

Graph Structural Features

lecture-3

Course on Graph Neural Networks (Winter Term 21/22)

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The Strength of Weak Ties [Granovetter 73]

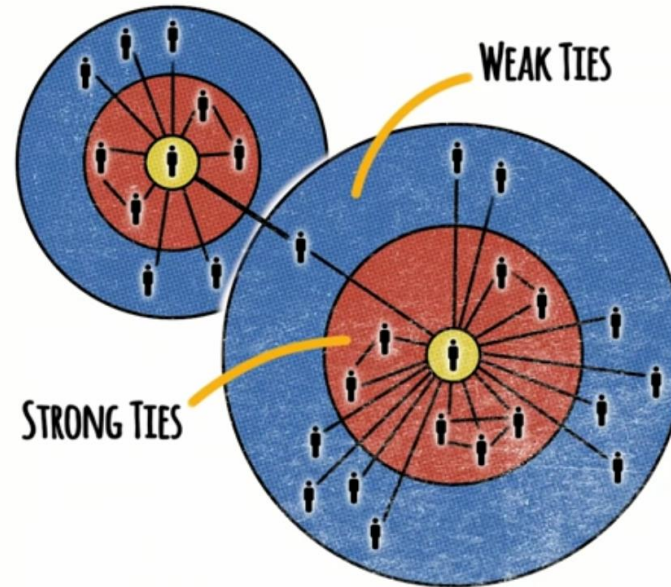
American Journal of Sociology, Volume 78, Issue 6 (May, 1973), 1360-1380.

The Strength of Weak Ties¹

Mark S. Granovetter
Johns Hopkins University

Analysis of social networks is suggested as a tool for linking micro and macro levels of sociological theory. The procedure is illustrated by elaboration of the macro implications of one aspect of small-scale interaction: the strength of dyadic ties. It is argued that the degree of overlap of two individuals' friendship networks varies directly with the strength of their tie to one another. The impact of this principle on diffusion of influence and information, mobility opportunity, and community organization is explored. Stress is laid on the cohesive power of weak ties. Most network models deal, implicitly, with strong ties, thus confining their applicability to small, well-defined groups. Emphasis on weak ties lends itself to discussion of relations *between* groups and to analysis of segments of social structure not easily defined in terms of primary groups.

A fundamental weakness of current sociological theory is that it does not relate micro-level interactions to macro-level patterns in any convincing way. Large-scale statistical, as well as qualitative, studies offer a good deal of insight into such macro phenomena as social mobility, community organization, and political structure. At the micro level, a large and increasing body of data and theory offers useful and illuminating ideas about what transpires within the confines of the small group. But how interaction in small groups aggregates to form large-scale patterns eludes us in most cases. I will argue, in this paper, that the analysis of processes in interpersonal

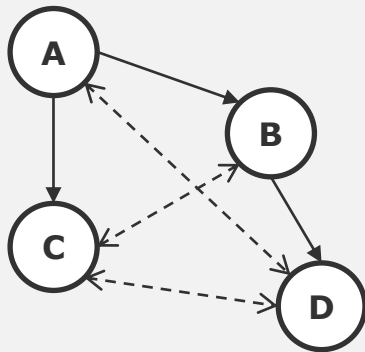


source: Interview with Mark Granovetter at Stanford -
<https://www.youtube.com/watch?v=g3bBajcR5fE&pbjreload=101>

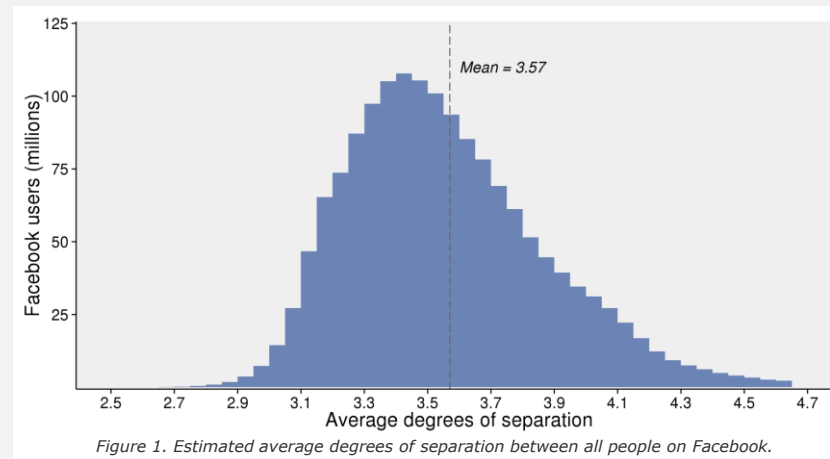
Interesting facts:

- Most people change jobs voluntarily
- 56% found new jobs through personal contacts
- 3/4 of the highest income categories
- More difficult to change if >5 years in a job
- People with 2 to 5 years in a job were more likely to find jobs through weak ties

Why?



Triads tend to form -> increasing the spread of information within a cluster



Shrinking average shortest paths

<https://research.fb.com/blog/2016/02/three-and-a-half-degrees-of-separation/>



Instant global communication

JJ Ying
<https://unsplash.com/photos/8bghKxNU1j0>

1. Structure of Graph

- Motifs – the building blocks
- Graphlets – the landscape
- Metrics
 - Centrality metrics
 - Structural membership metrics
 - Homophily metrics (Assortativity and Neighborhood)

2. Clustering

- Community detection
- Spectral clustering

Network-level metrics

- Average node degree (degree distribution)
- Average clustering
- Average path length (diameter)
- Node connectivity (distribution among components)

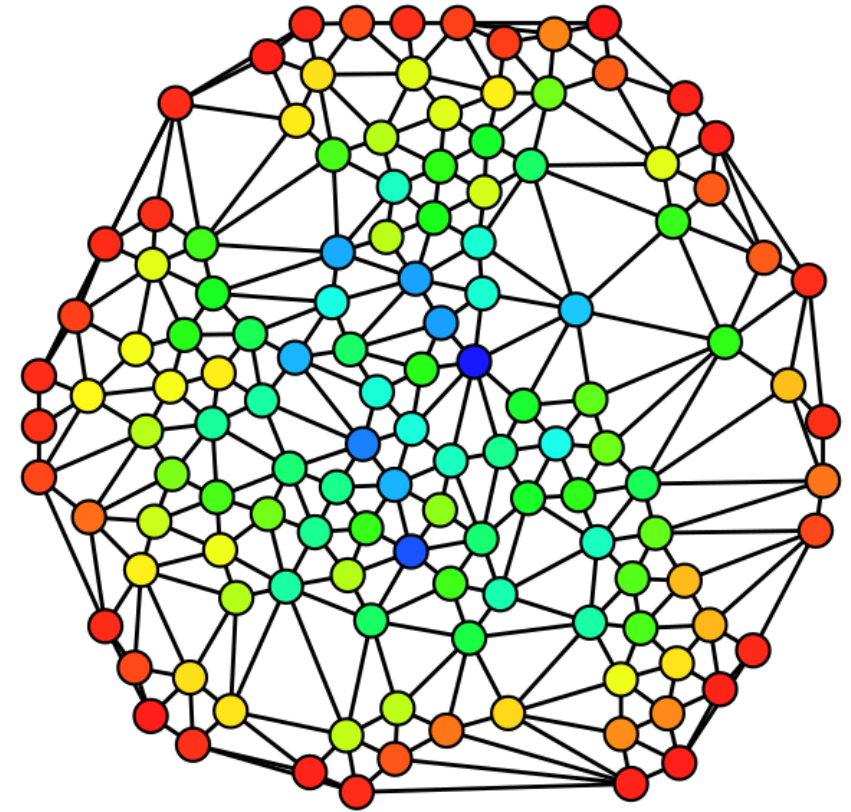
Node-level metrics

- Centrality (degree-based): Katz, PageRank
- Centrality (path-based): closeness and betweenness

Pair-wise metrics

- Edge-overlap
- Node equivalence (Regular and Structural)
- Node similarity

- Eccentricity $e(n_i)$: the maximum distance between nodes n_i and any other node
- Diameter (d): largest $e(n_i)$ for across all n_i
- Radius (r): smallest $e(n_i)$ for across all n_i
 - Central node: $e(n_i) = r$
 - Graph center: $\forall n_i | e(n_i) = r$
 - Graph periphery: $\forall n_i | e(n_i) = d$



source: Wikipedia

Centrality: node degree

source: Wikipedia

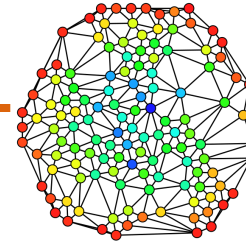
Eigenvector Centrality: importance of a node (x_i) depends on importance (x_j) of its neighbors

$$x_i = k^{-1} \sum_j x_j$$

Or use the Adjacency matrix A : $x_i = k^{-1} \sum_j A_{ij} x_j$, $x = k^{-1} Ax$, $Ax = kx$
 x = eigenvector of A
 k = from the i th eigenvalue of the leading eigenvector x ,
 $k = \frac{1}{\lambda_2}$, where λ_2 is the largest non-negative eigenvalue
(From the Perron-Frobenius Theorem).

Katz Centrality: $x_i = k^{-1} \sum_j A_{ij} x_j + \beta$, where $\beta = \text{constant}$

PageRank: $x_i = k^{-1} \sum_j A_{ij} \frac{x_j}{k_j^{\text{out}}} + \beta$, where k_j^{out} = outdegree of node j



source: Wikipedia

Closeness-Centrality:

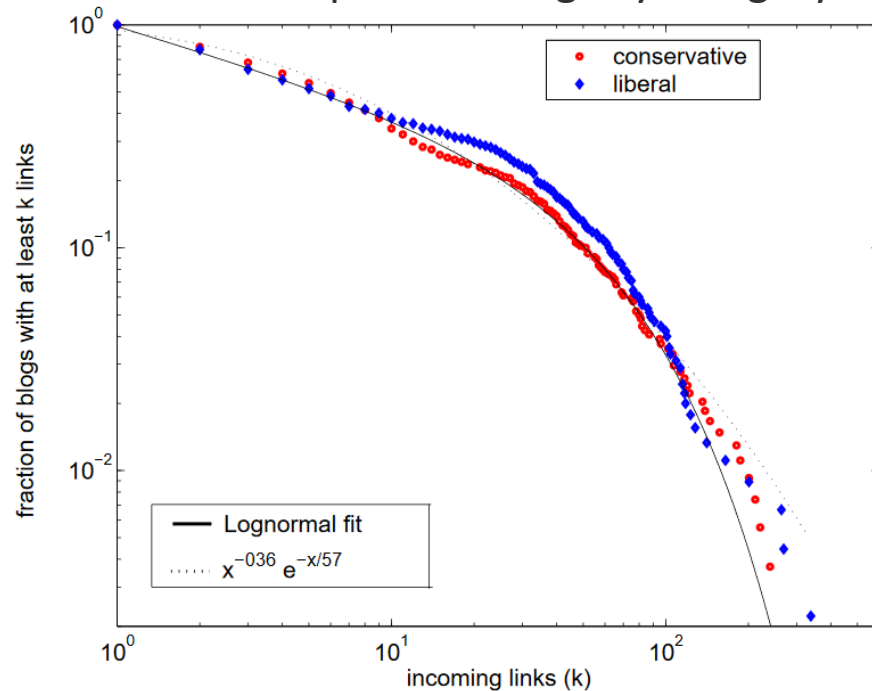
$x_i = \frac{1}{\sum_j d(i,j)}$ or take the harmonic mean $\sum_j \frac{1}{d(i,j)}$ (solves $d = \infty$)

Betweenness-Centrality:

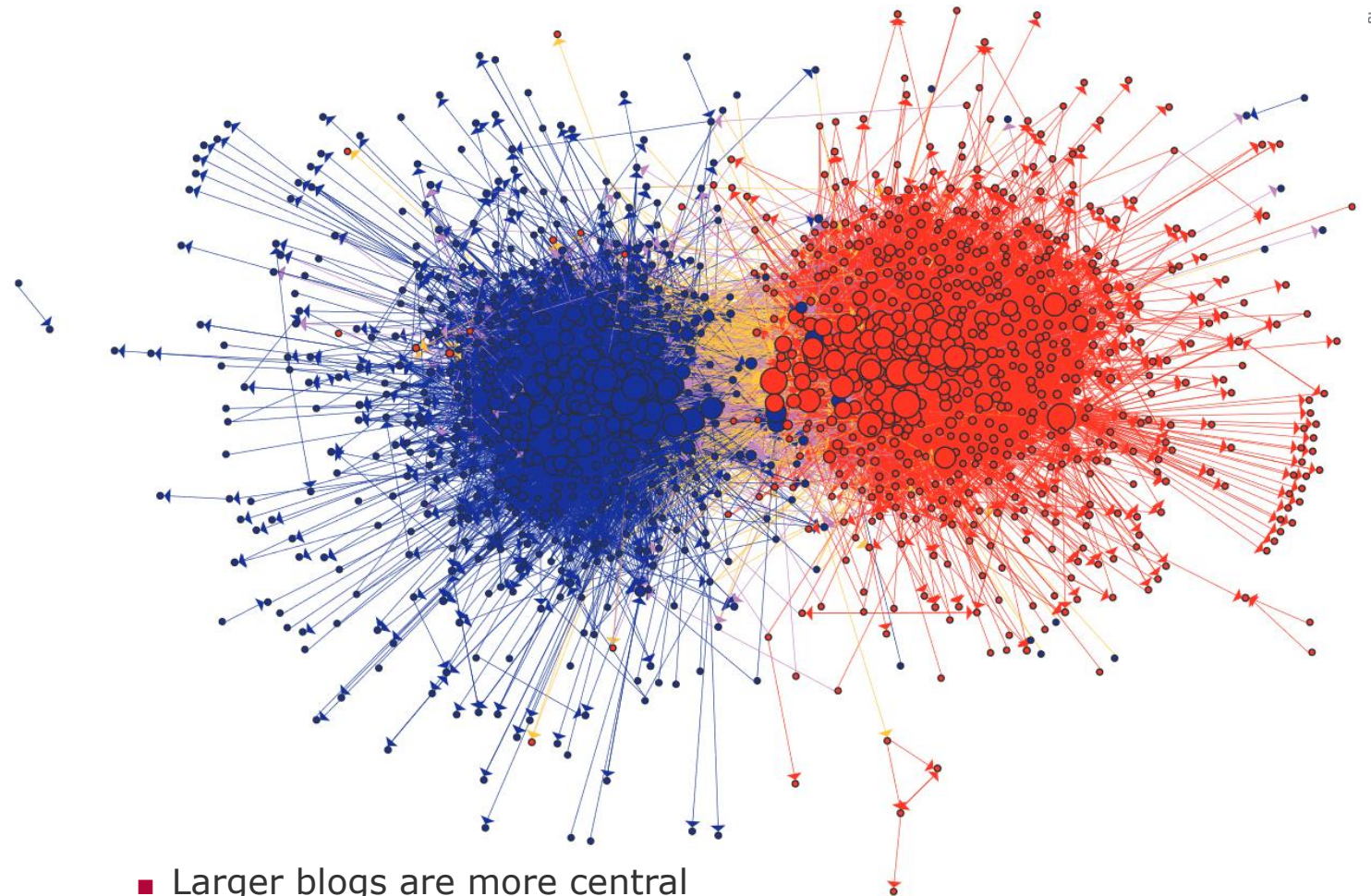
$x_i = \sum_{s \rightarrow t, s \neq t} n_{st}^i$, where n_{st}^i is the shortest path between s and t that goes through node i (n^i).

Political Blogosphere [Adamic & Glance 2005]

Cumulative distribution of incoming links for political blogs by category

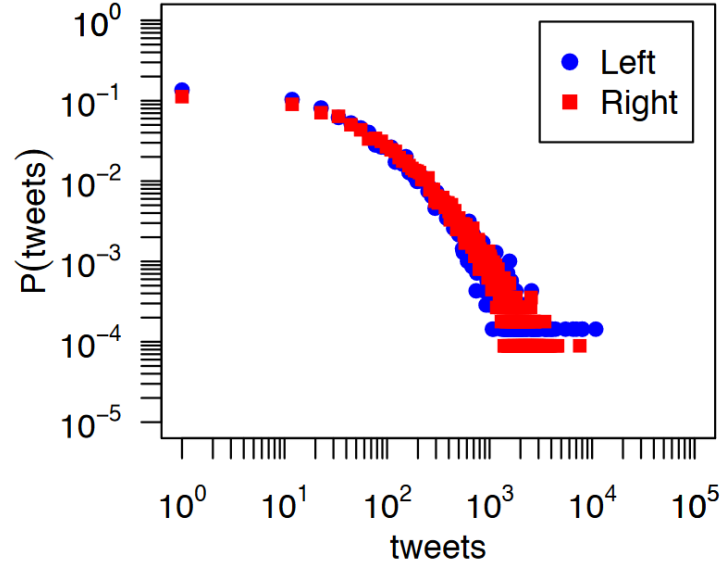


Similar distributions can be fit with lognormal or exponential functions.

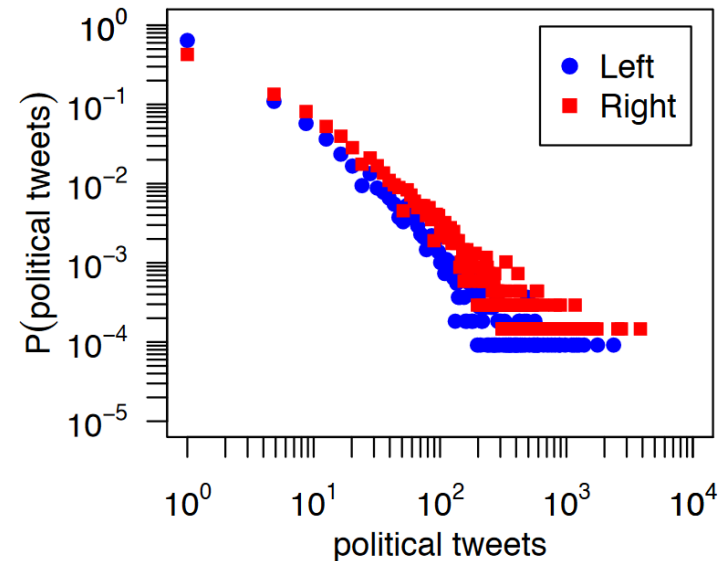


- Larger blogs are more central
- Homophily
- Yellow links show blogs from opposite views commenting on each other

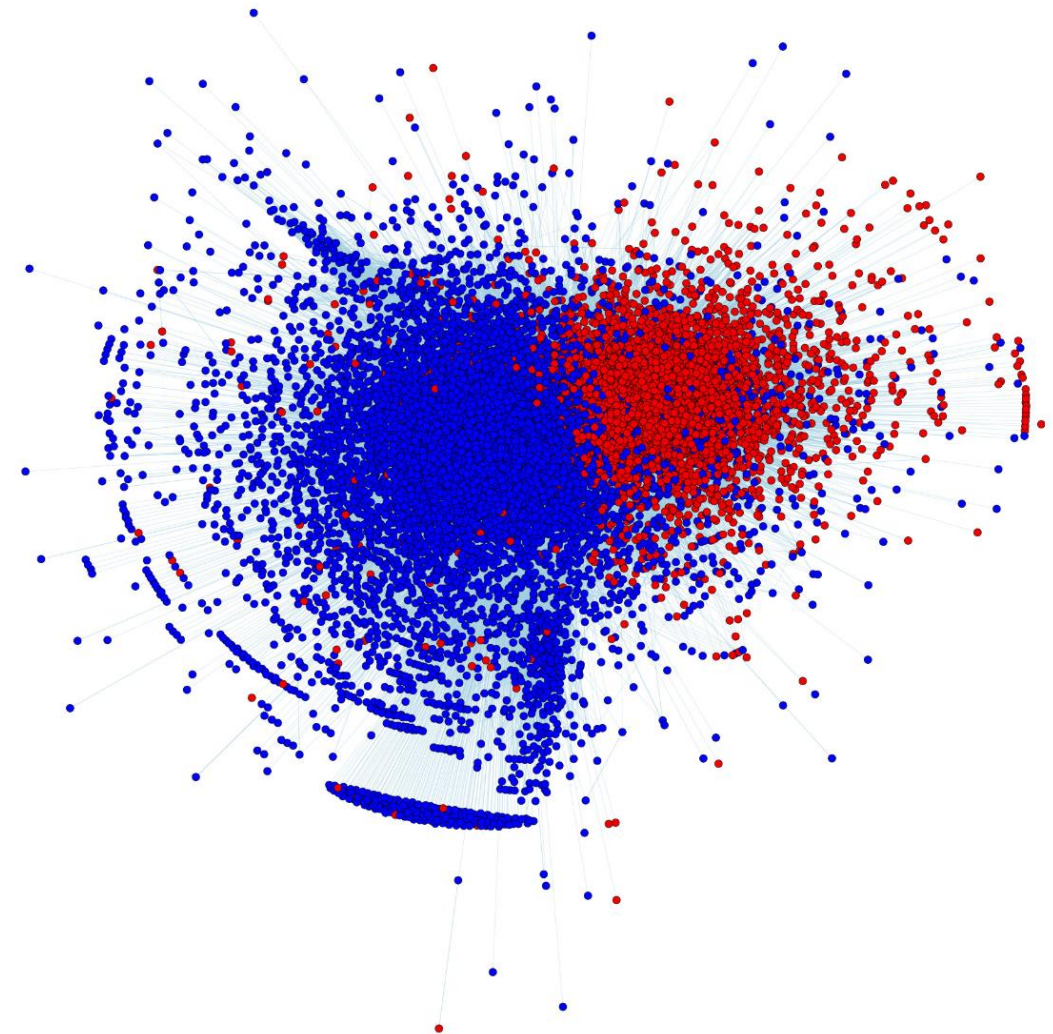
Partisan Asymmetries in Twitter [Conover et al. 2012]

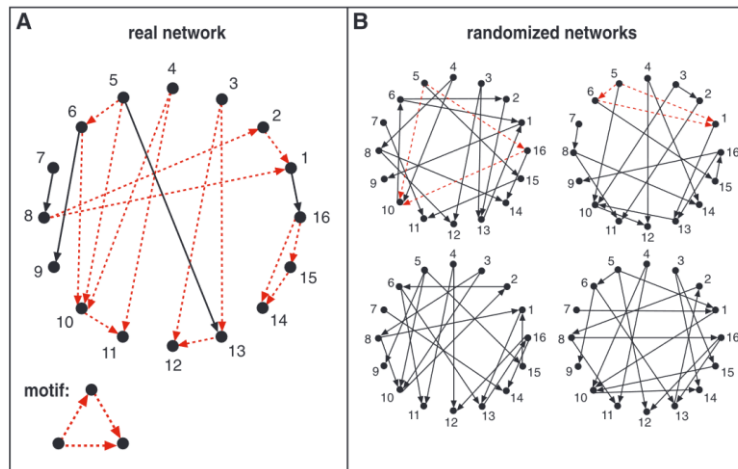
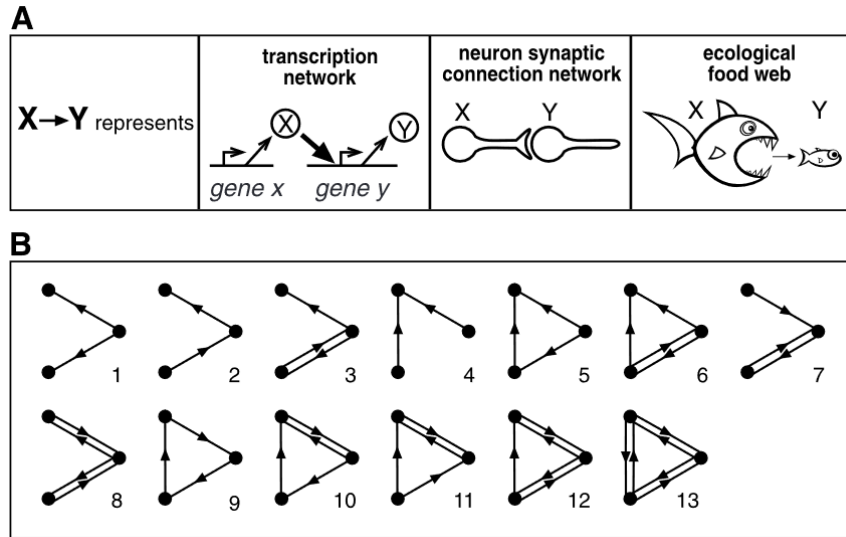


Both groups produce same amount of tweets per capita
tweets = number of tweets a user posts
P(tweets) probability of a user



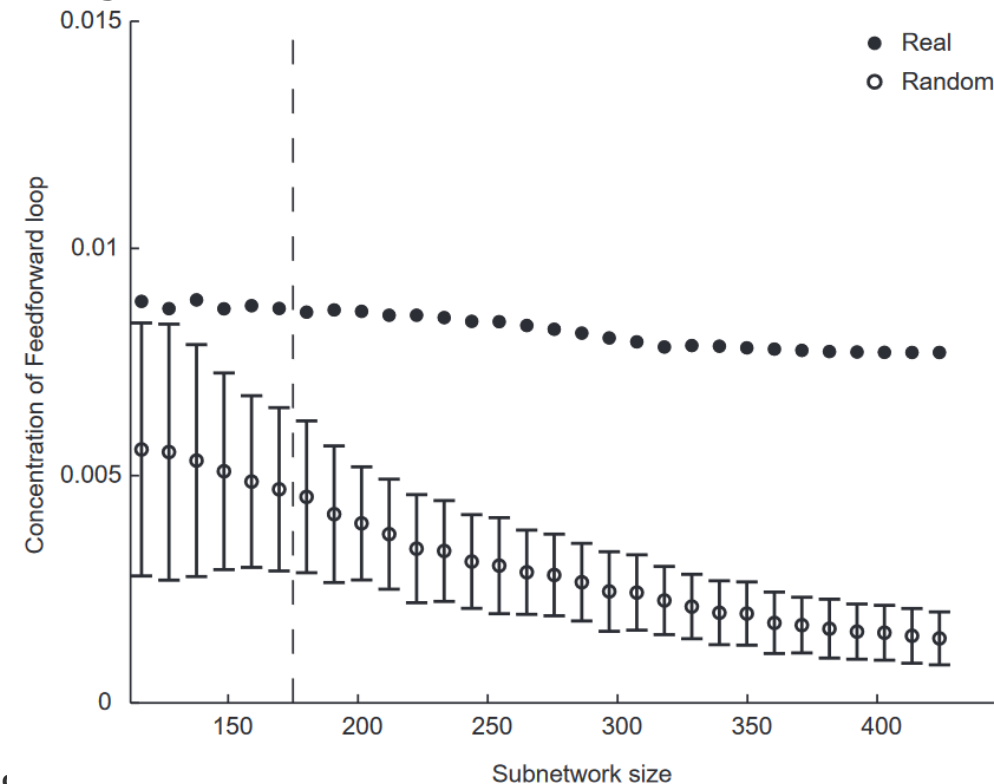
Right-leaning produce 2x more political content
One or more political hash tags
• Right-leaning= 22% of tweets
• Left-leaning= 12% of tweets





Remarks

- Number of motifs grow exponentially with the number of edges
- Real networks tend to be rich in motifs, whereas Random networks not.
- As Real networks evolve, their motif count remains stable, whereas in Random networks, it collapses.
- This might suggest that motifs provide structure to the proper functioning of these networks



Motifs in real networks

Biological

Technological

| Network | Nodes | Edges | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score |
|--|-------|-------|-------------------|---------------------------------|---------|-------------------|---------------------------------|---------|-------------------|---------------------------------|---------|
| Gene regulation (transcription) | | | | Feed-forward loop | | | Bi-fan | | | | |
| <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 | | | |
| Neurons | | | | Feed-forward loop | | | Bi-fan | | | Bi-parallel | |
| <i>C. elegans</i> † | 252 | 509 | 125 | 90 ± 10 | 3.7 | 127 | 55 ± 13 | 5.3 | 227 | 35 ± 10 | 20 |
| Food webs | | | | Three chain | | | Bi-parallel | | | | |
| 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 | | | |

| Network | Nodes | Edges | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score | N_{real} | $N_{\text{rand}} \pm \text{SD}$ | Z score |
|---|---------|--------|-------------------|---------------------------------------|---------|-------------------|---------------------------------|---------|-------------------|---------------------------------|---------|
| Electronic circuits (forward logic chips) | | | | Feed-forward loop | | | Bi-fan | | | Bi-parallel | |
| 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 |
| Electronic circuits (digital fractional multipliers) | | | | Three-node feedback loop | | | Bi-fan | | | Four-node feedback loop | |
| 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 |
| World Wide Web | | | | Feedback with two mutual dyads | | | Fully connected triad | | | Uplinked mutual dyad | |
| nd.edu§ | 325,729 | 1.46e6 | 1.1e5 | 2e3 ± 1e2 | 800 | 6.8e6 | 5e4 ± 4e2 | 15,000 | 1.2e6 | 1e4 ± 2e2 | 5000 |

Motif counting – ESU (FANMOD) algorithm [Wernicke 2006]

Algorithm: ENUMERATESUBGRAPHS(G, k) (ESU)

Input: A graph $G = (V, E)$ and an integer $1 \leq k \leq |V|$.

Output: All size- k subgraphs in G .

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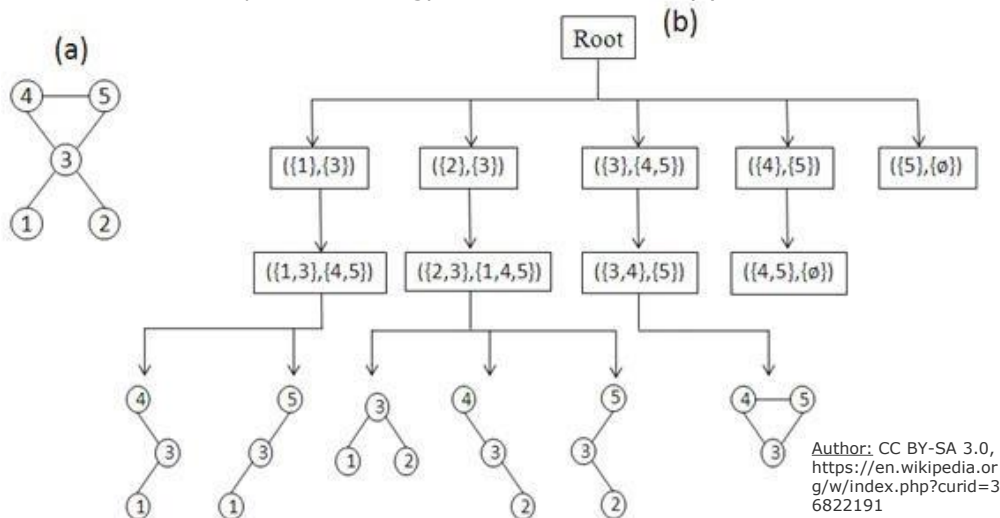
01 for each vertex  $v \in V$  do
02    $V_{Extension} \leftarrow \{u \in N(\{v\}) : u > v\}$ 
03   call EXTENDSUBGRAPH( $\{v\}, V_{Extension}, v$ )
04 return
    
```

EXTENDSUBGRAPH($V_{Subgraph}, V_{Extension}, v$)

```

E1 if  $|V_{Subgraph}| = k$  then output  $G[V_{Subgraph}]$  and return
E2 while  $V_{Extension} \neq \emptyset$  do
E3   Remove an arbitrarily chosen vertex  $w$  from  $V_{Extension}$ 
E4    $V'_{Extension} \leftarrow V_{Extension} \cup \{u \in N_{excl}(w, V_{Subgraph}) : u > v\}$ 
E5   call EXTENDSUBGRAPH( $V_{Subgraph} \cup \{w\}, V'_{Extension}, v$ )
E6 return
    
```

[Wernicke 2006] Wernicke S (2006). "Efficient detection of network motifs". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. **3** (4): 347–359.



Author: CC BY-SA 3.0,
<https://en.wikipedia.org/w/index.php?curid=6822191>

EXT set of all the nodes that :

1. are adjacent to at least one of the nodes in SUB (guarantees expansion is a connected graph)
2. their numerical labels must be larger than the label of first element in SUB. (guarantees termination)

Many other algorithms have been developed and tested

| Networks ↓ | Size → Algorithms ↓ | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|------------|------------------------|-------|------|-------|--------|--------|---------|----------|-----------|
| | | | | | | | | | |
| E. coli | Kavosh | 0.30 | 1.84 | 14.91 | 141.98 | 1374.0 | 13173.7 | 121110.3 | 1120560.1 |
| | FANMOD | 0.81 | 2.53 | 15.71 | 132.24 | 1205.9 | 9256.6 | - | - |
| | Mavisto | 13532 | - | - | - | - | - | - | - |
| | Mfinder | 31.0 | 297 | 23671 | - | - | - | - | - |
| Electronic | Kavosh | 0.08 | 0.36 | 8.02 | 11.39 | 77.22 | 422.6 | 2823.7 | 18037.5 |
| | FANMOD | 0.53 | 1.06 | 4.34 | 24.24 | 160 | 967.99 | - | - |
| | Mavisto | 210.0 | 1727 | - | - | - | - | - | - |
| | Mfinder | 7 | 14 | 109.8 | 2020.2 | - | - | - | - |
| Social | Kavosh | 0.04 | 0.23 | 1.63 | 10.48 | 69.43 | 415.66 | 2594.19 | 14611.23 |
| | FANMOD | 0.46 | 0.84 | 3.07 | 17.63 | 117.43 | 845.93 | - | - |
| | Mavisto | 393 | 1492 | - | - | - | - | - | - |
| | Mfinder | 12 | 49 | 798 | 181077 | - | - | - | - |

Caveats

- Stability of a network structure not necessary imply function stability [Ingram et al. 2006]
- Network structure not always imply function [Voigt et al. 2005]
- Static analysis might hide the relationship between structure and function
 - Temporal network motifs have been investigated [Braha & Bar-Yam 2009][Holme & Saramäki 2012]

[Braha & Bar-Yam 2009] Braha D., Bar-Yam Y. (2009). "Time-Dependent Complex Networks: Dynamic Centrality, Dynamic Motifs, and Cycles of Social Interactions." In: Gross T., Sayama H. (eds) *Adaptive Networks. Understanding Complex Systems*. Springer, Berlin, Heidelberg

[Holme & Saramäki 2012] Holme, P., & Saramäki, J. (2012). Temporal networks. *Physics reports*, 519(3), 97-125.

[Ingram et al. 2006] Ingram PJ, Stumpf MP, Stark J (2006). "Network motifs: structure does not determine function". *BMC Genomics*. 7: 108.

[Voigt et al. 2005] Voigt CA, Wolf DM, Arkin AP (2005). "The Bacillus subtilis sin operon: an evolvable network motif". *Genetics*. 169 (3): 1187-1202.

Goal: find clusters of motifs,

How: find clusters that minimize the number of motif that are cut

Definitions

Motif-cuts: number of motifs whose at least one edge is cut by the clustering

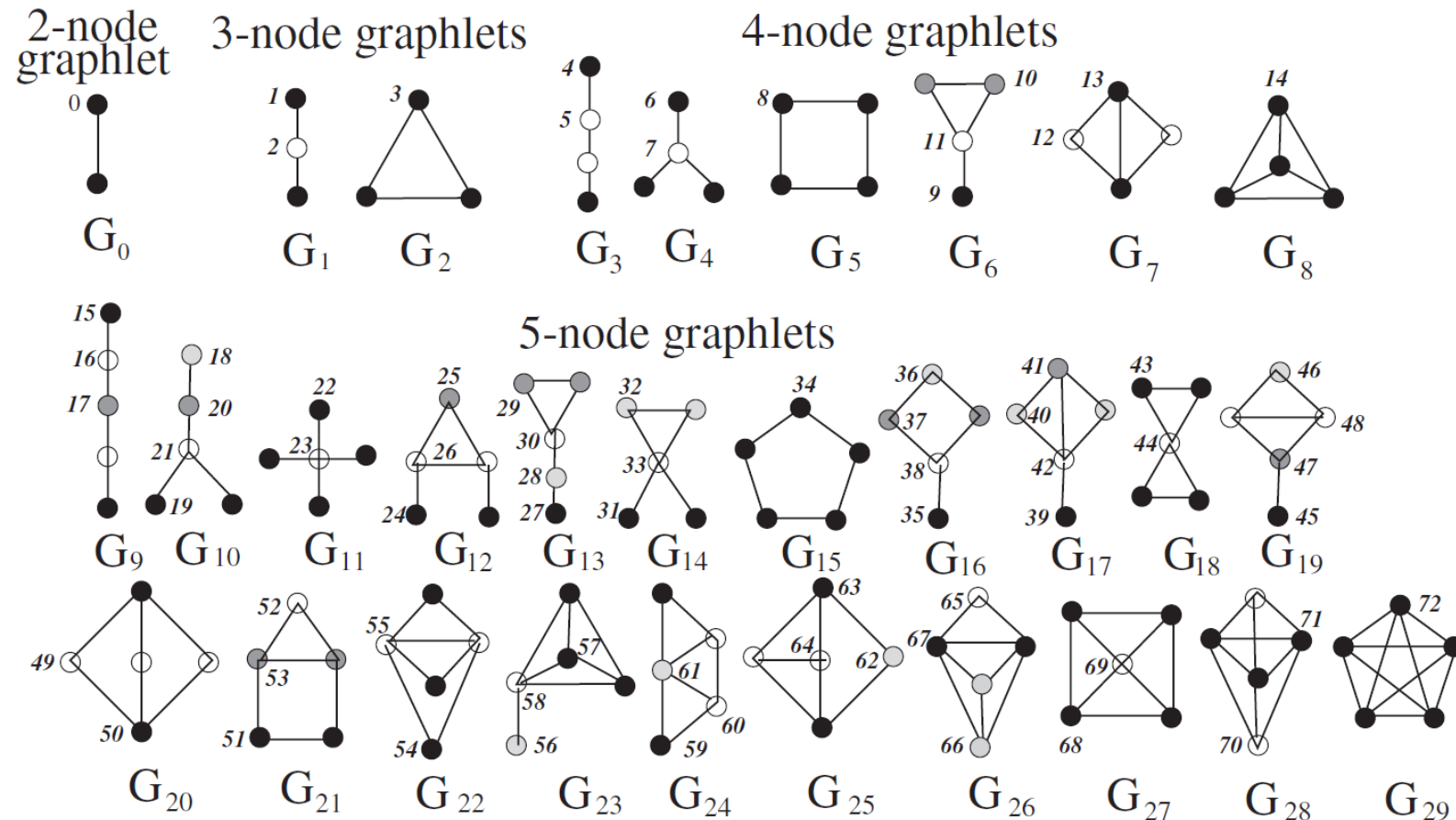
Motif-volume: number of nodes participating in a certain motif type

Motif Conductance: $\phi_M(S) = \frac{\text{MotifCuts}}{\text{MotifVolume}}$, where S is the set of nodes that minimizes conductance.

This is an NP-Hard problem... One approximation is the **Motif-based Spectral Clustering**:

- Step-1 Preprocessing – create a weighted graph W by counting the number of times a motif edge appears
- Step-2 Decomposition – use standard spectral clustering on the Weighted graph
- Step-3 Grouping – same as spectral clustering

Lu, Zhenqi, Johan Wahlström, and Arye Nehorai. "Community detection in complex networks via clique conductance." *Scientific reports* 8.1 (2018): 1-16.



Automorphism orbits $0, 1, 2, \dots, 72$ for the thirty 2, 3, 4, and 5-node graphlets G_0, G_1, \dots, G_{29} . In a graphlet G_i , $i \in \{0, 1, \dots, 29\}$, nodes belonging to the same orbit are of the same shade

Modularity (Q) fraction of the edges within the given groups minus the expected such fraction if edges were distributed at random. It is defined as [Newman 2004]:

$$Q = \frac{1}{2m} \sum_{i,j} \left(A_{i,j} - \frac{k_i k_j}{2m} \right) \delta(c_i, c_j),$$

Actual connection between i and j

If nodes were randomly connected (null model)

where:

m = total number of edges

$A_{i,j}$ = weight of the edge between i and j

$k_i = \sum_j A_{i,j}$ is sum of the weighted edges attached to node i

c_i = community of node i

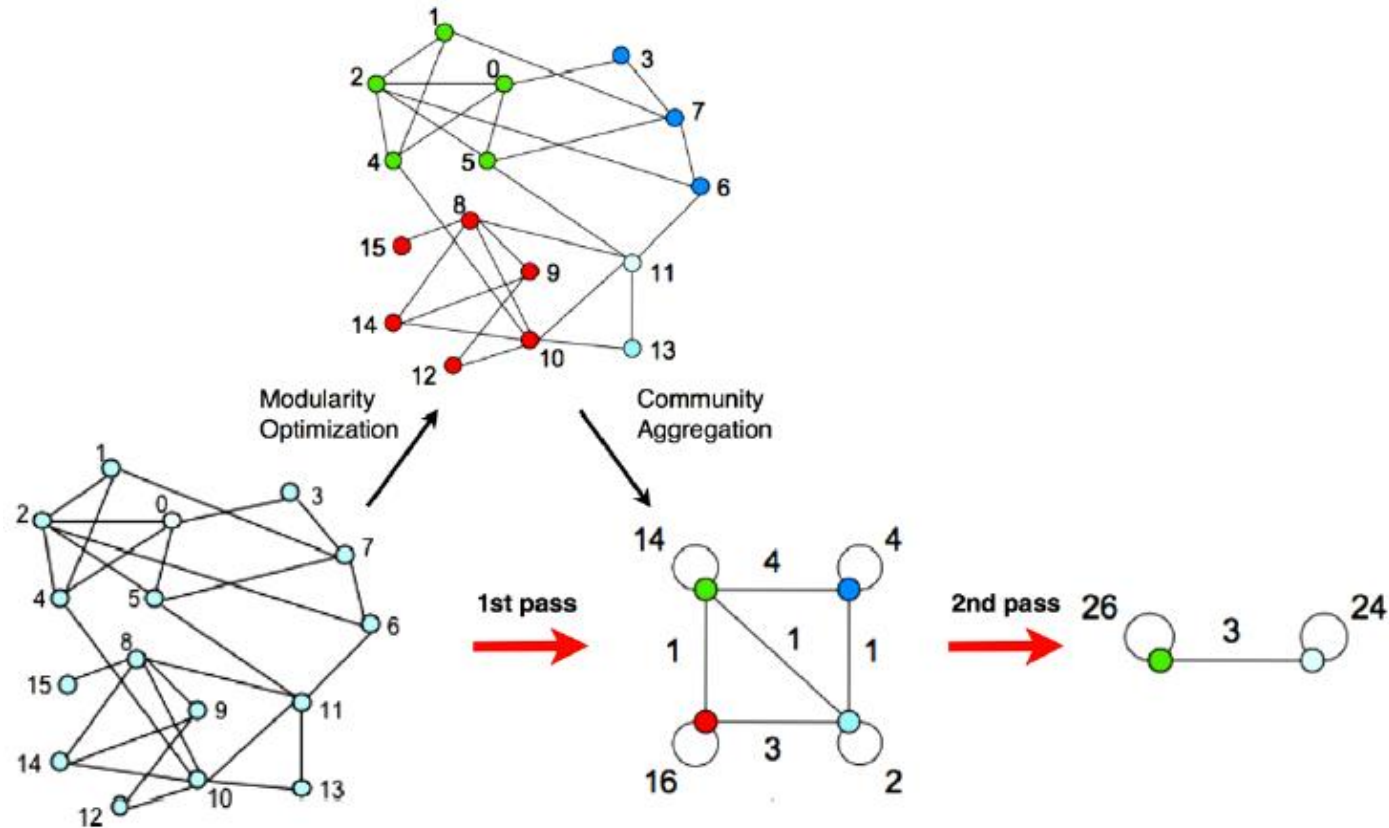
$\delta(c_i, c_j) = 1$ if i and $j \in$ same community c

[Newman 2004] Newman, Mark EJ. "Analysis of weighted networks." *Physical review E* 70.5 (2004): 056131.

[Blondel et al. 2008] Blondel, Vincent D., et al. (2008), "Fast unfolding of communities in large networks.", *Journal of statistical mechanics: theory and experiment*, 2008(9), pp.1-13.

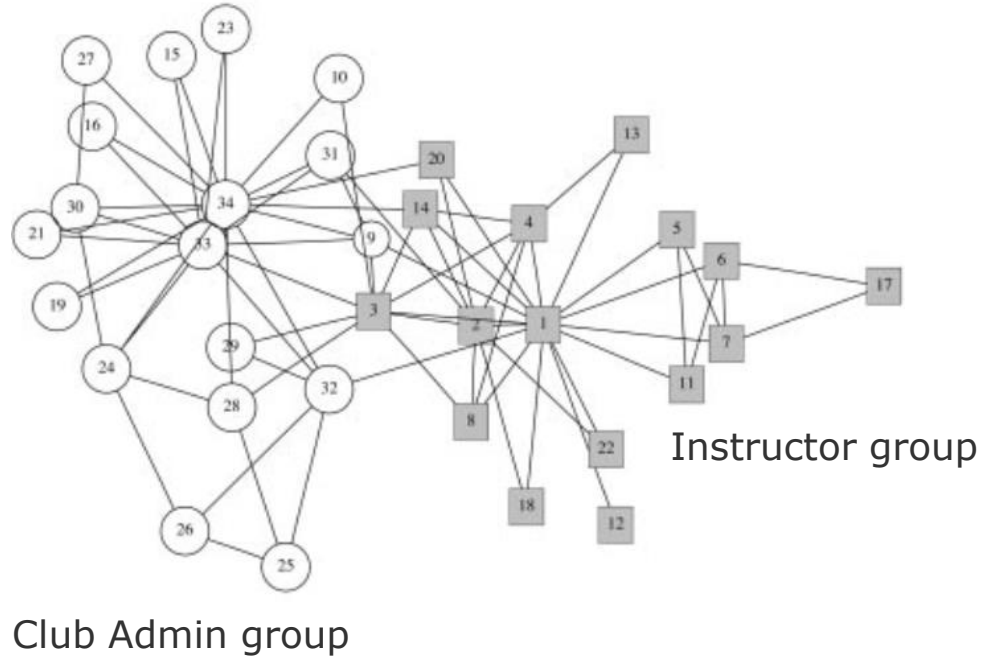
Louvain Algorithm

Iterate until find the lowest modularity value

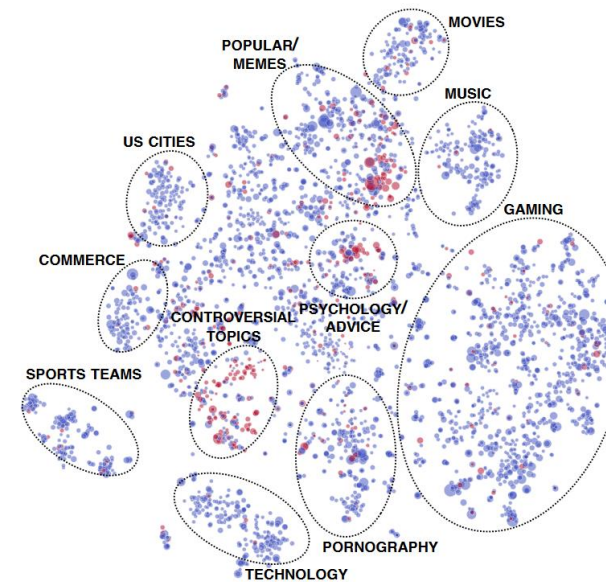


Community structure

Zachary's Karate Club Split
[Girvan et al. 2002]



Reddit Communities
[Kumar, et al. 2018]



[Girvan et al. 2002] Girvan, Michelle, and Mark EJ Newman. "Community structure in social and biological networks." *Proceedings of the national academy of sciences* 99.12 (2002): 7821-7826.

[Kumar et al. 2018] Kumar, S., Hamilton, W. L., Leskovec, J., & Jurafsky, D. (2018, April). Community interaction and conflict on the web. In *Proceedings of the 2018 World Wide Web Conference* (pp. 933-943).

1. Build Graph Laplacian representation:

Laplacian matrix (L) = Adjacency matrix (A) – Degree matrix (D)

2. Reduce Dimensionality:

Compute eigenvalues and eigenvectors of the L matrix

Use eigenvectors to map nodes to a reduced representation

3. Categorize:

Use the new representation, assign nodes to clusters

Further resources

Short Tutorial on Graph Laplacian:

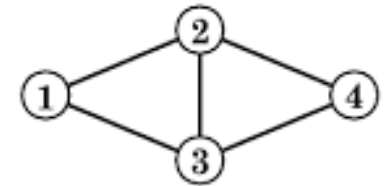
<https://csustan.csustan.edu/~tom/Clustering/GraphLaplacian-tutorial.pdf>

Lecture Slides: http://graphics.stanford.edu/courses/cs468-10-fall/LectureSlides/16_spectral_methods1.pdf

Tutorial on Spectral Clustering:

https://www.cs.cmu.edu/~aarti/Class/10701/readings/Luxburg06_TR.pdf

$$D = \begin{bmatrix} 2 & 0 & 0 & 0 \\ 0 & 3 & 0 & 0 \\ 0 & 0 & 3 & 0 \\ 0 & 0 & 0 & 2 \end{bmatrix}$$



$$A = \begin{bmatrix} 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 0 & 1 & 1 & 0 \end{bmatrix}$$

$$L = \begin{bmatrix} 2 & -1 & -1 & 0 \\ -1 & 3 & -1 & -1 \\ -1 & -1 & 3 & -1 \\ 0 & -1 & -1 & 2 \end{bmatrix}$$

$$L = A - D$$

Algorithm: Spectral graph partitioning - normalized cuts

Input: adjacency matrix **A**

Output: class indicator vector **v**

compute **D** = *diag(deg(A))*;

compute **L** = **D** – **A**;

solve for second smallest eigenvector:

min cut: **Lx** = $\lambda \mathbf{x}$;

normalized cut : **Lx** = $\lambda \mathbf{Dx}$;

set **s** = *sign(x₂)*

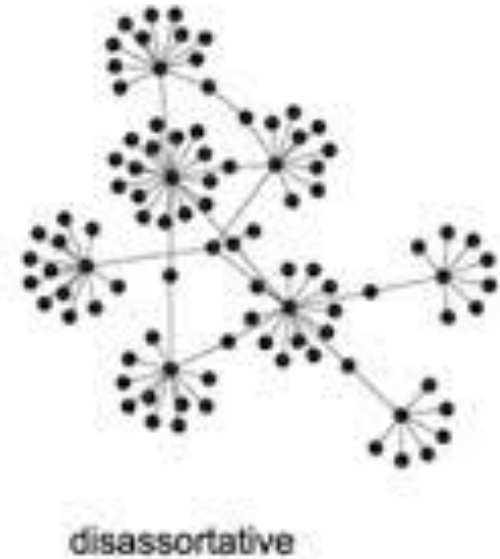
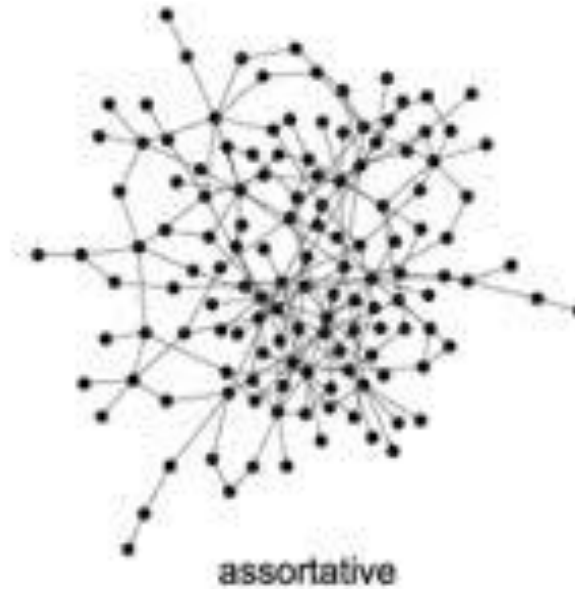
Definition: Preference to attach to nodes that are similar [Newman 2003]

Assortativity Coefficient (Pearson Correlation)

$$r(\alpha, \beta) = \frac{\sum_i (j_i^\alpha - \bar{j}^\alpha)(k_i^\beta - \bar{k}^\beta)}{\sqrt{\sum_i (j_i^\alpha - \bar{j}^\alpha)^2} \sqrt{\sum_i (k_i^\beta - \bar{k}^\beta)^2}}.$$

Neighborhood Connectivity

$$\langle k_{nn} \rangle = \sum_{k'} k' P(k' | k), \text{ where } P(k' | k)$$



[Newman 2003] Newman, M. E. J. (2003). "Mixing patterns in networks". *Physical Review E. American Physical Society (APS)*. **67** (2):

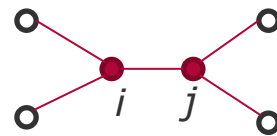
Structural equivalence

- Jaccard Similarity (intersection)
- Cosine Similarity (distance)
- Pearson Correlation
- Euclidean Distance (dissimilarity)
- Node overlap

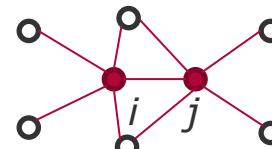
$$j_{ij} = \frac{n_{ij}}{k_i + k_j - n_{ij}}$$

$$\sigma_{ij} = \frac{n_{ij}}{\sqrt{k_i k_j}}$$

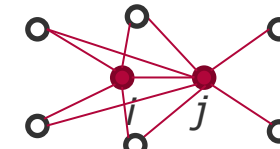
$$o_{i,j} = \frac{|(N_i \cap N_j) \setminus \{i, j\}|}{|(N_i \cup N_j) \setminus \{i, j\}|}$$



$$o_{ij} = 0$$



$$o_{ij} = 1/3$$



$$o_{ij} = 2/3$$

Regular equivalence

Nodes that do not necessarily share neighbors, but have similar features

Please enroll (if you did not yet).

Initial understanding about your graph data

1. What are possible the edges and nodes of your network?
2. What types of networks w.r.t. edge directionality?
3. What type of networks w.r.t. to node types?
4. Is your network possibly assortative, disassortative, or neither?
5. Which centrality metrics might make sense for you?
6. Are there communities/clusters that can be used as features?
7. Do you believe your graph will present high or low cluster coefficient?
8. What about the network diameter (low or high)?

END