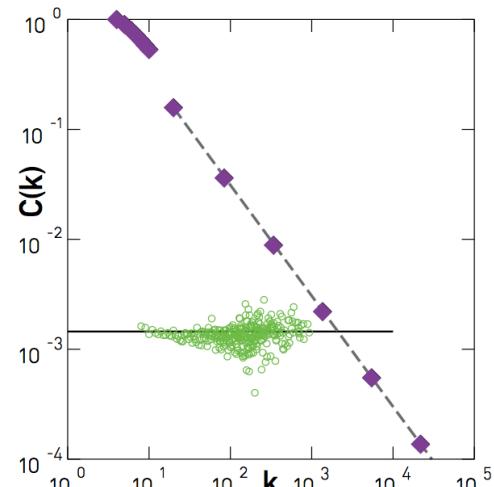


1. Scale-free

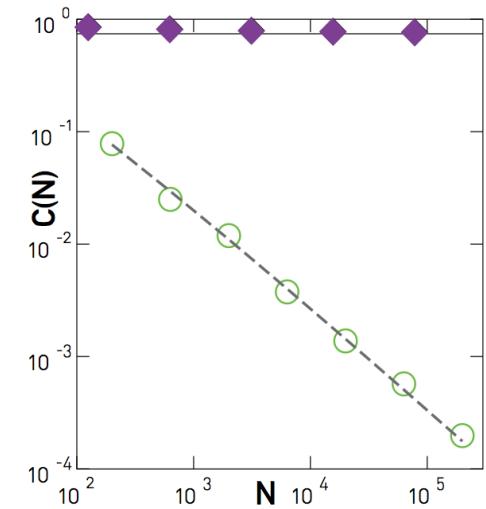
$$\gamma = 1 + \frac{\ln 5}{\ln 4} = 2.161$$

**2. Scaling clustering coefficient (DGM)**

$$C(k) \sim k^{-1}$$

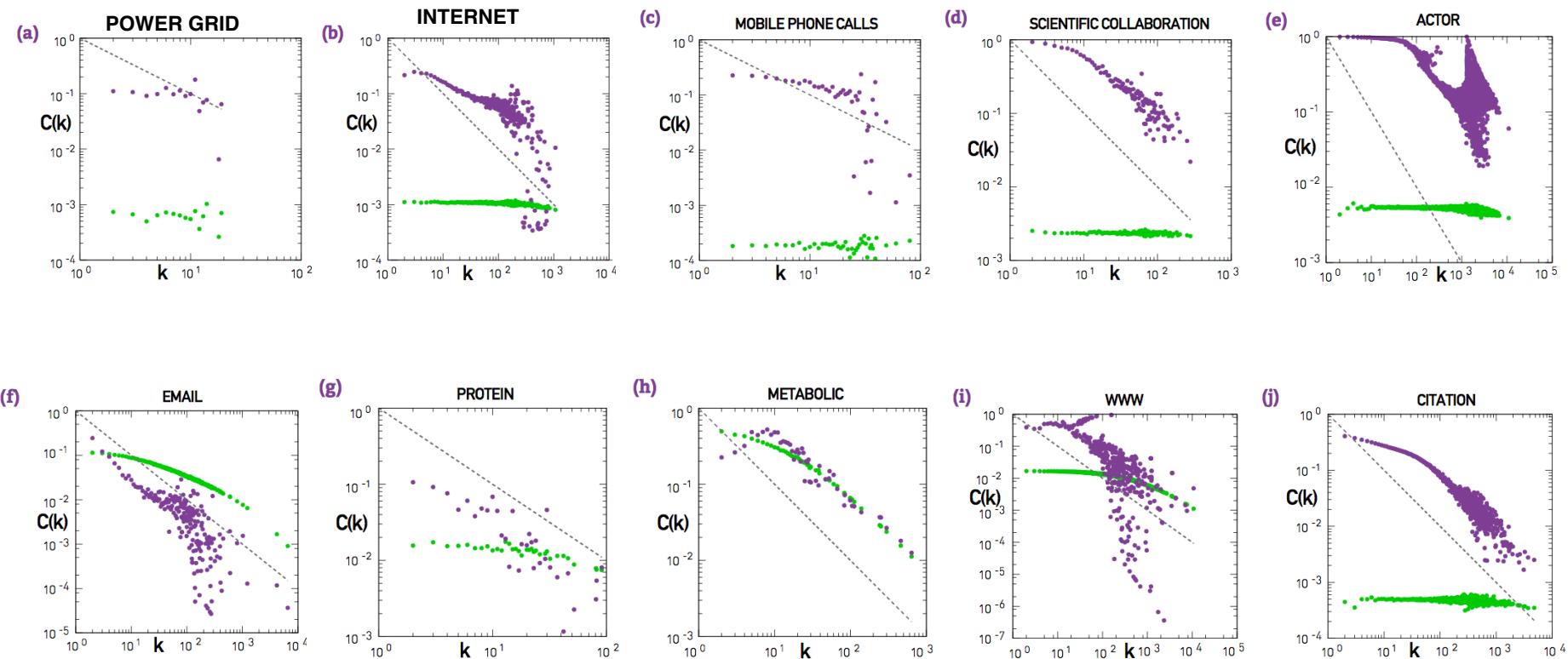
**3. Clustering coefficient independent of N**

$$C(N) = \text{const.}$$



Section 4

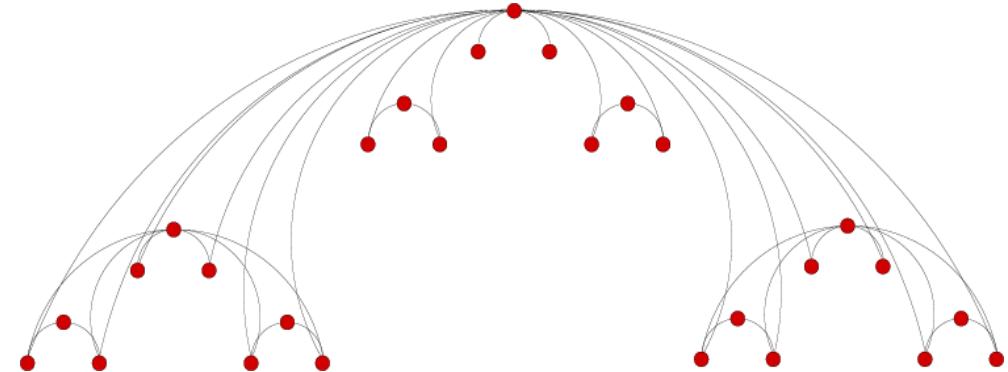
Hierarchy in real networks



HIERARCHICAL MODELS

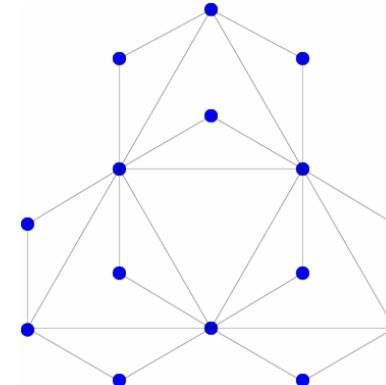
$$\gamma = \frac{\ln 3}{\ln 2}$$

- Barabási, Ravasz, Vicsek, Physica A 2003



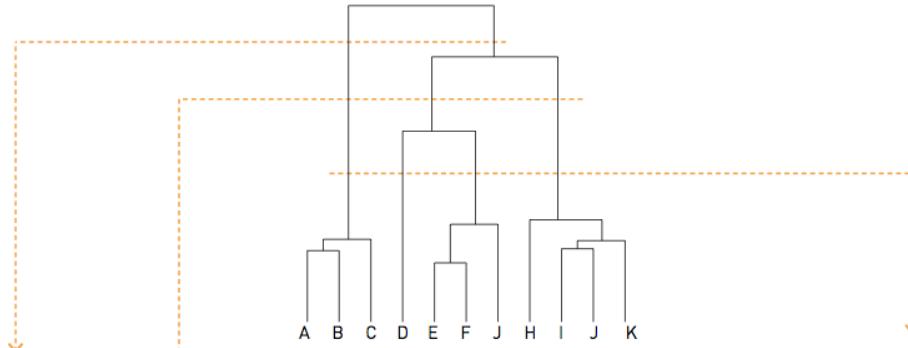
- Dorogovtsev, Goltsev, Mendes, 2001

$$\gamma = 1 + \frac{\ln 3}{\ln 2}$$

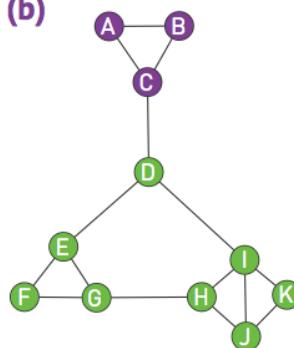


Where to “cut”?

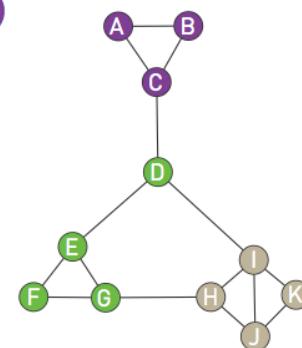
(a)



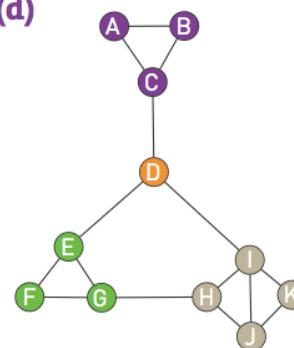
(b)



(c)



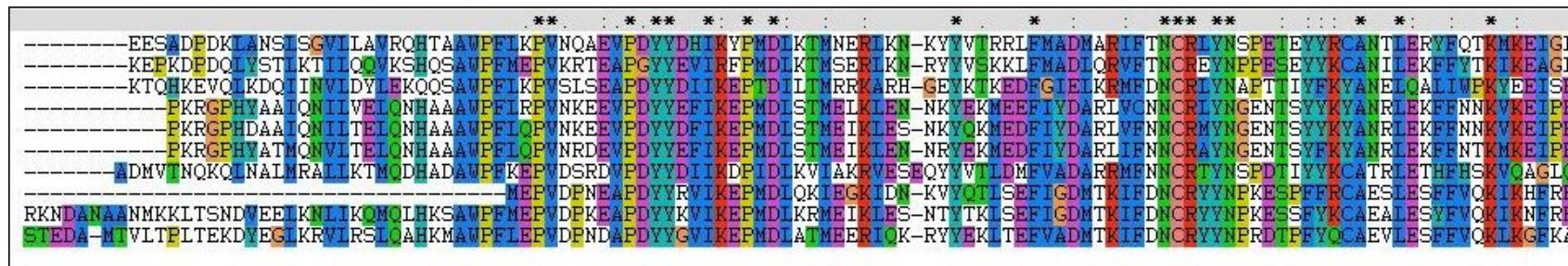
(d)



Phylogenetic dendograms

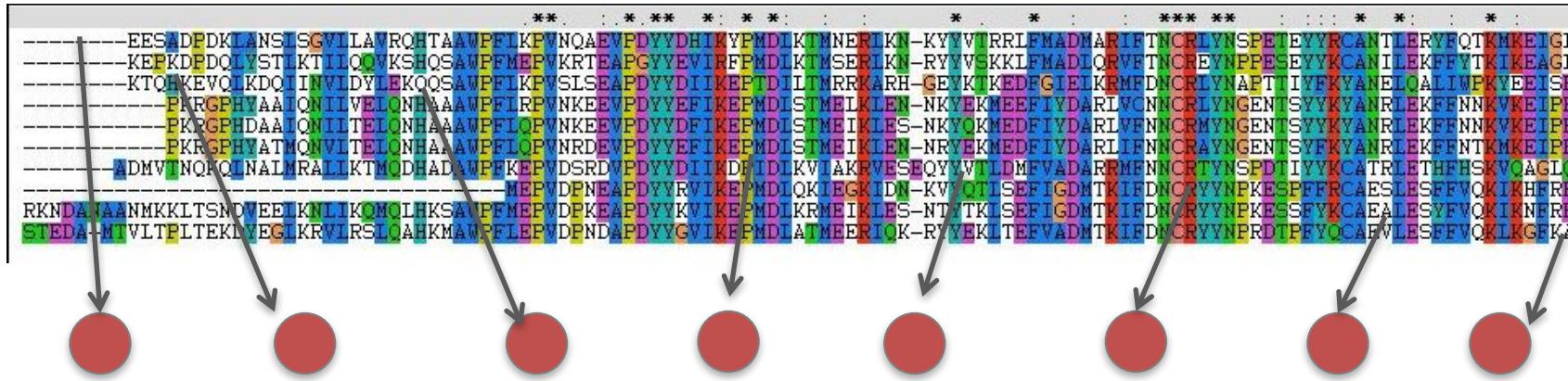
In bioinformatics, clusters and dendrograms have been studied for a long time.

For example, the sequences of the same protein or gene in different species are selected, and compared with each other.



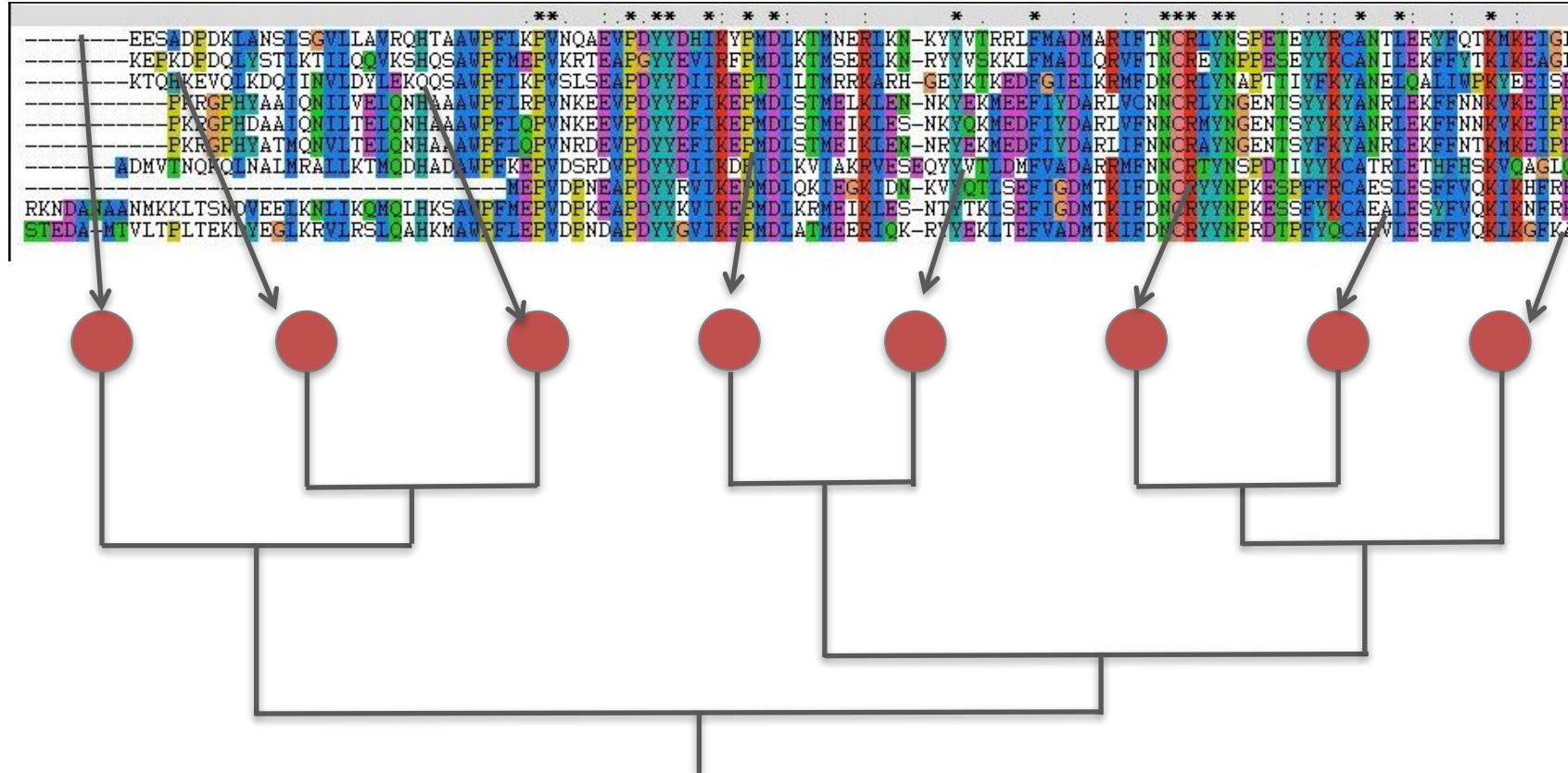
Phylogenetic dendograms

A similarity matrix is constructed between these sequences, by looking at how many aminoacids/nucleotides stay in place

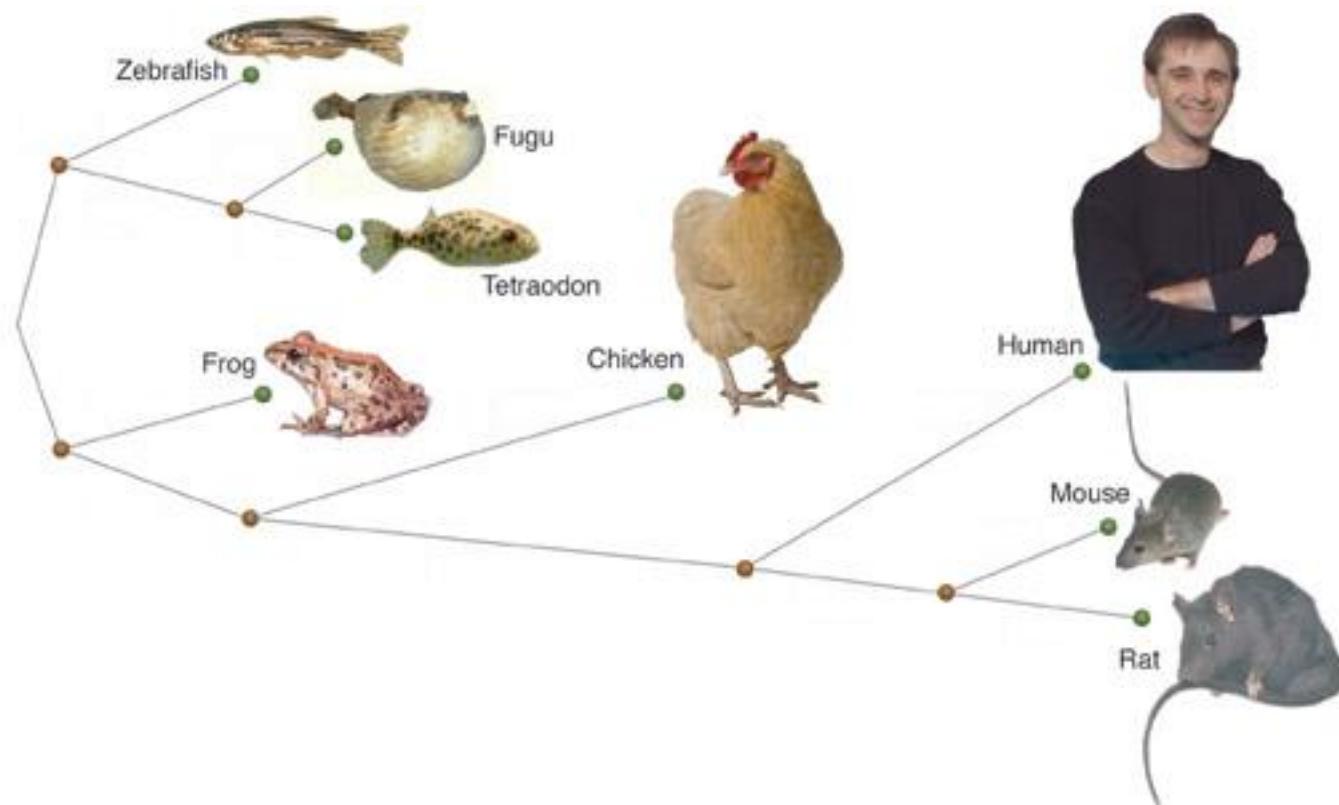


Phylogenetic dendograms

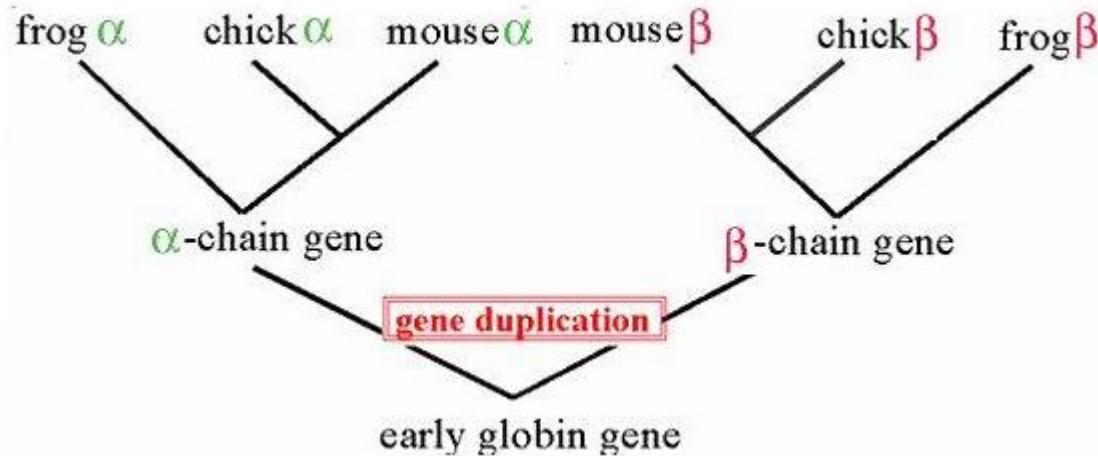
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Phylogenetic dendograms



Phylogenetic dendograms



Modularity

H4: *Random Hypothesis*

Randomly wired networks are not expected to have a community structure.

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Randomly wired networks are not expected to have a community structure.

Imagine a partition in n_c communities $\{C_c, c = 1, n_c\}$

Modularity
$$M(C_c) = \frac{1}{2L} \sum_{i,j=1}^N (A_{ij} - P_{ij})\delta(C_i - C_j)$$

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Original data

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$$\text{Modularity} \quad M(C_c) = \frac{1}{2L} \sum_{i,j=1}^N (A_{ij} - P_{ij}) \delta(C_i - C_j)$$

Original data

Expected connections,
a model

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Original data Expected connections, a model Relative to a specific partition

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Original data Expected connections,
a model Relative to a specific
partition

- Random network $P_{ij} = 2Lp_i p_j = \frac{k_i k_j}{2L}$
- Modularity is a measure associated to a partition

Another way of writing M

$$M(C_c) = \frac{1}{2L} \sum_{i,j=1}^N (A_{ij} - P_{ij})\delta(C_i - C_j) \quad P_{ij} = 2Lp_i p_j = \frac{k_i k_j}{2L}$$

We can rewrite the first term as

$$\frac{1}{2L} \sum_{i,j=1}^N A_{ij}\delta(C_i - C_j) = \sum_{c=1}^{n_c} \frac{1}{2L} \sum_{i,j \in C_c} A_{ij} = \sum_{c=1}^{n_c} \frac{l_c}{L}$$

where L_C is the number of links within C . In a similar fashion, the second term becomes

$$\frac{1}{2L} \sum_{i,j} \frac{k_i k_j}{2L} \delta(C_i - C_j) = \sum_{c=1}^{n_c} \frac{1}{(2L)^2} \sum_{i,j \in C_c} k_i k_j = \sum_{c=1}^{n_c} \frac{k_c^2}{4L^2}$$

Finally we get:

$$M(C_c) = \sum_{c=1}^{n_c} \left[\frac{l_c}{L} - \left(\frac{k_c}{2L} \right)^2 \right]$$

H5: Maximal Modularity Hypothesis

The partition with the maximum modularity M for a given network offers the optimal community structure

H5: Maximal Modularity Hypothesis

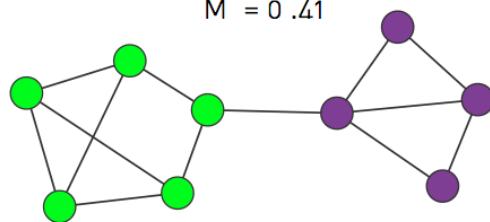
The partition with the maximum modularity M for a given network offers the optimal community structure

Goal

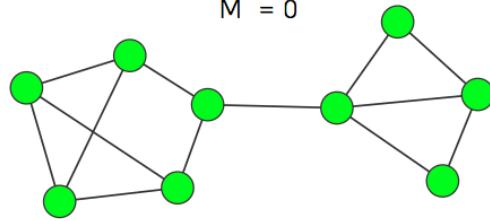
Find $\{C_c, c = 1, n_c\}$ that maximizes M

Which partition $\{C_c, c = 1, n_c\}$?

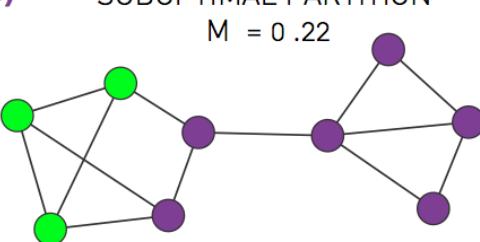
(a) OPTIMAL PARTITION
 $M = 0.41$



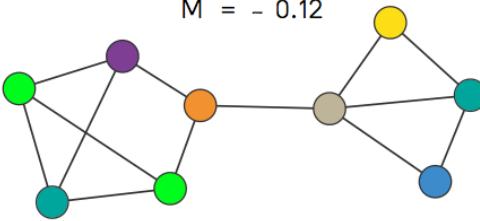
(c) SINGLE COMMUNITY
 $M = 0$



(b) SUBOPTIMAL PARTITION
 $M = 0.22$



(d) NEGATIVE MODULARITY
 $M = -0.12$



- *Optimal partition*, that maximizes the modularity.
- *Sub-optimal* but positive modularity.
- *Negative Modularity*: If we assign each node to a different community.
- *Zero modularity*: Assigning all nodes to the same community, independent of the network structure.
- *Modularity is size dependent*

A *greedy algorithm*, which iteratively joins nodes if the move increases the new partition's modularity.

Step 1. Assign each node to a community of its own. Hence we start with N communities.

Step 2. Inspect each pair of communities connected by at least one link and compute the modularity variation obtained if we merge these two communities.

Step 3. Identify the community pairs for which ΔM is the largest and merge them. Note that modularity of a particular partition is always calculated from the full topology of the network.

Step 4. Repeat step 2 until all nodes are merged into a single community.

Step 5. Record for each step and select the partition for which the modularity is maximal.

Which partition $\{C_c, c = 1, n_c\}$?

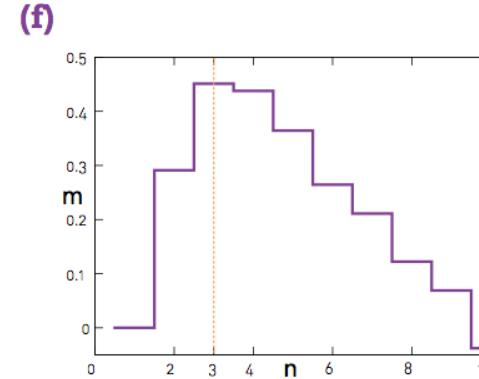
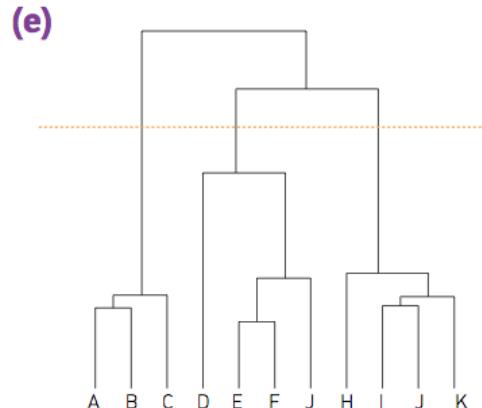
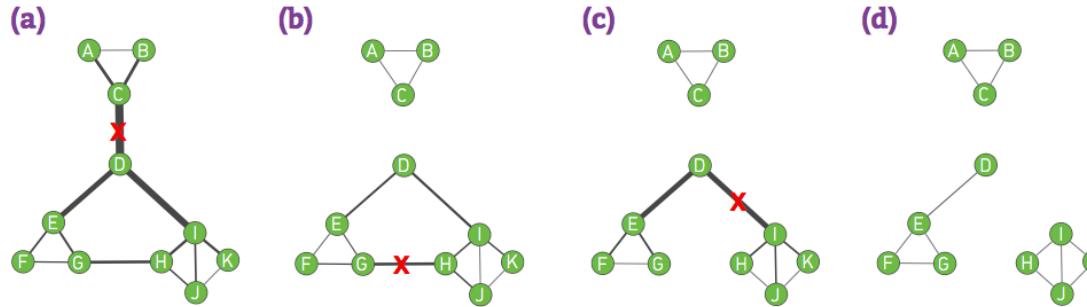
- It can be used to design new algorithms, aiming at maximizing M
- Modularity can be used to compare different partitions provided by other algorithms, like hierarchical clustering

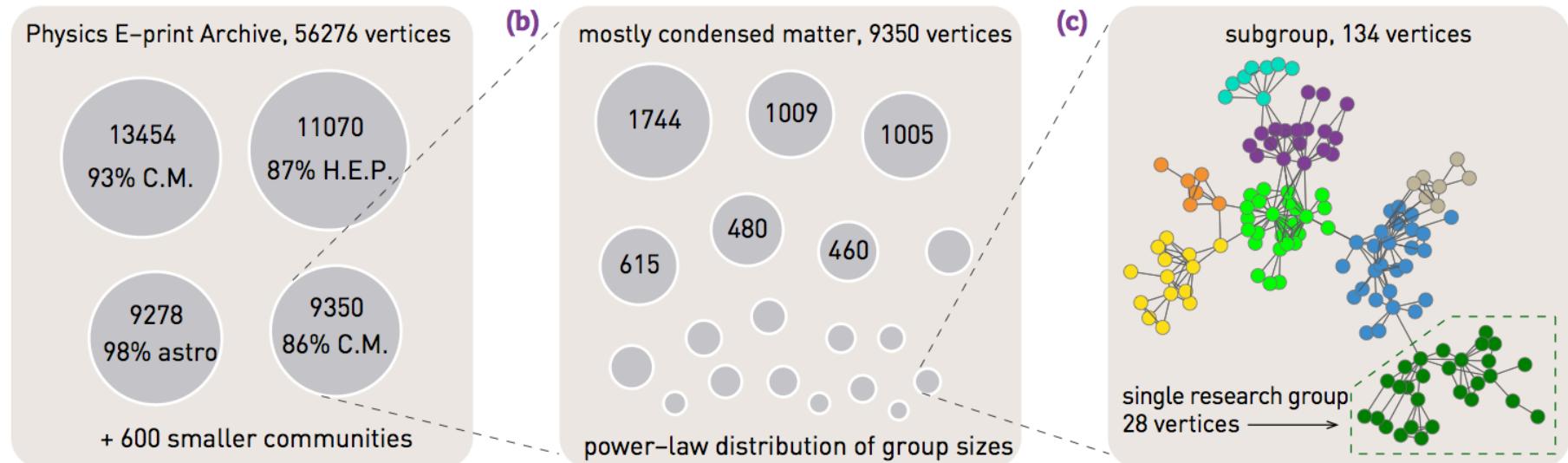
Section 4

Modularity for the Girvan-Newman

Which partition $\{C_c, c = 1, n_c\}$?

$$M(C_c) = \sum_{c=1}^{n_c} \left[\frac{l_c}{L} - \left(\frac{k_c}{2L} \right)^2 \right]$$

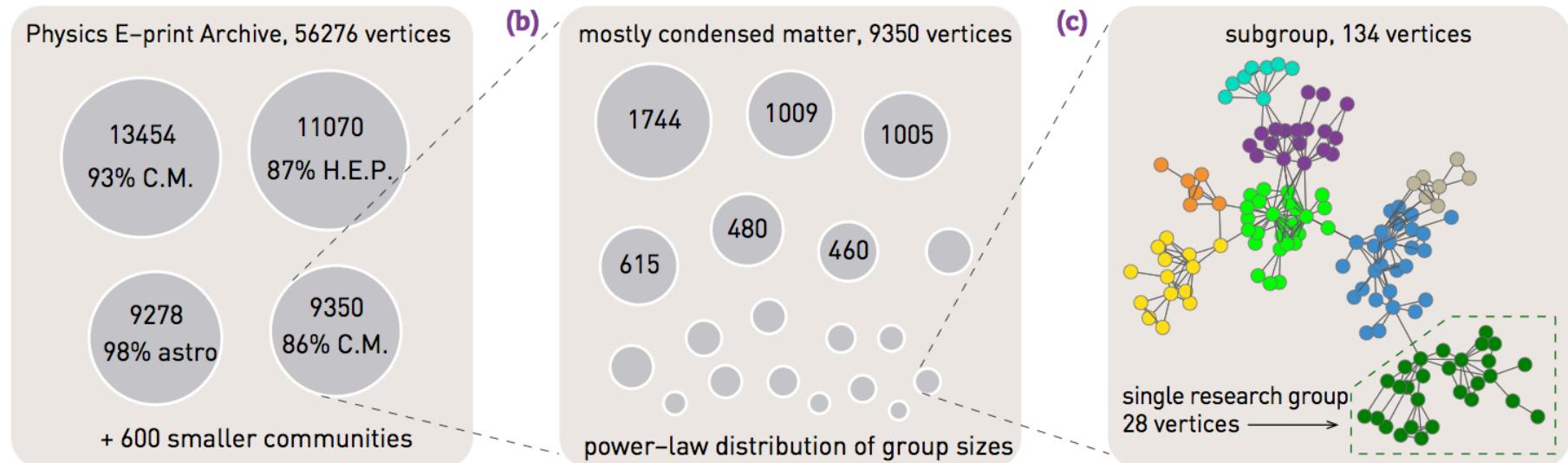




Computational complexity:

- Step 1-2 (calculation of ΔM for L links): $O(L)$
- Step 3 (matrix update): $O(N)$
- Step 4 ($N-1$ community merges): $O((L + N)N)$

for sparse networks

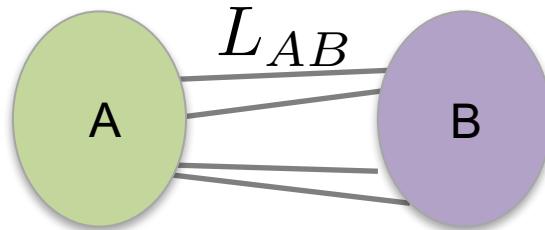


Computational complexity:

- Step 1-2 (calculation of ΔM for L links): $O(L)$
- Step 3 (matrix update): $O(N)$
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for sparse networks $O(N^2)$

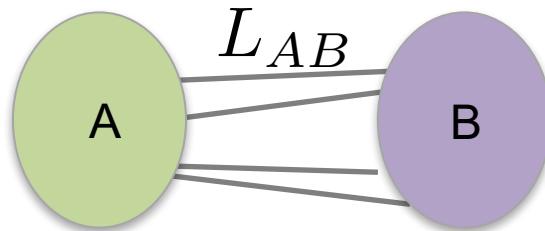
Resolution limit



$$\Delta M_{AB} = \frac{L_{AB}}{L} - \frac{k_A k_B}{2L^2},$$

k_A and k_B total degree in A and B

Resolution limit

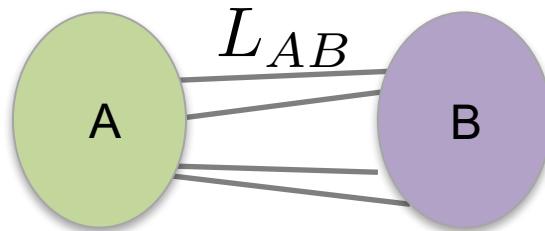


$$\Delta M_{AB} = \frac{L_{AB}}{L} - \frac{k_A k_B}{2L^2},$$

k_A and k_B total degree in A and B

If $\frac{k_A k_B}{2L} < 1$ and $L_{AB} \geq 1$

Resolution limit



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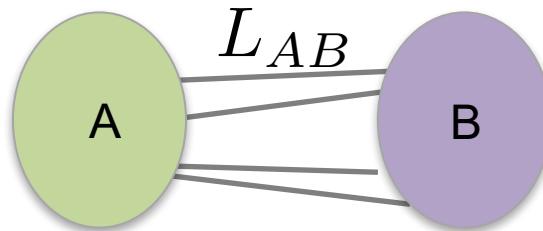
If $\frac{k_A k_B}{2L} < 1$ and $L_{AB} \geq 1$



$$\Delta M_{AB} > 0$$

We merge A and B to maximize modularity.

Resolution limit



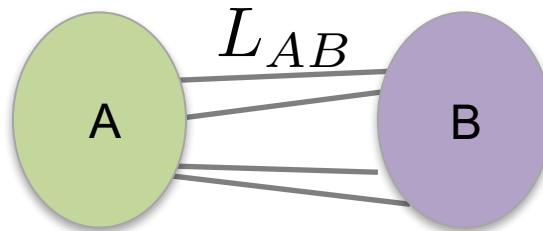
$$\Delta M_{AB} = \frac{L_{AB}}{L} - \frac{k_A k_B}{2L^2},$$

k_A and k_B total degree in A and B

If $\frac{k_A k_B}{2L} < 1$ and $L_{AB} \geq 1$ → $\Delta M_{AB} > 0$ We merge A and B to maximize modularity.

Assuming $k_A \sim k_B = k$ → $k \leq \sqrt{2L}$

Resolution limit



$$\Delta M_{AB} = \frac{L_{AB}}{L} - \frac{k_A k_B}{2L^2},$$

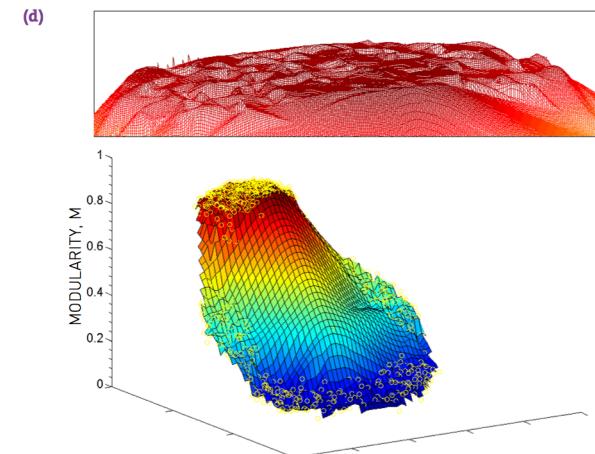
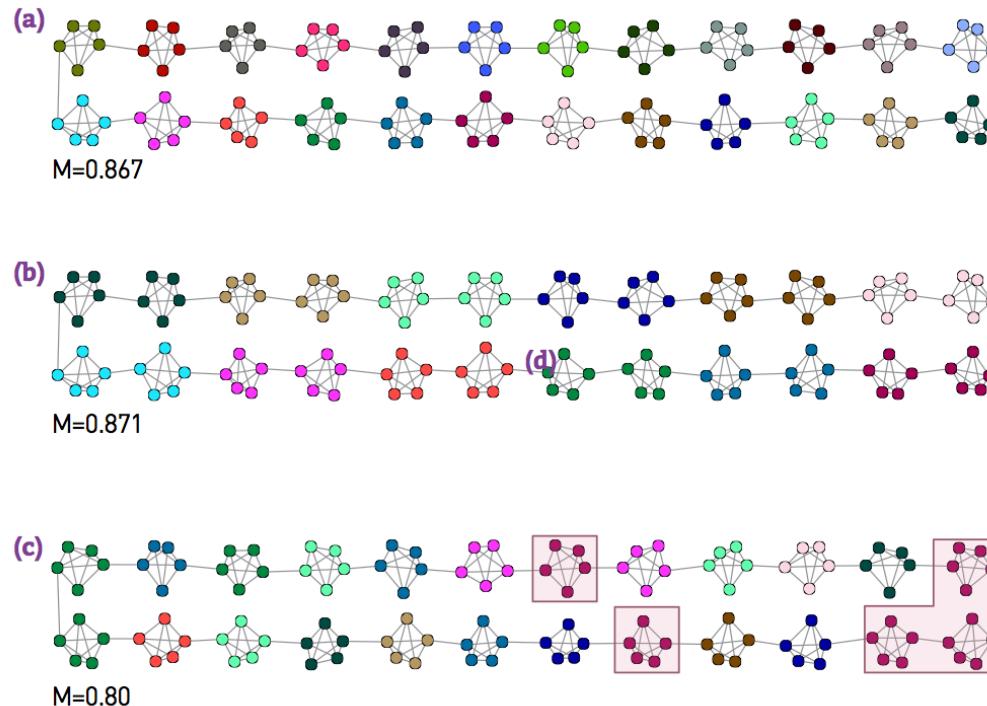
k_A and k_B total degree in A and B

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Assuming $k_A \sim k_B = k$ → $k \leq \sqrt{2L}$

Modularity has a resolution limit, as it cannot detect communities smaller than this size.

One maximum?



Null models

$$M(C_c) = \frac{1}{2L} \sum_{i,j=1}^N (A_{ij} - P_{ij}) \delta(C_i - C_j)$$



Expected connections,
a model

→ P_{ij} can take into account weights

S. Fortunato, *Phys. Rep.* 486 (2010)

→ P_{ij} can take into account directions

S. Fortunato, *Phys. Rep.* 486 (2010)

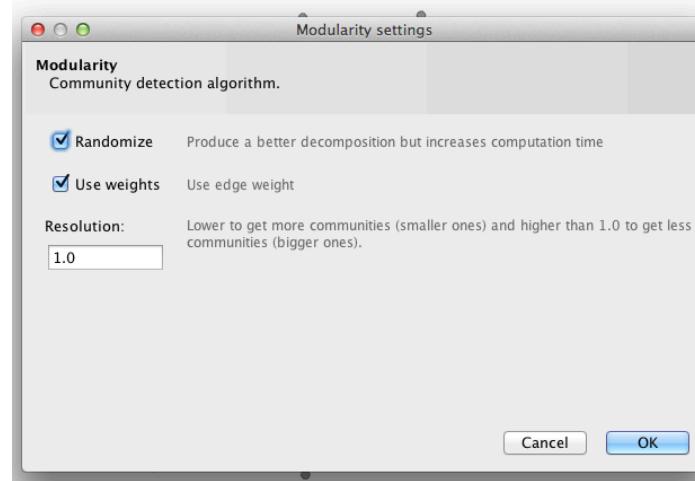
→ P_{ij} can take into account attributes or space

P. Expert et al., *PNAS* 108 (2011)

Section 5

Online Resources (Modularity)

→ Gephi



R assigns self-loops to nodes to increase or decrease the aversion of nodes to form communities

→ NetworkX

`community.best_partition(graph, partition=None)` 1

Compute the partition of the graph nodes which maximises the modularity (or try..) using the Louvain heuristics

This is the partition of highest modularity, i.e. the highest partition of the dendrogram generated by the Louvain algorithm.

Finds the partition that maximizes modularity (considers weights and direction)

`community.modularity(partition, graph)`

Compute the modularity of a partition of a graph

Calculates the modularity of the partition you provide

The greedy algorithm is neither particularly fast nor particularly successful at maximizing M .

Scalability: Due to the sparsity of the adjacency matrix, the update of the matrix involves a large number of useless operations. The use of data structures for sparse matrices can decrease the complexity of the computational algorithm to , which allows us to analyze is of networks up to nodes. See

"Fast Modularity" Community Structure Inference Algorithm

<http://cs.unm.edu/~aaron/research/fastmodularity.htm> for the code.

A fast greedy algorithm was proposed by Blondel and collaborators, that can process networks with millions of nodes. For the description of the algorithm see

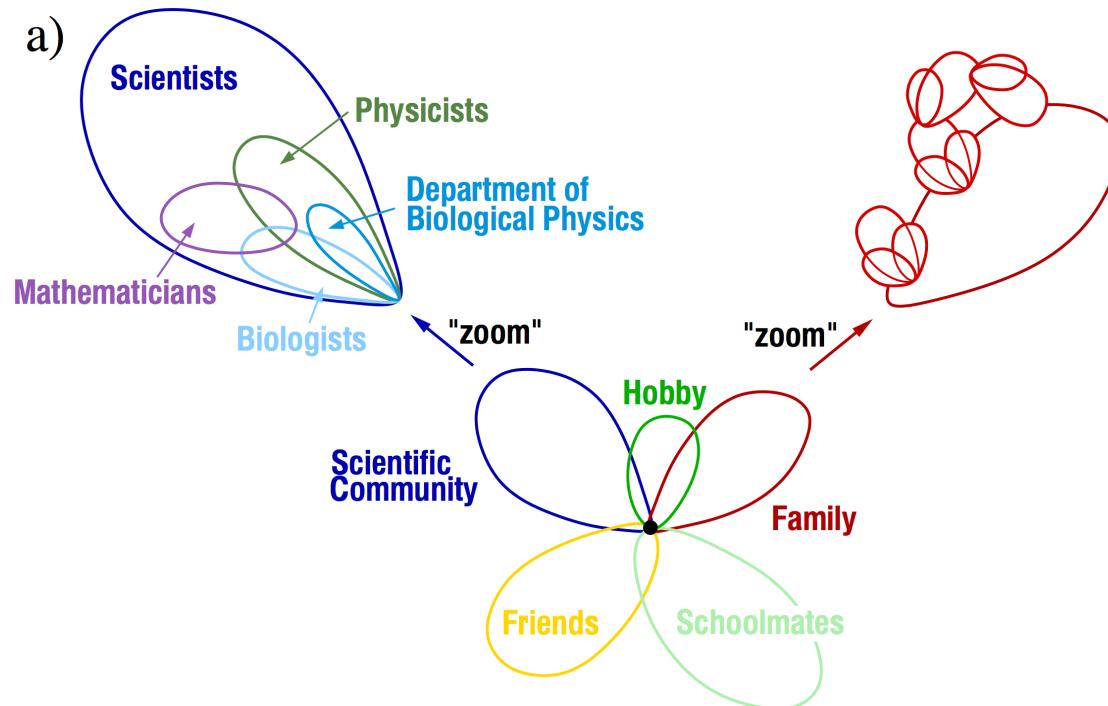
Louvain method: Finding communities in large networks

<https://sites.google.com/site/findcommunities/> for the code.

Overlapping Communities

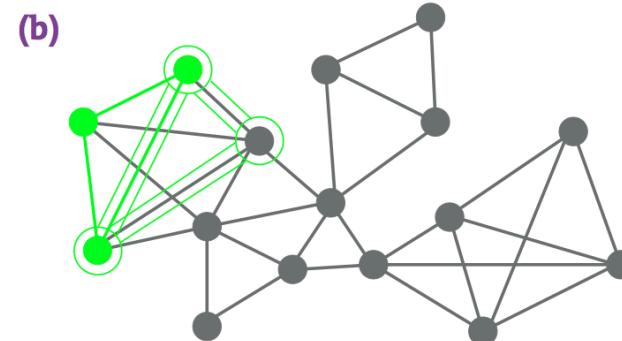
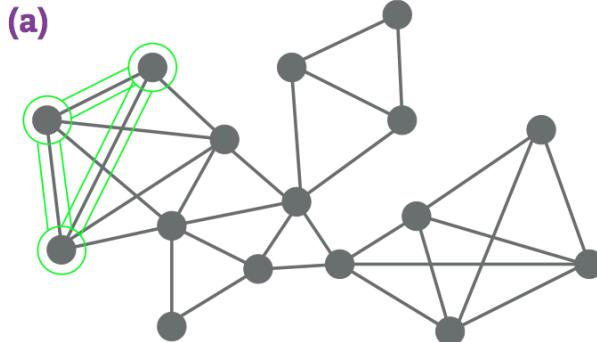
Section 5

Overlapping Communities

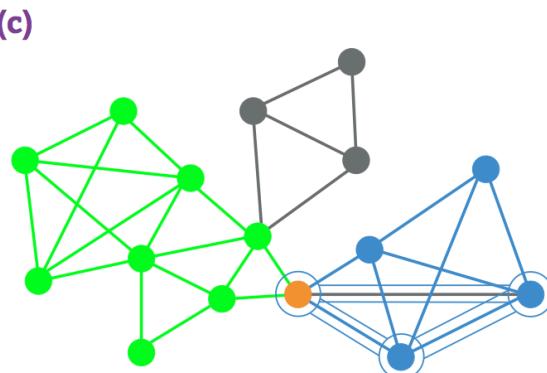


Section 5

Clique Percolation (CFinder)

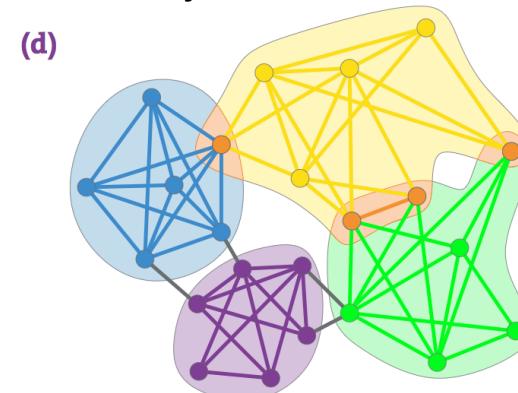


Start with a k -clique (complete subgraphs of k nodes), a 3-clique for example



A k -clique community is the largest connected subgraph obtained by the union of all adjacent k -cliques

Start “rolling” the clique over adjacent cliques. Two k -cliques are considered adjacent if they share $k-1$ nodes



Other k -cliques that can not be reached from a particular clique correspond to other clique-communities

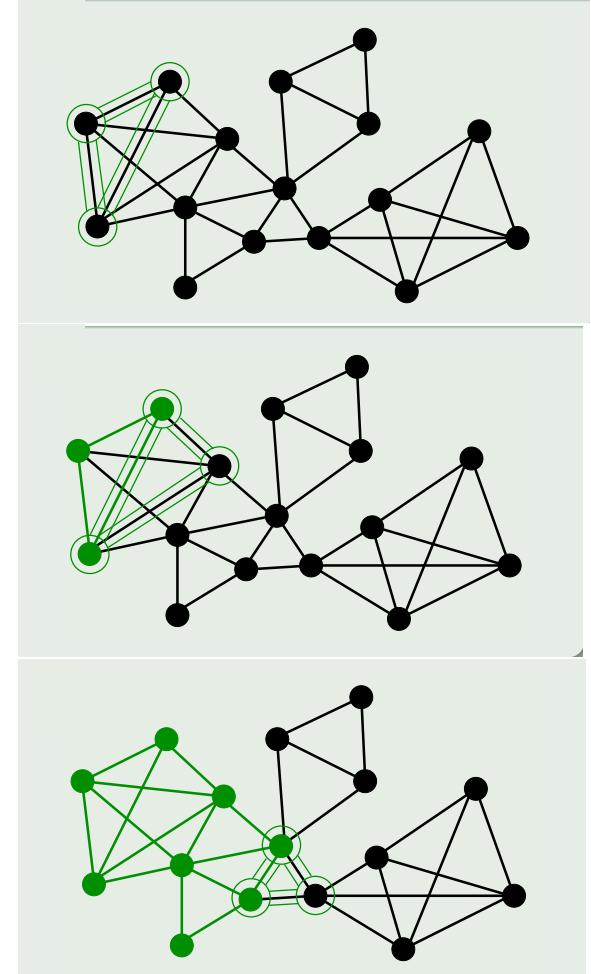
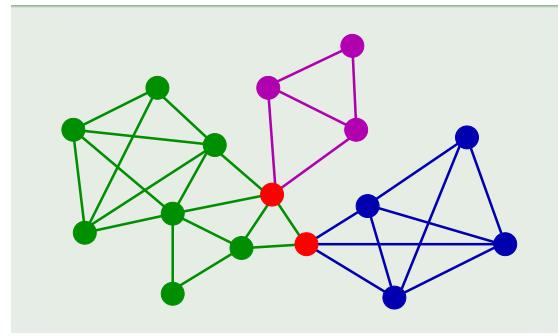
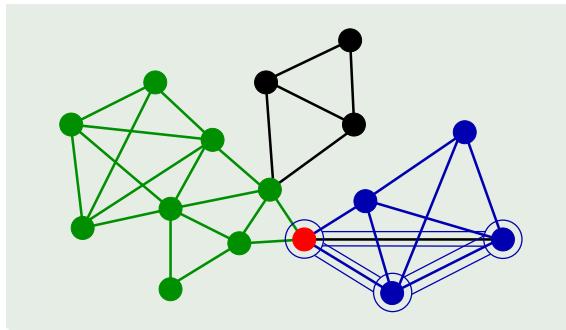
G. Palla et al., *Nature* 435 (2005).

A.-L. Barabási, *Network Science: Communities*.

Section 6

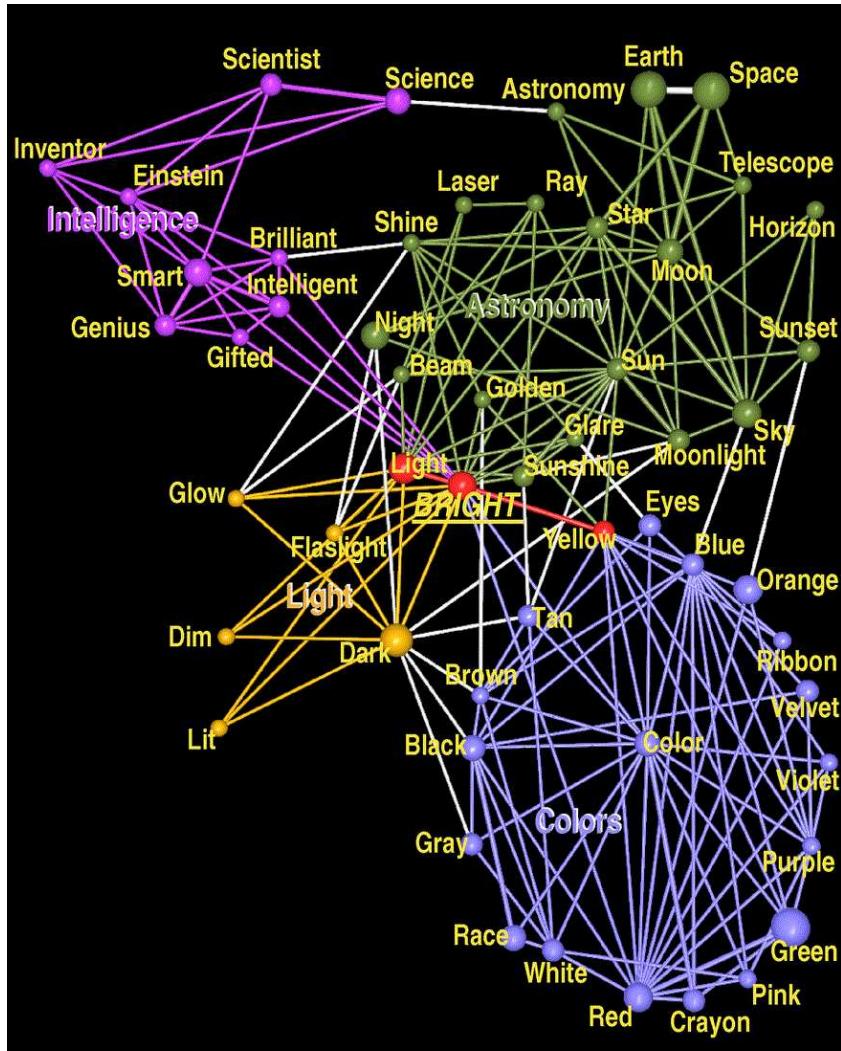
Clique Percolation

- Other k -cliques that can not be reached from a particular k -clique correspond to other k -clique-communities



Section 5

Overlapping Communities



Bright:

- community containing light-related words (*glow* or *dark*);
 - community capturing different colors (*yellow*, *brown*)
 - community consisting of astronomical terms (*sun*, *ray*).
 - community linked to intelligence (*gifted*, *brilliant*).

Notice that if a random network is sufficiently dense, there are cliques of varying order.

Notice that if a random network is sufficiently dense, there are cliques of varying order.

A k -clique community emerges in a random graph only if the connection probability exceeds the threshold:

$$k = 2 \quad p_c(k) \sim 1/N$$

$$k = 3 \quad p_c(k) = 1/\sqrt{2N}$$

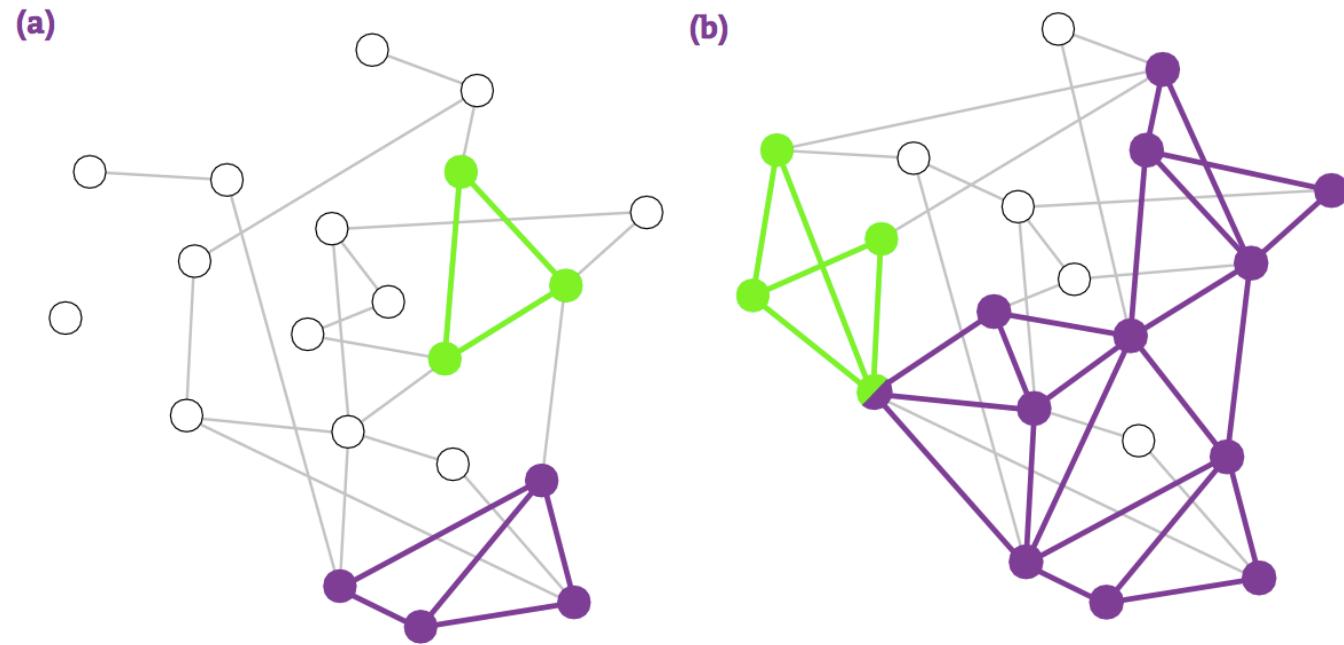
$$p_c(k) = \frac{1}{[(k-1)N]^{1/(k-1)}}$$

Section 5

Could CP communities emerge by chance?

$$k = 3 \quad p_c(k) = 1/\sqrt{2N}$$

$$N=20 \quad p_c=0.16$$



Random networks with

$$p=0.13 (< p_c)$$

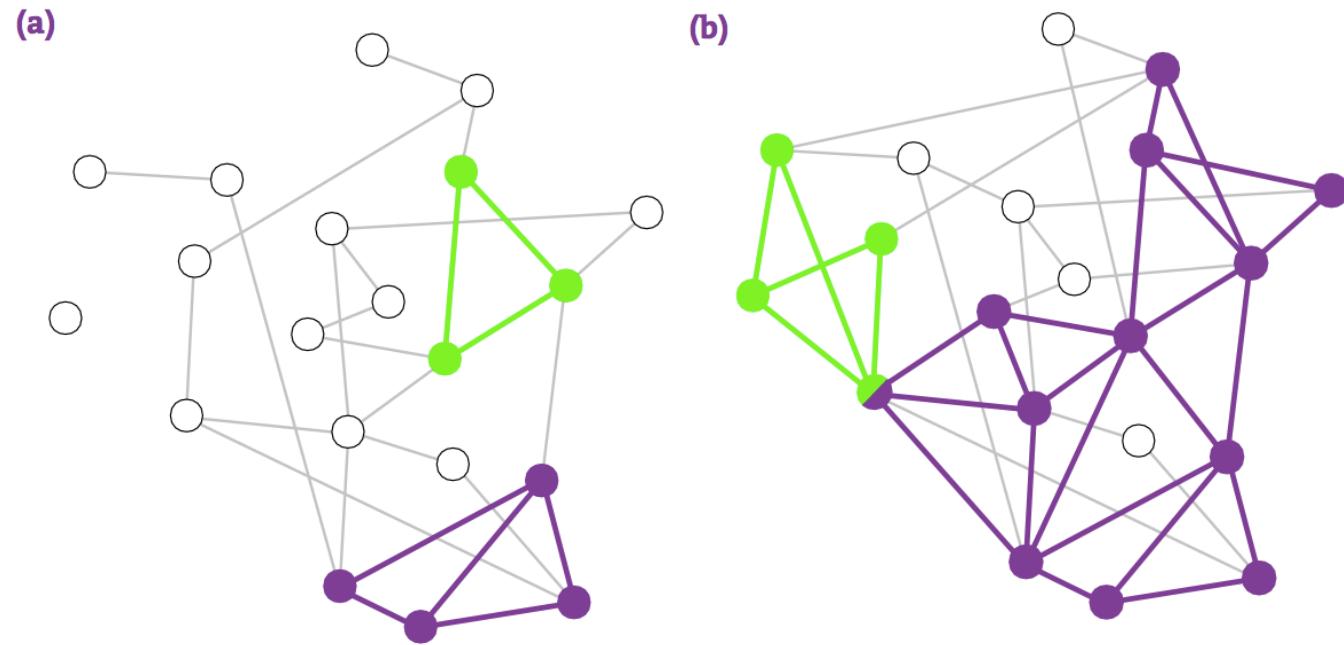
$$p=0.22 (> p_c)$$

Section 5

Could CP communities emerge by chance?

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$$N=20 \quad p_c=0.16$$



Random networks with

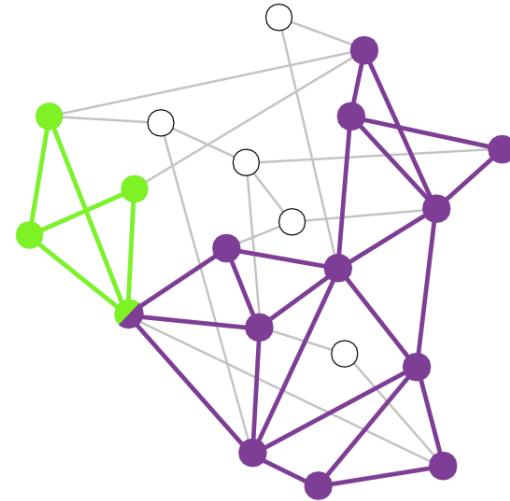
$$p=0.13 (< p_c)$$

$$p=0.22 (> p_c)$$

**Compare your Cfinder output with that you obtain
in a random graph with same N and p !**

I. Derényi et al., PRL 94 (2005).

A.-L. Barabási, *Network Science: Communities*.



Computational complexity:

- Finding maximal cliques require exponential time.
- However the algorithm has to find only k -cliques, which can be done in polynomial time

Section 5

Online Resources (CFinder)

→ The **CFinder** software package that implements the Clique Percolation Method can be downloaded at

www.cfinder.org

The screenshot shows the homepage of the CFinder website. At the top left, it says "CURRENT VERSION: CFinder 2.0.6". Below that is a red button with "Requires Java >>". The main title "Clusters & Communities" is in bold, with the subtitle "overlapping dense groups in networks" underneath. A navigation bar below the title includes "Download CFinder", "Manual", "Network Data", "Publications", and "WebCFinder". On the left, there's a sidebar with links for "Home", "Download Software", "Network Data", "Publications", "Support FAQ", "Manual", "Contact us", "People", and "Links". The main content area contains text about CFinder's purpose and its application to social groups, along with a "Download" link for "Software | Manual | Publications". Below this is a paragraph about clusters. To the right are two network visualizations: one showing nodes like "Scientist", "Science", "Astronomy", "Earth", "Space", "Laser", "Ray", "Star", "Telescope", "Horizon", "Sun", "Moon", "Night", "Galaxy", "Astronomer", "Brilliant", "Gifted", "Smart", "Genius", "Intelligence", "Inventor", and "Einstein"; and another smaller network graph.

→ **NetworkX**

Communities

K-Clique

`k_clique_communities (G, k[, cliques])`

Find k-clique communities in graph using the percolation method.

- Nodes tend to belong to multiple communities
- Links tend to be specific, capturing the nature of the relationship between two nodes.

Social networks, a link may indicate:

- they are in the same family
- they work together
- they share a hobby.

Biological networks:

each interaction of a protein is responsible for a different function, uniquely defining the protein's role in the cell

→ Define a hierarchical algorithm based on similarity of links

1. Define link similarity

$$S(e_{ik}, e_{jk}) = \frac{|n_+(i) \cap n_+(j)|}{|n_+(i) \cup n_+(j)|}$$

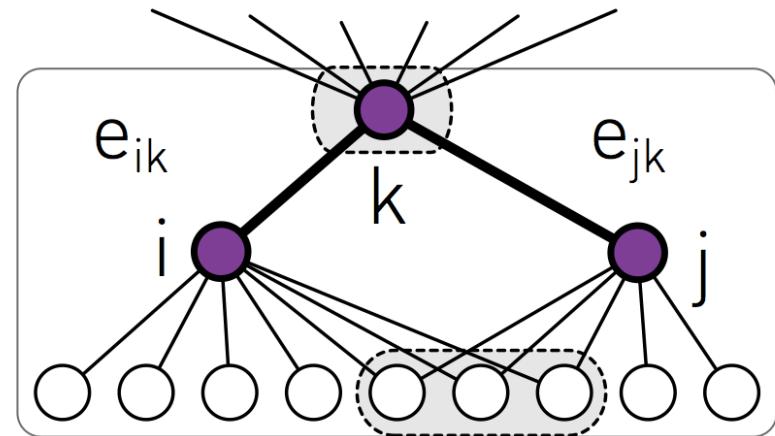
$n_+(i)$: the list of the neighbors of node i , including itself.

S measures the relative number of common neighbors i and j have.

$$\begin{aligned} |n_+(i) \cap n_+(j)| &= 4 \\ |n_+(i) \cup n_+(j)| &= 12 \end{aligned}$$

$$S(e_{ik}, e_{jk}) = \frac{1}{3}$$

(a)



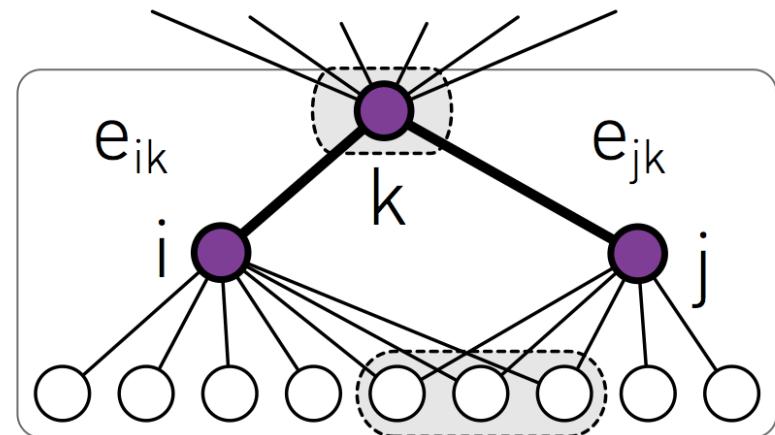
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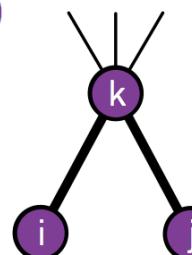
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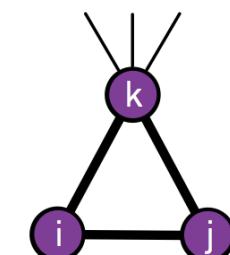
(a)



(b)



(c)

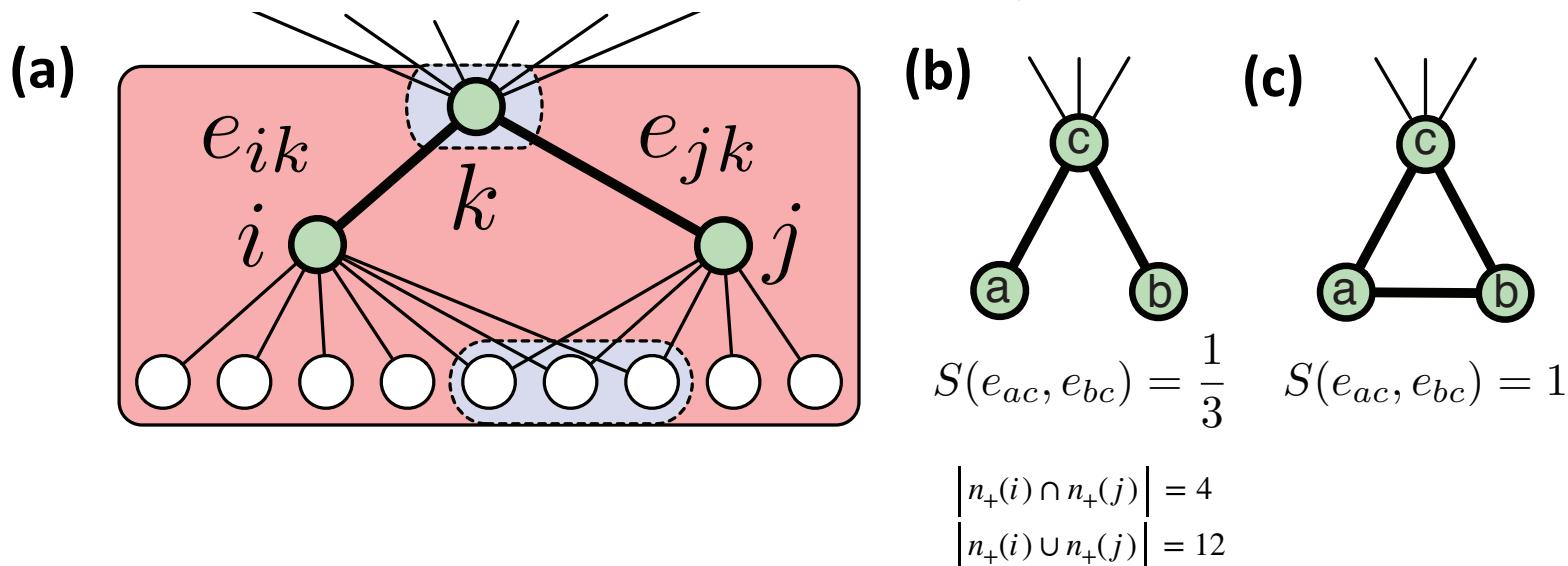


$$S(e_{ik}, e_{jk}) = \frac{1}{3} \quad S(e_{ik}, e_{jk}) = 1$$

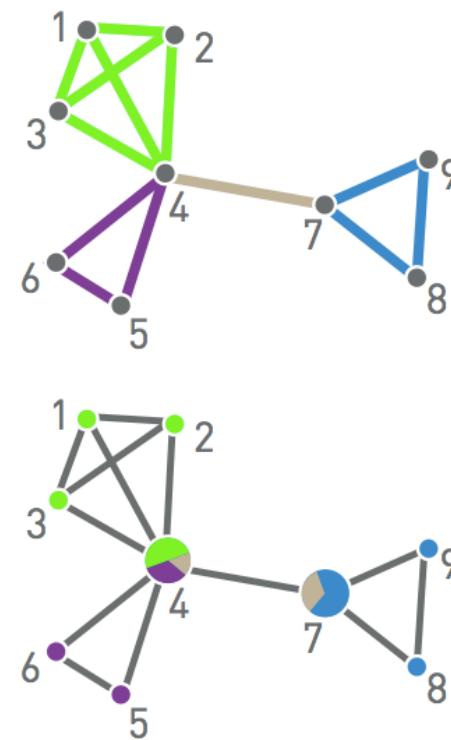
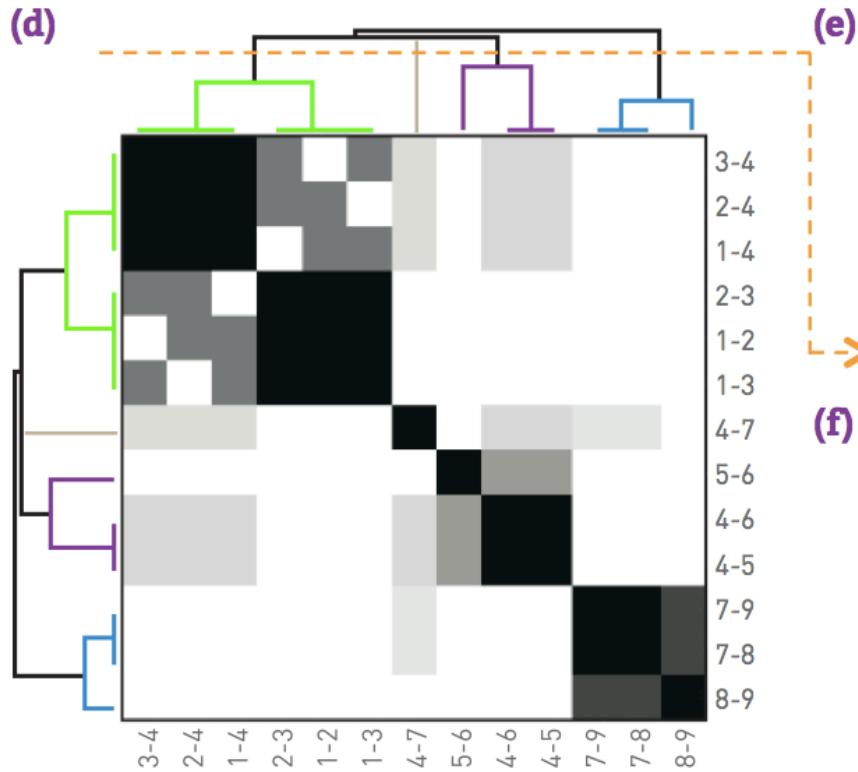
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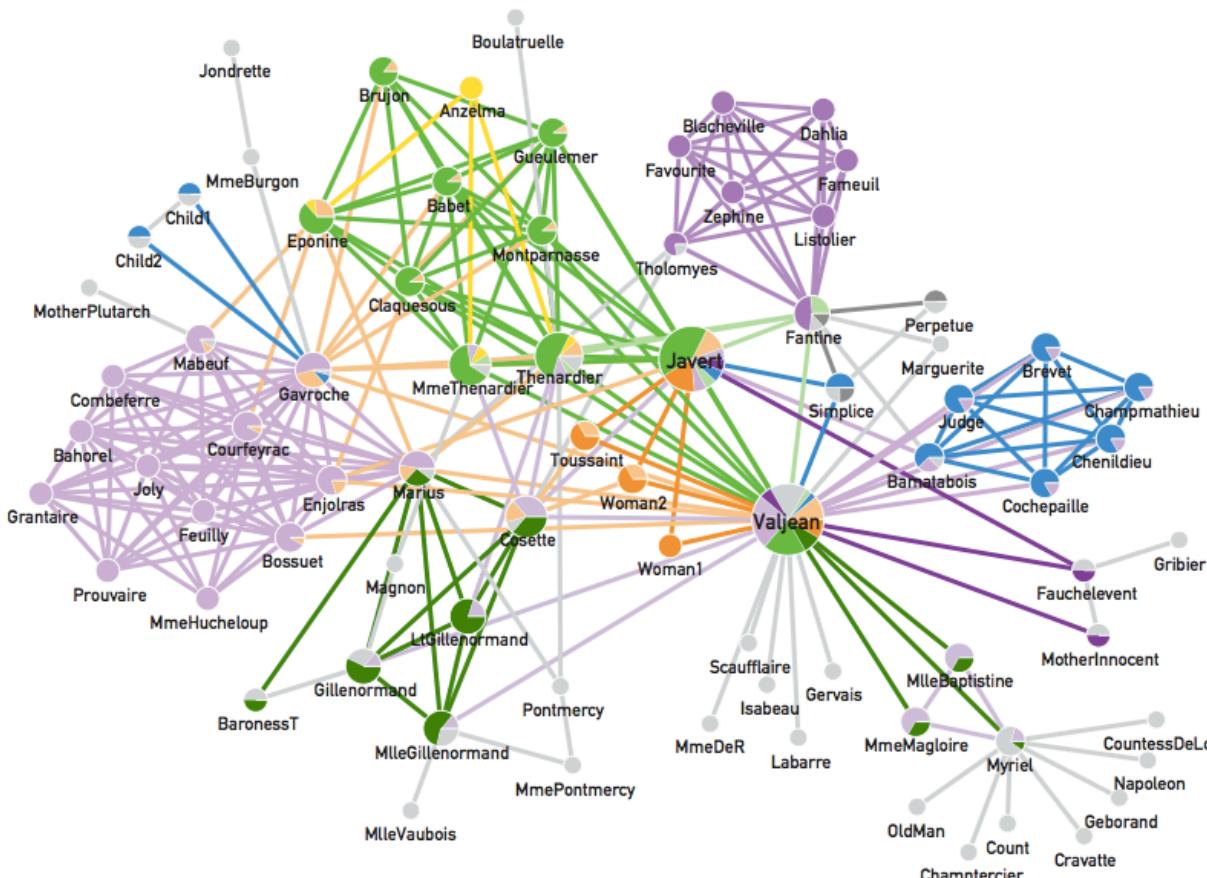


2. Apply hierarchical clustering (agglomerative, single linkage)



Section 5

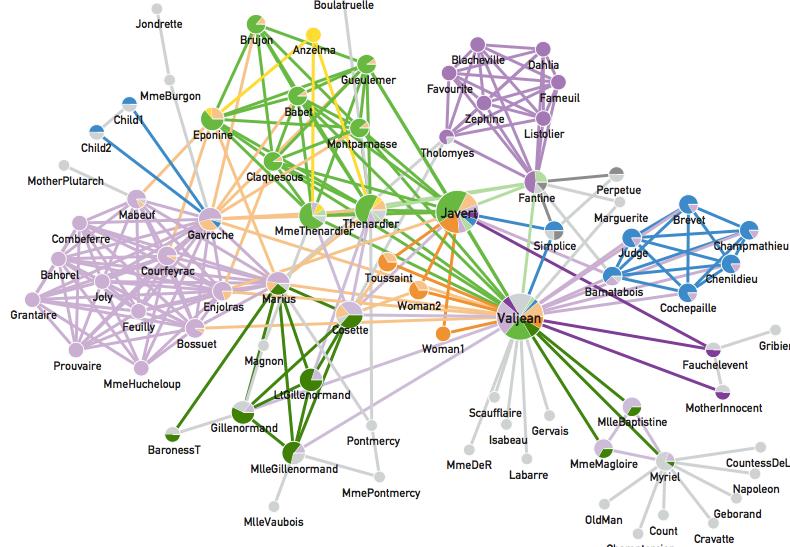
Link Clustering



The network of characters in Victor Hugo's 1862 novel *Les Misérables*. Two characters are connected if they interact directly with each other in the story. The link colors indicate the clusters, grey nodes corresponding to single-link clusters. Each node is depicted as a pie-chart, illustrating its membership in multiple communities. Not surprisingly, the main character, Jean Valjean, has the most diverse community membership

Section 5

Link Clustering



Computational complexity:

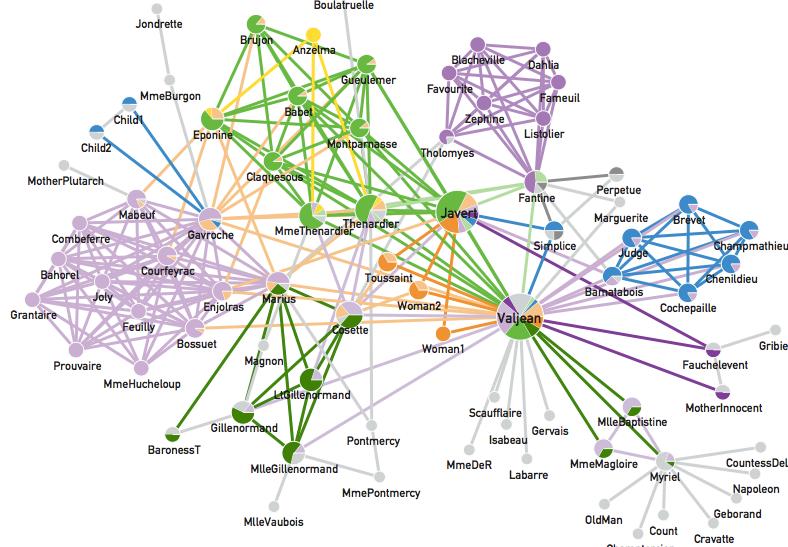
- Step 1: Comparison between two links requires $\max(k_1, k_2)$ steps. For scale free networks the step has complexity
- Step 2: hierarchical clustering requires $O(L^2)$

Ahn, Bragow and Lehmann, *Nature* 466 (2010).

A.-L. Barabási, *Network Science: Communities*.

Section 5

Link Clustering

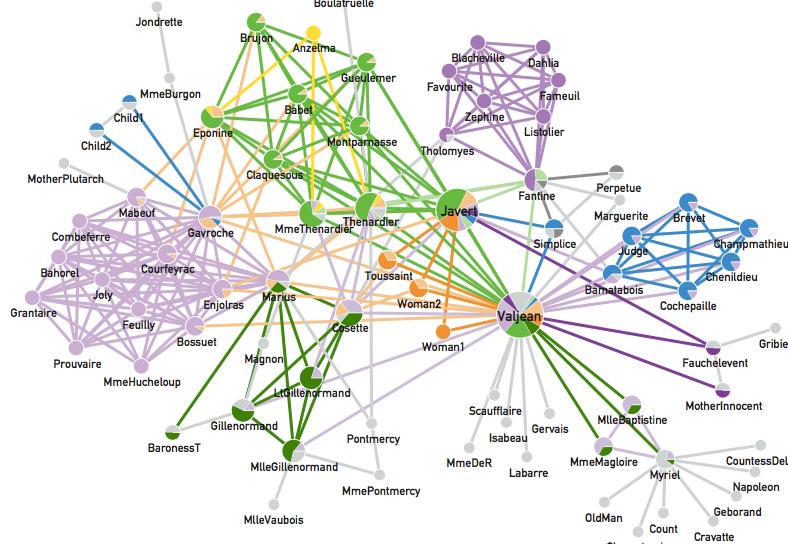


Computational complexity:

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Section 5

Link Clustering



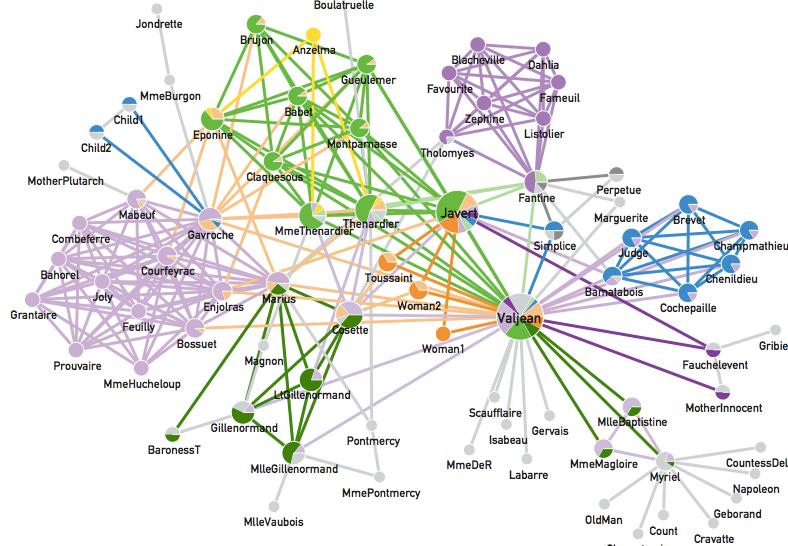
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for sparse networks

Section 5

Link Clustering



Computational complexity:

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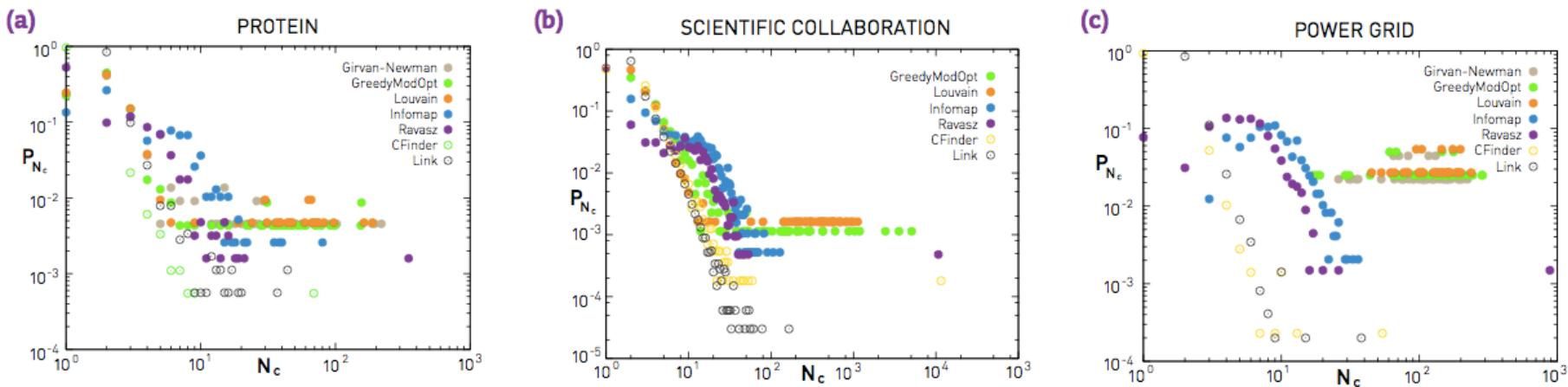
for sparse networks $\rightarrow O(N^2)$

Ahn, Bragow and Lehmann, *Nature* 466 (2010).

A.-L. Barabási, *Network Science: Communities*.

Characterizing Communities

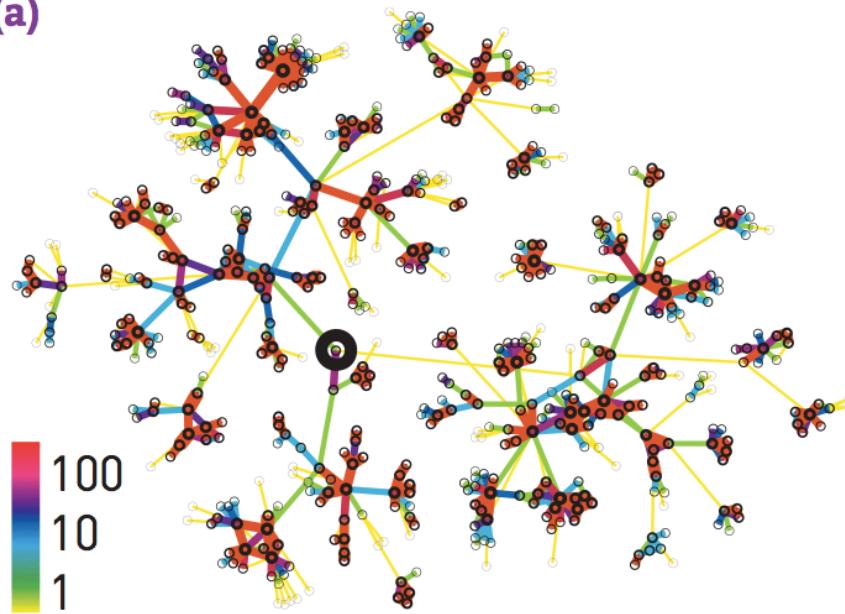
Community size is distributed according to a power-law



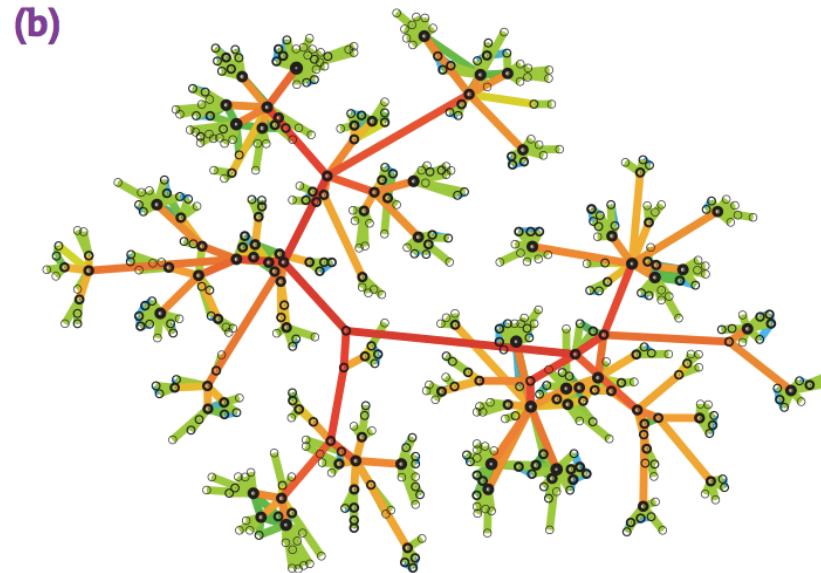
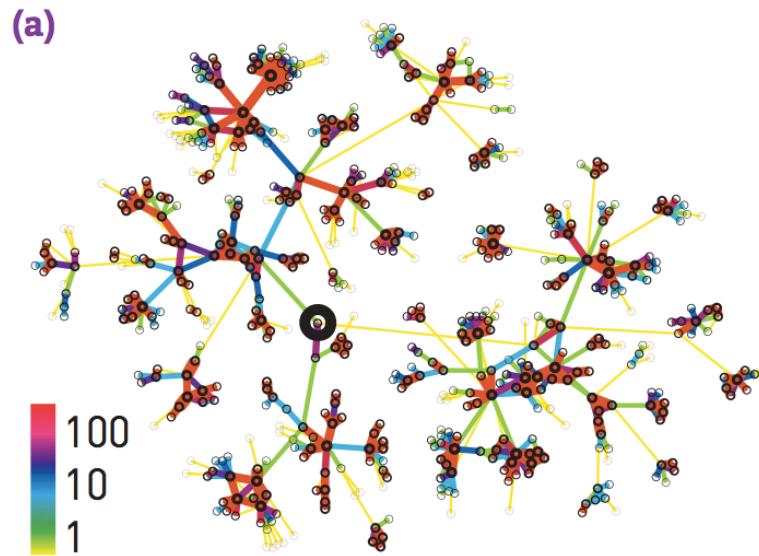
Not a subproduct of algorithms

Weights can help identifying communities

(a)



Weights can help identifying communities

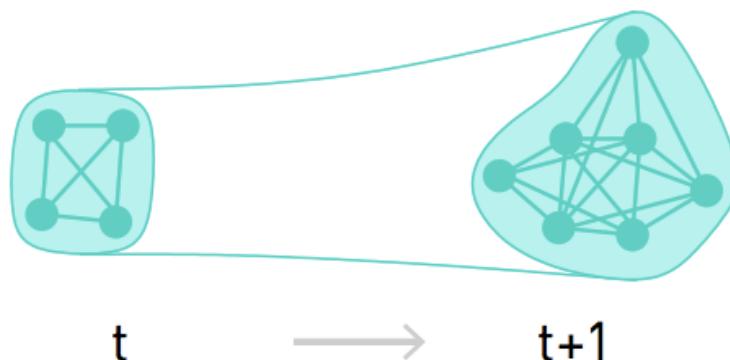


Caution!

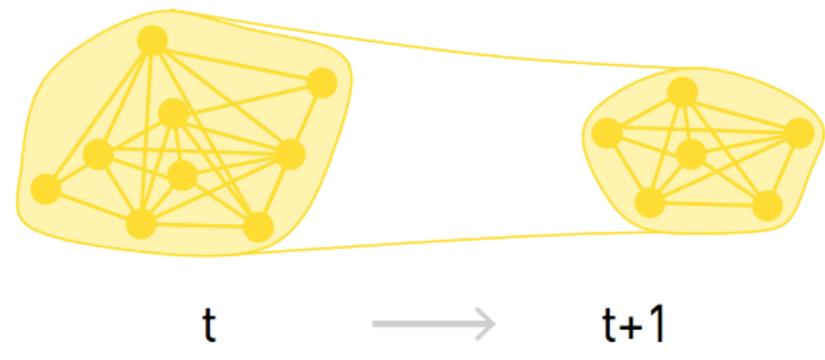
- In social networks (a), the weak tie hypothesis says that communities are connected by links with smaller weight
- In transport systems, high betweenness links (correlates with weight, (b)) connect different communities

Community evolution

GROWTH



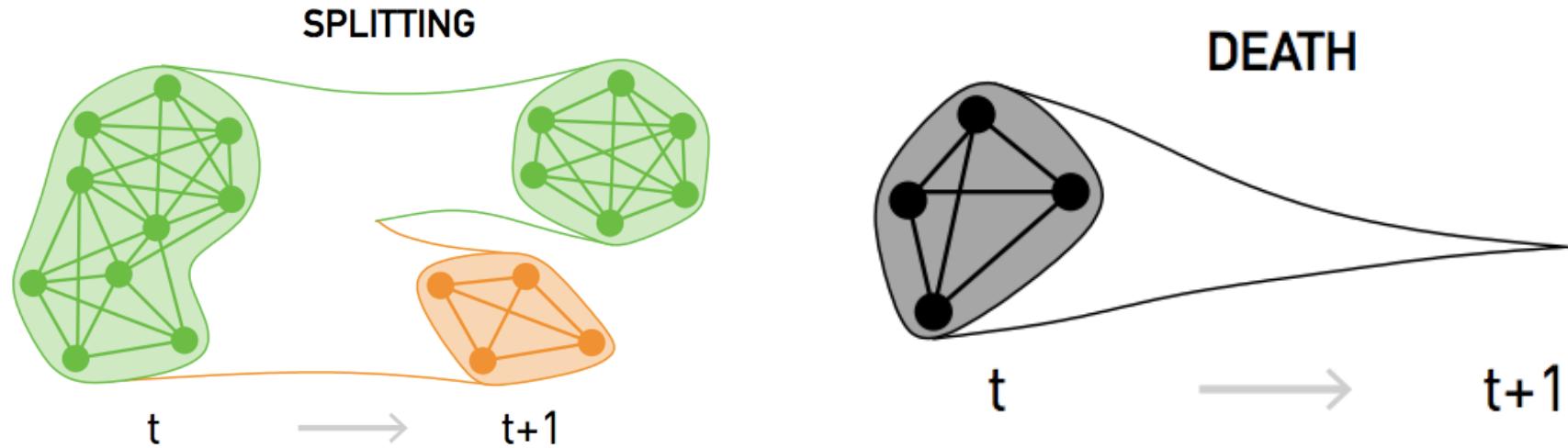
CONTRACTION



Probability that a node joins a community grows with the # of links the node has with the community

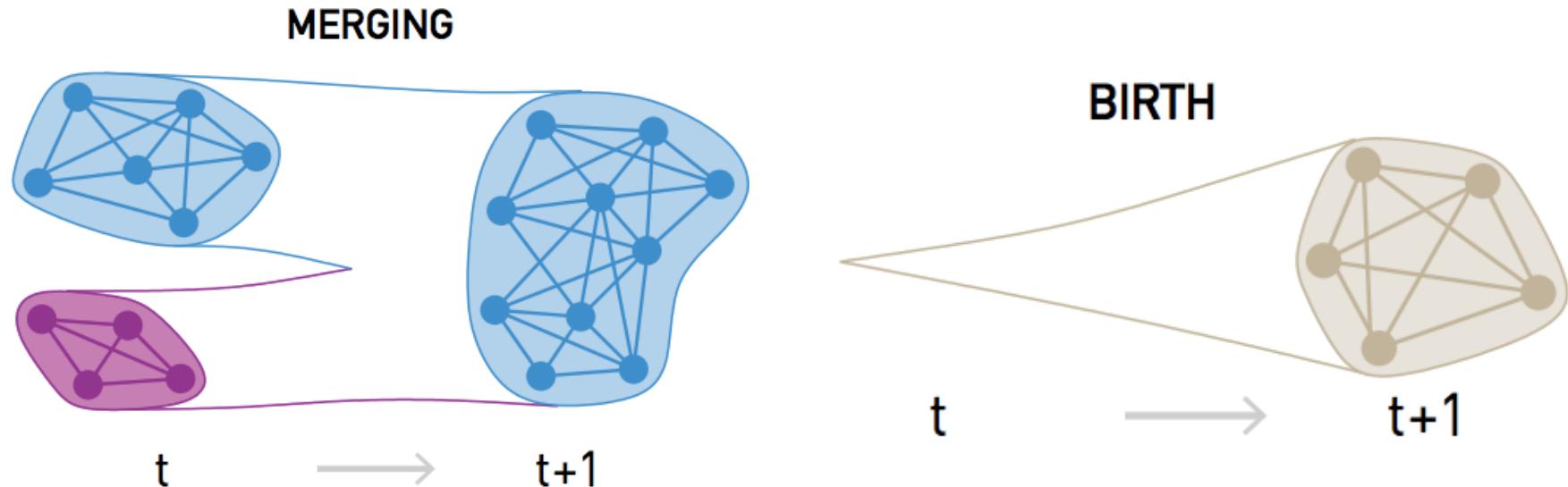
Node with fewer links within the community are more likely to leave than those with more links

Community evolution



Probability that a community disintegrates increases with the aggregate link weights to nodes outside the community

Community evolution



Older communities tend to be larger

Newman-Girvan (NG) Benchmark

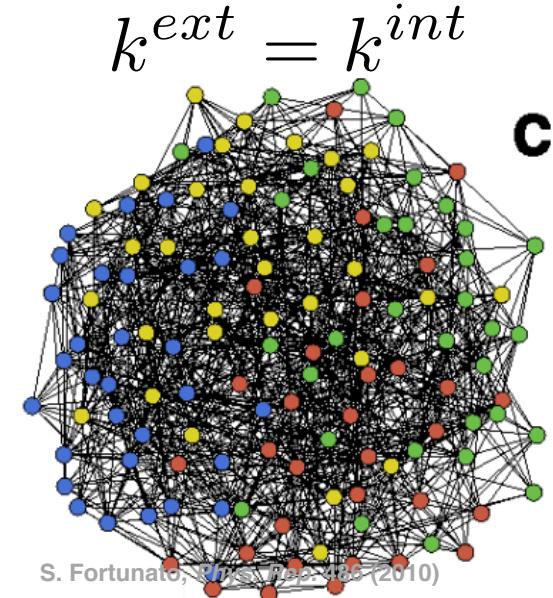
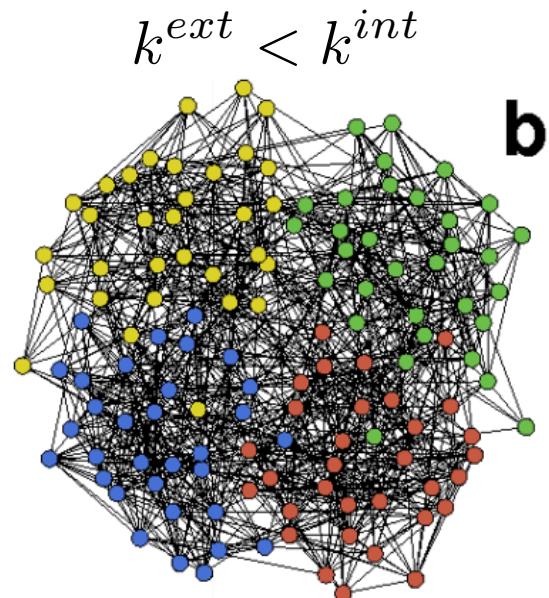
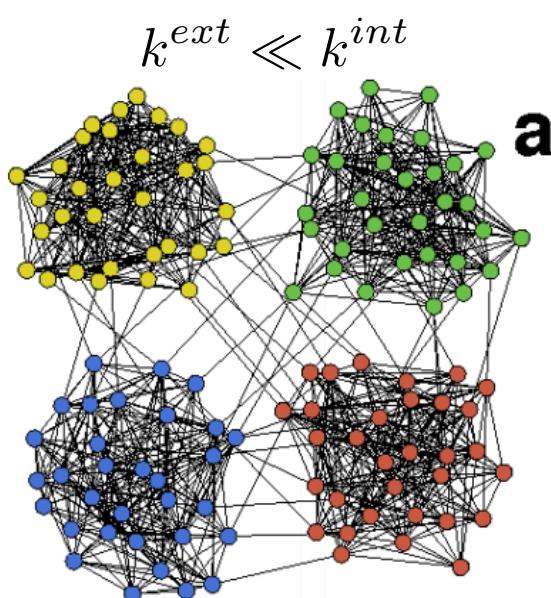
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Newman-Girvan (NG) Benchmark

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$$k^{ext}$$
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Measuring Accuracy

Information theory approach: if two partitions are similar, one needs very little information to infer one partition given the other. We can use the mutual information

$$I(\{C_1\}, \{C_2\}) = \sum_{C_1} \sum_{C_2} p(C_1, C_2) \log \frac{p(C_1, C_2)}{p(C_1)p(C_2)}$$

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Joint probability that a randomly chosen node belongs to community C_1 in the first partition and C_2 in the second

$$p(C_1, C_2) = \frac{\text{how many nodes that are in } C_1 \text{ are also in } C_2}{\text{sum over all possible pairs } C_1 \text{ and } C_2} = \frac{N_{C_1 C_2}}{\sum_{C_1, C_2} N_{C_1 C_2}}$$

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Probability that a randomly chosen node belongs to community C_1

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Measuring Accuracy

The mutual information is not ideal as a similarity measure as it is: in fact, given a partition C , all partitions derived from C by further partitioning its clusters would all have the same mutual information with C , even though they could be very different from each other. In this case the mutual information would simply equal the entropy $H(X)$, because the conditional entropy would be systematically zero. Also the measure is not normalized.

$$I_n (\{C_1\}, \{C_2\}) = \frac{2I (\{C_1\}, \{C_2\})}{H (\{C_1\}) + H (\{C_2\})}$$

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Shannon entropy

$$H (\{C_1\}) = \sum_{C_1} p (C_1) \log p (C_1)$$

Measuring Accuracy

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→ $I_n = 0$ If the communities are independent

Section 7

Testing Communities

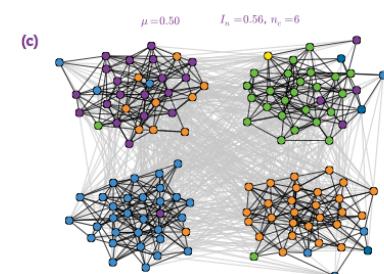
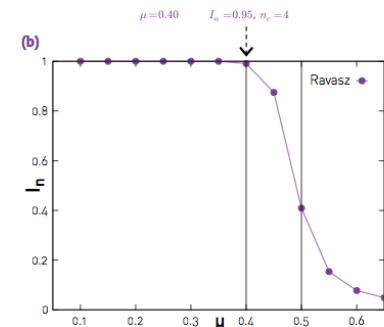
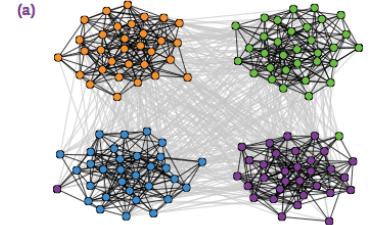
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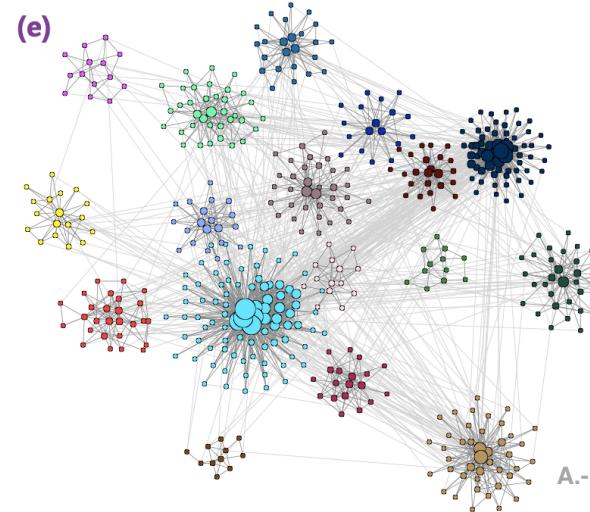
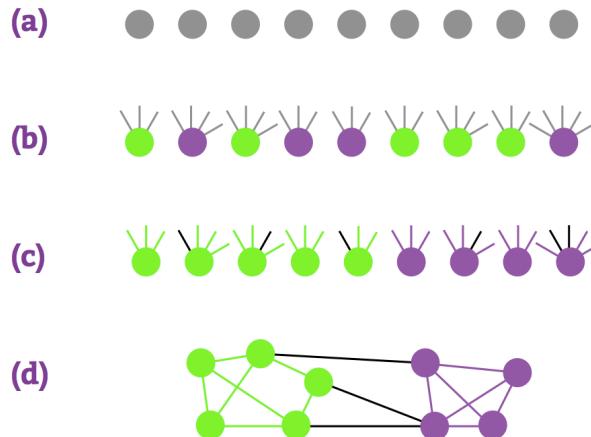
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Lancichinetti-Fortunato-Radicchi (LFR) Benchmark

Lancichinetti-Fortunato-Radicchi (LFR) Benchmark

- N nodes in N_C communities, taken from $P_{Nc} \sim N_C^{-\xi}$
- Each node is assigned a degree k from $P_k \sim k^{-r}$
- Each node i is assigned to a community, and receives an internal degree $(1-\mu)k_i$ and an external degree μk_i .
- Connect randomly nodes, according to the constraints above, until there are no more free stubs



Section 7

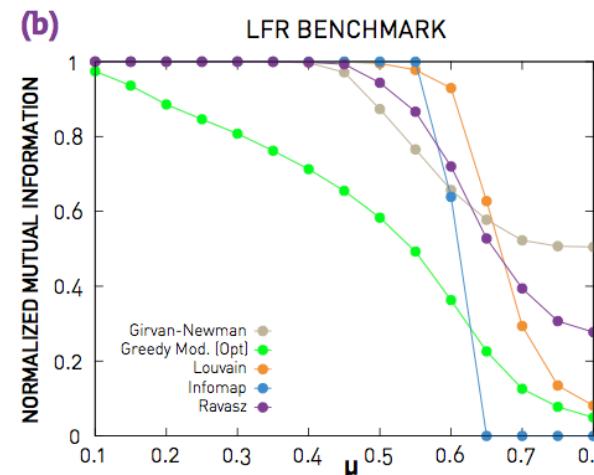
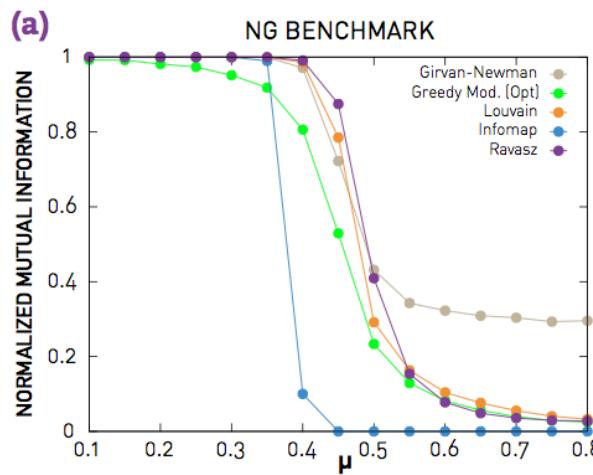
Testing Communities

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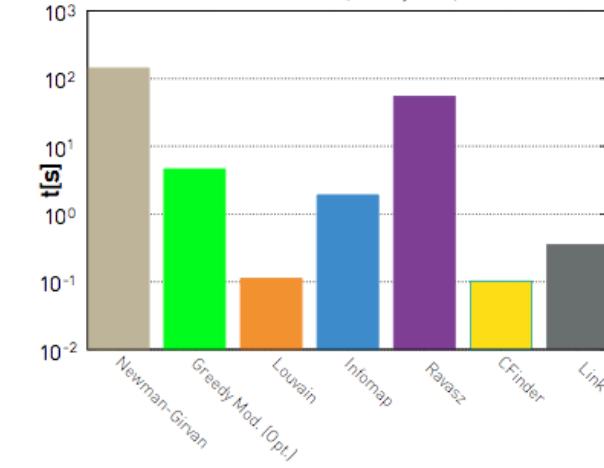
Section 7

Testing Communities

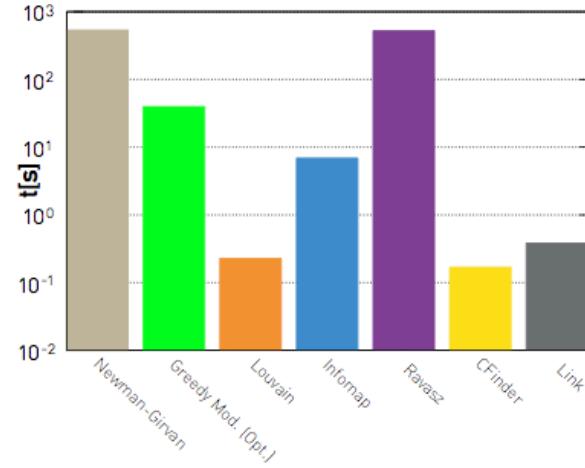
Speed

NAME	NATURE	COMP.
Ravasz	Hierarchical Agglomerative	$O(N^3)$
Girvan-Newman	Hierarchical Divisive	$O(N^3)$
Greedy Modularity	Modularity Optimization	$O(N^3)$
Greedy Modularity	Modularity Optimization	$O(N \log^2 N)$
Louvain	Modularity Optimization	$O(N \log N)$
Infomap	Flow Optimization	$O(N \log N)$
Clique Percolation	Overlapping Communities	$Exp(N)$
Link Clustering CFinder	Hierarchical Agglomerative; Overlapping Communities	$O(N^3)$

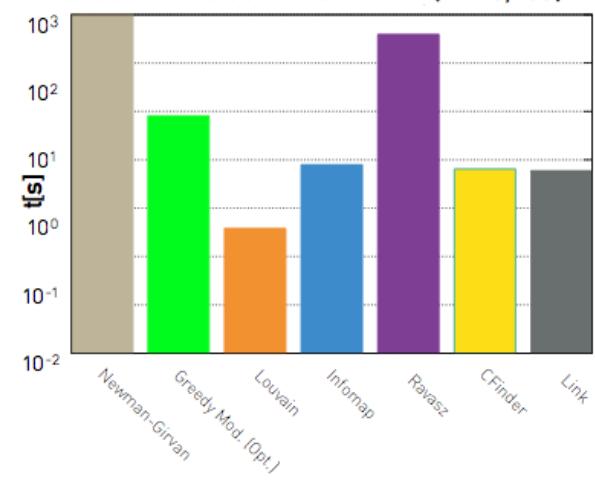
PROTEIN (N=2,018)



POWER GRID (N=4,941)

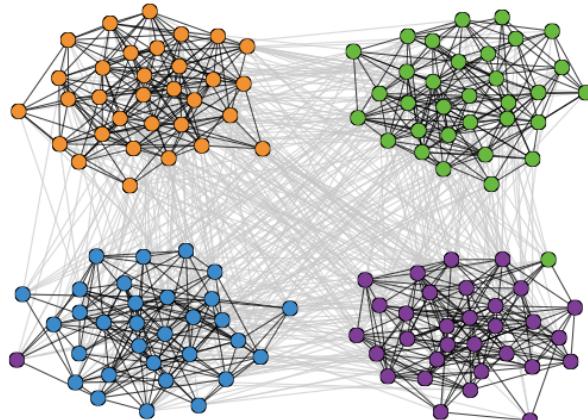


SCIENTIFIC COLLABORATION (N=23,133)

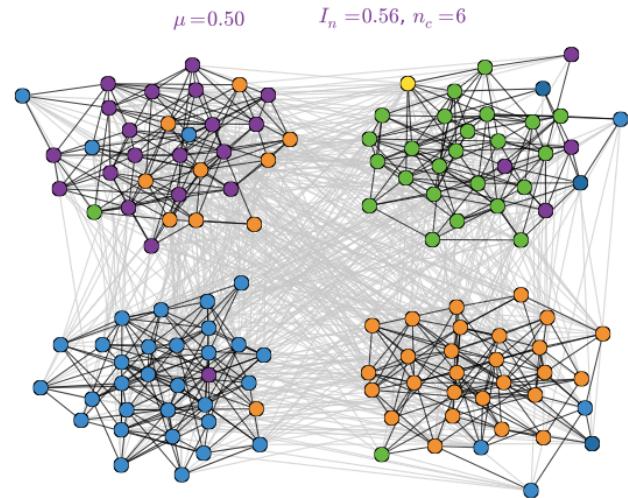


Ravasz algorithm on NG Benchmark

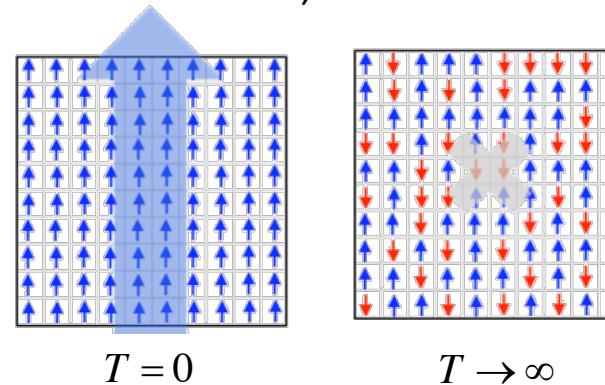
(a)

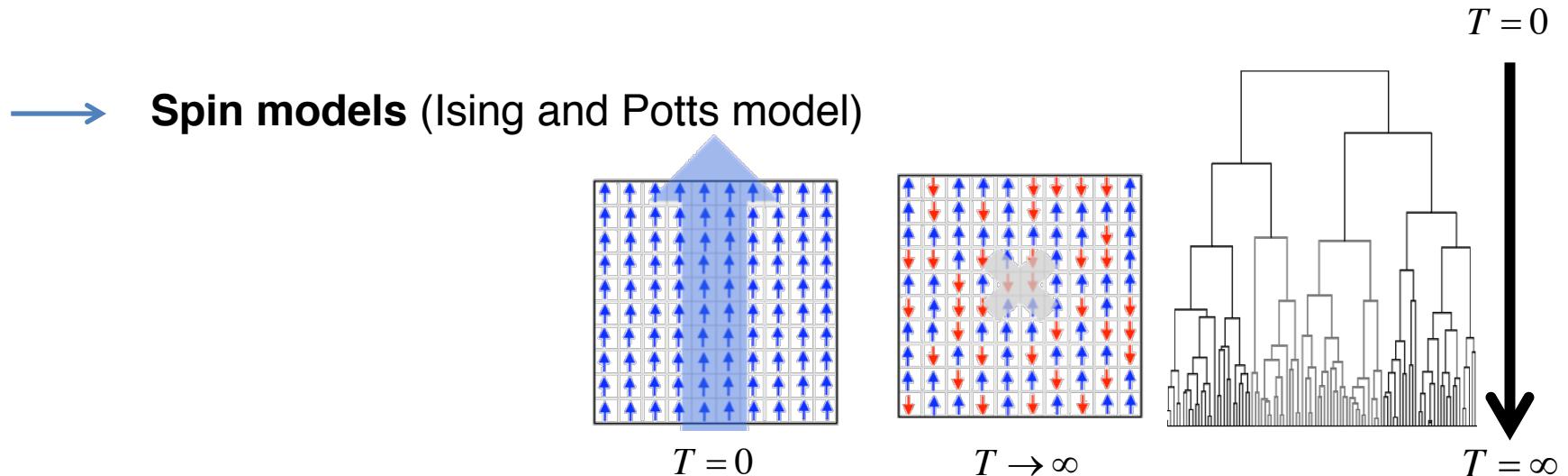
 $\mu = 0.40$ $I_n = 0.95, n_c = 4$

(c)

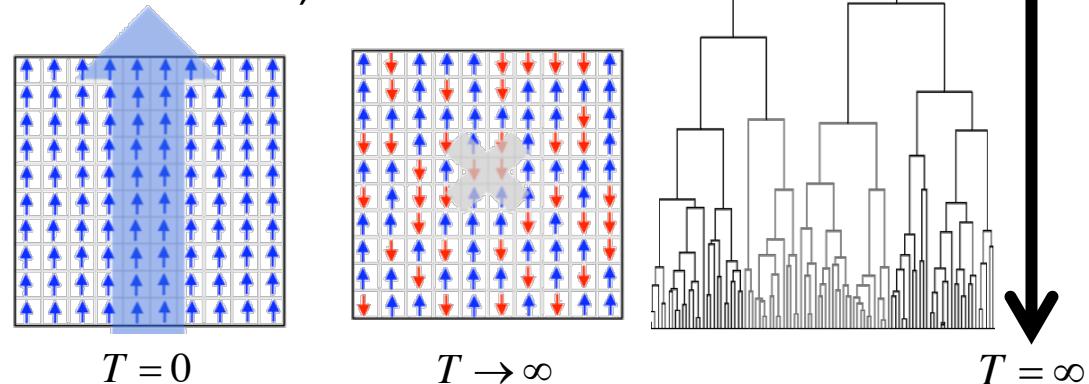


→ Spin models (Ising and Potts model)

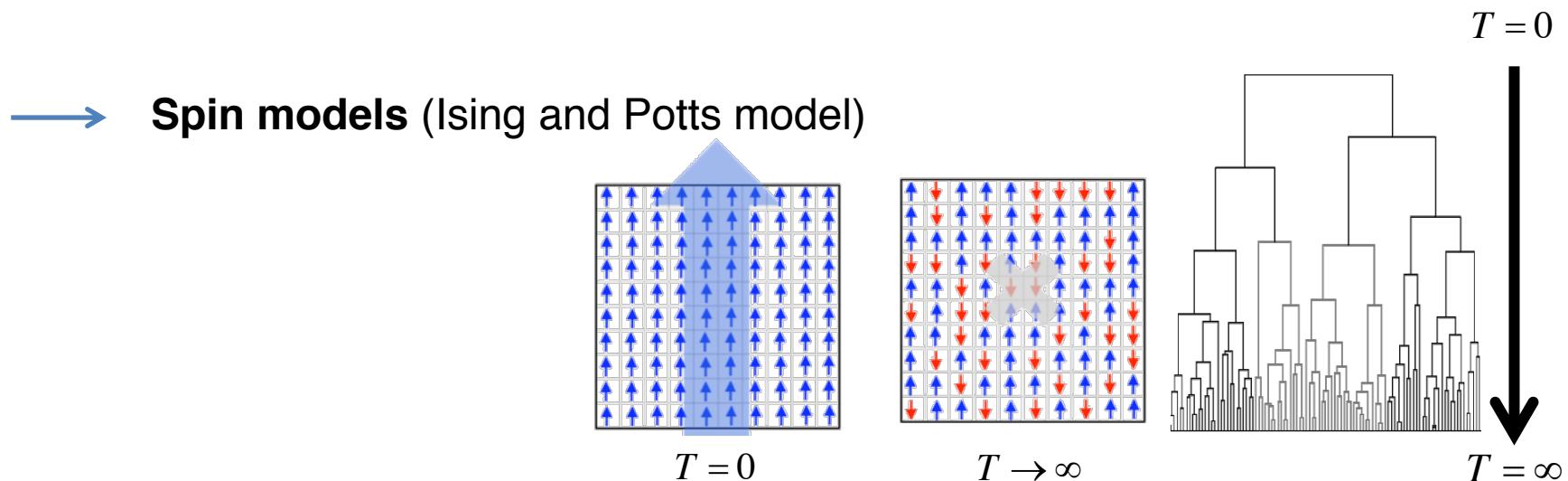




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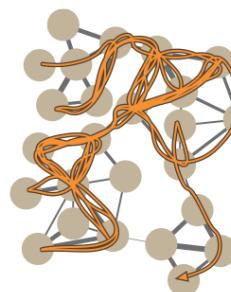


→ **Synchronization**. Each node is an oscillator (for example, Kuramoto). Nodes that are in the same community synchronize with each other sooner



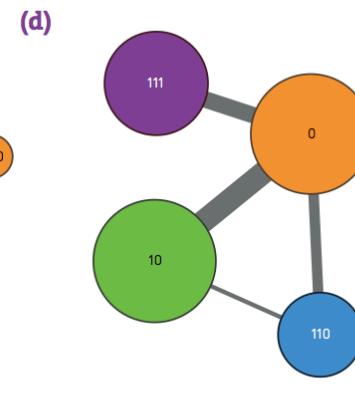
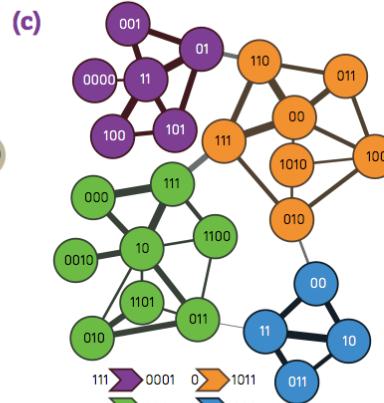
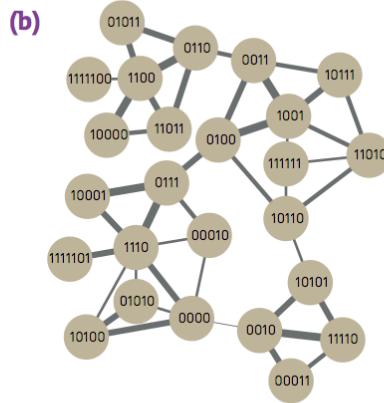
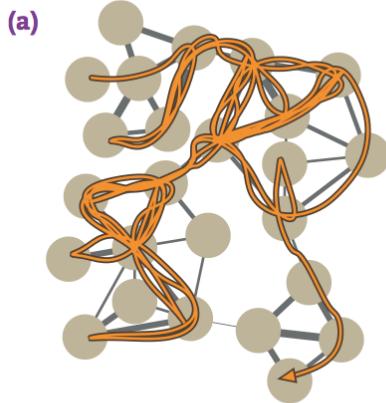
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→ **Random Walks** (Infomap)



Section 6

Infomap



```

1111100 1100 0110 11011 10000 11011 0110 0011 10111 1001 0011
1001 0100 0111 10001 1110 0111 10001 0111 1110 0000 1110 10001
0111 1110 0111 1110 111101 1110 0000 10100 0000 1110 10001 0111
0111 1110 0111 1110 111101 1110 0000 10100 0000 1110 10001 0111
0100 1010 11010 10111 1001 0100 1001 10111 1001 0100 10100
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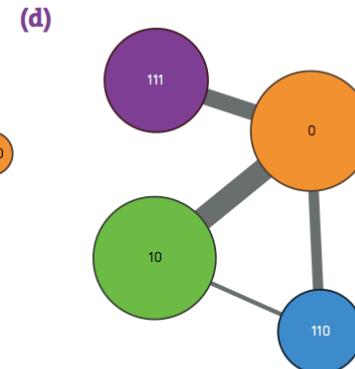
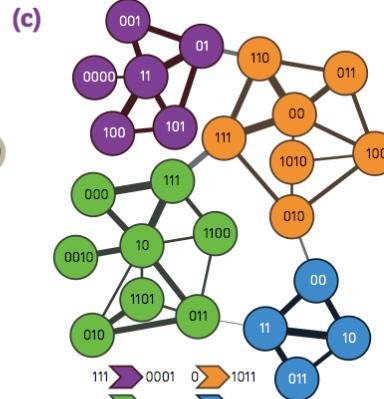
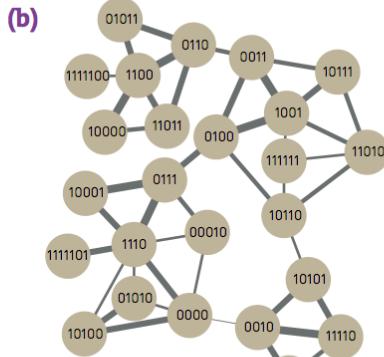
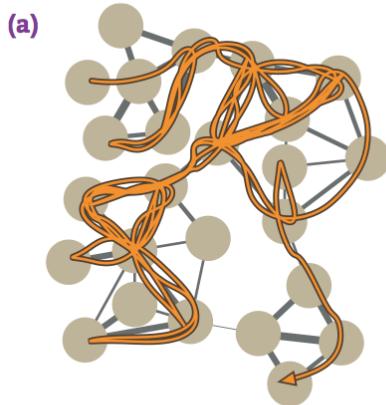
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111 0000 10 110 010 101 100 011 010 111 10 111 10 0010 10 011 010
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 00 111 00 111 00 111
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 1011
10 111 000 10 000 111 0001 0 111 010 101 011 00 111 00 111 00 111 00 111 00 111
  
```

```

111 0000 11 01 101 100 101 01 0001 0 110 011 00 110 00 111 1011 10
111 0000 10 110 010 101 100 011 010 111 10 111 10 0010 10 011 010
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 00 111 00 111 00 111
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 1011
10 111 000 10 000 113 0001 0 111 010 101 011 00 111 00 111 00 111 00 111 00 111
  
```

Section 6

Infomap



```
1111100 1100 0110 11011 10000 11011 0110 0011 10111 1001 0011  
1001 0100 0111 10001 1110 0111 10001 0111 1110 0000 1110 10001  
0111 1110 0111 1110 1111101 1110 0000 10100 0000 1110 10001 0111  
0100 1010 11010 10111 1001 0100 1001 10111 1001 0100 1001 0100  
0011 0100 0011 0110 11011 0110 0011 0100 1001 10111 0011 0100  
0111 10001 11001 1110 1111101 1110 0000 10110 0100 10111 1001 0100  
0011 1110 11011 1111 0110 101 0001 0110 1111 0011 110 1111 1011
```

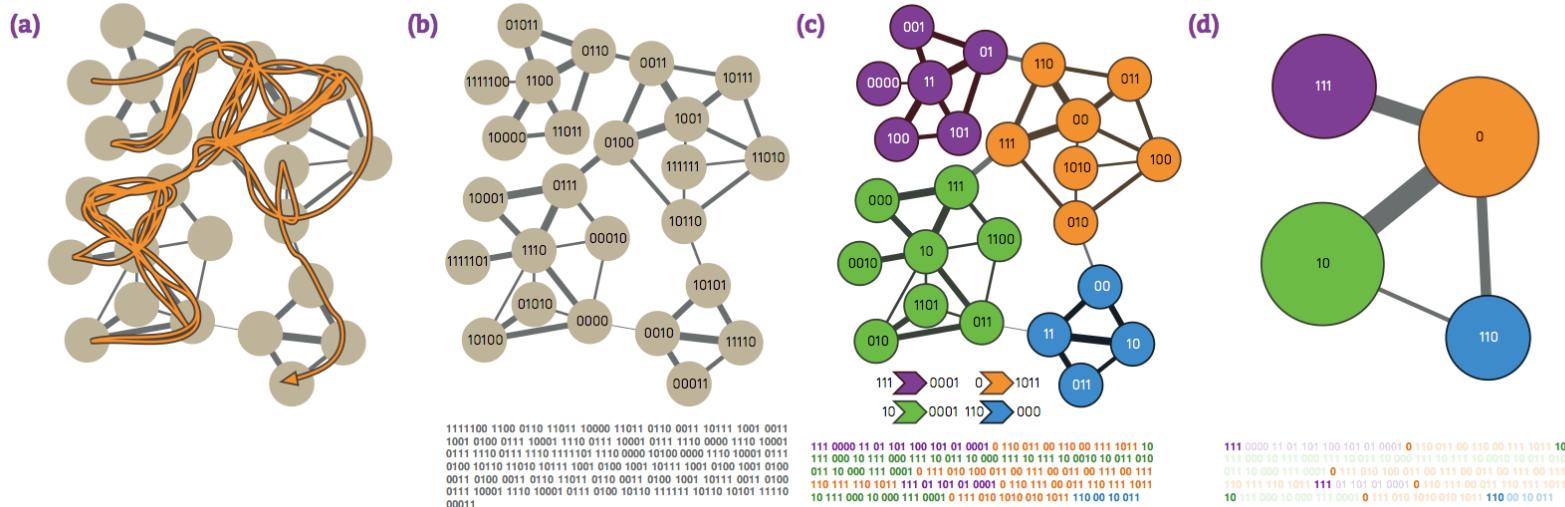
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111 000 10 111 100 110 011 00 110 011 10 0010 111 10 111 10 0010 10 011 010  
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 00 111 00 111 00 111 00 111  
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 111 1011  
10 111 000 10 000 111 0001 0 111 010 1010 010 1011 110 00 10 011
```

```
111 0000 11 01 101 100 101 01 0001 0 110 011 00 110 00 111 1011 10  
111 000 10 111 100 110 011 00 110 011 10 0010 111 10 111 10 0010 10 011 010  
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 00 111 00 111 00 111 00 111  
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 111 1011  
10 111 000 10 000 111 0001 0 111 010 1010 010 1011 110 00 10 011
```

Maximize the map equation: $L(C) = qH(Q) + \sum_{i=1}^{n_c} p^i H(p^i).$

Section 6

infomap



Maximize the map equation:

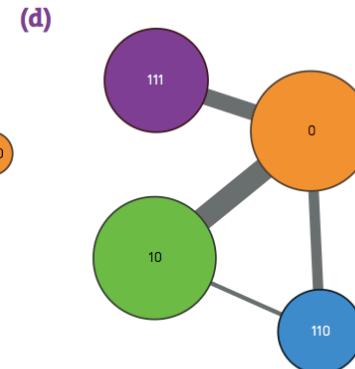
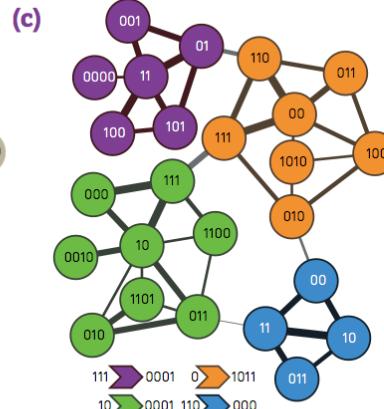
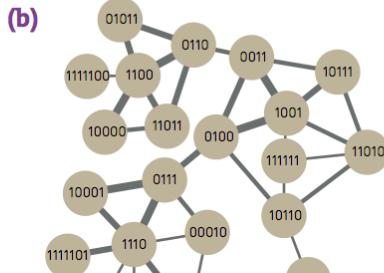
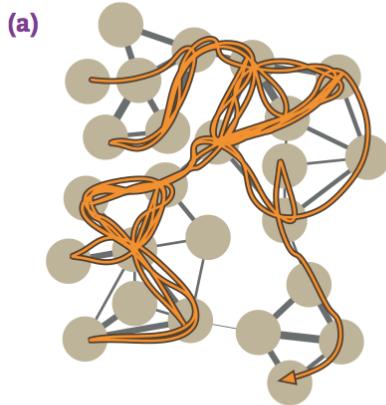
$$L(C) = qH(Q) + \sum_{i=1}^{n_c} p^i H(p^i).$$

Info to describe **between module** movements

Info to describe **within module** movements

Section 6

Infomap



```
1111100 1100 0110 11011 10000 11011 0110 0011 10111 1001 0011  
1001 0100 0111 10001 1110 0111 10001 0111 1110 0000 1110 10001  
0111 1110 0111 1110 1111101 1110 0000 10100 0000 1110 10001 0111  
0100 1010 11010 10111 1001 0100 1001 10111 1001 0100 10100  
0011 0100 0011 0110 11011 0110 0011 0100 1001 10111 0011 0100  
0111 1001 1100 1110 10001 0111 0100 10110 10111 10110 10111 0100  
00011
```

```
111 0000 11 01 101 100 101 01 0001 0 110 011 00 110 00 111 1011 10  
111 0000 10 111 00 10 10 011 0 10 011 0 111 10 111 10 0010 10 011 010  
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 0 111 00 111 00 111  
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 1011  
10 111 000 10 000 111 0001 0 111 010 1010 010 1011 110 00 10 011
```

```
111 0000 11 01 101 100 101 01 0001 0 110 011 00 110 00 111 1011 10  
111 0000 10 111 00 10 011 0 10 011 0 111 10 111 10 0010 10 011 010  
011 10 000 111 0001 0 111 010 100 011 00 111 00 011 0 111 00 111 00 111  
110 111 110 1011 111 01 101 01 0001 0 110 111 00 011 110 111 1011  
10 111 000 10 000 113 0001 0 111 010 1010 010 1011 110 00 10 011
```

Maximize the map equation:

$$L(C) = qH(Q) + \sum_{i=1}^{n_c} p^i H(p^i).$$

Info to describe **between module** movements

Info to describe **within module** movements

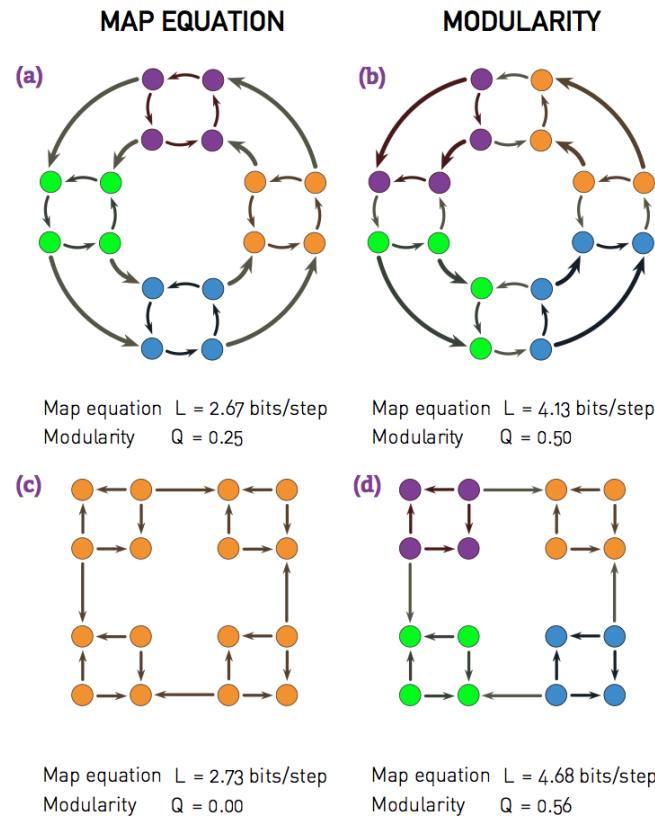
Code: <http://www.mapequation.org/>

S. Fortunato, *Phys. Rep.* 486 (2010)

A.-L. Barabási, *Network Science: Communities*.

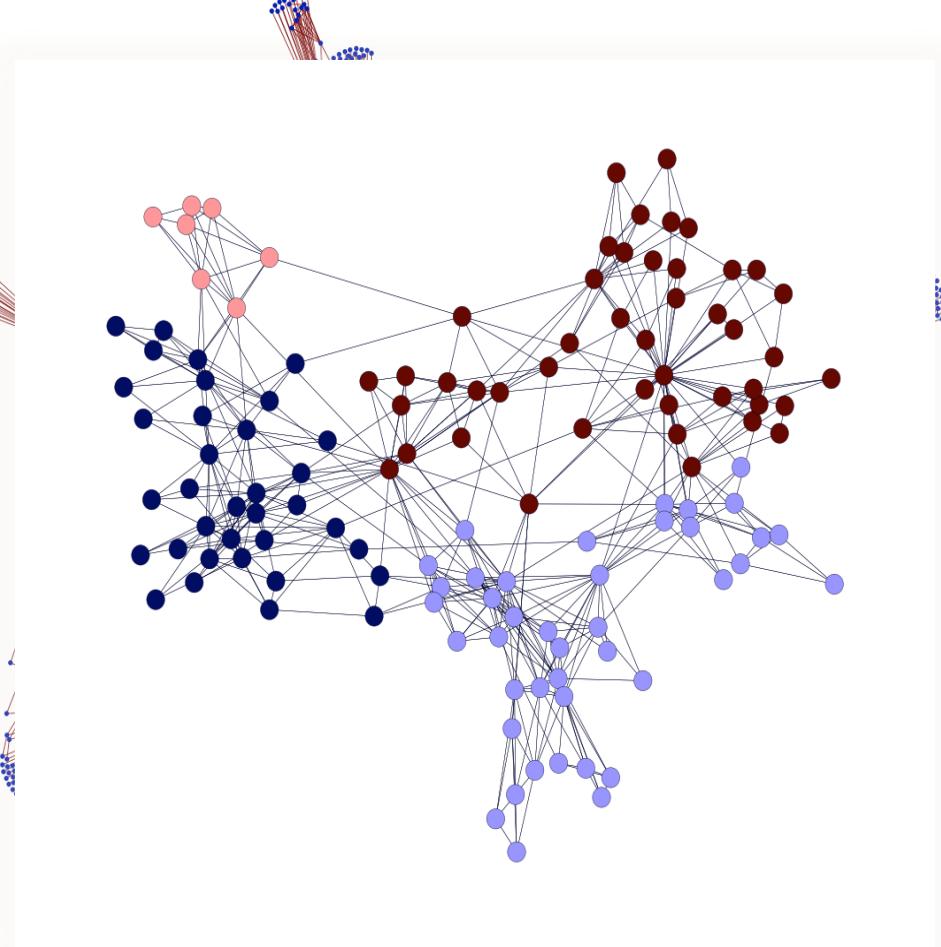
Section 6

Map Equation vs Modularity



Summary

ZOOMING INTO NETWORKS



Section 8

Summary

→ **How do we know that a network has communities?**

- **How do we know that a network has communities?**
- **We have a number of hypothesis...**

H1 (Fundamental Hypothesis): A network's community structure is uniquely encoded in its wiring diagram

H2 (Connectedness Hypothesis): A community corresponds to a connected subgraph.

H3 (Density Hypothesis): A community corresponds to locally dense neighborhood of a network.

H4 (Random Hypothesis): Randomly wired networks are not expected to have a community structure.

H5 (Maximal Modularity Hypothesis): The partition with the maximum modularity offers the best community structure, where modularity is given by

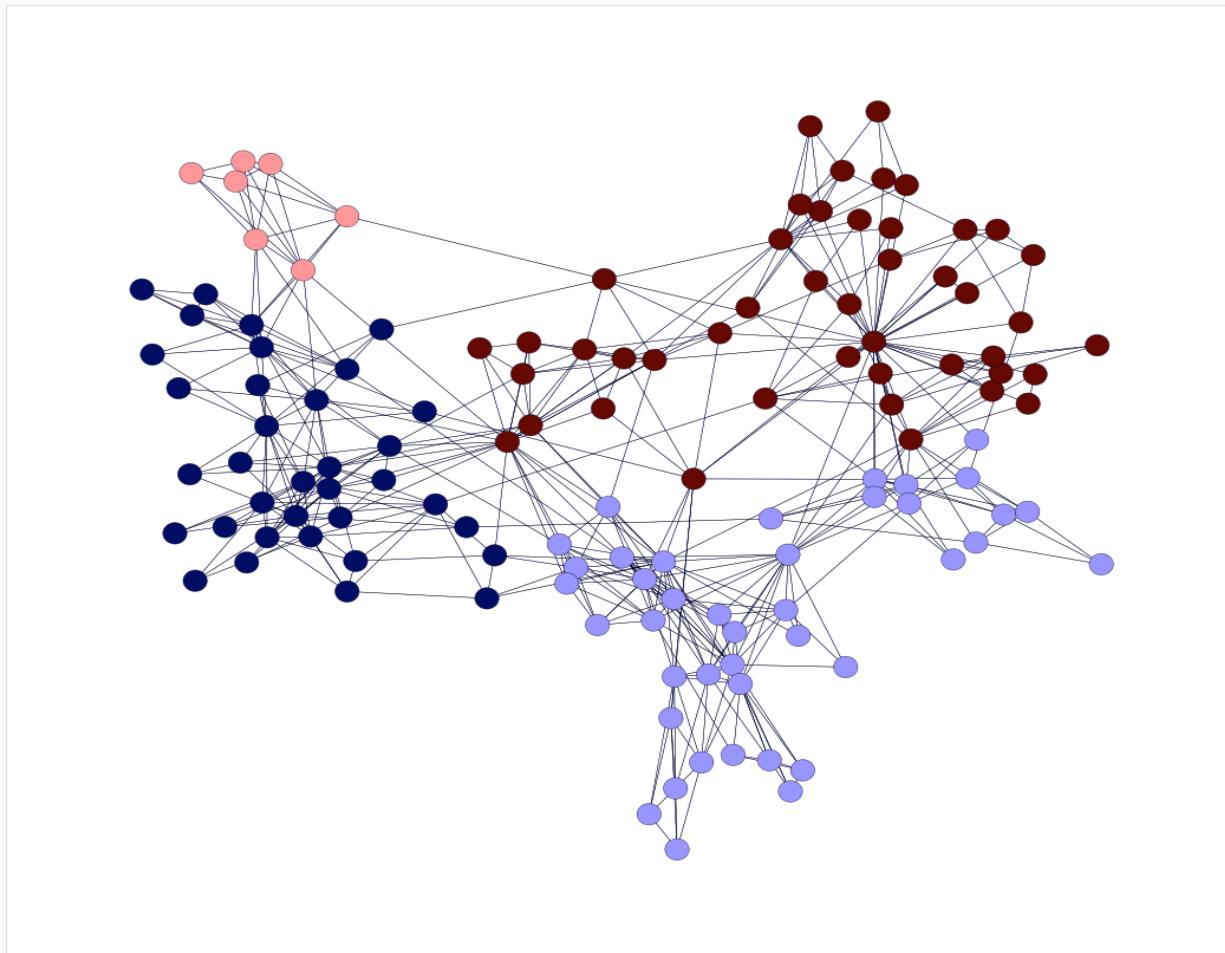
$$M = \sum_{c=1}^n \left[\frac{l_c}{L} - \left(\frac{d_c}{2L} \right)^2 \right].$$

- **How do we know that a network has communities?**
- **We have a number of hypothesis... can we prove them (hypothesis vs theorems)?**
 - H1 (Fundamental Hypothesis)
 - H2 (Connectedness Hypothesis)
 - H3 (Density Hypothesis)
 - H4 (Random Hypothesis)
 - H5 (Maximal Modularity Hypothesis)
- **Force all nodes into communities?**

Community identification relies on several fundamental hypotheses, pertaining to the nature of communities:

- (i) *Connectedness Hypothesis*: A community corresponds to a connected subgraph.
- (ii) *Density Hypothesis*: A community corresponds to locally dense neighborhood of a network.
- (iii) *Random Hypothesis*: Randomly wired networks are not expected to have a community structure.
- (iv) *Maximal Modularity Hypothesis*: The partition with the maximum modularity offers the best community structure, where modularity is given by

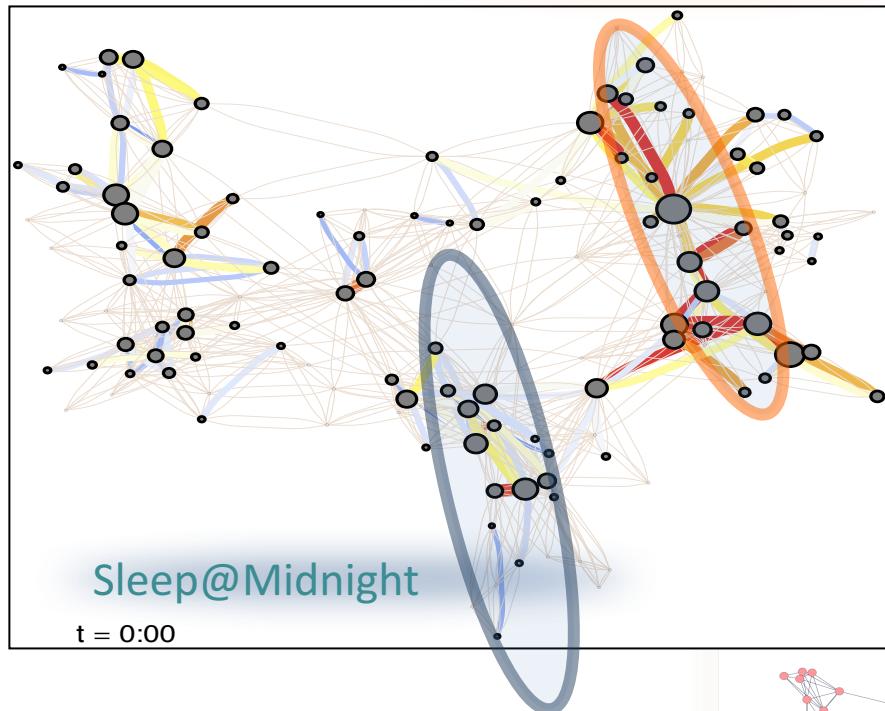
$$M = \sum_{c=1}^n \left[\frac{l_c}{L} - \left(\frac{d_c}{2L} \right)^2 \right].$$



Section 8

Summary

Busy@Midnight

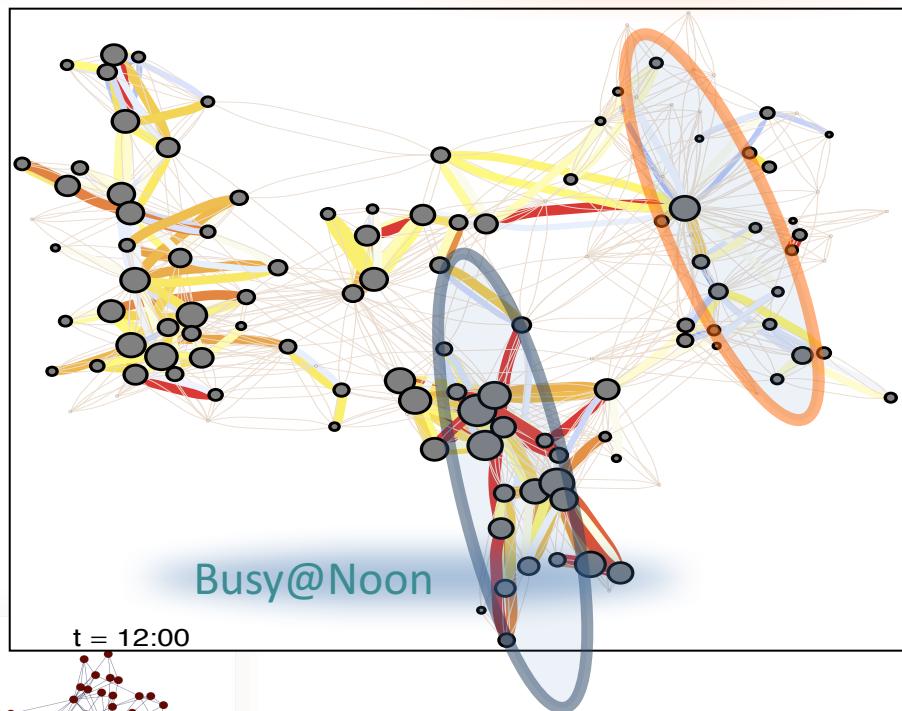


Sleep@Midnight

$t = 0:00$

Midnight

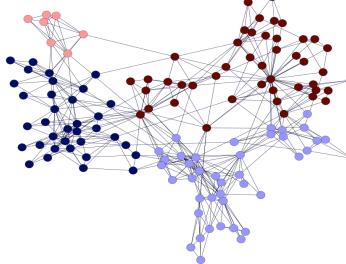
Sleep@Noon



Busy@Noon

$t = 12:00$

Noon



CALLING PATTERNS AT MIDNIGHT AND NOON

