



## Community Analysis

SOCIAL  
MEDIA  
MINING



# Social Community



## [real-world] community

A group of individuals with common *economic, social, or political* interests or characteristics, often living in *relative proximity*.

# Why analyze communities?

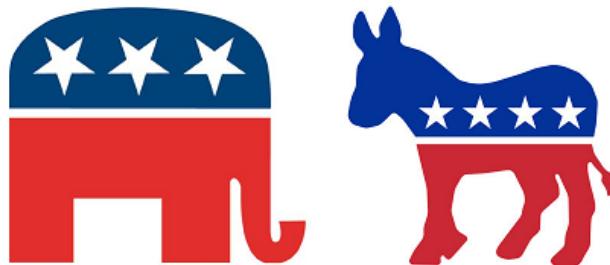
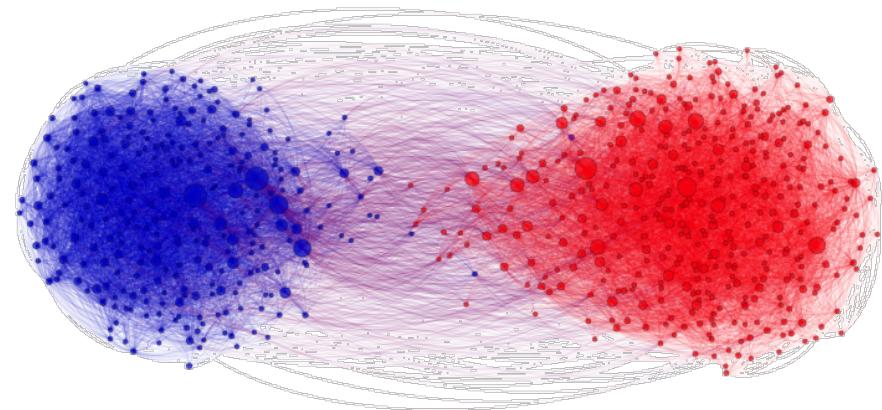


**Analyzing communities helps better understand users**

- Users form groups based on their interests

**Groups provide a clear global view of user interactions**

- E.g., find polarization



**Some behaviors are only observable in a group setting and not on an individual level**

- Some republican can **agree** with some democrats, but their parties can **disagree**

# Social Media Communities

- **Formation:**
  - When like-minded users on social media form a link and start interacting with each other
- **More Formal Formation:**
  1. A set of at least two nodes sharing some interest, and
  2. Interactions with respect to that interest.
- Social Media Communities
  - **Explicit (*emic*)**: formed by user subscriptions
  - **Implicit (*etic*)**: implicitly formed by social interactions
    - **Example:** individuals calling Canada from the United States
    - Phone operator considers them one community for promotional offers
- Other community names: *group, cluster, cohesive subgroup, or module*

# Examples of Explicit Social Media Communities

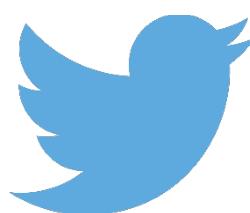


Facebook has groups and communities. Users can

- post messages and images,
- can comment on other messages,
- can like posts, and
- can view activities of other users



In Google+, Circles represent communities



In Twitter, communities form as lists.

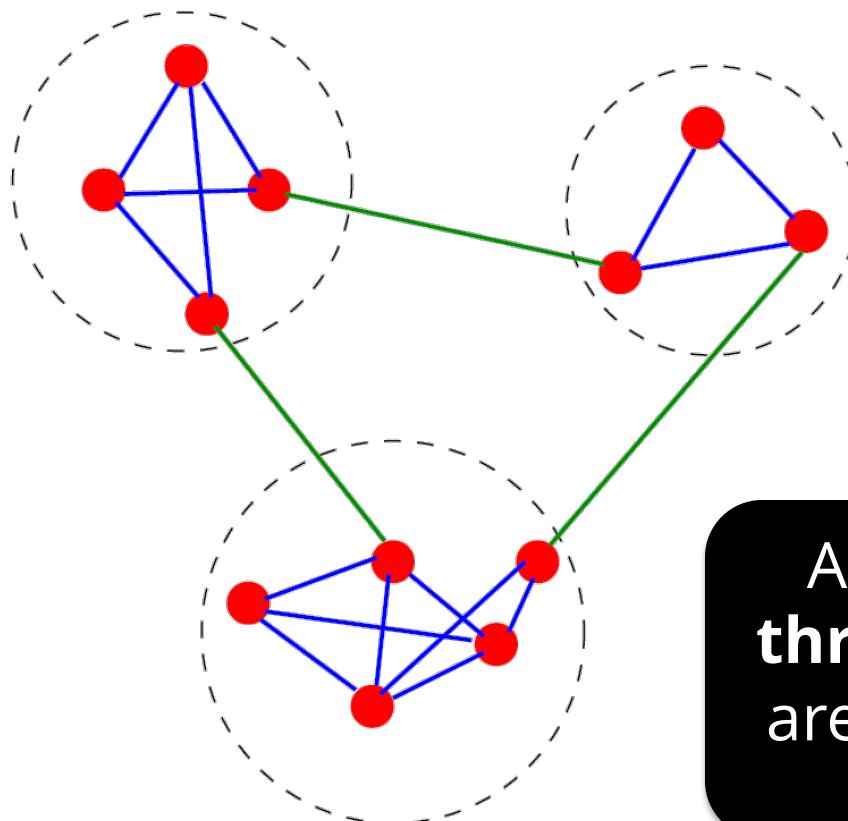
- Users join lists to receive information in the form of tweets



LinkedIn provides *Groups* and *Associations*.

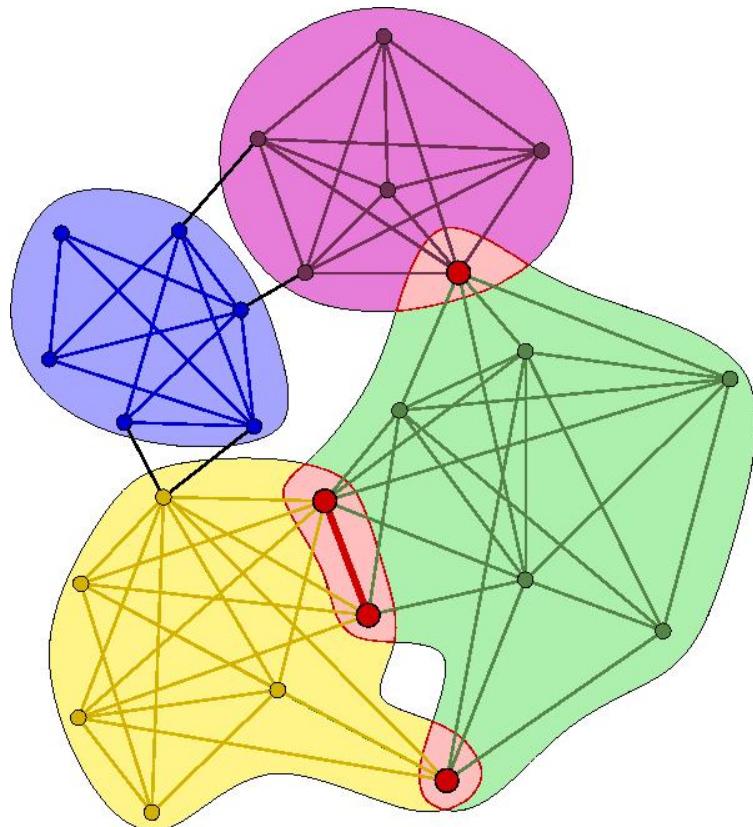
- Users can join professional groups where they can post and share information related to the group

# Finding Implicit Communities: An Example

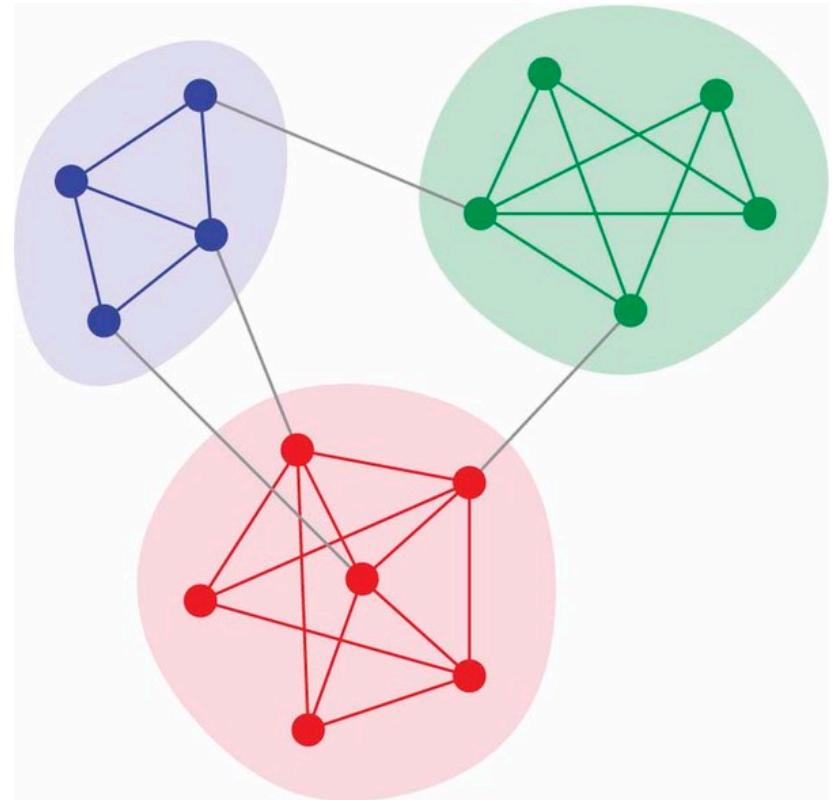


A simple graph in which  
**three** implicit communities  
are found, enclosed by the  
dashed circles

# Overlapping vs. Disjoint Communities



Overlapping Communities

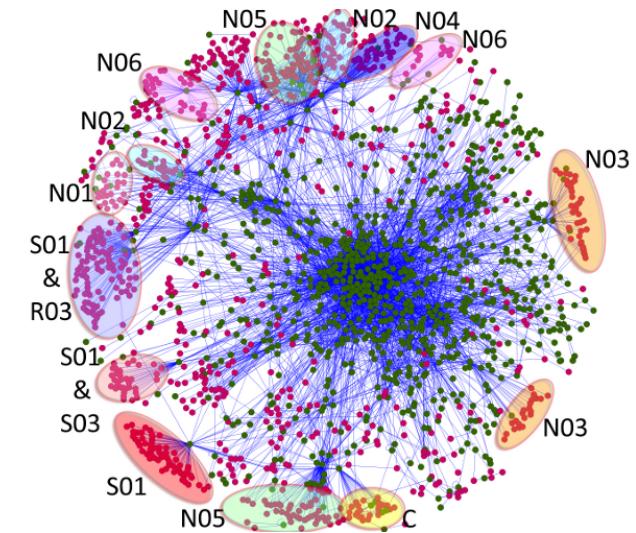


Disjoint Communities

# Implicit communities in other domains

## Protein-protein interaction networks

- Communities are likely to group proteins having the same specific function within the cell



## World Wide Web

- Communities may correspond to groups of pages dealing with the same or related topics

## Metabolic networks

- Communities may be related to functional modules such as cycles and pathways

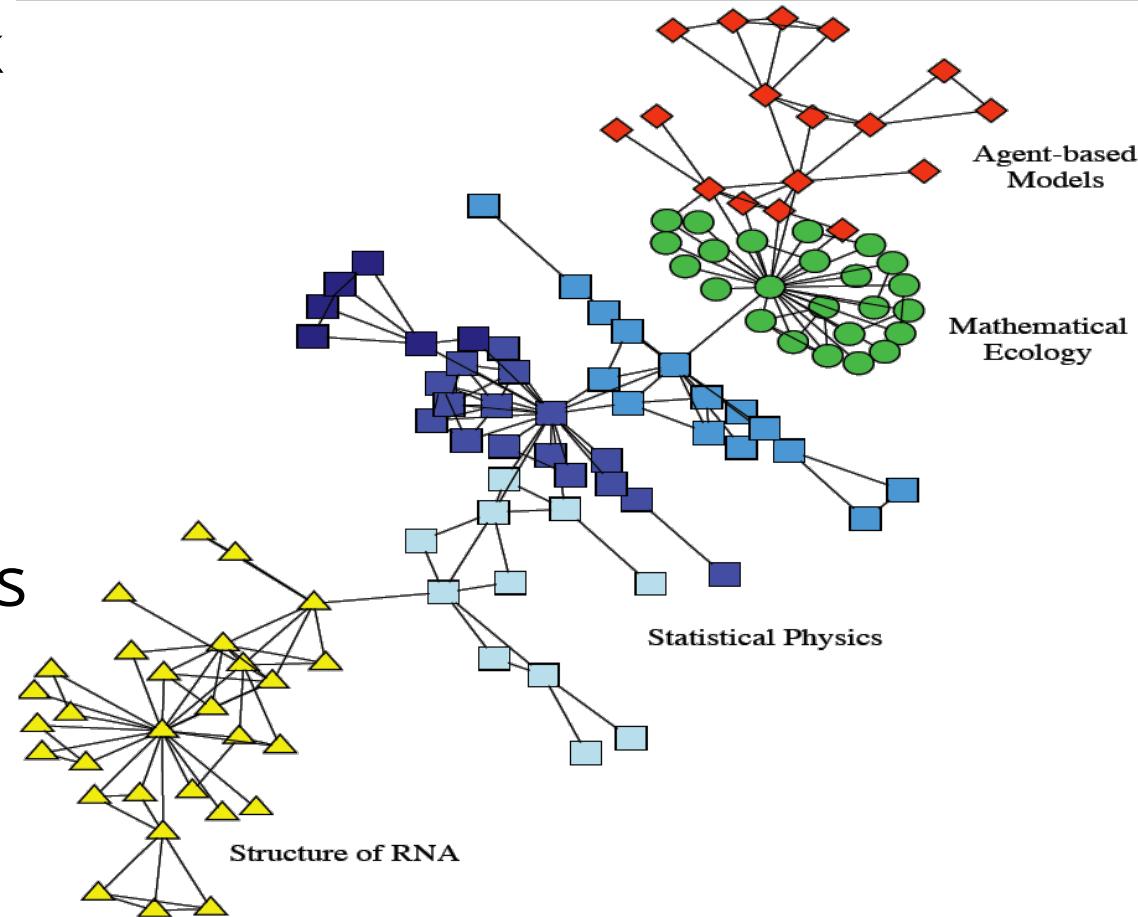
## Food webs

- Communities may identify compartments

# Real-world Implicit Communities

Collaboration network  
between scientists  
working at the  
Santa Fe Institute.

The colors indicate  
high level communities  
and correspond to  
research divisions of  
the institute



# What is Community Analysis?

- **Community detection**
  - Discovering implicit communities
- **Community evolution**
  - Studying temporal evolution of communities
- **Community evaluation**
  - Evaluating Detected Communities

# Community Detection

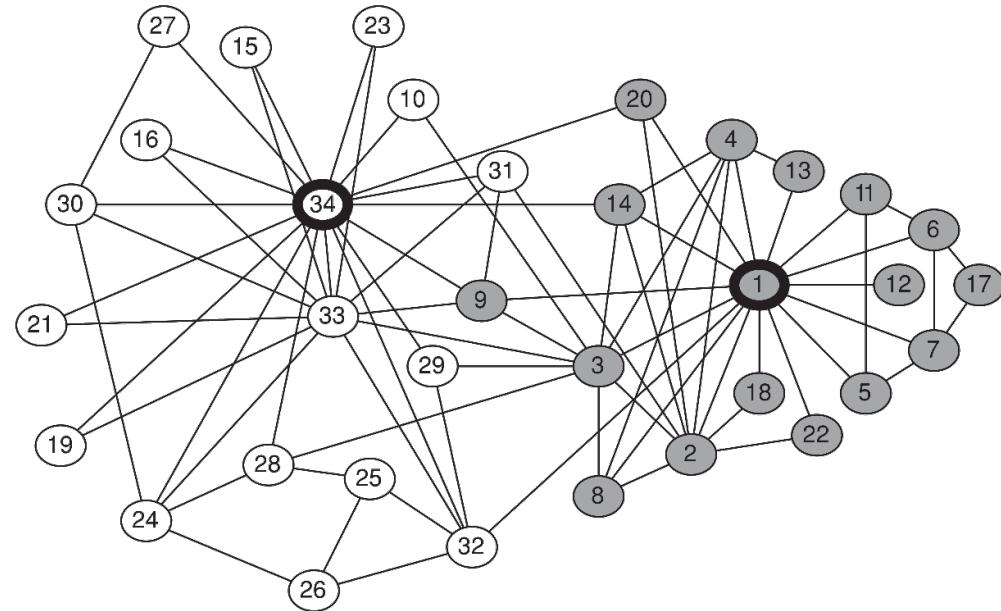
# What is community detection?

- The process of finding clusters of nodes (“*communities*”)
  - With **Strong** internal connections and
  - **Weak** connections between different communities
- Ideal decomposition of a large graph
  - Completely disjoint communities
  - There are no interactions between different communities.
- In practice,
  - find community partitions that are maximally decoupled.

# Why Detecting Communities is Important?

## Zachary's karate club

Interactions between  
34 members of a  
karate club  
for over two years



- The club members split into two groups (**gray** and **white**)
- Disagreement between the administrator of the club (node **34**) and the club's instructor (node **1**),
- The members of one group left to start their own club

**The same communities can be  
found using community detection**

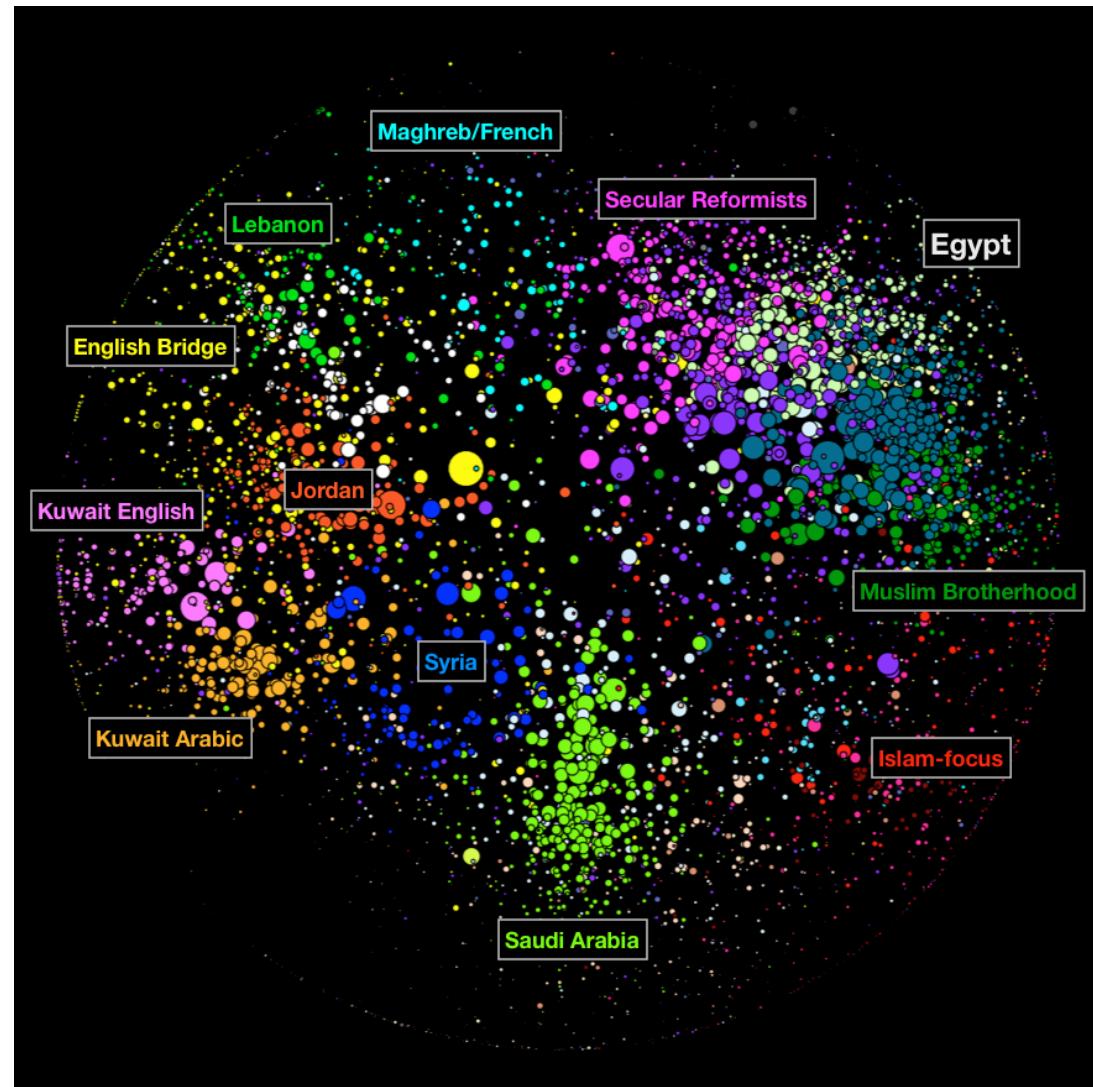
# Why Community Detection?

## Network Summarization

- A community can be considered as a summary of the whole network
- Easier to visualize and understand

## Preserve Privacy

- [Sometimes] a community can reveal some properties without releasing the individuals' privacy information.



# Community Detection vs. Clustering

## Clustering

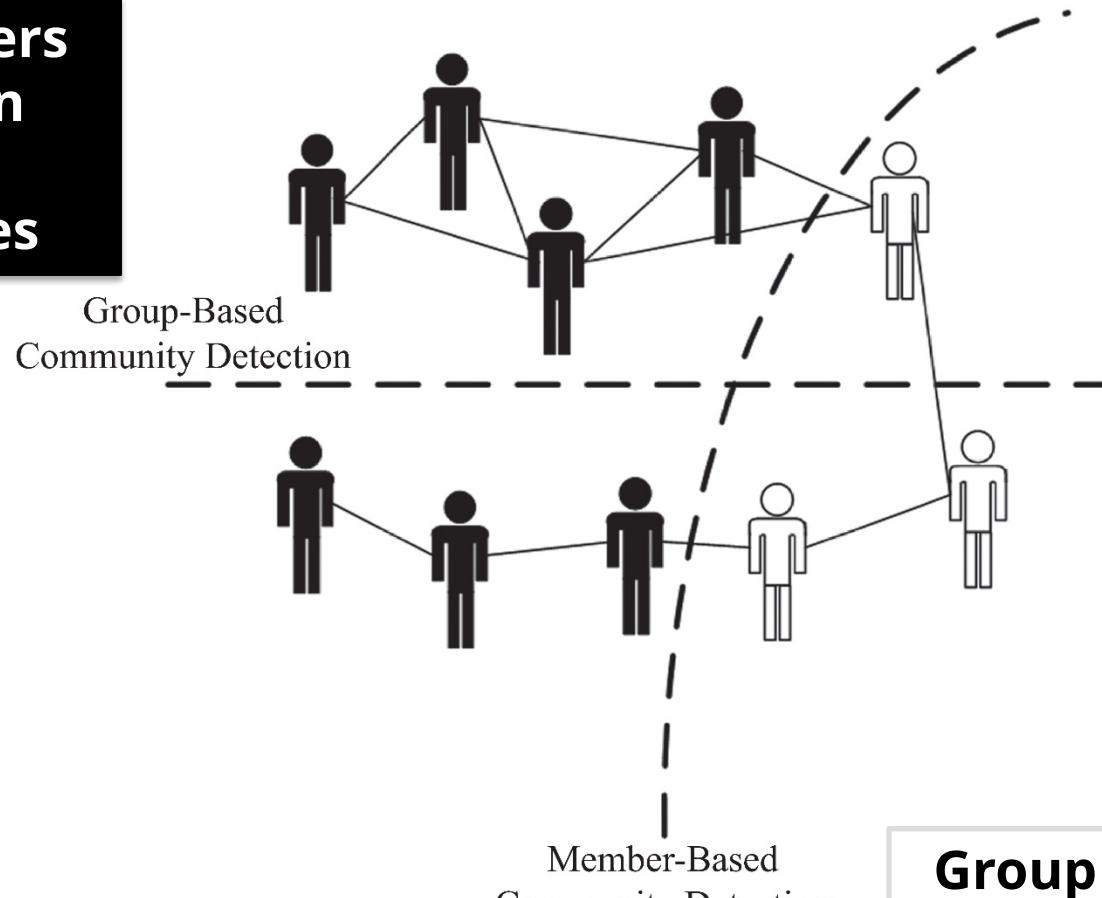
- Data is often non-linked (matrix rows)
- Clustering works on the distance or similarity matrix, e.g.,  $k$ -means.
- If you use  $k$ -means with adjacency matrix rows, you are only considering the ego-centric network

## Community detection

- Data is linked (a graph)
- Network data tends to be “discrete”, leading to algorithms using the graph property directly
  - $k$ -clique, quasi-clique, or edge-betweenness

# Community Detection Algorithms

**Group Users  
based on  
Group  
attributes**



**Group Users  
based on  
Member  
attributes**

# Member-Based Community Detection

# Member-Based Community Detection

- Look at node characteristics; and
- Identify nodes with similar characteristics and consider them a community

## ***Node Characteristics***

### ***A. Degree***

- Nodes with same (or similar) degrees are in one community
- Example: cliques

### ***B. Reachability***

- Nodes that are close (small shortest paths) are in one community
- Example:  $k$ -cliques,  $k$ -clubs, and  $k$ -clans

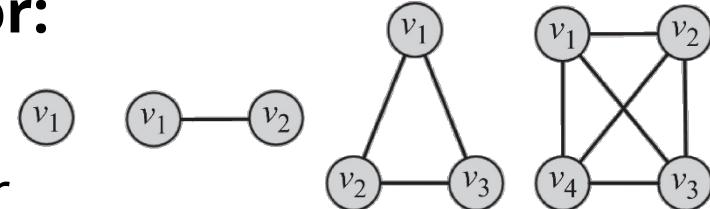
### ***C. Similarity***

- Similar nodes are in the same community

# A. Node Degree

## Most common subgraph searched for:

- **Clique**: a maximum complete subgraph in which all nodes inside the subgraph adjacent to each other



Find communities by searching for

1. **The maximum clique**:  
the one with the largest number of vertices, or
2. **All maximal cliques**:  
cliques that are not subgraphs of a larger clique; i.e., cannot be further expanded

To overcome this, we can

- I. Brute Force
- II. Relax cliques
- III. Use cliques as the core for larger communities

Both problems are NP-hard

# I. Brute-Force Method

Can find all the maximal cliques in the graph

For each vertex  $v_x$ , we find the maximal clique that contains node  $v_x$

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**Algorithm 1** Brute-Force Clique Identification

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**Require:** Adjacency Matrix  $A$ , Vertex  $v_x$

```
1: return Maximal Clique  $C$  containing  $v_x$ 
2: CliqueStack =  $\{\{v_x\}\}$ , Processed =  $\{\}$ ;
3: while CliqueStack not empty do
4:    $C = \text{pop}(\text{CliqueStack})$ ;  $\text{push}(\text{Processed}, C)$ ;
5:    $v_{last} = \text{Last node added to } C$ ;
6:    $N(v_{last}) = \{v_i | A_{v_{last}, v_i} = 1\}$ .
7:   for all  $v_{temp} \in N(v_{last})$  do
8:     if  $C \cup \{v_{temp}\}$  is a clique then
9:        $\text{push}(\text{CliqueStack}, C \cup \{v_{temp}\})$ ;
10:      end if
11:    end for
12:  end while
13: Return the largest clique from Processed
```

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## Impractical for large networks:

- For a complete graph of only 100 nodes, the algorithm will generate at least  $2^{99} - 1$  different cliques starting from any node in the graph

# Enhancing the Brute-Force Performance

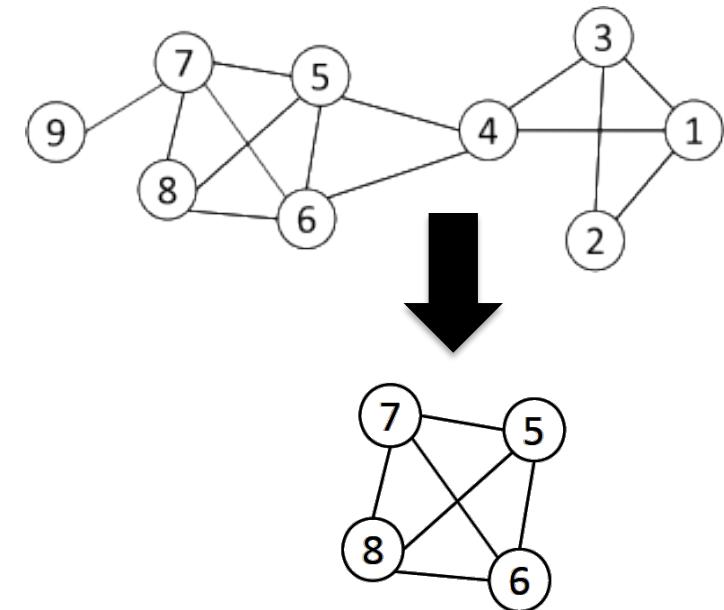
[Systematic] Pruning can help:

- When searching for cliques of size  $k$  or larger
- If the clique is found, each node should have a degree equal to or more than  $k - 1$
- We can first prune all nodes (and edges connected to them) with degrees less than  $k - 1$ 
  - More nodes will have degrees less than  $k - 1$
  - Prune them recursively
- For large  $k$ , many nodes are pruned as social media networks follow a power-law degree distribution

# Maximum Clique: Pruning...

**Example.** to find a clique  $\geq 4$ , remove all nodes with degree  $\leq (4 - 1) - 1 = 2$

- Remove nodes 2 and 9
- Remove nodes 1 and 3
- Remove node 4



Even with pruning, cliques are less desirable

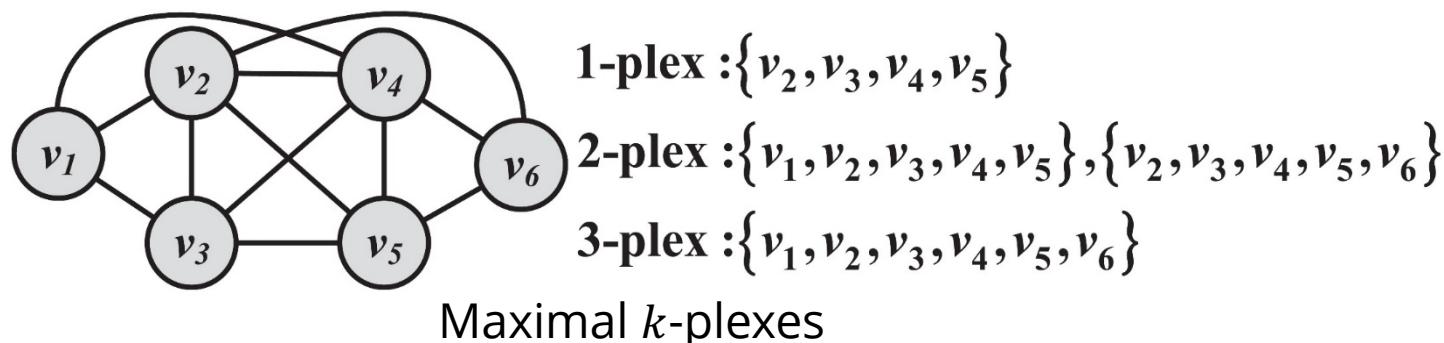
- Cliques are **rare**
- A clique of 1000 nodes, has  $999 \times 1000 / 2$  edges
  - **A single edge removal** destroys the clique
  - That is less than 0.0002% of the edges!

## II. Relaxing Cliques

- **$k$ -plex**: a set of vertices  $V$  in which we have

$$d_v \geq |V| - k, \forall v \in V$$

- $d_v$  is the degree of  $v$  in the induced subgraph
  - Number of nodes from  $V$  that are connected to  $v$
- Clique of size  $k$  is a  $1$ -plex
- Finding the maximum  $k$ -plex: **NP-hard**
  - In practice, relatively easier due to smaller search space.



# More Cliques Relaxing...

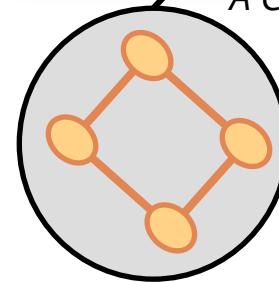
- **$k$ -core:** a maximal connected subgraph in which all vertices have degree at least  $k$ 
  - Difference with  $k$ -plex?
- **$k$ -shell:** nodes that are part of the  $k$ -core, but are not part of the  $(k + 1)$ -core.

## Questions

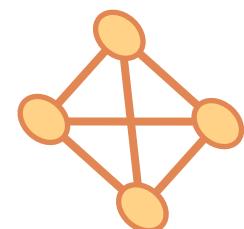
- 0-core?
- 0-shell?
- 1-core?
- $k$ -cores of the complete graph?



A Clique that wants to relax



A 2-plex or a 2-core?

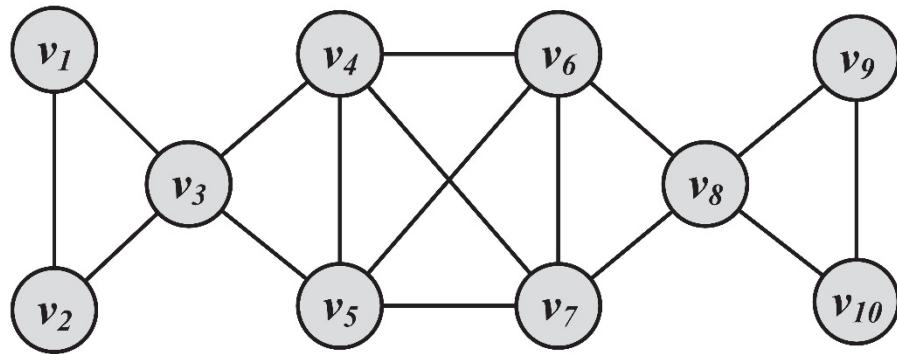


# III. Using Cliques as a seed of a Community

## Clique Percolation Method (CPM)

- Uses cliques as seeds to find larger communities
  - CPM finds overlapping communities
- 
- **Input**
    - A parameter  $k$ , and a network
  - **Procedure**
    - Find out all cliques of size  $k$  in the given network
    - Construct a clique graph.
      - Two cliques are adjacent if they share  $k - 1$  nodes
    - Each connected components in the clique graph form a community

# Clique Percolation Method: Example



(a) Graph

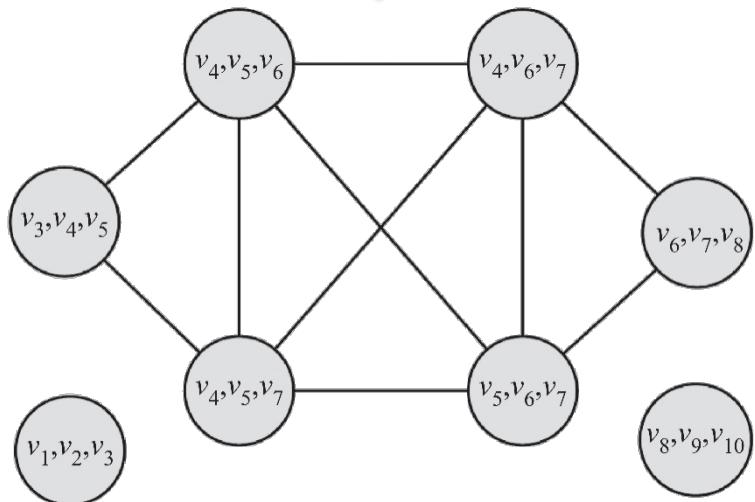
## Cliques of size 3:

$\{v_1, v_2, v_3\}, \{v_3, v_4, v_5\},$   
 $\{v_4, v_5, v_6\}, \{v_4, v_5, v_7\},$   
 $\{v_4, v_6, v_7\}, \{v_5, v_6, v_7\},$   
 $\{v_6, v_7, v_8\}, \{v_8, v_9, v_{10}\}$



## Communities:

$\{v_1, v_2, v_3\},$   
 $\{v_8, v_9, v_{10}\},$   
 $\{v_3, v_4, v_5, v_6, v_7, v_8\}$



(b) CPM Clique Graph

## B. Node Reachability

### The two extremes

Nodes are assumed to be in the same community

1. If there is a path between them (regardless of the distance) or
2. They are so close as to be immediate neighbors.

**How? Find using BFS/DFS**

**Challenge:** most nodes are in one community (giant component)

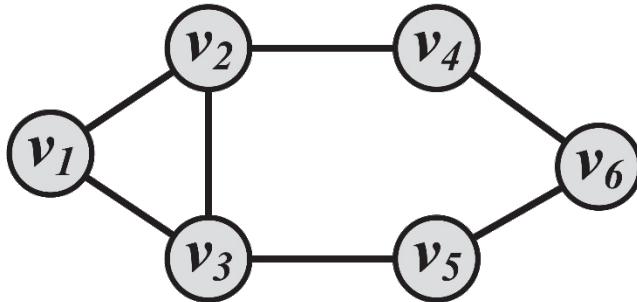
**How? Finding Cliques**

**Challenge:** Cliques are challenging to find and are rarely observed

**Solution:** find communities that are in between **cliques** and **connected components** in terms of connectivity and have small shortest paths between their nodes

# Special Subgraphs

1. ***k*-Clique**: a **maximal** subgraph in which the largest shortest path distance between any nodes is less than or equal to  $k$
2. ***k*-Club**: follows the same definition as a  $k$ -clique
  - **Additional Constraint**: nodes on the shortest paths should be part of the subgraph (i.e., diameter)
3. ***k*-Clan**: a  $k$ -clique where for all shortest paths within the subgraph the distance is equal or less than  $k$ .
  - All  $k$ -clans are  $k$ -cliques, but not vice versa.



2-cliques :  $\{v_1, v_2, v_3, v_4, v_5\}, \{v_2, v_3, v_4, v_5, v_6\}$

2-clubs :  $\{v_2, v_3, v_4, v_5, v_6\}, \{v_1, v_2, v_3, v_4\}, \{v_1, v_2, v_3, v_5\}$

2-clans :  $\{v_2, v_3, v_4, v_5, v_6\}$

# More Special Subgraphs!



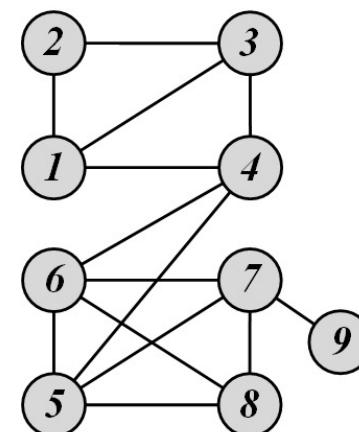
- ***k*-truss:** the largest subgraph where all edges belong to  $k - 2$  triangles
- What is the relationship between a ***k*-core** and ***k*-truss**?

# C. Node Similarity

- Similar (or most similar) nodes are assumed to be in the same community.
  - A classical clustering algorithm (e.g.,  $k$ -means) is applied to node similarities to find communities.
- Node similarity can be defined
  - Using the similarity of node neighborhoods (**Structural Equivalence**) – Ch. 3
  - Similarity of social circles (**Regular Equivalence**) – Ch. 3

**Structural equivalence:** two nodes are structurally equivalent iff. they are connecting to the same set of actors

*Nodes 1 and 3 are  
structurally equivalent,  
So are nodes 5 and 7.*



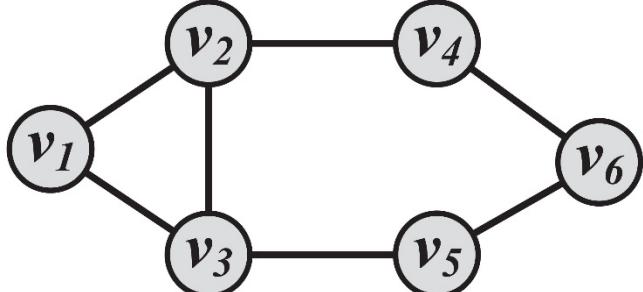
# Node Similarity (Structural Equivalence)

**Jaccard Similarity**

$$\sigma_{\text{Jaccard}}(v_i, v_j) = \frac{|N(v_i) \cap N(v_j)|}{|N(v_i) \cup N(v_j)|}$$

**Cosine similarity**

$$\sigma_{\text{Cosine}}(v_i, v_j) = \frac{|N(v_i) \cap N(v_j)|}{\sqrt{|N(v_i)||N(v_j)|}}$$



$$\sigma_{\text{Jaccard}}(v_2, v_5) = \frac{|\{v_1, v_3, v_4\} \cap \{v_3, v_6\}|}{|\{v_1, v_3, v_4, v_6\}|} = 0.25$$

$$\sigma_{\text{Cosine}}(v_2, v_5) = \frac{|\{v_1, v_3, v_4\} \cap \{v_3, v_6\}|}{\sqrt{|\{v_1, v_3, v_4\}||\{v_3, v_6\}|}} = 0.40$$

# Group-Based Community Detection

# Group-Based Community Detection

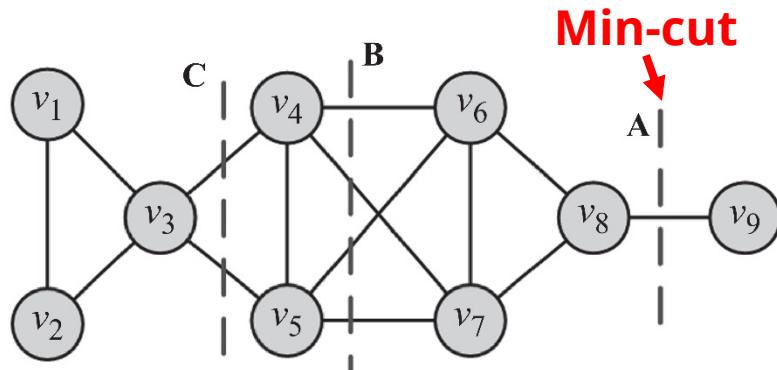
Group-based community detection: finding communities that have certain **group properties**

## Group Properties:

- I. **Balanced**: Spectral clustering
- II. **Robust**:  $k$ -connected graphs
- III. **Modular**: Modularity Maximization
- IV. **Dense**: Quasi-cliques
- V. **Hierarchical**: Hierarchical clustering

# I. Balanced Communities

- Community detection can be thought of *graph clustering*
- Graph clustering:** we cut the graph into several partitions and assume these partitions represent communities
- Cut:** partitioning (*cut*) of the graph into two (or more) sets (*cutsets*)
  - The size of the cut is the number of edges that are being cut
- Minimum cut (min-cut) problem:** find a graph partition such that the number of edges between the two sets is minimized



Min-cuts can be computed efficiently using the max-flow min-cut theorem

Min-cut often returns an imbalanced partition, with one set being a singleton

# Ratio Cut and Normalized Cut

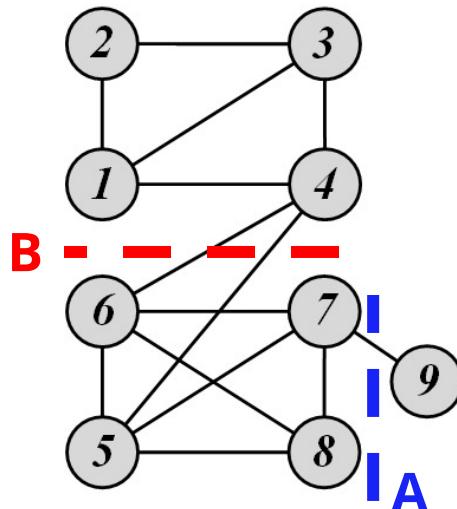
- To mitigate the min-cut problem we can change the objective function to consider community size

$$\text{Ratio Cut}(P) = \frac{1}{k} \sum_{i=1}^k \frac{\text{cut}(P_i, \bar{P}_i)}{|P_i|}$$

$$\text{Normalized Cut}(P) = \frac{1}{k} \sum_{i=1}^k \frac{\text{cut}(P_i, \bar{P}_i)}{\text{vol}(P_i)}$$

- $\bar{P}_i = V - P_i$  is the complement cut set
- $\text{cut}(P_i, \bar{P}_i)$  is the size of the cut
- $\text{vol}(P_i) = \sum_{v \in P_i} d_v$

# Ratio Cut & Normalized Cut: Example



## For Cut A

$$\text{Ratio Cut}(\{1, 2, 3, 4, 5, 6, 7, 8\}, \{9\}) = \frac{1}{2}(\frac{1}{1} + \frac{1}{8}) = 9/16 = 0.56$$

$$\text{Normalized Cut}(\{1, 2, 3, 4, 5, 6, 7, 8\}, \{9\}) = \frac{1}{2}(\frac{1}{1} + \frac{1}{27}) = 14/27 = 0.52$$

## For Cut B

$$\text{Ratio Cut}(\{1, 2, 3, 4\}, \{5, 6, 7, 8, 9\}) = \frac{1}{2}(\frac{2}{4} + \frac{2}{5}) = 9/20 = 0.45 < 0.56$$

$$\text{Normalized Cut}(\{1, 2, 3, 4\}, \{5, 6, 7, 8, 9\}) = \frac{1}{2}(\frac{2}{12} + \frac{2}{16}) = 7/48 = 0.15 < 0.52$$

Both ratio cut and normalized cut prefer a balanced partition

# Spectral Clustering

## Reformulating ratio cut (or normalized cut) in matrix format

- Let  $X_{ij} = 1$ , when node  $i$  is member of community  $j$ ; 0, otherwise
- Let  $D = \text{diag}(d_1, d_2, \dots, d_n)$  be the diagonal degree matrix
- The  $i$ th entry on the diagonal of  $X^TAX$  is **the number of edges that are inside community  $i$ .**
- The  $i$ th element on the diagonal of  $X^TDX$  is **the number of edges that are connected to members of community  $i$ .**
- The  $i$ th element on the diagonal of  $X^T(D - A)X$  is **the number of edges in the cut that separates community  $i$  from other nodes.**

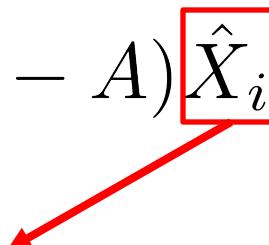
The  $i$ th diagonal element of  $X^T(D - A)X$  is equivalent to  $\text{cut}(P_i, \bar{P}_i)$

# Spectral Clustering

So ratio cut is

$$\begin{aligned}\text{Ratio Cut}(P) &= \frac{1}{k} \sum_{i=1}^k \frac{\text{cut}(P_i, \bar{P}_i)}{|P_i|} \\ &= \frac{1}{k} \sum_{i=1}^k \frac{X_i^T (D - A) X_i}{X_i^T X_i} \\ &= \frac{1}{k} \sum_{i=1}^k \hat{X}_i^T (D - A) \hat{X}_i\end{aligned}$$

$\hat{X}_i = \hat{X}_i / (\hat{X}_i^T \hat{X}_i)^{1/2}$



# Spectral Clustering

Both ratio/normalized cut can be reformulated as

$$\min_{\hat{X}} \text{Tr}(\hat{X}^T L \hat{X})$$

$$L = \begin{cases} D - A & \text{Ratio Cut Laplacian, i.e., Unnormalized Laplacian} \\ I - D^{-1/2} A D^{-1/2} & \text{Normalized Laplacian for Normalized Cut.} \end{cases}$$

$D = \text{diag}(d_1, d_2, \dots, d_n)$  is a diagonal degree matrix

- Spectral relaxation:

$$\begin{aligned} & \min_{\hat{X}} \text{Tr}(\hat{X}^T L \hat{X}) \\ & s.t. \quad \hat{X}^T \hat{X} = I_k \end{aligned}$$

**Optimal Solution**

**$\hat{X}$  is the top eigenvectors with the smallest eigenvalues**

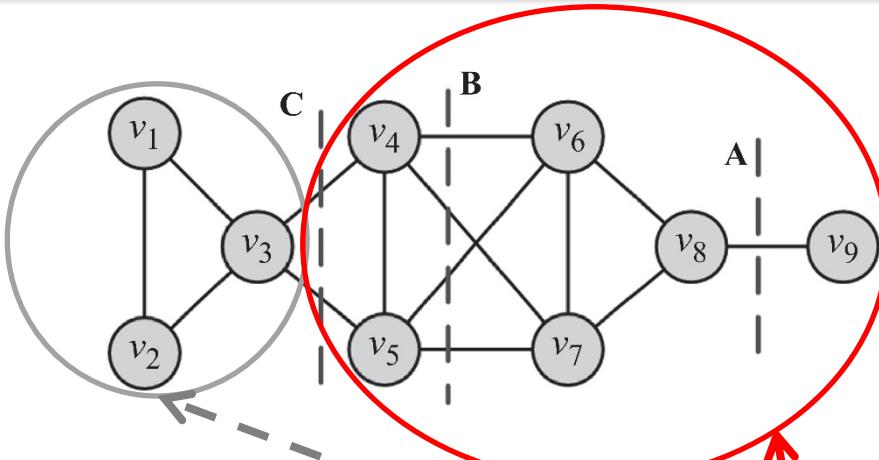
# Recovering Integer Membership Values

- Because we performed spectral relaxation, the matrix obtained is not integer valued
- To recover  $X$  from  $\hat{X}$  we can run  $k$ -means on  $\hat{X}$

# Spectral Clustering: Example

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

$$D = \text{diag}(2, 2, 4, 4, 4, 4, 4, 3, 1)$$



Two communities:  
 $\{v_1, v_2, v_3\}$   
 $\{v_4, v_5, v_6, v_7, v_8, v_9\}$

$$L = D - A = \begin{bmatrix} 2 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & -1 & 4 & -1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 4 & -1 & -1 & -1 & 0 & 0 \\ 0 & 0 & -1 & -1 & 4 & -1 & -1 & 0 & 0 \\ 0 & 0 & 0 & -1 & -1 & 4 & -1 & -1 & 0 \\ 0 & 0 & 0 & -1 & -1 & -1 & 4 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & -1 & 3 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 1 \end{bmatrix}$$

2 Eigenvectors  
i.e., we want  
2 communities

$$\begin{bmatrix} 0.53 & -0.46 \\ 0.33 & -0.46 \\ 0.33 & -0.26 \\ 0.33 & 1.16 \times 10^{-16} \\ 0.33 & 1.16 \times 10^{-16} \\ 0.33 & 0.13 \\ 0.33 & 0.13 \\ 0.33 & 0.33 \\ 0.33 & 0.59 \end{bmatrix}$$

k-means,  $k = 2$

## Laplacian and Diffusion:

- Consider a substance that diffuses from node to node on a graph (e.g., gas or fluid)
- The substance quantity for node  $j$  is  $\varphi(j)$
- The diffusion depends on the difference in quantity between nodes
  - e.g., gas pressure difference
- Then we have

$$\frac{d\phi_i}{dt} = \alpha \sum_j A_{ji}(\phi_j - \phi_i)$$

# Laplacian and Diffusion

$$\begin{aligned}\frac{d\phi_i}{dt} &= \alpha \sum_j A_{ji}(\phi_j - \phi_i) \\&= \alpha \sum_j A_{ji}\phi_j - \alpha \sum_j A_{ji}\phi_i \\&= \alpha \sum_j A_{ji}\phi_j - \alpha\phi_i \sum_j A_{ji} \\&= \alpha \sum_j A_{ji}\phi_j - \alpha\phi_i d_i \\&= \alpha \sum_j (A_{ji} - \delta_{ij}d_i)\phi_j \quad \longrightarrow -L_{ij} \\ \frac{d\phi}{dt} &= -\alpha L\phi \quad \longrightarrow \quad \frac{d\phi}{dt} + \alpha L\phi = 0\end{aligned}$$

Why do we call it the Laplacian? As this is equivalent to heat equation  
 $(\frac{d\varphi}{dt} + \alpha\nabla^2\varphi = 0)$  and  $L$  replaces the Laplace operator  $\nabla^2$

# Laplacian and Diffusion

$$\frac{d\phi}{dt} + \alpha L\phi = 0$$

State  $\varphi(t)$  in terms of eigenvalue-eigenvectors of  $L$   
–  $L$  is symmetric and has real eigenvalues.

$$\phi(t) = \sum_i w_i(t) v_i \quad \text{Some coefficient!}$$

$$\sum_i \left( \frac{dw_i(t)}{dt} + \alpha \lambda_i w_i(t) \right) v_i = 0$$

Eigenvalues are orthogonal, so right multiply by any  $v_j$

$$\forall i, \frac{dw_i(t)}{dt} + \alpha \lambda_i w_i(t) = 0$$

$$w_i(t) = w_i(0) e^{-\alpha \lambda_i t}$$

## II. Robust Communities

- The goal is find subgraphs robust enough such that removing some edges or vertices does not disconnect the subgraph
- **$k$ -vertex connected ( $k$ -connected) graph:**
  - $k$  is the minimum number of nodes that must be removed to disconnect the graph
- **$k$ -edge connected:** at least  $k$  edges must be removed to disconnect the graph
- Examples:
  - Complete graph of size  $n$ : unique  $n$ -connected graph
  - A cycle: 2-connected graph

### III. Modular Communities

Consider a graph  $G(V, E)$ , where the degrees are known beforehand however edges are not

- Consider two vertices  $v_i$  and  $v_j$  with degrees  $d_i$  and  $d_j$ .

What is an expected number of edges between  $v_i$  and  $v_j$ ?

- For any edge going out of  $v_i$  randomly the probability of this edge getting connected to vertex  $v_j$  is

$$\frac{d_j}{\sum_i d_i} = \frac{d_j}{2m}$$

# Modularity and Modularity Maximization

- Given a degree distribution, we know the expected number of edges between any pairs of vertices
- We assume that real-world networks should be far from random. Therefore, the more distant they are from this randomly generated network, the more structural they are.
- Modularity defines this distance and modularity maximization tries to maximize this distance

# Normalized Modularity

Consider a partitioning of the data  $P = (P_1, P_2, P_3, \dots, P_k)$

For partition  $P_x$ , this distance can be defined as

$$\sum_{i,j \in P_x} A_{ij} - \frac{d_i d_j}{2m}$$

This distance can be generalized for a partitioning  $P$

$$\sum_{x=1}^k \sum_{i,j \in P_x} A_{ij} - \frac{d_i d_j}{2m}$$

The normalized version of this distance is defined as **Modularity**

$$Q = \frac{1}{2m} \sum_{x=1}^k \sum_{i,j \in P_x} A_{ij} - \frac{d_i d_j}{2m}$$

# Modularity Maximization

Modularity matrix

$$B = A - dd^T / 2m$$

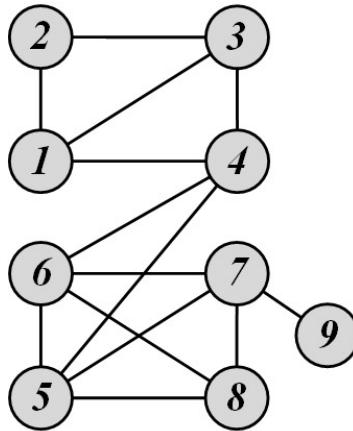
$d \in \mathbb{R}^{n \times 1}$  is the degree vector for all nodes

Reformulation of the modularity

$$Q = \frac{1}{2m} \text{Tr}(X^T BX)$$

- $X \in \mathbb{R}^{n \times k}$  is the indicator (partition membership) function:
  - $X_{ij} = 1$  iff.  $v_i \in P_j$
- Similar to Spectral clustering,
  - We relax  $X$  to be orthogonal, i.e., matrix  $\hat{X}$
  - The optimal solution for  $\hat{X}$  is the top  $k$  eigenvectors of  $B$ .
  - To recover the original  $X$ , we can run  $k$ -means on  $\hat{X}$
- **Difference:** in Modularity, the top  $k$  eigenvalues have to be positive!

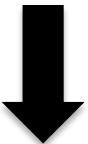
# Modularity Maximization: Example



**Two Communities:**  
 $\{1, 2, 3, 4\}$   
and  
 $\{5, 6, 7, 8, 9\}$

$$B = A - dd^T / 2m$$

$$B_{ij} = A_{ij} - d_i d_j / 2m$$



$$B = \begin{bmatrix} -0.32 & 0.79 & 0.68 & 0.57 & -0.43 & -0.43 & -0.43 & -0.32 & -0.11 \\ 0.79 & -0.14 & 0.79 & -0.29 & -0.29 & -0.29 & -0.29 & -0.21 & -0.07 \\ 0.68 & 0.79 & -0.32 & 0.57 & -0.43 & -0.43 & -0.43 & -0.32 & -0.11 \\ 0.57 & -0.29 & 0.57 & -0.57 & 0.43 & 0.43 & -0.57 & -0.43 & -0.14 \\ -0.43 & -0.29 & -0.43 & 0.43 & -0.57 & 0.43 & 0.43 & 0.57 & -0.14 \\ -0.43 & -0.29 & -0.43 & 0.43 & 0.43 & -0.57 & 0.43 & 0.57 & -0.14 \\ -0.43 & -0.29 & -0.43 & -0.57 & 0.43 & 0.43 & -0.57 & 0.57 & 0.86 \\ -0.32 & -0.21 & -0.32 & -0.43 & 0.57 & 0.57 & 0.57 & -0.32 & -0.11 \\ -0.11 & -0.07 & -0.11 & -0.14 & -0.14 & -0.14 & 0.86 & -0.11 & -0.04 \end{bmatrix}$$

Modularity Matrix

*k*-means



2 eigenvectors

$$\begin{bmatrix} 0.44 & -0.00 \\ 0.38 & 0.23 \\ 0.44 & -0.00 \\ 0.17 & -0.48 \\ -0.29 & -0.32 \\ -0.29 & -0.32 \\ -0.38 & 0.34 \\ -0.34 & -0.08 \\ -0.14 & 0.63 \end{bmatrix}$$

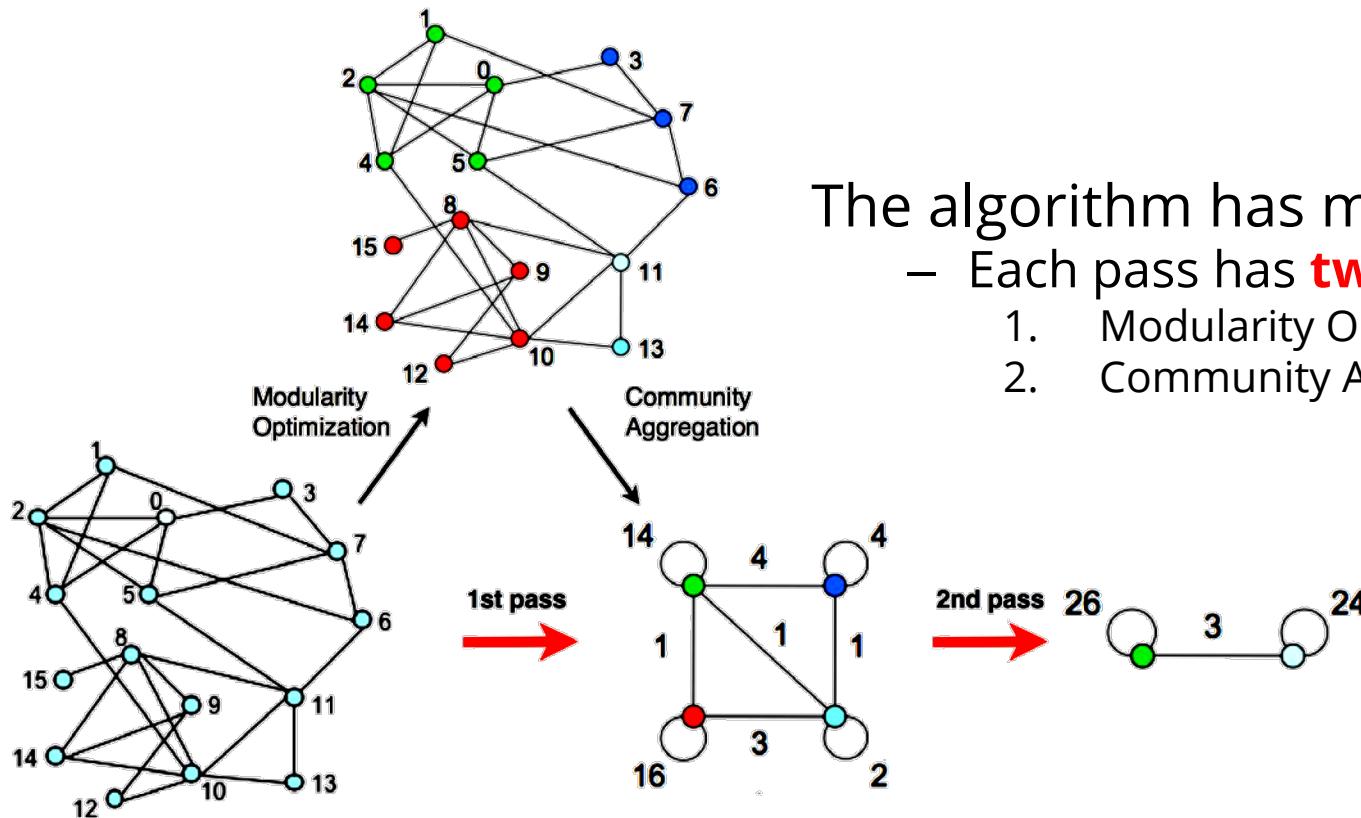


# Making Modularity Optimization Faster

- The matrix method discussed is slow and does not scale to millions of nodes (and billions of edges)
- We can perform greedy optimization of modularity to speed-up the process
- Louvain Method
  - A greedy modularity optimization method for community detection
    - Invented when all authors affiliated with ***Université catholique de Louvain (UCL)***



# Louvain Method



The algorithm has multiple passes

- Each pass has **two phases**
  1. Modularity Optimization
  2. Community Aggregation

*Image from*

Blondel, Vincent D., Jean-Loup Guillaume, Renaud Lambiotte, and Etienne Lefebvre. "Fast unfolding of communities in large networks." *Journal of statistical mechanics: theory and experiment* 2008, no. 10 (2008): P10008.

# Louvain Method

Start with a weighted network where all nodes are in their own communities (i.e., n communities)

## First Phase:

- For each node  $v_i$ ,
  - For all neighbors  $v_j \in N(v_i)$ :
    - compute the modularity gain if  $v_i$  is removed from its community and placed in the community of  $v_j$ .
  - Find the community with the maximum modularity gain
  - If the maximum gain is positive, remove  $v_i$  from its community, and place it in that community
  - If no positive gain, do not change communities
- Repeat until no node changes its community

# Important Points about Phase I

- A point can be considered multiple times
- A Local Minima of modularity maximization is achieved in phase I
- Phase I is order dependent
  - The modularity achieved is more or less stable and is less dependent on the initial order
  - The computation time depends on the initial order.



## Second Phase:

- Build a new network
  - Nodes are communities
  - Edges are the edges between nodes in the corresponding communities (weights are sum of the weights)
  - Self-loops represent edges within the community
- The algorithm creates hierarchies of communities
- It usually ends in less than 10 passes
- It is seems to be an  $O(n \log n)$  algorithm

# Why is it fast?

$$Q = \frac{1}{2m} \sum_{x=1}^k \sum_{i,j \in P_x} A_{ij} - \frac{d_i d_j}{2m}$$

$$\delta(x, y) = \begin{cases} 0, & \text{if } x \neq y \\ 1, & \text{if } x = y \end{cases}$$

Modularity can be restated as

$$Q = \frac{1}{2m} \sum_{i,j} [A_{ij} - \frac{d_i d_j}{2m}] \delta(c_i, c_j)$$

Kronecker delta function

community of node  $i$

Consider node  $i$ , in an isolated community,  
when it moves to community  $C$

- The gain in modularity can be computed easily

$$\Delta Q = [\frac{\sum_{in}}{2m} + 2\sum_{i,in} - (\frac{\sum_{total} + d_i}{2m})^2] - [\frac{\sum_{in}}{2m} - (\frac{\sum_{total}}{2m})^2 - (\frac{d_i}{2m})^2]$$

Edges within  $C$

Edges between  $i$  and  $C$

All edges connected to  
members of  $C$

## IV. Dense Communities: $\gamma$ -dense

- The density of a graph defines how close a graph is to a clique

$$\gamma = \frac{|E|}{\binom{|V|}{2}}$$

- A subgraph  $G(V, E)$  is a  $\gamma$ -dense (or quasi-clique) if

$$|E| \geq \gamma \binom{|V|}{2}$$

- A 1-dense graph is a clique
- We can find quasi-cliques using the brute force algorithm discussed previously, but there are more efficient methods.

# Finding Maximal $\gamma$ -dense Quasi-Cliques

We can use a two-step procedure consisting of “local search” and “heuristic pruning”

## Local search

- Sample a subgraph, and find a maximal  $\gamma$ -dense quasi-clique
  - A greedy approach is to expand a quasi-clique by all of its high-degree neighbors until the density drops below  $\gamma$

## Heuristic pruning

- For a  $\gamma$ -dense quasi-clique of size  $k$ , we recursively remove nodes with degree less than  $\gamma k$  and incident edges
  - We can start from low-degree nodes and recursively remove all nodes with degree less than  $\gamma k$

# V. Hierarchical Communities

- Previous methods consider communities at a single level
  - Communities may have hierarchies.
    - Each community can have sub/super communities.
  - Hierarchical clustering deals with this scenario and generates community hierarchies.
- Initially  $n$  members are considered as either 1 or  $n$  communities in hierarchical clustering. These communities are gradually
  - merged (**agglomerative hierarchical clustering**) or
  - split (**divisive hierarchical clustering**)

# Hierarchical Community Detection

- **Goal:** build a hierarchical structure of communities based on network topology
- Allow the analysis of a network at different resolutions
- Representative approaches:
  - Divisive Hierarchical Clustering
  - Agglomerative Hierarchical clustering

# Divisive Hierarchical Clustering

- Divisive clustering
  - Partition nodes into several sets
  - Each set is further divided into smaller ones
  - Network-centric partition can be applied for the partition
- One particular example:

**Girvan-Newman Algorithm:** recursively remove the “weakest” links within a “community”

- Find the edge with the weakest link
- Remove the edge and update the corresponding strength of each edge
- Recursively apply the above two steps until a network is discomposed into a desired number of connected components.
- Each component forms a community

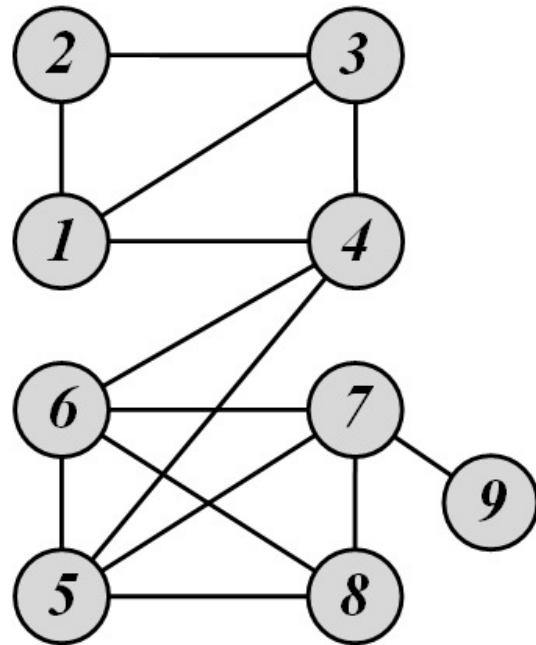
# Edge Betweenness

- To determine weakest links, the algorithm uses **edge betweenness**.

**Edge betweenness** is the number of shortest paths that pass along with the edge

- Edge betweenness measures the “bridgeness” of an edge between two communities
- The edge with high betweenness tends to be the bridge between two communities.

# Edge Betweenness: Example

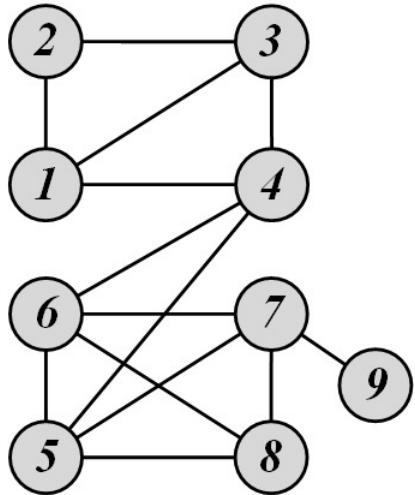


The edge betweenness of  $e(1, 2)$  is  $6/2 + 1 = 4$ , as all the shortest paths from 2 to  $\{4, 5, 6, 7, 8, 9\}$  have to either pass  $e(1, 2)$  or  $e(2, 3)$ , and  $e(1, 2)$  is the shortest path between 1 and 2

# The Girvan-Newman Algorithm

1. Calculate edge betweenness for all edges in the graph.
2. Remove the edge with the highest betweenness.
3. Recalculate betweenness for all edges affected by the edge removal.
4. Repeat until all edges are removed.

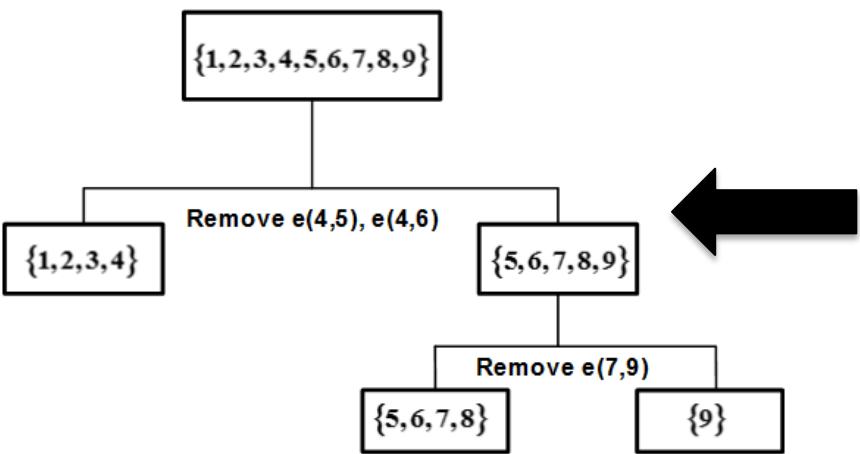
# Edge Betweenness Divisive Clustering: Example



Initial betweenness value

	1	2	3	4	5	6	7	8	9
1	0	4	1	9	0	0	0	0	0
2	4	0	4	0	0	0	0	0	0
3	1	4	0	9	0	0	0	0	0
4	9	0	9	0	10	10	0	0	0
5	0	0	0	10	0	1	6	3	0
6	0	0	0	10	1	0	6	3	0
7	0	0	0	0	6	6	0	2	8
8	0	0	0	0	3	3	2	0	0
9	0	0	0	0	0	0	8	0	0

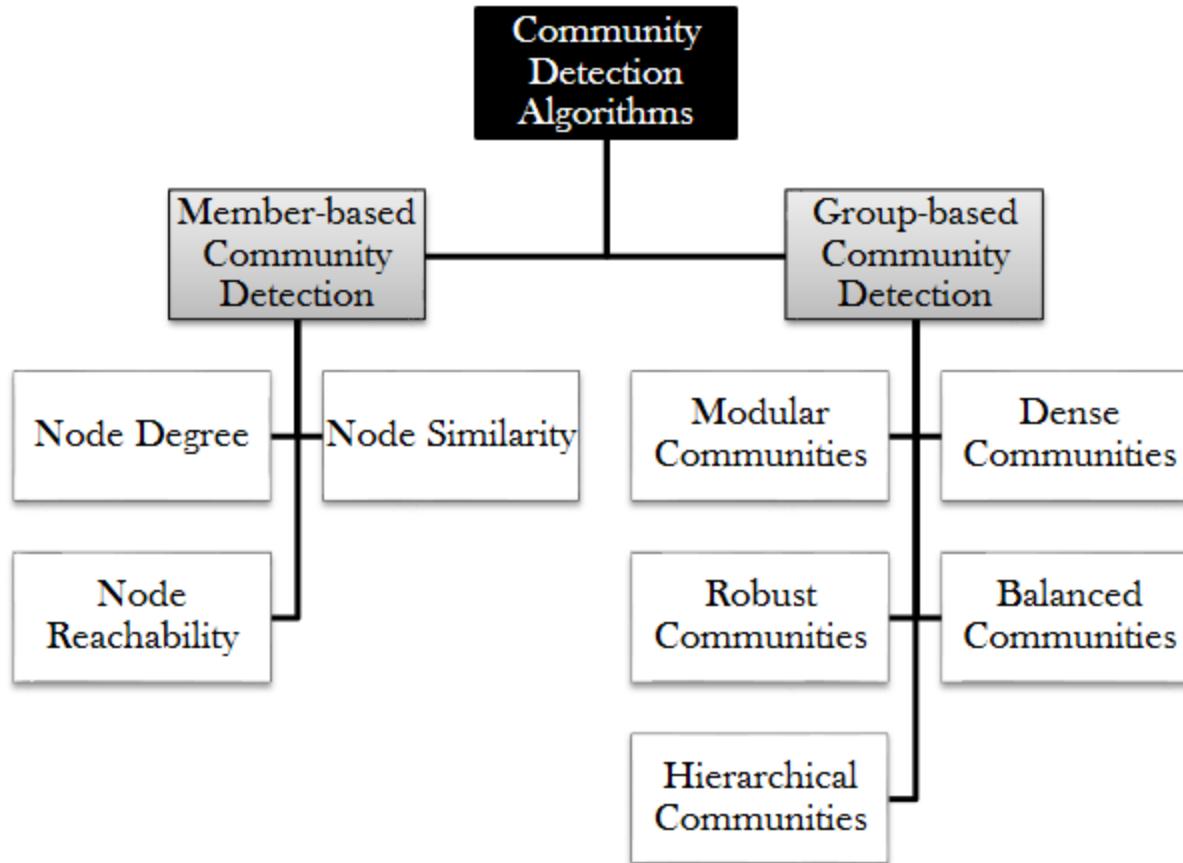
the first edge that needs to be removed is  $e(4, 5)$  ( or  $e(4, 6)$  )



By removing  $e(4, 5)$ , we compute the edge betweenness once again; this time,  $e(4, 6)$  has the highest betweenness value: 20.

This is because all shortest paths between nodes {1,2,3,4} to nodes {5,6,7,8,9} must pass  $e(4, 6)$ ; therefore, it has betweenness  $4 \times 5 = 20$ .

# Community Detection Algorithms



# Community Evolution

# Network and Community Evolution

- How does a **network** change over time?
- How does a **community** change over time?
- What properties do you expect to remain roughly constant?
- What properties do you expect to change?
- For example,
  - Where do you expect new edges to form?
  - Which edges do you expect to be dropped?

# How Networks Evolve?

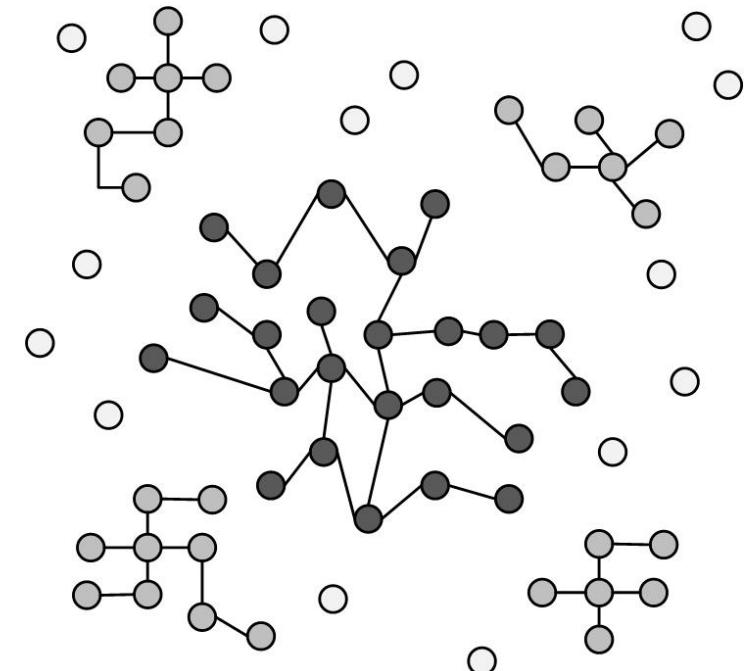
# Network Growth Patterns

1. Network Segmentation
2. Graph Densification
3. Diameter Shrinkage

# 1. Network Segmentation

- Often, in evolving networks, segmentation takes place, where the large network is decomposed over time into three parts

- Giant Component:** As network connections stabilize, a giant component of nodes is formed, with a large proportion of network nodes and edges falling into this component.
- Stars:** These are isolated parts of the network that form star structures. A star is a tree with one internal node and  $n$  leaves.
- Singltons:** These are orphan nodes disconnected from all nodes in the network.



## 2. Graph Densification

- The density of the graph increases as the network grows
  - The number of edges increases faster than the number of nodes does

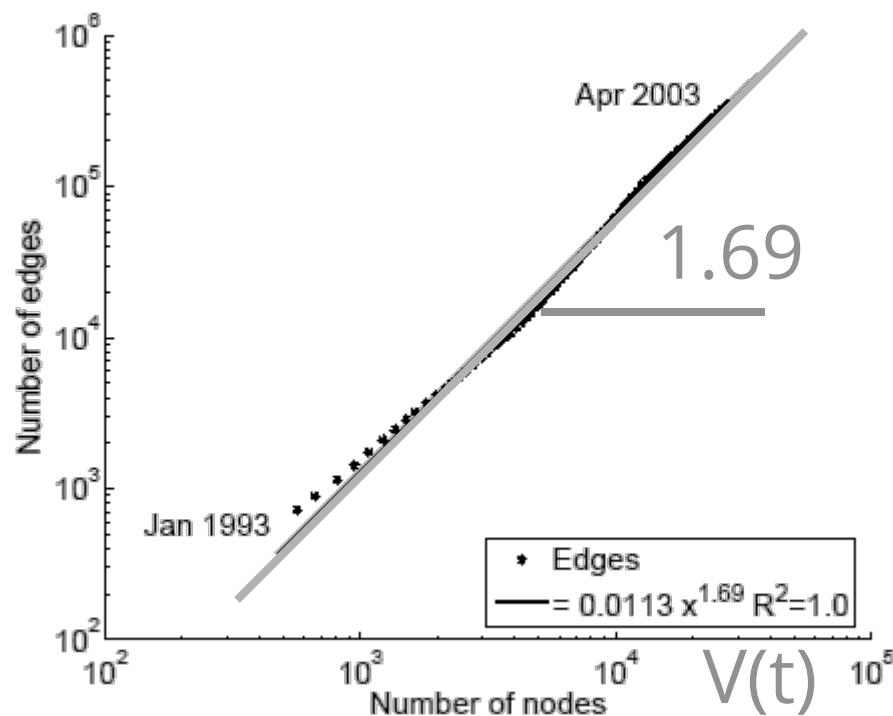
$$E(t) \propto V(t)^\alpha$$

- Densification exponent:  $1 \leq \alpha \leq 2$ :
  - $\alpha = 1$ : linear growth – constant out-degree
  - $\alpha = 2$ : quadratic growth – clique

$E(t)$  and  $V(t)$  are numbers of edges and nodes respectively at time  $t$

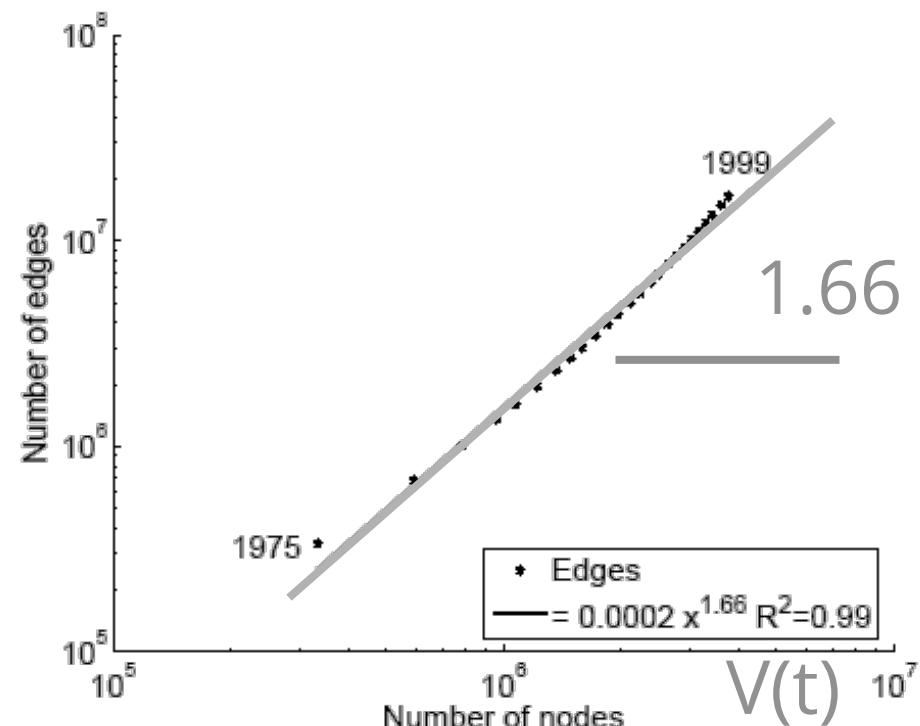
# Densification in Real Networks

$E(t)$



**Physics Citations**

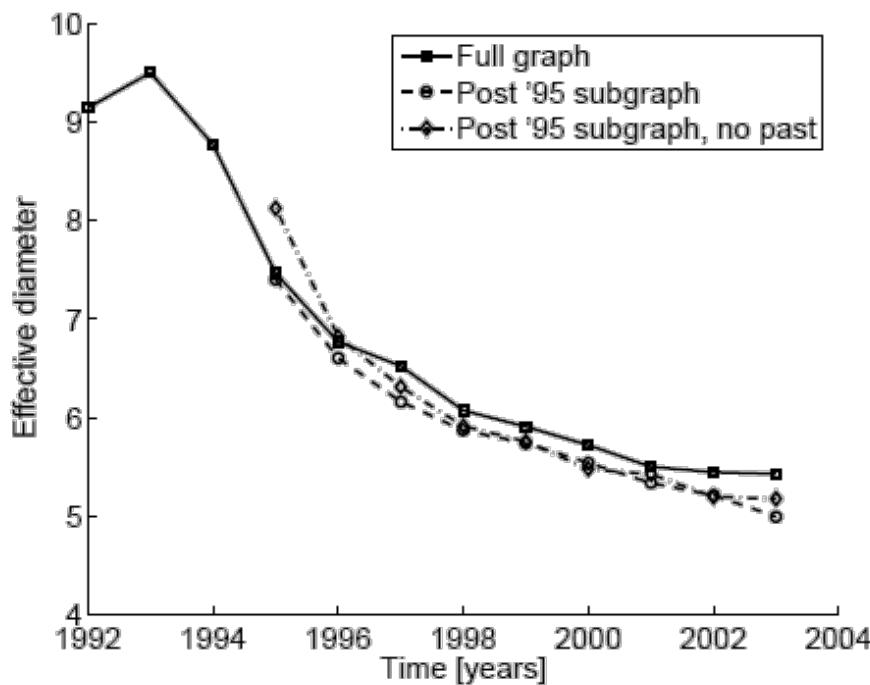
$E(t)$



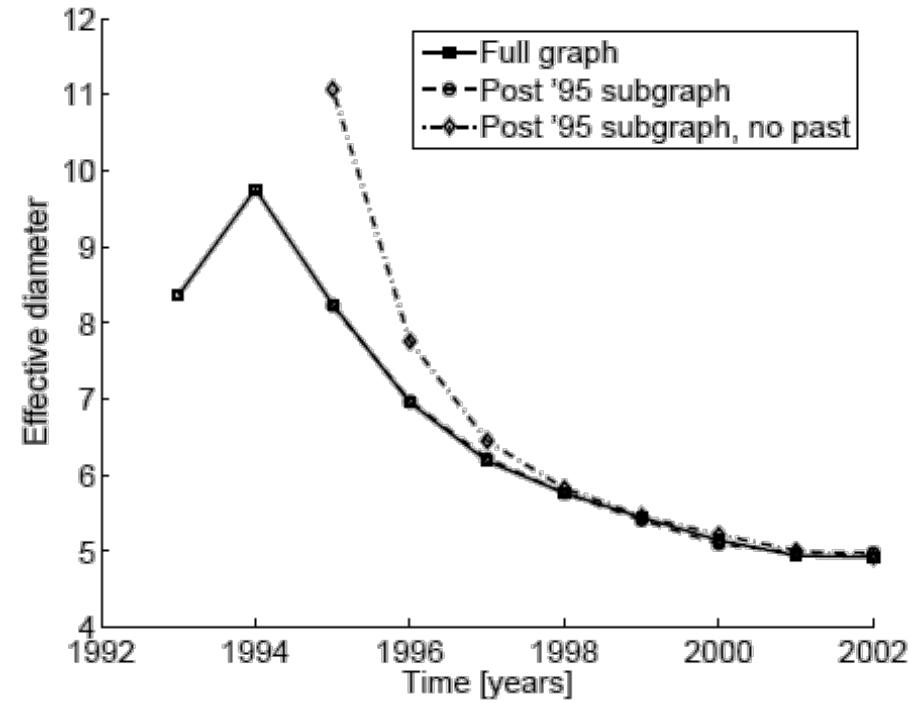
**Patent Citations**

### 3. Diameter Shrinking

- In networks diameter shrinks over time



ArXiv citation graph

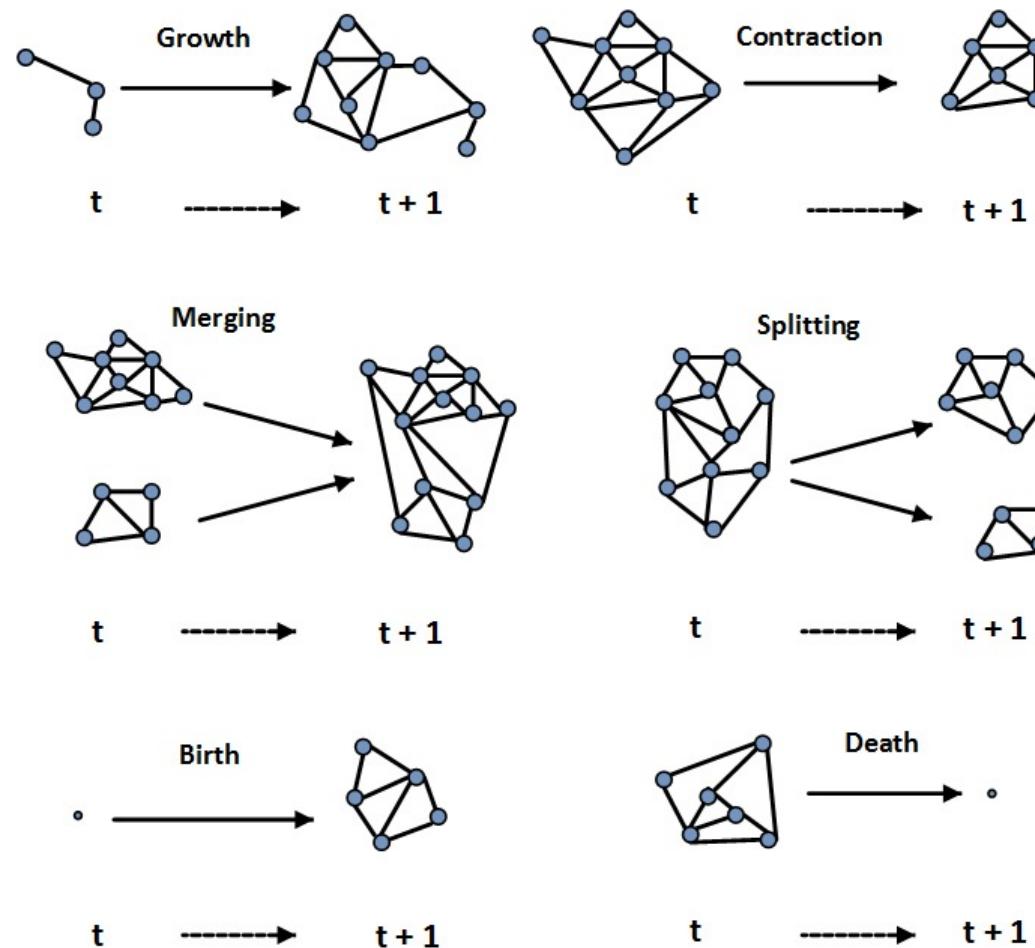


Affiliation Network

# How Communities Evolve?

# Community Evolution

- Communities also expand, shrink, or dissolve in dynamic networks



# Community Detection in Evolving Networks

# Extending Previous Methods

1. Take  $t$  snapshots of the network,  $G_1, G_2, \dots, G_t$  where  $G_i$  is a snapshot at time  $i$
2. Perform a static community detection algorithm (all methods discussed before) on all snapshots independently
3. Assign community members based on communities found in all  $t$  time stamps.
  - E.g., Assign nodes to communities based on voting (assign nodes to communities they belong to the most over time)

**Unstable in highly dynamic networks as community memberships are always changing**

# Evolutionary Clustering

- Assume that communities don't change most of the time
- Minimize an objective function that considers
  - **Snapshot Cost.** Communities at different times (**SC**)
  - **Temporal Cost.** How communities evolve (**TC**)
- Objective function is defined as

$$Cost = \alpha SC + (1 - \alpha) TC$$

$$0 \leq \alpha \leq 1$$

# Evolutionary Clustering

- If we use spectral clustering for each snapshot
- Then,  $Cost_t$ , the objective function at time  $t$  is

$$\begin{aligned} Cost_t &= \alpha SC + (1 - \alpha) TC \\ &= \alpha \operatorname{Tr}(X_t^T L X_t) + (1 - \alpha) TC \end{aligned}$$

- $X_t$  is the community membership matrix at  $t$
- To define TC we can use  $TC = \|X_t - X_{t-1}\|^2$
- Challenges with this definition
  - Assumes that we have the same number of communities at time  $t - 1$  and  $t$
  - $X_t$  is non-unique (any orthogonal transformation is still a solution)

# Evolutionary Clustering

- We can define TC as

$$\begin{aligned}TC &= \frac{1}{2} \left\| X_t X_t^T - X_{t-1} X_{t-1}^T \right\|^2, \\&= \frac{1}{2} \text{Tr} \left( (X_t X_t^T - X_{t-1} X_{t-1}^T)^T (X_t X_t^T - X_{t-1} X_{t-1}^T) \right), \\&= \frac{1}{2} \text{Tr} \left( X_t X_t^T X_t X_t^T - 2X_t X_t^T X_{t-1} X_{t-1}^T + X_{t-1} X_{t-1}^T X_{t-1} X_{t-1}^T \right), \\&= \text{Tr} \left( I - X_t X_t^T X_{t-1} X_{t-1}^T \right), & \text{Tr}(AB) = \text{Tr}(BA) \\&= \text{Tr} \left( I - X_t^T X_{t-1} X_{t-1}^T X_t \right)\end{aligned}$$

- Hence cost will be

$$\begin{aligned}Cost_t &= \alpha \text{Tr} \left( X_t^T L X_t \right) + (1 - \alpha) \frac{1}{2} \left\| X_t X_t^T - X_{t-1} X_{t-1}^T \right\|^2, \\&= \alpha \text{Tr} \left( X_t^T L X_t \right) + (1 - \alpha) \text{Tr} \left( I - X_t^T X_{t-1} X_{t-1}^T X_t \right), \\&= \alpha \text{Tr} \left( X_t^T L X_t \right) + (1 - \alpha) \text{Tr} \left( X_t^T I X_t - X_t^T X_{t-1} X_{t-1}^T X_t \right), \\&= \text{Tr} \left( X_t^T \alpha L X_t \right) + \text{Tr} \left( X_t^T (1 - \alpha) I X_t - X_t^T (1 - \alpha) X_{t-1} X_{t-1}^T X_t \right).\end{aligned}$$

# Evolutionary Clustering

- Assuming Normalized Laplacian is used

$$L = I - D_t^{-1/2} A_t D_t^{-1/2}$$

$$\begin{aligned} Cost_t &= Tr\left(X_t^T \alpha \left(I - D_t^{-1/2} A_t D_t^{-1/2}\right) X_t\right) \\ &\quad + Tr\left(X_t^T (1-\alpha) I X_t - X_t^T (1-\alpha) X_{t-1} X_{t-1}^T X_t\right), \\ &= Tr\left(X_t^T \left(I - \alpha D_t^{-1/2} A_t D_t^{-1/2} - (1-\alpha) X_{t-1} X_{t-1}^T\right) X_t\right), \\ &= Tr(X_t \hat{L} X_t) \end{aligned}$$

$$\hat{L} = I - \alpha D_t^{-1/2} A_t D_t^{-1/2} - (1-\alpha) X_{t-1} X_{t-1}^T$$

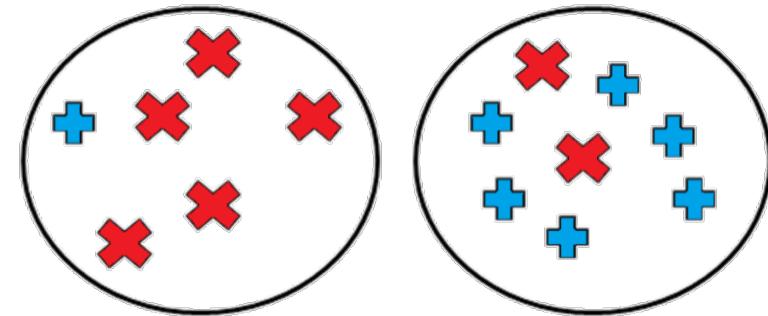
**Similar to Spectral Clustering  
 $X_t$  can be obtained by taking the top eigenvectors of  $\hat{L}$**

# Community Evaluation

# Evaluating the Communities

We are given objects of two different kinds (+, ×)

- **The perfect community:** all objects inside the community are of the same type
- **Evaluation with ground truth**
- **Evaluation without ground truth**



# Evaluation with Ground Truth

- When ground truth is available
  - We have partial knowledge of what communities should look like
  - We are given the correct community (clustering) assignments
- **Measures**
  - Precision and Recall, or F-Measure
  - Purity
  - Normalized Mutual Information (NMI)

# Precision and Recall

$$Precision = \frac{\text{Relevant and retrieved}}{\text{Retrieved}}$$

$$Recall = \frac{\text{Relevant and retrieved}}{\text{Relevant}}$$

$$P = \frac{TP}{TP + FP}$$

$$R = \frac{TP}{TP + FN}$$

## True Positive (TP) :

- When similar members are assigned to the same communities
- A **correct** decision.

## True Negative (TN) :

- When dissimilar members are assigned to different communities
- A **correct** decision

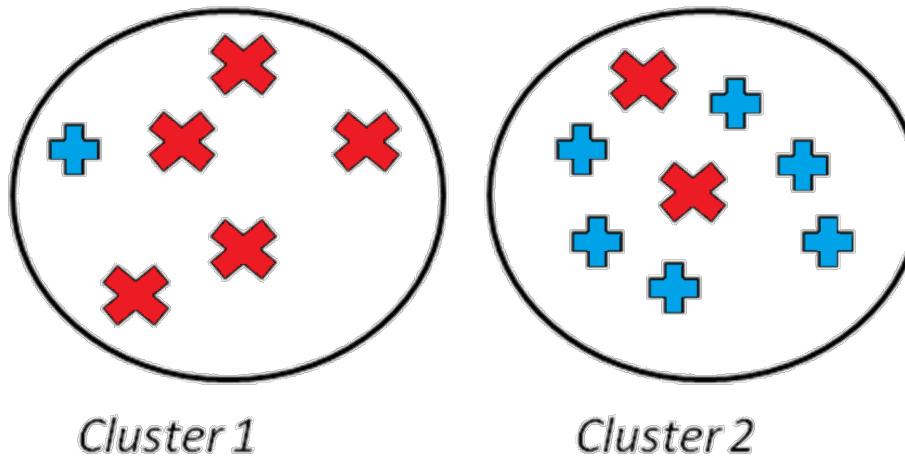
## False Negative (FN) :

- When similar members are assigned to different communities
- An **incorrect** decision

## False Positive (FP) :

- When dissimilar members are assigned to the same communities
- An **incorrect** decision

# Precision and Recall: Example



$$TP = \binom{5}{2} + \binom{6}{2} + \binom{2}{2} = 26,$$

$$FP = (5 \times 1) + (6 \times 2) = 17,$$

$$FN = (5 \times 2) + (6 \times 1) = 16,$$

$$TN = (6 \times 5) + (2 \times 1) = 32.$$

$$P = \frac{26}{26+17} = 0.60$$

$$R = \frac{26}{26+16} = 0.61$$

# F-Measure

Either  $P$  or  $R$  measures one aspect of the performance,

- To integrate them into one measure, we can use the harmonic mean of precision of recall

$$F = 2 \cdot \frac{P \cdot R}{P + R}$$

For the example earlier,

$$F = 2 \times \frac{0.6 \times 0.61}{0.6 + 0.61} = 0.60$$

# Purity

We can assume the majority of a community represents the community

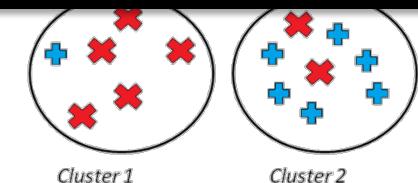
- We use the label of the majority against the label of each member to evaluate the communities

Purity can be easily **tampered** by

- Points being singleton communities (of size 1); or by
- Very large communities

$$Purity = \frac{1}{N} \sum_{i=1}^k \max_j |C_i \cap L_j|$$

- $k$ : the number of communities
- $N$ : total number of nodes,
- $L_j$ : the set of instances with label  $j$  in all communities
- $C_i$ : the set of members in community  $i$



purity is:  $\frac{6+5}{14} = 0.78$

# Mutual Information

- **Mutual information (MI).** The amount of information that two random variables share.
  - By knowing one of the variables, it measures the amount of uncertainty reduced regarding the others

$$MI = I(H, L) = \sum_{h \in H} \sum_{l \in L} \frac{n_{h,l}}{n} \log \frac{n \cdot n_{h,l}}{n_h n_l}$$

- $L$  and  $H$  are labels and found communities;
- $n_h$  and  $n_l$  are the number of data points in community  $h$  and with label  $l$ , respectively;
- $n_{h,l}$  is the number of nodes in community  $h$  and with label  $l$ ; and  $n$  is the number of nodes

# Normalizing Mutual Information (NMI)

- Mutual information (MI) is unbounded
- To address this issue, we can normalize MI
- How? We know that 
$$MI \leq \min(H(L), H(H)),$$
$$(MI)^2 \leq H(H)H(L).$$
$$MI \leq \sqrt{H(H)} \sqrt{H(L)}.$$
- $H(\cdot)$  is the entropy function

$$H(L) = - \sum_{l \in L} \frac{n_l}{n} \log \frac{n_l}{n}$$

$$H(H) = - \sum_{h \in H} \frac{n_h}{n} \log \frac{n_h}{n}.$$

# Normalized Mutual Information

## Normalized Mutual Information

$$NMI = \frac{MI}{\sqrt{H(L)} \sqrt{H(H)}}.$$

$$NMI = \frac{\sum_{h \in H} \sum_{l \in L} n_{h,l} \log \frac{n \cdot n_{h,l}}{n_h n_l}}{\sqrt{(\sum_{h \in H} n_h \log \frac{n_h}{n})(\sum_{l \in L} n_l \log \frac{n_l}{n})}}.$$

We can also define it as

Note that  $MI < 1/2(H(H) + H(L))$

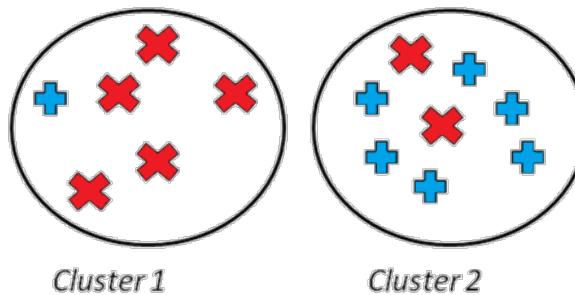
$$NMI = \frac{I(H; L)}{\frac{1}{2}(H(L) + H(H))}$$

# Normalized Mutual Information

$$NMI = \frac{\sum_{h,l} n_{h,l} \log \frac{n \cdot n_{h,l}}{n_h n_l}}{\sqrt{(\sum_h n_h \log \frac{n_h}{n})(\sum_l n_l \log \frac{n_l}{n})}}$$

- where  $l$  and  $h$  are known (with labels) and found communities, respectively
  - $n_h$  and  $n_l$  are the number of members in the community  $h$  and  $l$ , respectively,
  - $n_{h,l}$  is the number of members in community  $h$  and labeled  $l$ ,
  - $n$  is the size of the dataset
- 
- **NMI** values close to one indicate high similarity between communities found and labels
  - Values close to zero indicate high dissimilarity between them

# Normalized Mutual Information: Example



Found communities (H)

- [1,1,1,1,1,1,2,2,2,2,2,2,2,2]

Actual Labels (L)

- [2,1,1,1,1,1,2,2,2,2,2,1,1]

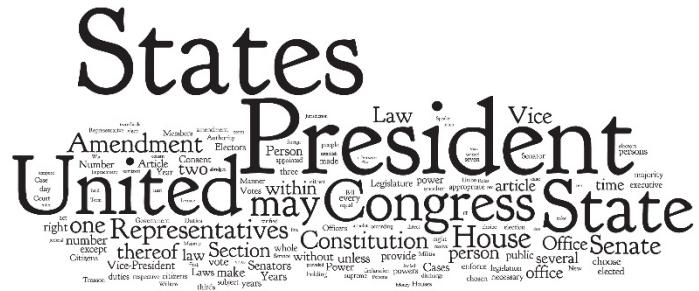
$n = 14$

	$n_h$
h=1	6
h=2	8

	$n_l$
$l = 1$	7
$l = 2$	7

$n_{h,l}$	$l = 1$	$l = 2$
h=1	5	1
h=2	2	6

# Evaluation without Ground Truth



(a) U.S. Constitution



(b) Sports

- **Evaluation with Semantics**

- A simple way of analyzing detected communities is to analyze other attributes (posts, profile information, content generated, etc.) of community members to see if there is a coherency among community members
  - The coherency is often checked via human subjects.
    - Or through labor markets: Amazon Mechanical Turk
  - To help analyze these communities, one can use word frequencies. By generating a list of frequent keywords for each community, human subjects determine whether these keywords represent a coherent topic.

- **Evaluation Using Clustering Quality Measures**

- Use clustering quality measures (SSE)
  - Use more than two community detection algorithms and compare the results and pick the algorithm with better quality measure