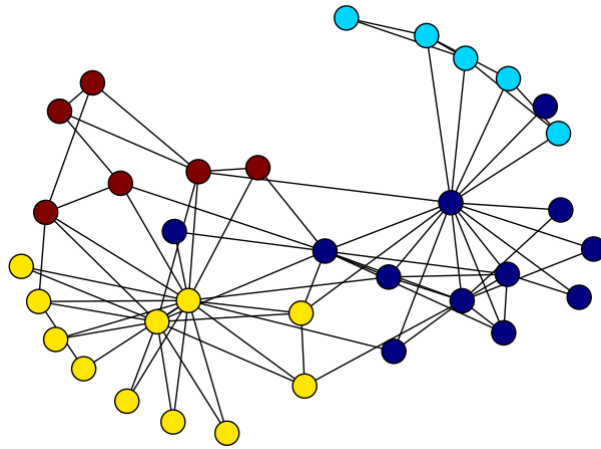


# Topological Analysis (2)



**Hiroki Sayama**  
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# Mesososcopic Structures

# K-core

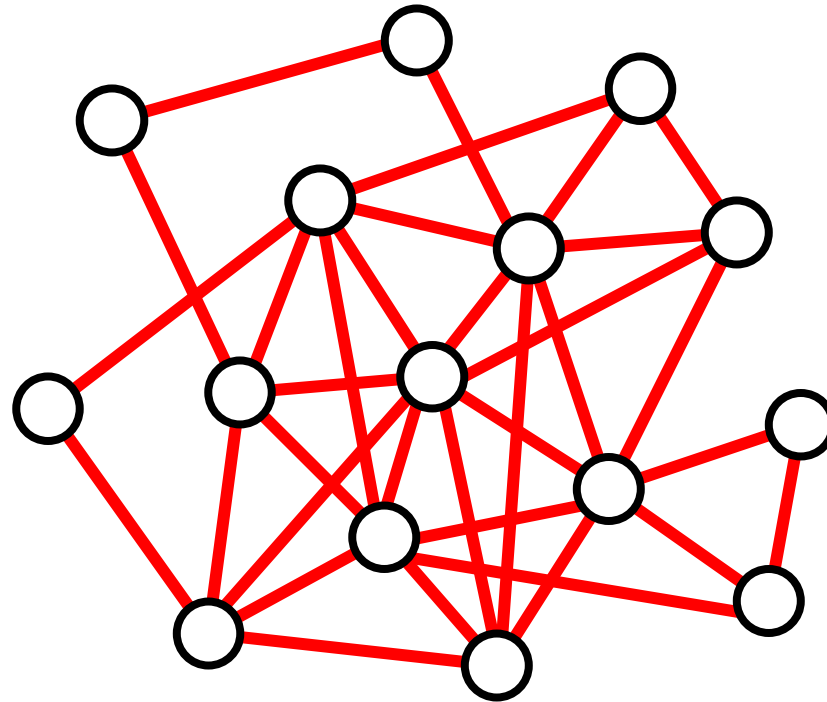
---

- A connected component of a network obtained by repeatedly deleting all the nodes whose degree is less than  $k$  until no more such nodes exist
  - Helps identify where the core cluster is
  - All nodes of a  $k$ -core have at least degree  $k$
  - The largest value of  $k$  for which a  $k$ -core exists is called “**degeneracy**” of the network

# Exercise

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- Find the  $k$ -core (with the largest  $k$ ) of the following network



# Coreness (core number)

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- A node's coreness (core number) is  $c$  if it belongs to a  $c$ -core but not  $(c+1)$ -core
- Indicates how strongly the node is connected to the network
- Classifies nodes into several layers
  - Useful for visualization

# Exercise

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- Obtain the  $k$ -core (for largest  $k$ ) of the Karate Club graph and visualize it
- Calculate the coreness of its nodes and plot its histogram
  
- Do the same for the (undirected) Supreme Court citation network

# Exercise

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- Visualize the Karate Club graph using the node coreness in NetworkX's "shell" layout algorithm



# Exercise

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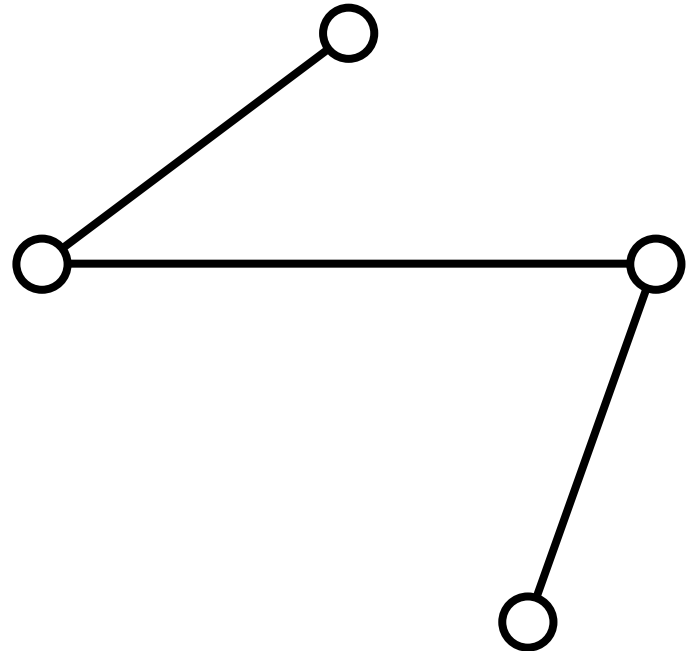
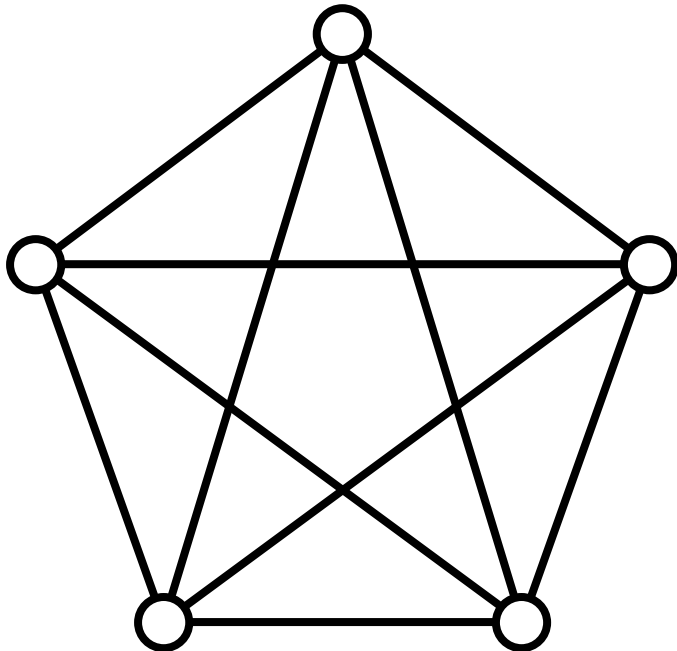
- Improve the previously implemented “node coreness”-based visualization method so that the number of edge crossings are heuristically minimized



# Subgraph

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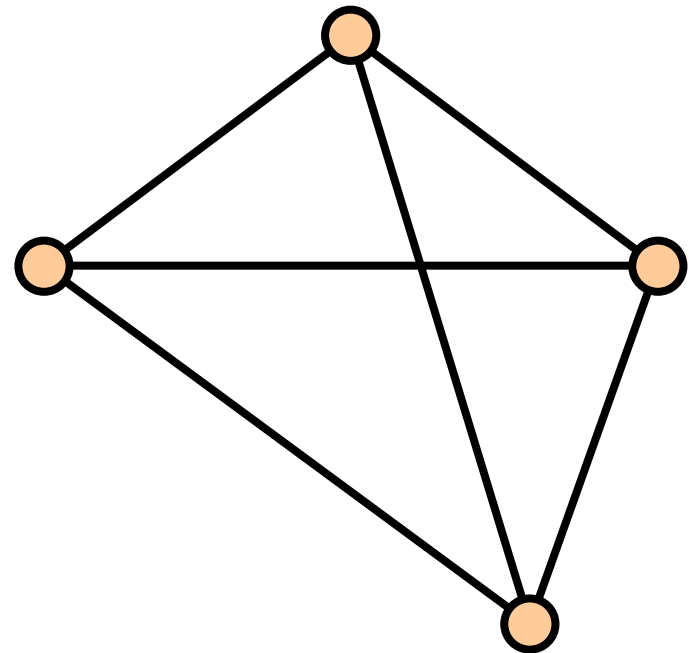
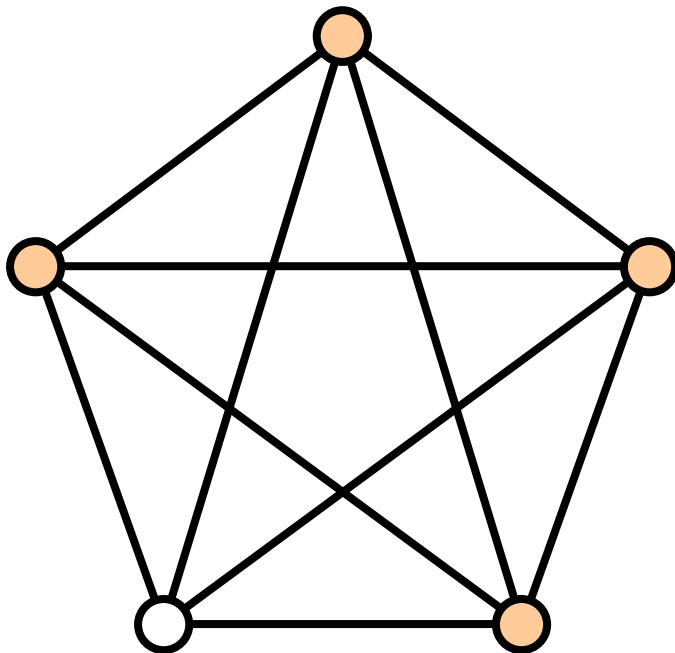
- A graph made of subsets of nodes and edges in the original graph



# Induced subgraph

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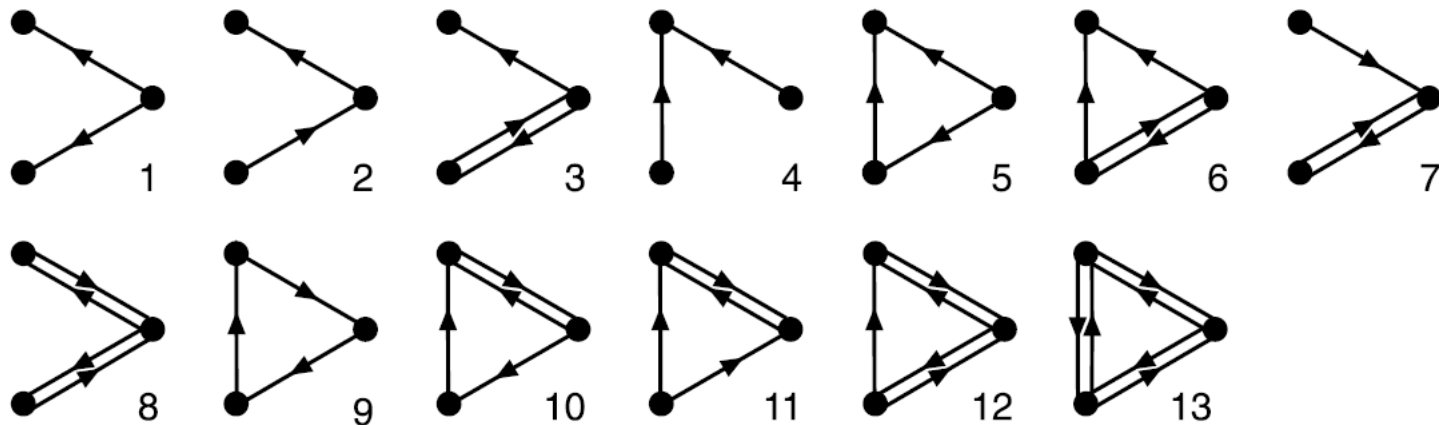
- A subgraph made of a subset of nodes and all edges among them



# Motifs

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- Small patterns of connections in a network whose number of appearance is significantly higher than those in randomized networks



(from Milo et al., Science 298: 824-827, 2002)

Network	Nodes	Edges	$N_{\text{real}}$	$N_{\text{rand}} \pm \text{SD}$	Z score	$N_{\text{real}}$	$N_{\text{rand}} \pm \text{SD}$	Z score	$N_{\text{real}}$	$N_{\text{rand}} \pm \text{SD}$	Z score
<b>Gene regulation (transcription)</b>				<b>Feed-forward loop</b>		<b>Bi-fan</b>					
<i>E. coli</i>	424	519	40	7 ± 3	10	203	47 ± 12	13			
<i>S. cerevisiae</i> *	685	1,052	70	11 ± 4	14	1812	300 ± 40	41			
<b>Neurons</b>				<b>Feed-forward loop</b>		<b>Bi-fan</b>		<b>Bi-parallel</b>			
<i>C. elegans</i> †	252	509	125	90 ± 10	3.7	127	55 ± 13	5.3	227	35 ± 10	20
<b>Food webs</b>				<b>Three chain</b>		<b>Bi-parallel</b>					
Little Rock	92	984	3219	3120 ± 50	2.1	7295	2220 ± 210	25			
Ythan	83	391	1182	1020 ± 20	7.2	1357	230 ± 50	23			
St. Martin	42	205	469	450 ± 10	NS	382	130 ± 20	12			
Chesapeake	31	67	80	82 ± 4	NS	26	5 ± 2	8			
Coachella	29	243	279	235 ± 12	3.6	181	80 ± 20	5			
Skipwith	25	189	184	150 ± 7	5.5	397	80 ± 25	13			
B. Brook	25	104	181	130 ± 7	7.4	267	30 ± 7	32			
<b>Electronic circuits (forward logic chips)</b>				<b>Feed-forward loop</b>		<b>Bi-fan</b>		<b>Bi-parallel</b>			
s15850	10,383	14,240	424	2 ± 2	285	1040	1 ± 1	1200	480	2 ± 1	335
s38584	20,717	34,204	413	10 ± 3	120	1739	6 ± 2	800	711	9 ± 2	320
s38417	23,843	33,661	612	3 ± 2	400	2404	1 ± 1	2550	531	2 ± 2	340
s9234	5,844	8,197	211	2 ± 1	140	754	1 ± 1	1050	209	1 ± 1	200
s13207	8,651	11,831	403	2 ± 1	225	4445	1 ± 1	4950	264	2 ± 1	200
<b>Electronic circuits (digital fractional multipliers)</b>				<b>Three-node feedback loop</b>		<b>Bi-fan</b>		<b>Four-node feedback loop</b>			
s208	122	189	10	1 ± 1	9	4	1 ± 1	3.8	5	1 ± 1	5
s420	252	399	20	1 ± 1	18	10	1 ± 1	10	11	1 ± 1	11
s838‡	512	819	40	1 ± 1	38	22	1 ± 1	20	23	1 ± 1	25
<b>World Wide Web</b>				<b>Feedback with two mutual dyads</b>		<b>Fully connected triad</b>		<b>Uplinked mutual dyad</b>			
nd.edu§	325,729	1.46e6	1.1e5	2e3 ± 1e2	800	6.8e6	5e4 ± 4e2	15,000	1.2e6	1e4 ± 2e2	5000

(from Milo et al., Science 298: 824-827, 2002)

# Unfortunately...

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- Motif counting is computationally costly and still being actively studied, so NetworkX does not have built-in motif counting tools
- You may use specialized software
  - mfinder, igraph
- You can write a code yourself
  - Use `itertools.combinations + subgraph + nx.is_isomorphic`

# Exercise

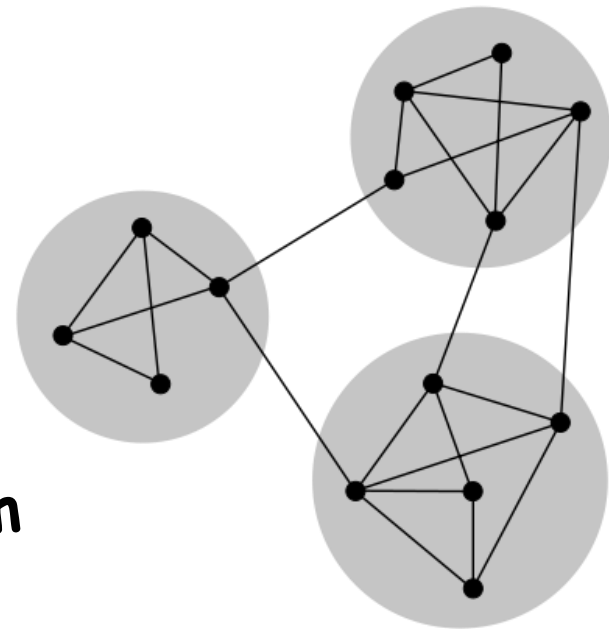
---

- Write a code that enumerates all the connected motifs in the Karate Club graph
- Compare the frequencies of each motif with those in randomized null model networks
- Which motif(s) are over-represented in the Karate Club graph?

# Community

---

- A subgraph of a network within which nodes are connected to each other more densely than to the outside
  - Still defined vaguely...
  - Various detection algorithms proposed
    - K-clique percolation
    - Hierarchical clustering
    - Girvan-Newman algorithm
    - Modularity maximization (e.g., Louvain method)



(diagram from Wikipedia)

# K-clique percolation method

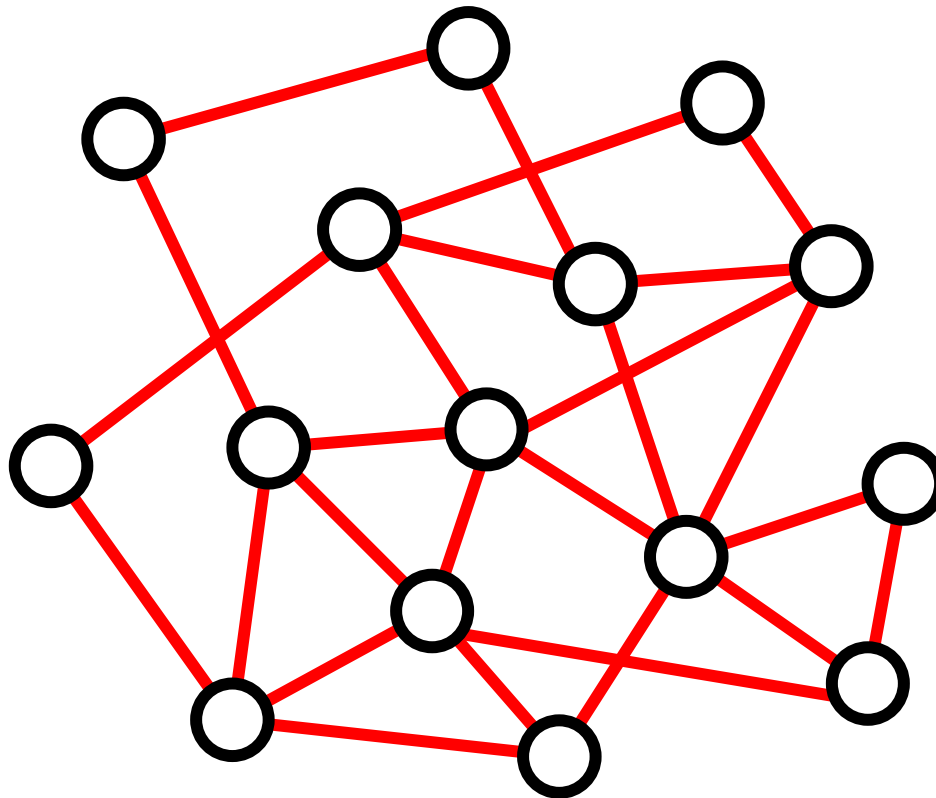
1. Choose a value for  $k$  (e.g., 4)
  2. Find all  $k$ -cliques (complete subgraphs of  $k$ -nodes) in the network
  3. Assume that two cliques belong to the same community if they share  $k-1$  nodes (“ $k$ -clique percolation”)
- This methods detect communities that potentially overlap



# Exercise

---

- Find communities in the following network by 3-clique percolation



# Exercise

---

- **Generate a random network made of 100 nodes and 250 links**
- **Calculate node positions using spring layout**
- **Visualize the original network & its  $k$ -clique communities (for  $k = 3$  or  $4$ ) using the same positions**

# Exercise

---

- Find  $k$ -clique communities in the (undirected) Supreme Court Citation Network
- Start with large  $k$  (say 100) and decrease it until you find a meaningful community

# Non-overlapping communities

---

- Other methods find ways to assign ALL the nodes to one and only one community
  - Community structure is a mapping from a node ID to a community ID
  - No community overlaps
  - No “stray” nodes

# Community detection by edge removals

---

- **Girvan-Newman method**

- Girvan, M., & Newman, M. E., PNAS, 99(12), 7821-7826, 2002.

- Gradually removes high betweenness centrality edges to break the network into pieces
  - Generates a hierarchical clustering dendrogram

# Exercise

---

- Visualize the sequence of the Karate Club graph decompositions by the Girvan-Newman method
- Which level of the decomposition makes the most sense?

# Modularity

---

- A quantity that characterizes how good a given community structure is in dividing the network

$$Q = \frac{|E_{in}| - |E_{in-R}|}{|E|}$$

- $|E_{in}|$ : # of links connecting nodes that belong to the same community
- $|E_{in-R}|$ : Estimated  $|E_{in}|$  if links were random

# Community detection based on modularity (1)

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- **Clauset-Newman-Moore method**
  - Clauset, A., Newman, M. E., & Moore, C. Physical Review E 70(6), 2004.
  - Starts with every node viewed as separate community
  - Gradually merges small communities until modularity no longer increases



# Exercise

---

- Use `nx.algorithms.community` to detect communities in the Karate Club graph using:
  - Girvan-Newman method
  - Clauset-Newman-Moore method
- Visualize the results and compare

# Community detection based on modularity (2)

---

- The Louvain method
  - Heuristic algorithm to construct communities that optimize modularity
    - Blondel et al. J. Stat. Mech. 2008 (10): P10008
- Python implementation by Thomas Aynaud available at:
  - <https://bitbucket.org/taynaud/python-louvain/>

# Exercise

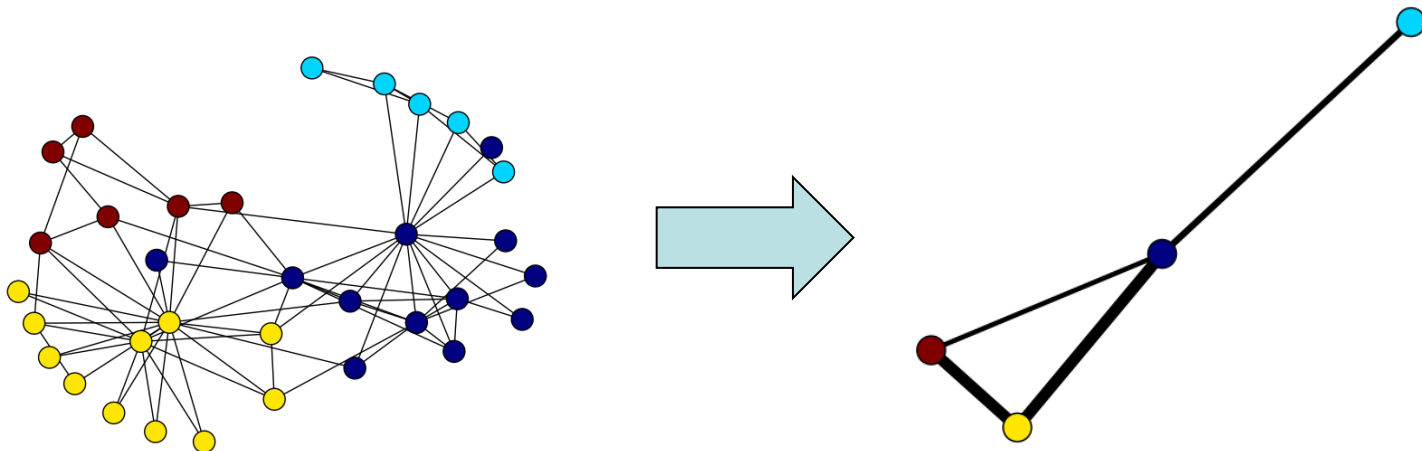
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- Detect community structure in the (undirected) Supreme Court Citation Network using the Louvain method
- Measure the modularity achieved
- How many communities are detected?
- How large is each community?

# Block model (quotient graph)

---

- Create a new, “coarse” network by aggregating nodes within each community into a meta-node
  - Meta-nodes contain original communities
  - Meta-edge weights show connections b/w communities



# Exercise

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- Create a block model of some real-world network by using its communities as partitions
- Visualize the block model with edge widths varied according to connections between communities

# Hierarchy

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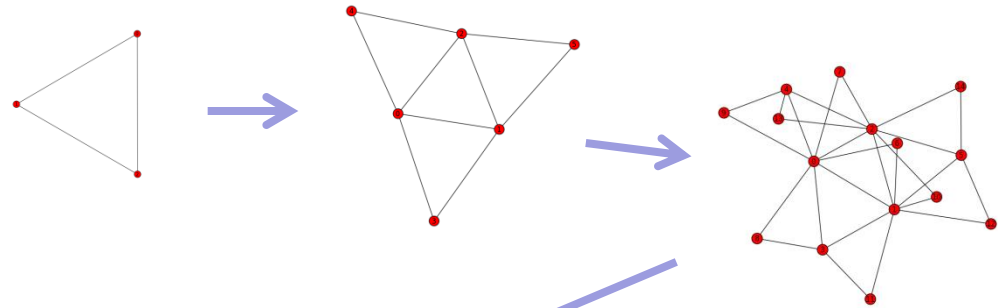
- Many real-world complex networks have many layers of modular structures forming a hierarchy
  - Community structures are not single-scale, but multiscale
  - Similar to fractals

# Deterministic scale-free networks

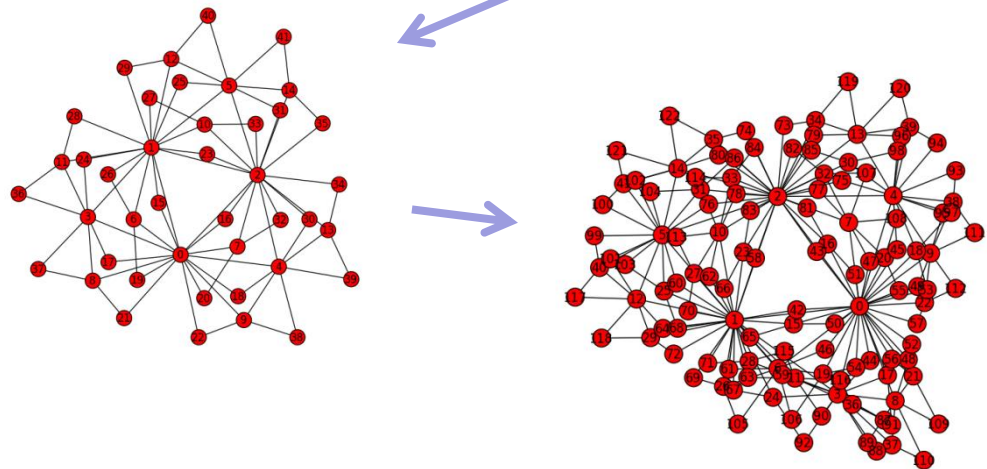
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- E.g. Dorogovtsev, Goltsev & Mendes 2002

- Scale-free degree distribution



- But still high clustering coefficients

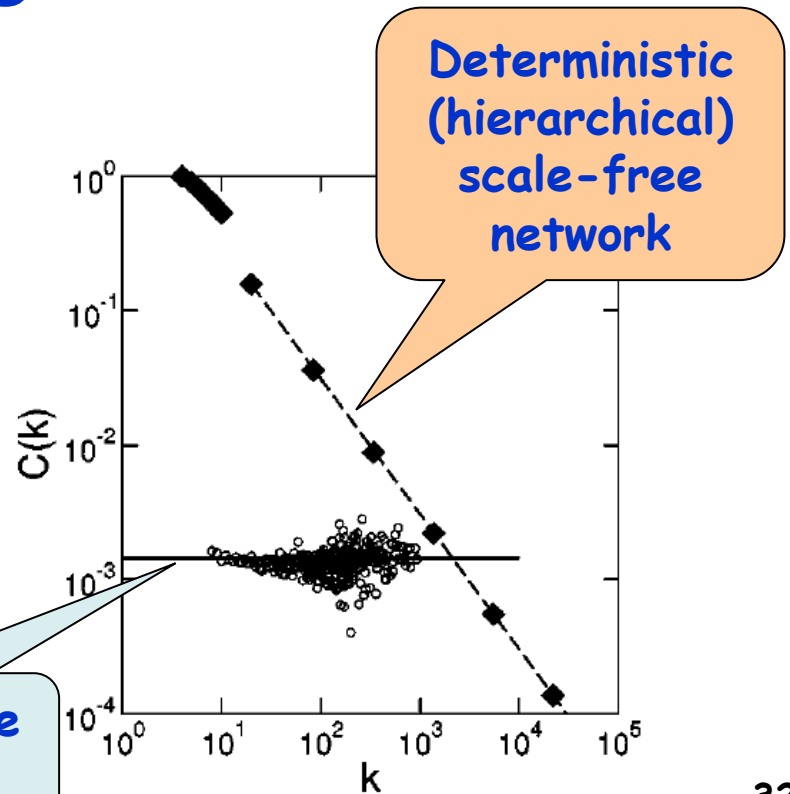


# Clustering coefficients and k

- Deterministic scale-free networks show another scaling law

(Dorogovtsev et al. 2002;  
Ravasz & Barabasi 2003)

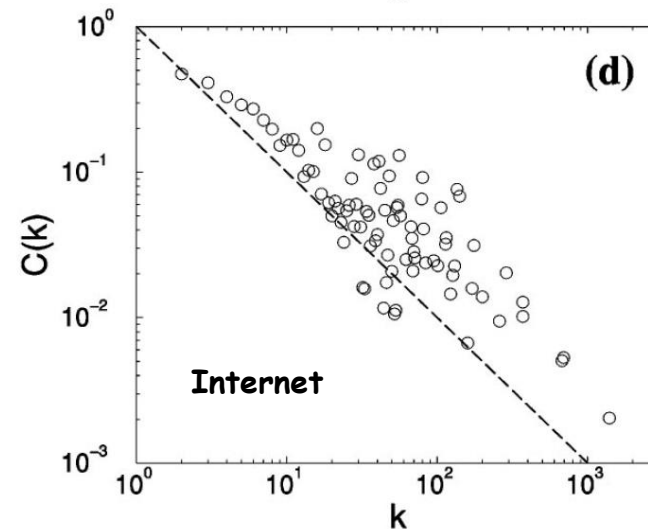
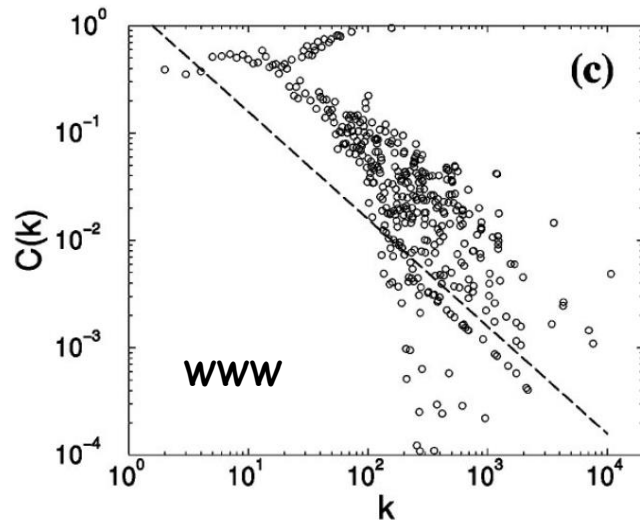
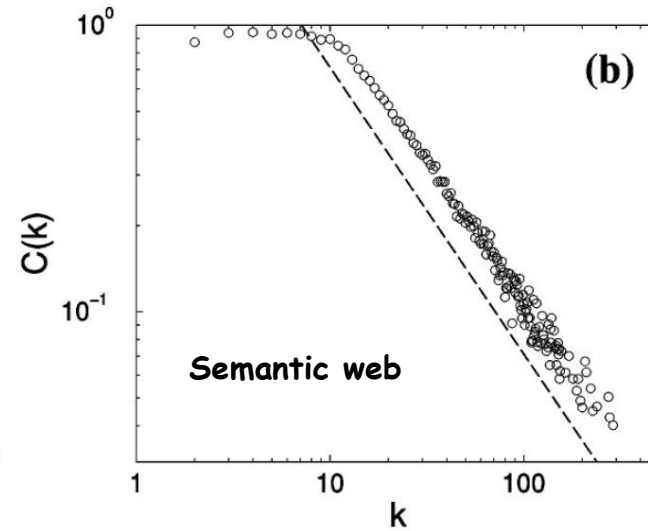
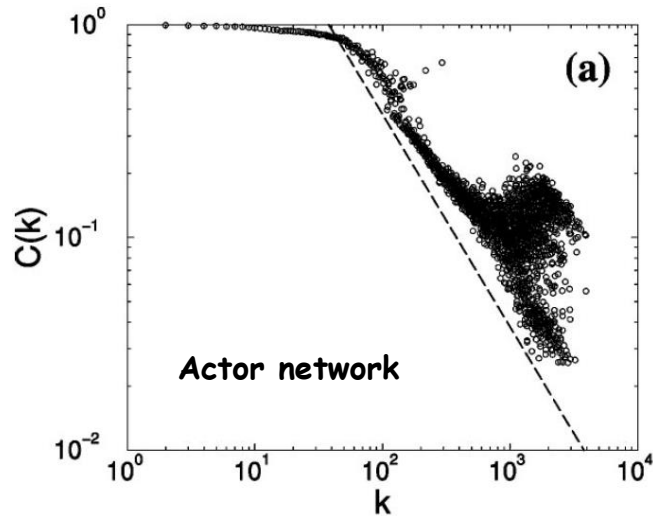
$$C(k) \sim k^{-1}$$



(from Ravasz & Barabasi 2003)



# $C(k)$ plots of real-world networks



(from Ravasz & Barabasi 2003)

# Exercise

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- Plot  $C(k)$  for several real-world network data and see if the inverse scaling law between  $k$  and  $C(k)$  appears or not