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Chapter 6

Community Analysis

In November 2010, a team of Dutch law enforcement agents dismantled a community of 30 million infected computers across the globe that were sending more than 3.6 billion daily spam mails. These distributed networks of infected computers are called *botnets*. The community of computers in a botnet transmit spam or viruses across the web without their owner's permission. The members of a botnet are rarely known; however, it is vital to identify these botnet communities and analyze their behavior to enhance internet security. This is an example of *community analysis*. In this chapter, we discuss community analysis in social media.

Also known as *groups*, *clusters*, or *cohesive subgroups*, communities have been studied extensively in many fields and, in particular, the social sciences. In social media mining, analyzing communities is essential. Studying communities in social media is important for many reasons. First, individuals often form groups based on their interests, and when studying individuals, we are interested in identifying these groups. Consider the importance of finding groups with similar reading tastes by an online book seller for recommendation purposes. Second, groups provide a clear global view of user interactions, whereas a local-view of individual behavior is often noisy and ad hoc. Finally, some behaviors are *only* observable in a group setting and not on an individual level. This is because the individual's behavior can fluctuate, but group collective behavior is more robust to change. Consider the interactions between two opposing political groups on social media. Two individuals, one from each group, can hold similar opinions on a subject, but what is important is that their

communities can exhibit opposing views on the same subject.

In this chapter, we discuss communities and answer the following three questions in detail:

1. *How can we detect communities?* This question is discussed in different disciplines, and in diverse forms. In particular, quantization in electrical engineering, discretization in statistics, and clustering in machine learning tackle a similar challenge. As discussed in Chapter 5, in clustering, data points are grouped together based on a similarity measure. In community detection, data points represent actors in social media, and similarity between these actors is often defined based on the interests these users share. The major difference between clustering and community detection is that in community detection, individuals are connected to others via a network of links, whereas in clustering, data points are not embedded in a network.

2. *How do communities evolve and how can we study evolving communities?* Social media forms a dynamic and evolving environment. Similar to real-world friendships, social media interactions evolve over time. People join or leave groups; groups expand, shrink, dissolve, or split over time. Studying the temporal behavior of communities is necessary for a deep understanding of communities in social media.

3. *How can we evaluate detected communities?* As emphasized in our botnet example, the list of community members (i.e., ground truth) is rarely known. Hence, community evaluation is a challenging task and often means to evaluating detected communities in the absence of ground truth.

Social Communities

Broadly speaking, a real-world community is a body of individuals with common economic, social, or political interests/characteristics, often living in relatively close proximity. A virtual community comes into existence when like-minded users on social media form a link and start interacting with each other. In other words, formation of any community requires (1) a set of at least two nodes sharing some interest and (2) interactions with respect to that interest.

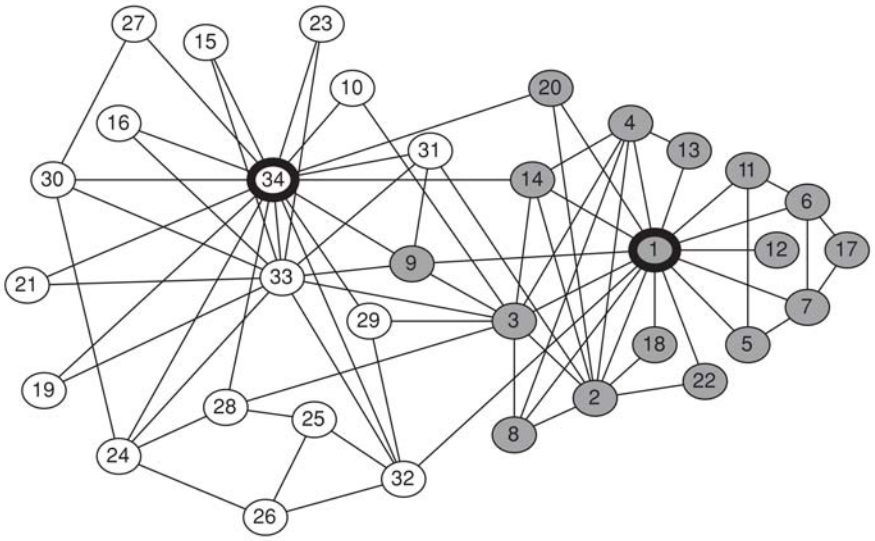


Figure 6.1: Zachary's Karate Club. Nodes represent karate club members and edges represent friendships. A conflict in the club divided the members into two groups. The color of the nodes denotes which one of the two groups the nodes belong to.

As a real-world community example, consider the interactions of a college karate club collected by Wayne Zachary in 1977. The example is often referred to as *Zachary's Karate Club* [309] in the literature. Figure 6.1 depicts the interactions in a college karate club over two years. The links show friendships between members. During the observation period, individuals split into two communities due to a disagreement between the club administrator and the karate instructor, and members of one community left to start their own club. In this figure, node colors demonstrate the communities to which individuals belong. As observed in this figure, using graphs is a convenient way to depict communities because color-coded nodes can denote memberships and edges can be used to denote relations. Furthermore, we can observe that individuals are more likely to be friends with members of their own group, hence, creating tightly knit components in the graph.

Zachary's Karate Club

Zachary's Karate Club is an example of two *explicit communities*. An explicit community, also known as an *emic* community, satisfies the following three criteria:

Explicit (emic) Communities

1. Community members understand that they are its members.
2. Nonmembers understand who the community members are.
3. Community members often have more interactions with each other than with nonmembers.

Implicit (etic) Communities

In contrast to explicit communities, in implicit communities, also known as *etic* communities, individuals tacitly interact with others in the form of an unacknowledged community. For instance, individuals calling Canada from the United States on a daily basis need not be friends and do not consider each other as members of the same explicit community. However, from the phone operator's point of view, they form an implicit community that needs to be marketed the same promotions. Finding implicit communities is of major interest, and this chapter focuses on finding these communities in social media.

Communities in social media are more or less representatives of communities in the real world. As mentioned, in the real world, members of communities are often geographically close to each other. The geographical location becomes less important in social media, and many communities on social media consist of highly diverse people from all around the planet. In general, people in real-world communities tend to be more similar than those of social media. People do not need to share language, location, and the like to be members of social media communities. Similar to real-world communities, communities in social media can be labeled as explicit or implicit. Examples of explicit communities in well-known social media sites include the following:

- **Facebook.** In Facebook, there exist a variety of explicit communities, such as *groups* and *communities*. In these communities, users can post messages and images, comment on other messages, like posts, and view activities of others.
- **Yahoo! Groups**. In Yahoo! groups, individuals join a group mailing list where they can receive emails from all or a selection of group members (administrators) directly.
- **LinkedIn.** LinkedIn provides its users with a feature called *Groups and Associations*. Users can join professional groups where they can post and share information related to the group.

Because these sites represent explicit communities, individuals have an understanding of when they are joining them. However, there exist implicit communities in social media as well. For instance, consider individuals with the same taste for certain movies on a movie rental site. These individuals are rarely all members of the same explicit community. However, the movie rental site is particularly interested in finding these implicit communities so it can better market to them by recommending movies similar to their tastes. We discuss techniques to find these implicit communities next.

6.1 Community Detection

As mentioned earlier, communities can be explicit (e.g., Yahoo! groups), or implicit (e.g., individuals who write blogs on the same or similar topics). In contrast to explicit communities, in many social media sites, implicit communities and their members are obscure to many people. Community detection finds these implicit communities.

In the simplest form, similar to the graph shown in Figure 6.1, community detection algorithms are often provided with a graph where nodes represent individuals and edges represent friendships between individual. This definition can be generalized. Edges can also be used to represent contents or attributes shared by individuals. For instance, we can connect individuals at the same location, with the same gender, or who bought the same product using edges. Similarly, nodes can also represent products, sites, and webpages, among others. Formally, for a graph $G(V, E)$, the task of community detection is to find a set of communities $\{C_i\}_{i=1}^{n}$ in a G such that $\cup_{i=1}^{n} C_i \subseteq V$.

6.1.1 Community Detection Algorithms

There are a variety of community detection algorithms. When detecting communities, we are interested in detecting communities with either (1) *specific members* or (2) *specific forms* of communities. We denote the former as *member-based community detection* and the latter as *group-based community detection*. Consider the network of 10 individuals shown in Figure 6.2 where 7 are wearing black t-shirts and 3 are wearing white ones. If we group individuals based on their t-shirt color, we end up having a

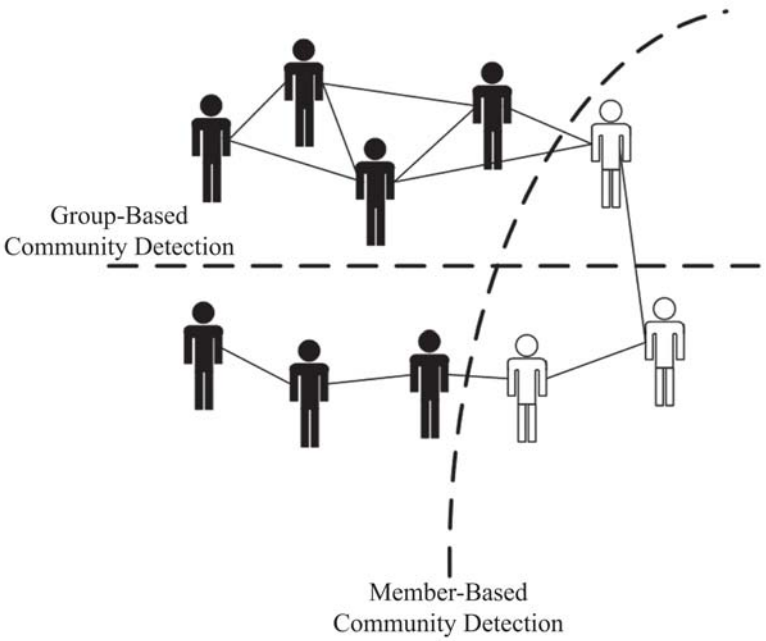


Figure 6.2: Community Detection Algorithms Example. Member-based community detection groups members based on their characteristics. Here, we divide the network based on color. In group-based community detection, we find communities based on group properties. Here, groups are formed based on the density of interactions among their members.

community of three and a community of seven. This is an example of member-based community detection, where we are interested in *specific members* characterized by their t-shirts' color. If we group the same set based on the density of interactions (i.e., internal edges), we get two other communities. This is an instance of group-based community detection, where we are interested in *specific communities* characterized by their interactions' density.

Member-based community detection uses community detection algorithms that group members based on attributes or measures such as similarity, degree, or reachability. In group-based community detection, we are interested in finding communities that are modular, balanced, dense, robust, or hierarchical.

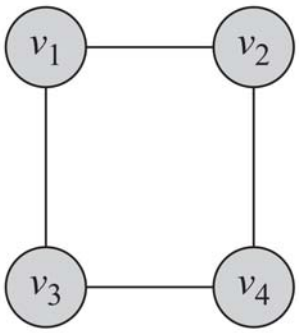


Figure 6.3: A 4-Cycle.

6.1.2 Member-Based Community Detection

The intuition behind member-based community detection is that members with the same (or similar) characteristics are more often in the same community. Therefore, a community detection algorithm following this approach should assign members with similar characteristics to the same community. Let us consider a simple example. We can assume that nodes that belong to a cycle form a community. This is because they share the same characteristic: being in the cycle. Figure 6.3 depicts a 4-cycle. For instance, we can search for all n-cycles in the graph and assume that they represent a community. The choice for n can be based on empirical evidence or heuristics, or n can be in a range $[\alpha_1, \alpha_2]$ for which all cycles are found. A well-known example is the search for 3-cycles (triads) in graphs.

In theory, any subgraph can be searched for and assumed to be a community. In practice, only subgraphs that have nodes with specific characteristics are considered as communities. Three general node characteristics that are frequently used are *node similarity*, *node degree (familiarity)*, and *node reachability*.

When employing node degrees, we seek subgraphs, which are often connected, such that each node (or a subset of nodes) has a certain node degree (number of incoming or outgoing edges). Our 4-cycle example follows this property, the degree of each node being two. In reachability, we seek subgraphs with specific properties related to paths existing between nodes. For instance, our 4-cycle instance also follows the reachability characteristic where all pairs of nodes can be reached via two independent paths. In node similarity, we assume nodes that are highly similar belong

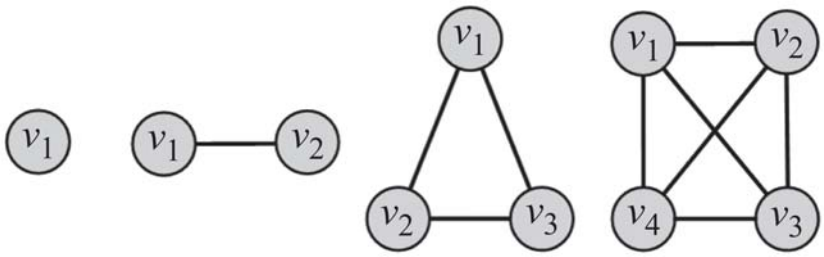


Figure 6.4: First Four Complete Graphs.

to the same community.

Node Degree

The most common subgraph searched for in networks based on node degrees is a *clique*. A clique is a maximum complete subgraph in which all pairs of nodes inside the subgraph are connected. In terms of the node degree characteristic, a clique of size k is a subgraph of k nodes where all node degrees in the induced subgraph are $k - 1$. The only difference between cliques and complete graphs is that cliques are subgraphs, whereas complete graphs contain the whole node set V. The simplest four complete graphs (or cliques, when these are subgraphs) are represented in Figure 6.4.

To find communities, we can search for the maximum clique (the one with the largest number of vertices) or for all maximal cliques (cliques that are not subgraphs of a larger clique; i.e., cannot be expanded further). However, both problems are NP-hard, as is verifying whether a graph contains a clique larger than size k. To overcome these theoretical barriers, for sufficiently small networks or subgraphs, we can (1) use brute force, (2) add some constraints such that the problem is relaxed and polynomially solvable, or (3) use cliques as the seed or core of a larger community.

Brute-force clique identification. The brute force method can find all maximal cliques in a graph. For each vertex v_x, we try to find the maximal clique that contains node v_x. The brute-force algorithm is detailed in Algorithm 6.1.

The algorithm starts with an empty stack of cliques. This stack is initialized with the node v_x that is being analyzed (a clique of size 1). Then, from the stack, a clique is popped (C). The last node added to clique C

Algorithm 6.1 Brute-Force Clique Identification

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=pop(CliqueStack); push(Processed,C);
5: v_{last} = 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** $C \bigcup \{v_{temp}\}$ is a clique **then**
9: push(CliqueStack, $C \bigcup \{v_{temp}\}$);
10: **end if**
11: **end for**
12: **end while**
13: Return the largest clique from Processed

is selected (v_{last}). All the neighbors of v_{last} are added to the popped clique C sequentially, and if the new set of nodes creates a larger clique (i.e., the newly added node is connected to all of the other members), then the new clique is pushed back into the stack. This procedure is followed until nodes can no longer be added.

The brute-force algorithm becomes impractical for large networks. For instance, 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 (why?).

The performance of the brute-force algorithm can be enhanced by pruning specific nodes and edges. If the cliques being searched for are of size k or larger, we can simply assume that the clique, if found, should contain nodes that have degrees equal to or more than $k - 1$. We can first prune all nodes (and edges connected to them) with degrees less than $k - 1$. Due to the power-law distribution of node degrees, many nodes exist with small degrees (1, 2, etc.). Hence, for a large enough k many nodes and edges will be pruned, which will reduce the computation drastically. This pruning works for both directed and undirected graphs.

Even with pruning, there are intrinsic properties with cliques that make them a less desirable means for finding communities. Cliques are rarely observed in the real world. For instance, consider a clique of 1,000 nodes.

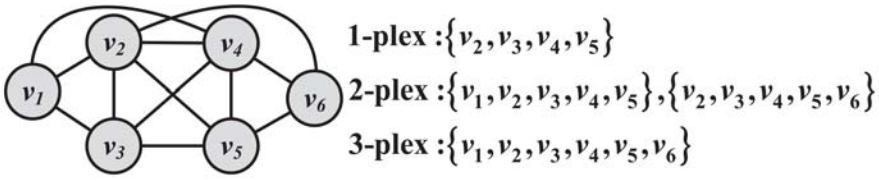


Figure 6.5: Maximal k-plexes for $k = 1, 2$, and 3.

This subgraph has $\frac{999 \times 1000}{2} = 499{,}500$ edges. A single edge removal from this many edges results in a subgraph that is no longer a clique. That represents less than 0.0002% of the edges, which makes finding cliques a challenging task.

In practice, to overcome this challenge, we can either relax the clique structure or use cliques as a seed or core of a community.

k-plex

Relaxing cliques. A well-known clique relaxation that comes from sociology is the k-plex concept. In a clique of size k, all nodes have the degree of $k-1$; however, in a k-plex, all nodes have a minimum degree that is not necessarily $k-1$ (as opposed to cliques of size k). For a set of vertices V, the structure is called a k-plex if we have

$$d_v \geq |V| - k, \forall v \in V, \tag{6.1}$$

where d_v is the degree of v in the induced subgraph (i.e., the number of nodes from the set V that are connected to v).

Clearly, a clique of size k is a 1-plex. As k gets larger in a k-plex, the structure gets increasingly relaxed, because we can remove more edges from the clique structure. Finding the maximum k-plex in a graph still tends to be NP-hard, but in practice, finding it is relatively easier due to smaller search space. Figure 6.5 shows maximal k-plexes for $k = 1$, 2, and 3. A k-plex is maximal if it is not contained in a larger k-plex (i.e., with more nodes).

Clique Percolation Method (CPM)

Using cliques as a seed of a community. When using cliques as a seed or core of a community, we assume communities are formed from a set of cliques (small or large) in addition to edges that connect these cliques. A well-known algorithm in this area is the clique percolation method (CPM) [225]. The algorithm is provided in Algorithm 6.2. Given parameter k, the

Algorithm 6.2 Clique Percolation Method (CPM)

Require: parameter k

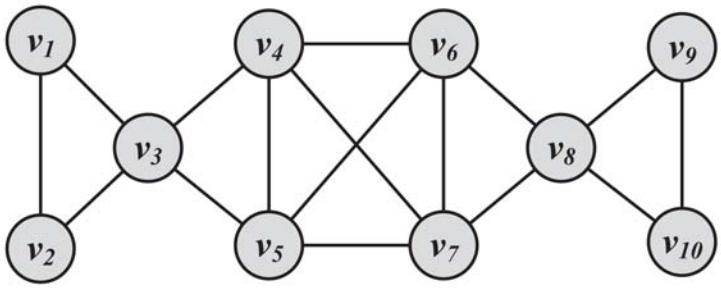
1: **return** Overlapping Communities
2: $Cliques_k$ = find all cliques of size k
3: Construct clique graph $G(V, E)$, where $|V| = |Cliques_k|$
4: $E = \{e_{ij} \mid$ clique i and clique j share $k-1$ nodes$\}$
5: Return all connected components of G

method starts by finding all cliques of size k. Then a graph is generated (clique graph) where all cliques are represented as nodes, and cliques that share $k-1$ vertices are connected via edges. Communities are then found by reporting the connected components of this graph. The algorithm searches for all cliques of size k and is therefore computationally intensive. In practice, when using the CPM algorithm, we often solve CPM for a small k. Relaxations discussed for cliques are desirable to enable the algorithm to perform faster. Lastly, CPM can return overlapping communities.

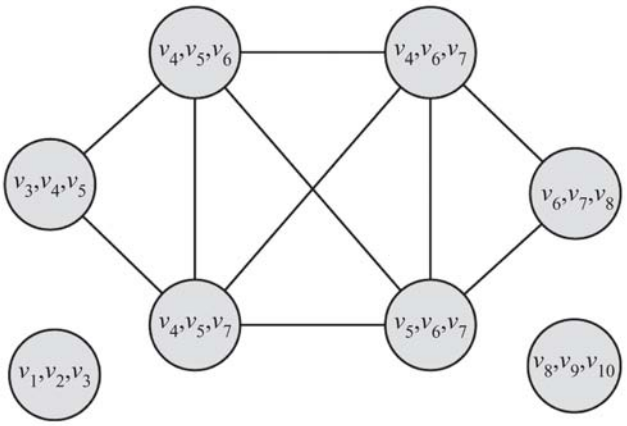
Example 6.1. *Consider the network depicted in Figure 6.6(a). The corresponding clique graph generated by the CPM algorithm for $k = 3$ is provided in Figure 6.6(b). All cliques of size $k = 3$ have been identified and cliques that share $k-1 = 2$ nodes are connected. Connected components are returned as communities ($\{v_1, v_2, v_3\}$, $\{v_8, v_9, v_{10}\}$, and $\{v_3, v_4, v_5, v_6, v_7, v_8\}$). Nodes v_3 and v_8 belong to two communities, and these communities are overlapping.*

Node Reachability

When dealing with reachability, we are seeking subgraphs where nodes are reachable from other nodes via a path. The two extremes of reachability are achieved when nodes are assumed to be in the same community if (1) there is a path between them (regardless of the distance) or (2) they are so close as to be immediate neighbors. In the first case, any graph traversal algorithm such as BFS or DFS can be used to identify connected components (communities). However, finding connected components is not very useful in large social media networks. These networks tend to have a large-scale connected component that contains most nodes, which are connected to each other via short paths. Therefore, finding connected components is less powerful for detecting communities in them. In the second case, when nodes are immediate neighbors of all other nodes, cliques



(a) Graph



(b) CPM Clique Graph

Figure 6.6: Clique Percolation Method (CPM) Example for $k = 3$.

are formed, and as discussed previously, finding cliques is considered a very challenging process.

To overcome these issues, we can find communities that are in between cliques and connected components in terms of connectivity and have small shortest paths between their nodes. There are predefined subgraphs, with roots in social sciences, with these characteristics. Well-known ones include the following:

k-Clique, *k*-Club, and *k*-Clan

- ***k*-Clique** is a maximal subgraph where the shortest path between any two nodes is always less than or equal to k. Note that in k-cliques, nodes on the shortest path should not necessarily be part of the subgraph.

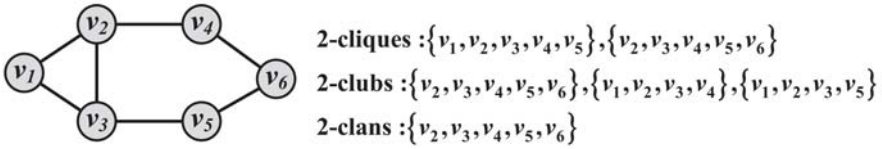


Figure 6.7: Examples of 2-Cliques, 2-Clubs, and 2-Clans.

- ***k*-Club** is a more restricted definition; it follows the same definition as *k*-cliques with the additional constraint that nodes on the shortest paths should be part of the subgraph.
- ***k*-Clan** is a *k*-clique where, for all shortest paths within the subgraph, the distance is less than or equal to *k*. All *k*-clans are *k*-cliques and *k*-clubs, but not vice versa. In other words,

$$k\text{-Clans} = k\text{-Cliques} \cap k\text{-Clubs}.$$

Figure 6.7 depicts an example of the three discussed models.

Node Similarity

Node similarity attempts to determine the similarity between two nodes v_i and v_j. Similar nodes (or most similar nodes) are assumed to be in the same community. Often, once the similarities between nodes are determined, a classical clustering algorithm (see Chapter 5) is applied to find communities. Determining similarity between two nodes has been addressed in different fields; in particular, the problem of *structural equivalence* in the field of sociology considers the same problem. In structural equivalence, similarity is based on the overlap between the neighborhood of the vertices. Let $N(v_i)$ and $N(v_j)$ be the neighbors of vertices v_i and v_j, respectively. In this case, a measure of vertex similarity can be defined as follows:

Structural Equivalence

$$\sigma(v_i, v_j) = |N(v_i) \cap N(v_j)|. \tag{6.2}$$

For large networks, this value can increase rapidly, because nodes may share many neighbors. Generally, similarity is attributed to a value that is bounded and usually in the range $[0, 1]$. For that to happen, various normalization procedures such as the Jaccard similarity or the cosine similarity

can be done:

$$\sigma_{\text{Jaccard}}(v_i, v_j) = \frac{|N(v_i) \cap N(v_j)|}{|N(v_i) \cup N(v_j)|}, \tag{6.3}$$

$$\sigma_{\text{Cosine}}(v_i, v_j) = \frac{|N(v_i) \cap N(v_j)|}{\sqrt{|N(v_i)||N(v_j)|}}. \tag{6.4}$$

Example 6.2. *Consider the graph in Figure 6.7. The similarity values between nodes v_2 and v_5 are*

$$\sigma_{\text{Jaccard}}(v_2, v_5) = \frac{|\{v_1, v_3, v_4\} \cap \{v_3, v_6\}|}{|\{v_1, v_3, v_4, v_6\}|} = 0.25, \tag{6.5}$$

$$\sigma_{\text{Cosine}}(v_2, v_5) = \frac{|\{v_1, v_3, v_4\} \cap \{v_3, v_6\}|}{\sqrt{|\{v_1, v_3, v_4\}||\{v_3, v_6\}|}} = 0.40. \tag{6.6}$$

In general, the definition of neighborhood $N(v_i)$ excludes the node itself (v_i). This, however, leads to problems with the aforementioned similarity values because nodes that are connected and do not share a neighbor will be assigned zero similarity. This can be rectified by assuming that nodes are included in their own neighborhood.

A generalization of structural equivalence is known as *regular equivalence*. Consider the situation of two basketball players in two different countries. Though sharing no neighborhood overlap, the social circles of these players (coach, players, fans, etc.) might look quite similar due to their social status. In other words, nodes are regularly equivalent when they are connected to nodes that are themselves similar (a self-referential definition). For more details on regular equivalence, refer to Chapter 3.

6.1.3 Group-Based Community Detection

When considering community characteristics for community detection, we are interested in communities that have certain group properties. In this section, we discuss communities that are balanced, robust, modular, dense, or hierarchical.

Balanced Communities

As mentioned before, community detection can be thought of as the problem of clustering in data mining and machine learning. Graph-based

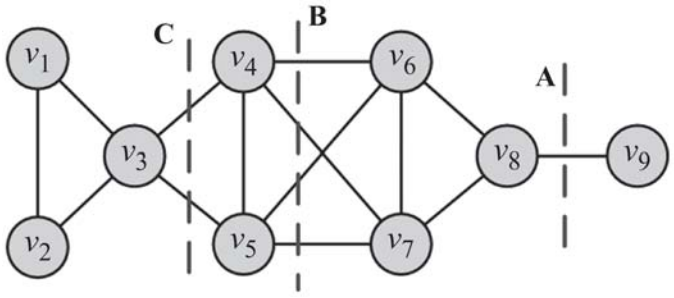


Figure 6.8: Minimum Cut (A) and Two More Balanced Cuts (B and C) in a Graph.

clustering techniques have proven to be useful in identifying communities in social networks. In graph-based clustering, we cut the graph into several partitions and assume these partitions represent communities.

Formally, a *cut* in a graph is a 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 and the summation of weights of edges that are being cut in a weighted graph. A *minimum cut* (min-cut) is a cut such that the size of the cut is minimized. Figure 6.8 depicts several cuts in a graph. For example, cut B has size 4, and A is the minimum cut. Minimum Cut

Based on the well-known *max-flow min-cut* theorem, the minimum cut of a graph can be computed efficiently. However, minimum cuts are not always preferred for community detection. Often, they result in cuts where a partition is only one node (singleton), and the rest of the graph is in the other. Typically, communities with balanced sizes are preferred. Figure 6.8 depicts an example where the minimum cut (A) creates unbalanced partitions, whereas, cut C is a more balanced cut.

To solve this problem, variants of minimum cut define an objective function, minimizing (or maximizing) that during the cut-finding procedure, results in a more balanced and natural partitioning of the data. Consider a graph $G(V, E)$. A partitioning of G into k partitions is a tuple $P = (P_1, P_2, P_3, \ldots, P_k)$, such that $P_i \subseteq V$, $P_i \cap P_j = \emptyset$ and $\bigcup_{i=1}^{k} P_i = V$. Then, the objective function for the ratio cut and normalized cut are defined as follows: Ratio cut and Normalized Cut

$$\text{Ratio Cut}(P) = \frac{1}{k} \sum_{i=1}^{k} \frac{\text{cut}(P_i, \bar{P}_i)}{|P_i|}, \tag{6.7}$$

$$\text{Normalized Cut}(P) = \frac{1}{k}\sum_{i=1}^{k}\frac{\text{cut}(P_i, \bar{P}_i)}{\text{vol}(P_i)}, \tag{6.8}$$

where $\bar{P}_i = V - P_i$ is the complement cut set, $cut(P_i, \bar{P}_i)$ is the size of the cut, and volume $vol(P_i) = \sum_{v \in P_i} d_v$. Both objective functions provide a more balanced community size by normalizing the cut size either by the number of vertices in the cutset or the volume (total degree).

Both the ratio cut and normalized cut can be formulated in a matrix format. Let matrix $X \in \{0,1\}^{|V| \times k}$ denote the *community membership* matrix, where $X_{i,j} = 1$ if node i is in community j; otherwise, $X_{i,j} = 0$. Let $D = \text{diag}(d_1, d_2, \ldots, d_n)$ represent the diagonal degree matrix. Then the i^{th} entry on the diagonal of $X^T AX$ represents the number of edges that are inside community i. Similarly, the ith element on the diagonal of $X^T DX$ represents the number of edges that are connected to members of community i. Hence, the i^{th} element on the diagonal of $X^T(D - A)X$ represents the number of edges that are in the cut that separates community i from all other nodes. In fact, the ith diagonal element of $X^T(D-A)X$ is equivalent to the summation term $cut(P_i, \bar{P}_i)$ in both the ratio and normalized cut. Thus, for ratio cut, we have

$$\begin{aligned}
\text{Ratio Cut}(P) &= \frac{1}{k}\sum_{i=1}^{k}\frac{\text{cut}(P_i, \bar{P}_i)}{|P_i|} && (6.9)\\
&= \frac{1}{k}\sum_{i=1}^{k}\frac{X_i^T(D-A)X_i}{X_i^T X_i} && (6.10)\\
&= \frac{1}{k}\sum_{i=1}^{k}\hat{X}_i^T(D-A)\hat{X}_i, && (6.11)
\end{aligned}$$

where $\hat{X}_i = X_i/(X_i^T X_i)^{1/2}$. A similar approach can be followed to formulate the normalized cut and to obtain a different $\hat{X}_i$. To formulate the summation in both the ratio and normalized cut, we can use the trace of matrix ($tr(\hat{X}) = \sum_{i=1}^{n}\hat{X}_{ii}$). Using the trace, the objectives for both the ratio and normalized cut can be formulated as trace-minimization problems,

$$\min_{\hat{X}} \text{Tr}(\hat{X}^T L\hat{X}), \tag{6.12}$$

where L is the *(normalized) graph Laplacian*, defined as follows:

$$L = \begin{cases} D - A & \text{Ratio Cut Laplacian (}\textit{Unnormalized Laplacian}\text{);} \\ I - D^{-1/2} A D^{-1/2} & \text{Normalized Cut Laplacian (}\textit{Normalized Laplacian}\text{).} \end{cases} \tag{6.13}$$

Normalized and Unnormalized Graph Laplacian

It has been shown that both ratio cut and normalized cut minimization are NP-hard; therefore, approximation algorithms using relaxations are desired. Spectral clustering is one such relaxation:

$$\min_{\hat{X}} \operatorname{Tr}(\hat{X}^T L \hat{X}), \tag{6.14}$$

$$s.t.\ \ \hat{X}^T \hat{X} = I_k. \tag{6.15}$$

Spectral Clustering

The solution to this problem is the top eigenvectors of L.[1] Given L, the top k eigenvectors corresponding to the smallest eigen values are computed and used as $\hat{X}$, and then k-means is run on $\hat{X}$ to extract communities memberships (X). The first eigenvector is meaningless (why?); hence, the rest of the eigenvectors ($k-1$) are used as k-means input.

Example 6.3. *Consider the graph in Figure 6.8. We find two communities in this graph using spectral clustering (i.e., $k = 2$). Then, we have*

$$D = diag(2, 2, 4, 4, 4, 4, 4, 3, 1). \tag{6.16}$$

The adjacency matrix A and the unnormalized laplacian L are

$$A = \begin{bmatrix} 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{bmatrix}, \tag{6.17}$$

[1] For more details refer to [56].

$$L = D - A = \begin{bmatrix} 2 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -1 & -1 & 4 & -1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 4 & -1 & -1 & -1 & 0 & 0 \\ 0 & 0 & -1 & -1 & 4 & -1 & -1 & 0 & 0 \\ 0 & 0 & 0 & -1 & -1 & 4 & -1 & -1 & 0 \\ 0 & 0 & 0 & -1 & -1 & -1 & 4 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & -1 & -1 & 3 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 1 \end{bmatrix}. \tag{6.18}$$

We aim to find two communities; therefore, we get two eigenvectors corresponding to the two smallest eigenvalues from L:

$$\hat{X} = \begin{array}{c} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \\ 7 \\ 8 \\ 9 \end{array} \begin{bmatrix} & \\ 0.33 & -0.46 \\ 0.33 & -0.46 \\ 0.33 & -0.26 \\ 0.33 & \approx 0.01 \\ 0.33 & \approx 0.01 \\ 0.33 & 0.13 \\ 0.33 & 0.13 \\ 0.33 & 0.33 \\ 0.33 & 0.59 \end{bmatrix}. \tag{6.19}$$

As mentioned, the first eigenvector is meaningless, because it assigns all nodes to the same community. The second is used with k-means; based on the vector signs, we get communities $\{1, 2, 3\}$ *and* $\{4, 5, 6, 7, 8, 9\}$.

Robust Communities

When seeking robust communities, our goal is to find subgraphs robust enough such that removing some edges or nodes does not disconnect the subgraph. A k-vertex connected graph (or k-connected) is an example of such a graph. In this graph, k is the minimum number of nodes that must

k-connected

be removed to disconnect the graph (i.e., there exist at least k independent paths between any pair of nodes). A similar subgraph is the k-edge graph, where at least k edges must be removed to disconnect the graph. An upper-bound analysis on *k-edge connectivity* shows that the minimum degree for any node in the graph should not be less than k (why?). For example, a complete graph of size n is a unique n-connected graph, and a cycle is a 2-connected graph.

Modular Communities

Modularity is a measure that defines how likely the community structure found is created at random. Clearly, community structures should be far from random. Consider an undirected graph $G(V, E)$, $|E| = m$ where the degrees are known beforehand, but edges are not. Consider two nodes v_i and v_j, with degrees d_i and d_j, respectively. What is the expected number of edges between these two nodes? Consider node v_i. For any edge going out of v_i randomly, the probability of this edge getting connected to node v_j is $\frac{d_j}{\sum_i d_i} = \frac{d_j}{2m}$. Because the degree for v_i is d_i, we have d_i number of such edges; hence, the expected number of edges between v_i and v_j is $\frac{d_i d_j}{2m}$. So, given a degree distribution, the expected number of edges between any pair of vertices can be computed. Real-world communities are far from random; therefore, the more distant they are from randomly generated communities, the more structure they exhibit. Modularity defines this distance, and modularity maximization tries to maximize this distance. Consider a partitioning of the graph G into k partitions, $P = (P_1, P_2, P_3, \ldots, P_k)$. For partition P_x, this distance can be defined as

Modularity

$$\sum_{v_i, v_j \in P_x} A_{ij} - \frac{d_i d_j}{2m}. \tag{6.20}$$

This distance can be generalized for partitioning P with k partitions,

$$\sum_{x=1}^{k} \sum_{v_i, v_j \in P_x} A_{ij} - \frac{d_i d_j}{2m}. \tag{6.21}$$

The summation is over all edges (m), and because all edges are counted twice ($A_{ij} = A_{ji}$), the normalized version of this distance is defined as

modularity [211]:

$$Q = \frac{1}{2m}\left(\sum_{x=1}^{k}\sum_{v_i,v_j\in P_x} A_{ij} - \frac{d_i d_j}{2m}\right). \tag{6.22}$$

We define the modularity matrix as $B = A - \mathbf{d}\mathbf{d}^T/2m$, where $\mathbf{d} \in \mathbb{R}^{n\times 1}$ is the degree vector for all nodes. Similar to spectral clustering matrix formulation, modularity can be reformulated as

$$Q = \frac{1}{2m}\text{Tr}(X^T B X), \tag{6.23}$$

where $X \in \mathbb{R}^{n\times k}$ is the indicator (partition membership) function; that is, $X_{ij} = 1$ iff. $v_i \in P_j$. This objective can be maximized such that the best membership function is extracted with respect to modularity. The problem is NP-hard; therefore, we relax X to $\hat{X}$ that has an orthogonal structure ($\hat{X}^T\hat{X} = I_k$). The optimal $\hat{X}$ can be computed using the top k eigenvectors of B corresponding to the largest positive eigenvalues. Similar to spectral clustering, to find X, we can run k-means on $\hat{X}$. Note that this requires that B has at least k positive eigenvalues.

Dense Communities

Often, we are interested in dense communities, which have sufficiently frequent interactions. These communities are of particular interest in social media where we would like to have enough interactions for analysis to make statistical sense. When we are measuring density in communities, the community may or may not be connected as long as it satisfies the properties required, assuming connectivity is not one such property. Cliques, clubs, and clans are examples of connected dense communities. Here, we focus on subgraphs that have the possibility of being disconnected. Density-based community detection has been extensively discussed in the field of clustering (see Chapter 5, Bibliographic Notes).

Graph Density

The density γ of a graph defines how close a graph is to a clique. In other words, the density γ is the ratio of the number of edges $|E|$ that graph G has over the maximum it can have $\binom{|V|}{2}$:

$$\gamma = \frac{|E|}{\binom{|V|}{2}}. \tag{6.24}$$

A graph $G = (V, E)$ is γ-dense if $|E| \geq \gamma\binom{|V|}{2}$. Note that a 1-dense graph is a clique. Here, we discuss the interesting scenario of connected dense graphs (i.e., quasi-cliques). A quasi-clique (or γ-clique) is a connected γ-dense graph. Quasi-cliques can be searched for using approaches previously discussed for finding cliques. We can utilize the brute-force clique identification algorithm (Algorithm 6.1) for finding quasi-cliques as well. The only part of the algorithm that needs to be changed is the part where the clique condition is checked (Line 8). This can be replaced with a quasi-clique checking condition. In general, because there is less regularity in quasi-cliques, searching for them becomes harder. Interested readers can refer to the bibliographic notes for faster algorithms.

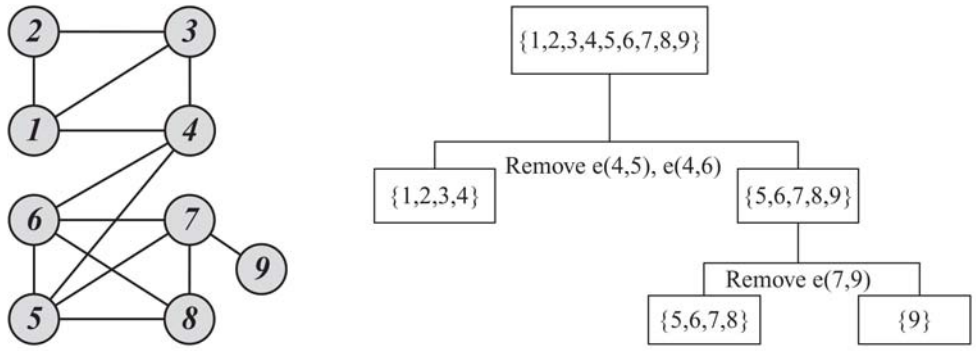
Quasi-Clique

Hierarchical Communities

All previously discussed methods have considered communities at a single level. In reality, it is common to have hierarchies of communities, in which each community can have sub/super communities. Hierarchical clustering deals with this scenario and generates community hierarchies. Initially, n nodes are considered as either 1 or n communities in hierarchical clustering. These communities are gradually merged or split (*agglomerative* or *divisive* hierarchical clustering algorithms), depending on the type of algorithm, until the desired number of communities are reached. A dendrogram is a visual demonstration of how communities are merged or split using hierarchical clustering. The Girvan-Newman [101] algorithm is specifically designed for finding communities using divisive hierarchical clustering.

The assumption underlying this algorithm is that, if a network has a set of communities and these communities are connected to one another with a few edges, then all shortest paths between members of different communities should pass through these edges. By removing these edges (at times referred to as *weak ties*), we can recover (i.e., disconnect) communities in a network. To find these edges, the Girvan-Newman algorithm uses a measure called *edge betweenness* and removes edges with higher edge betweenness. For an edge e, edge betweenness is defined as the number of shortest paths between node pairs (v_i, v_j) such that the shortest path between v_i and v_j passes through e. For instance, in Figure 6.9(a), edge betweenness for edge $e(1, 2)$ is $6/2 + 1 = 4$, because 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. Formally, the Girvan-Newman algorithm

Edge Betweenness



(a) Graph (b) Dendrogram

Figure 6.9: An Example of Girvan-Newman Algorithm Example: (a) graph and (b) its hierarchical clustering dendrogram based on edge betweenness.

Girvan-Newman Algorithm

is as follows:

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.

Example 6.4. *Consider the graph depicted in Figure 6.9(a). For this graph, the edge-betweenness values are as follows:*

$$\left[\begin{array}{c|ccccccccc} & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 \\ \hline 1 & 0 & 4 & 1 & 9 & 0 & 0 & 0 & 0 & 0 \\ 2 & 4 & 0 & 4 & 0 & 0 & 0 & 0 & 0 & 0 \\ 3 & 1 & 4 & 0 & 9 & 0 & 0 & 0 & 0 & 0 \\ 4 & 9 & 0 & 9 & 0 & 10 & 10 & 0 & 0 & 0 \\ 5 & 0 & 0 & 0 & 10 & 0 & 1 & 6 & 3 & 0 \\ 6 & 0 & 0 & 0 & 10 & 1 & 0 & 6 & 3 & 0 \\ 7 & 0 & 0 & 0 & 0 & 6 & 6 & 0 & 2 & 8 \\ 8 & 0 & 0 & 0 & 0 & 3 & 3 & 2 & 0 & 0 \\ 9 & 0 & 0 & 0 & 0 & 0 & 0 & 8 & 0 & 0 \end{array}\right]. \tag{6.25}$$

Therefore, by following the algorithm, 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*

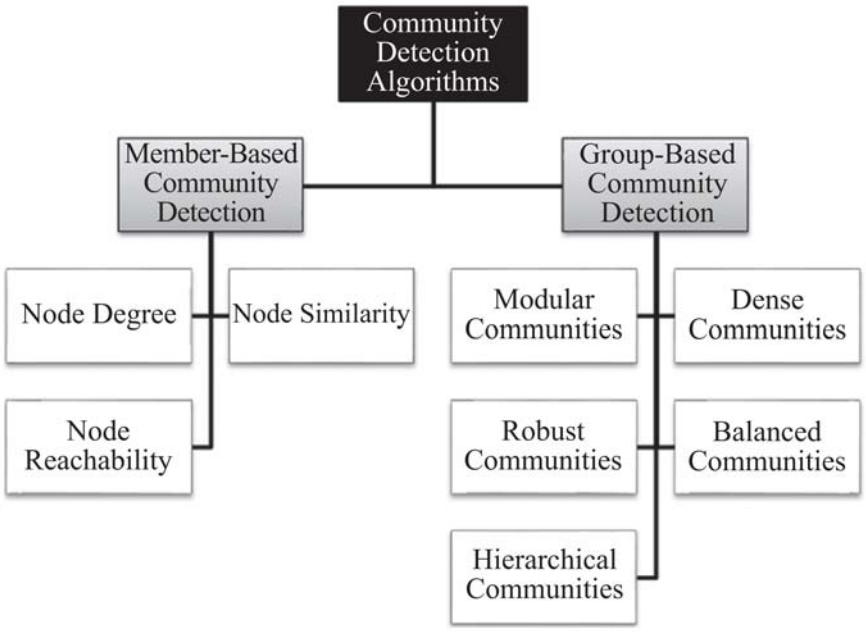


Figure 6.10: Community Detection Algorithms.

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* $4 \times 5 = 20$*. By following the first few steps of the algorithm, the dendrogram shown in Figure 6.9(b) and three disconnected communities* $(\{1,2,3,4\}, \{5,6,7,8\}, \{9\})$ *can be obtained.*

We discussed various community detection algorithms in this section. Figure 6.10 summarizes the two categories of community detection algorithms.

6.2 Community Evolution

Community detection algorithms discussed so far assume that networks are static; that is, their nodes and edges are fixed and do not change over time. In reality, with the rapid growth of social media, networks and their internal communities change over time. Earlier community detection algorithms have to be extended to deal with evolving networks. Before

analyzing evolving networks, we need to answer the question, *How do networks evolve?* In this section, we discuss how networks evolve in general and then how communities evolve over time. We also demonstrate how communities can be found in these evolving networks.

6.2.1 How Networks Evolve

Large social networks are highly dynamic, where nodes and links appear or disappear over time. In these evolving networks, many interesting patterns are observed; for instance, when distances (in terms of shortest path distance) between two nodes increase, their probability of getting connected decreases.[2] We discuss three common patterns that are observed in evolving networks: segmentation, densification, and diameter shrinkage.

Network Segmentation

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

1. **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.
2. **Stars**: These are isolated parts of the network that form star structures. A star is a tree with one internal node and n leaves.
3. **Singletons**: These are orphan nodes disconnected from all nodes in the network.

Figure 6.11 depicts a segmented network and these three components.

Graph Densification

It is observed in evolving graphs that the density of the graph increases as the network grows. In other words, the number of edges increases faster than the number of nodes. This phenomenon is called *densification*. Let $V(t)$ denote nodes at time t and let $E(t)$ denote edges at time t,

$$|E(t)| \propto |V(t)|^{\alpha}. \tag{6.26}$$

[2] See [154] for details.

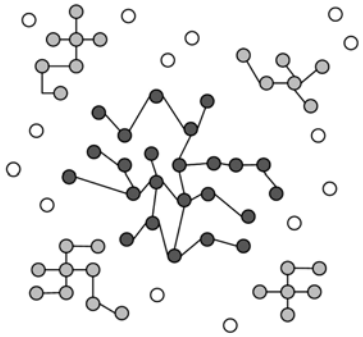


Figure 6.11: Network Segmentation. The network is decomposed into a giant component (dark gray), star components (medium gray), and singletons (light gray).

If densification happens, then we have $1 \leq \alpha \leq 2$. There is linear growth when $\alpha = 1$, and we get clique structures when $\alpha = 2$ (why?). Networks exhibit α values between 1 and 2 when evolving. Figure 6.12 depicts a log-log graph for densification for a physics citation network and a patent citation network. During the evolution process in both networks, the number of edges is recorded as the number of nodes grows. These recordings show that both networks have $\alpha \approx 1.6$ (i.e., the log-log graph of $|E|$ with respect to $|V|$ is a straight line with slope 1.6). This value also implies that when V is given, to realistically model a social network, we should generate $O(|V|^{1.6})$ edges.

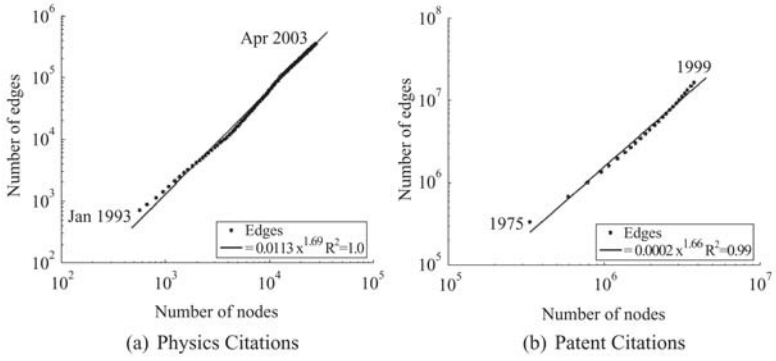


Figure 6.12: Graph Densification (from [167]).

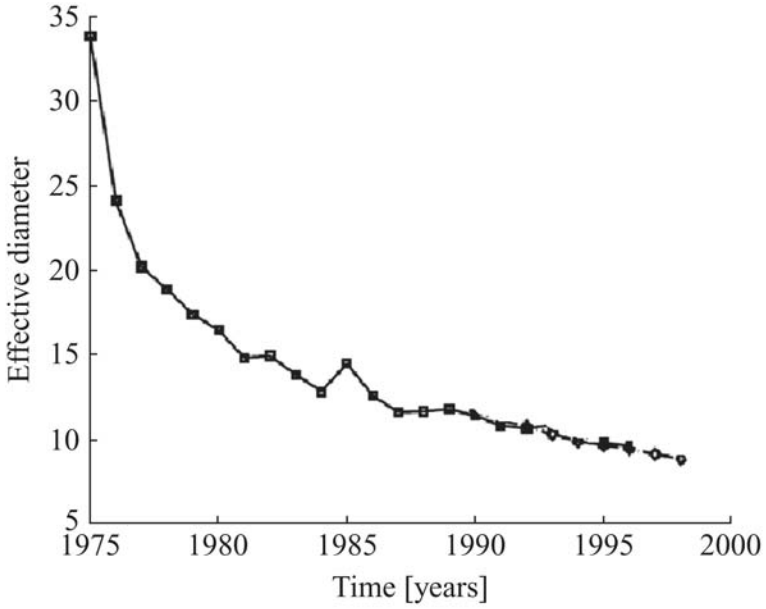


Figure 6.13: Diameter Shrinkage over Time for a Patent Citation Network (from [167]).

Diameter Shrinkage

Another property observed in large networks is that the network diameter shrinks in time. This property has been observed in random graphs as well (see Chapter 4). Figure 6.13 depicts the diameter shrinkage for the same patent network discussed in Figure 6.12.

In this section we discussed three phenomena that are observed in evolving networks. Communities in evolving networks also evolve. They appear, grow, shrink, split, merge, or even dissolve over time. Figure 6.14 depicts different situations that can happen during community evolution.

Both networks and their internal communities evolve over time. Given evolution information (e.g., when edges or nodes are added), how can we study evolving communities? And can we adapt static (nontemporal) methods to use this temporal information? We discuss these questions next.

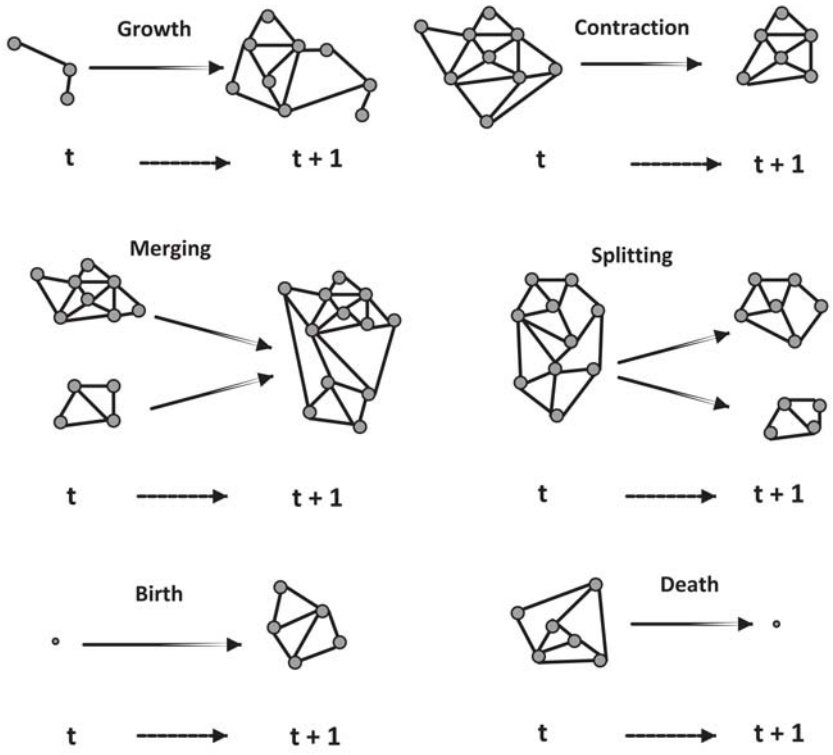


Figure 6.14: Community Evolution (reproduced from [226]).

6.2.2 Community Detection in Evolving Networks

Consider an instant messaging (IM) application in social media. In these IM systems, members become "available" or "offline" frequently. Consider individuals as nodes and messages between them as edges. In this example, we are interested in finding a community of individuals who send messages to one another frequently. Clearly, community detection at any time stamp is not a valid solution because interactions are limited at any point in time. A valid solution to this problem needs to use temporal information and interactions between users over time. In this section, we present community detection algorithms that incorporate temporal information. To incorporate temporal information, we can extend previously discussed static methods as follows:

1. Take t snapshots of the network, $G_1, G_2, \ldots, G_t$, where G_i is a snapshot at time i.

2. Perform a static community detection algorithm on all snapshots independently.

3. Assign community members based on communities found in all t different time stamps. For instance, we can assign nodes to communities based on voting. In voting, we assign nodes to communities they belong to the most over time.

Unfortunately, this method is unstable in highly dynamic networks because community memberships are always changing. An alternative is to use evolutionary clustering.

Evolutionary Clustering

In evolutionary clustering, it is assumed that communities do not change most of the time; hence, it tries to minimize an objective function that considers both communities at different time stamps (snapshot cost or SC) and how they evolve throughout time (temporal cost or TC). Then, the objective function for evolutionary clustering is defined as a linear combination of the snapshot cost and temporal cost (SC and TC),

$$Cost = \alpha\ SC + (1 - \alpha)\ TC, \tag{6.27}$$

where $0 \leq \alpha \leq 1$. Let us assume that spectral clustering (discussed in Section 6.1.3) is used to find communities at each time stamp. We know that the objective for spectral clustering is $Tr(X^T L X)$ s.t. $X^T X = I_m$, so we will have the objective function at time t as

$$\begin{aligned} Cost_t &= \alpha\ SC + (1 - \alpha)\ TC, & (6.28)\\ &= \alpha\ Tr(X_t^T L X_t) + (1 - \alpha)\ TC, & (6.29) \end{aligned}$$

where X_t is the community membership matrix at time t. To define TC, we can compute the distance between the community assignments of two snapshots:

$$TC = \|X_t - X_{t-1}\|^2. \tag{6.30}$$

Unfortunately, this requires both X_t and X_{t-1} to have the same number of columns (number of communities). Moreover, X_t is not unique and

can change by orthogonal transformations;[3] therefore, the distance value $\|X_t - X_{t-1}\|^2$ can change arbitrarily. To remove the effect of orthogonal transformations and allow different numbers of columns, TC is defined as

$$\begin{aligned} TC &= \frac{1}{2}\|X_t X_t^T - X_{t-1}X_{t-1}^T\|^2, \\ &= \frac{1}{2}Tr((X_t X_t^T - X_{t-1}X_{t-1}^T)^T(X_t X_t^T - X_{t-1}X_{t-1}^T)), \\ &= \frac{1}{2}Tr(X_t X_t^T X_t X_t^T - 2X_t X_t^T X_{t-1}X_{t-1}^T + X_{t-1}X_{t-1}^T X_{t-1}X_{t-1}^T), \\ &= Tr(I - X_t X_t^T X_{t-1}X_{t-1}^T), \\ &= Tr(I - X_t^T X_{t-1}X_{t-1}^T X_t), \end{aligned} \tag{6.31}$$

where $\frac{1}{2}$ is for mathematical convenience, and $Tr(AB) = Tr(BA)$ is used. Therefore, evolutionary clustering objective can be stated as

$$\begin{aligned} Cost_t &= \alpha\, Tr(X_t^T L X_t) + (1-\alpha)\,\frac{1}{2}\|X_t X_t^T - X_{t-1}X_{t-1}^T\|^2, \\ &= \alpha\, Tr(X_t^T L X_t) + (1-\alpha)\, Tr(I - X_t^T X_{t-1}X_{t-1}^T X_t), \\ &= \alpha\, Tr(X_t^T L X_t) + (1-\alpha)\, Tr(X_t^T I X_t - X_t^T X_{t-1}X_{t-1}^T X_t), \\ &= Tr(X_t^T \alpha L X_t) + Tr(X_t^T(1-\alpha) I X_t - X_t^T(1-\alpha) X_{t-1}X_{t-1}^T X_t). \end{aligned} \tag{6.32}$$

Assuming the normalized Laplacian is used in spectral clustering, $L = I - D_t^{-1/2} A_t D_t^{-1/2}$,

$$\begin{aligned} Cost_t &= Tr(X_t^T \alpha(I - D_t^{-1/2} A_t D_t^{-1/2})\, X_t) \\ &\quad + Tr(X_t^T\, (1-\alpha)\, I\, X_t - X_t^T\, (1-\alpha)\, X_{t-1}\, X_{t-1}^T\, X_t), \\ &= Tr(X_t^T\, (I - \alpha D_t^{-1/2} A_t D_t^{-1/2} - (1-\alpha)\, X_{t-1}X_{t-1}^T)\, X_t), \\ &= Tr(X_t \hat{L} X_t), \end{aligned} \tag{6.33}$$

where $\hat{L} = I - \alpha D_t^{-1/2} A_t D_t^{-1/2} - (1-\alpha) X_{t-1}X_{t-1}^T$. Similar to spectral clustering, X_t can be obtained by taking the top eigenvectors of $\hat{L}$.

[3] Let X be the solution to spectral clustering. Consider an orthogonal matrix Q (i.e., $QQ^T = I$). Let $Y = XQ$. In spectral clustering, we are maximizing $Tr(X^T L X) = Tr(X^T L X Q Q^T) = Tr(Q^T X^T L X Q) = Tr((XQ)^T L (XQ)) = Tr(Y^T L Y)$. In other words, Y is another answer to our trace-maximization problem. This proves that the solution X to spectral clustering is non-unique under orthogonal transformations Q.

Figure 6.15: Community Evaluation Example. Circles represent communities, and items inside the circles represent members. Each item is represented using a symbol, +, ×, or △, that denotes the item's true label.

Note that at time t, we can obtain X_t directly by solving spectral clustering for the laplacian of the graph at time t, but then we are not employing any temporal information. Using evolutionary clustering and the new laplacian $\hat{L}$, we incorporate temporal information into our community detection algorithm and disallow user memberships in communities at time t: X_t to change dramatically from X_{t-1}.

6.3 Community Evaluation

When communities are found, one must evaluate how accurately the detection task has been performed. In terms of evaluating communities, the task is similar to evaluating clustering methods in data mining. Evaluating clustering is a challenge because ground truth may not be available. We consider two scenarios: when ground truth is available and when it is not.

6.3.1 Evaluation with Ground Truth

When ground truth is available, we have at least partial knowledge of what communities should look like. Here, we assume that we are given the correct community (clustering) assignments. We discuss four measures: precision and recall, F-measure, purity, and normalized mutual information (NMI). Consider Figure 6.15, where three communities are found and the points are shown using their true labels.

Precision and Recall

Community detection can be considered a problem of assigning all similar nodes to the same community. In the simplest case, any two similar nodes should be considered members of the same community. Based on our assignments, four cases can occur:

1. True Positive (**TP**) Assignment: when similar members are assigned to the same community. This is a *correct* decision.

2. True Negative (**TN**) Assignment: when dissimilar members are assigned to different communities. This is a *correct* decision.

3. False Negative (**FN**) Assignment: when similar members are assigned to different communities. This is an *incorrect* decision.

4. False Positive (**FP**) Assignment: when dissimilar members are assigned to the same community. This is an *incorrect* decision.

Precision (P) and Recall (R) are defined as follows,

$$P = \frac{TP}{TP + FP}, \tag{6.34}$$

$$R = \frac{TP}{TP + FN}. \tag{6.35}$$

Precision defines the fraction of pairs that have been correctly assigned to the same community. Recall defines the fraction of pairs that the community detection algorithm assigned to the same community of all the pairs that should have been in the same community.

Example 6.5. *We compute these values for Figure 6.15. For TP, we need to compute the number of pairs with the same label that are in the same community. For instance, for label $\times$ and community 1, we have $\binom{5}{2}$ such pairs. Therefore,*

$$TP = \underbrace{\binom{5}{2}}_{\text{Community 1}} + \underbrace{\binom{6}{2}}_{\text{Community 2}} + \underbrace{(\binom{4}{2} + \binom{2}{2})}_{\text{Community 3}} = 32. \tag{6.36}$$

For FP, we need to compute dissimilar pairs that are in the same community. For instance, for community 1, this is $(5 \times 1 + 5 \times 1 + 1 \times 1)$*. Therefore,*

$$FP = \underbrace{(5 \times 1 + 5 \times 1 + 1 \times 1)}_{\text{Community 1}} + \underbrace{(6 \times 1)}_{\text{Community 2}} + \underbrace{(4 \times 2)}_{\text{Community 3}} = 25. \quad (6.37)$$

FN computes similar members that are in different communities. For instance, for label +, this is $(6 \times 1 + 6 \times 2 + 2 \times 1)$*. Similarly,*

$$FN = \underbrace{(5 \times 1)}_{\times} + \underbrace{(6 \times 1 + 6 \times 2 + 2 \times 1)}_{+} + \underbrace{(4 \times 1)}_{\triangle} = 29. \quad (6.38)$$

Finally, TN computes the number of dissimilar pairs in dissimilar communities:

$$\begin{aligned} TN = & \underbrace{(\overbrace{5 \times 6}^{\times,+} + \overbrace{1 \times 1}^{+,\times} + \overbrace{1 \times 6}^{\triangle,+} + \overbrace{1 \times 1}^{\triangle,\times})}_{\text{Communities 1 and 2}} \\ & + \underbrace{(\overbrace{5 \times 4}^{\times,\triangle} + \overbrace{5 \times 2}^{\times,+} + \overbrace{1 \times 4}^{+,\triangle} + \overbrace{1 \times 2}^{\triangle,+})}_{\text{Communities 1 and 3}} \\ & + \underbrace{(\overbrace{6 \times 4}^{+,\triangle} + \overbrace{1 \times 2}^{\times,+} + \overbrace{1 \times 4}^{\times,\triangle})}_{\text{Communities 2 and 3}} = 104. \end{aligned} \quad (6.39)$$

Hence,

$$P = \frac{32}{32 + 25} = 0.56 \quad (6.40)$$

$$R = \frac{32}{32 + 29} = 0.52. \quad (6.41)$$

F-Measure

To consolidate precision and recall into one measure, we can use the harmonic mean of precision and recall:

$$F = 2 \cdot \frac{\mathrm{P} \cdot \mathrm{R}}{\mathrm{P} + \mathrm{R}}. \quad (6.42)$$

Computed for the same example, we get $F = 0.54$.

Purity

In purity, we assume that the majority of a community represents the community. Hence, we use the label of the majority of the community against the label of each member of the community to evaluate the algorithm. For instance, in Figure 6.15, the majority in Community 1 is ×; therefore, we assume majority label × for that community. The purity is then defined as the fraction of instances that have labels equal to their community's majority label. Formally,

$$Purity = \frac{1}{N} \sum_{i=1}^{k} \max_{j} |C_i \cap L_j|, \tag{6.43}$$

where k is the number of communities, N is the total number of nodes, L_j is the set of instances with label j in all communities, and C_i is the set of members in community i. In the case of our example, purity is $\frac{5+6+4}{20} = 0.75$.

Normalized Mutual Information

Purity can be easily manipulated to generate high values; consider when nodes represent singleton communities (of size 1) or when we have very large pure communities (ground truth = majority label). In both cases, purity does not make sense because it generates high values.

A more precise measure to solve problems associated with purity is the normalized mutual information (NMI) measure, which originates in information theory. Mutual information (MI) describes the amount of information that two random variables share. In other words, by knowing one of the variables, MI measures the amount of uncertainty reduced regarding the other variable. Consider the case of two independent variables; in this case, the mutual information is zero because knowing one does not help in knowing more information about the other. Mutual information of two variables X and Y is denoted as $I(X, Y)$. We can use mutual information to measure the information one clustering carries regarding the ground truth. It can be calculated using Equation 6.44, where 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.

$$MI = I(X, Y) = \sum_{h \in H} \sum_{l \in L} \frac{n_{h,l}}{n} \log \frac{n \cdot n_{h,l}}{n_h n_l} \tag{6.44}$$

Unfortunately, mutual information is unbounded; however, it is common for measures to have values in range [0,1]. To address this issue, we can normalize mutual information. We provide the following equation, without proof, which will help us normalize mutual information,

$$MI \leq min(H(L), H(H)), \tag{6.45}$$

where $H(\cdot)$ is the entropy function,

$$H(L) = -\sum_{l \in L} \frac{n_l}{n} \log \frac{n_l}{n} \tag{6.46}$$

$$H(H) = -\sum_{h \in H} \frac{n_h}{n} \log \frac{n_h}{n}. \tag{6.47}$$

From Equation 6.45, we have $MI \leq H(L)$ and $MI \leq H(H)$; therefore,

$$(MI)^2 \leq H(H)H(L). \tag{6.48}$$

Equivalently,

$$MI \leq \sqrt{H(H)}\sqrt{H(L)}. \tag{6.49}$$

Equation 6.49 can be used to normalize mutual information. Thus, we introduce the NMI as

$$NMI = \frac{MI}{\sqrt{H(L)}\sqrt{H(H)}}. \tag{6.50}$$

By plugging Equations 6.47, 6.46, and 6.44 into 6.50,

$$NMI = \frac{\sum_{h \in H} \sum_{l \in L} n_{h,l} \log \frac{n \cdot n_{h,l}}{n_h n_l}}{\sqrt{(\sum_{h \in H} n_h \log \frac{n_h}{n})(\sum_{l \in L} n_l \log \frac{n_l}{n})}}. \tag{6.51}$$

An NMI value close to one indicates high similarity between communities found and labels. A value close to zero indicates a long distance between them.

(a) U.S . Constitution (b) Sports

Figure 6.16: Tag Clouds for Two Communities.

6.3.2 Evaluation without Ground Truth

When no ground truth is available, we can incorporate techniques based on semantics or clustering quality measures to evaluate community detection algorithms.

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. For example, the Amazon Mechanical Turk platform[4] allows defining this task on its platform for human workers and hiring individuals from all around the globe to perform tasks such as community evaluation. 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. A more focused and single-topic set of keywords represents a coherent community. Tag clouds are one way of demonstrating these topics. Figure 6.16 depicts two coherent tag clouds for a community related to the U.S. Constitution and another for sports. Larger words in these tag clouds represent higher frequency of use.

Evaluation Using Clustering Quality Measures

When experts are not available, an alternative is to use clustering quality measures. This approach is commonly used when two or more commu-

[4]http://www.mturk.com.

nity detection algorithms are available. Each algorithm is run on the target network, and the quality measure is computed for the identified communities. The algorithm that yields a more desirable quality measure value is considered a better algorithm. SSE (sum of squared errors) and inter-cluster distance are some of the quality measures. For other measures refer to Chapter 5.

We can also follow this approach for evaluating a single community detection algorithm; however, we must ensure that the clustering quality measure used to evaluate community detection is different from the measure used to find communities. For instance, when using node similarity to group individuals, a measure other than node similarity should be used to evaluate the effectiveness of community detection.

6.4 Summary

In this chapter, we discussed community analysis in social media, answering three general questions: (1) how can we detect communities, (2) how do communities evolve and how can we study evolving communities, and (3) how can we evaluate detected communities? We started with a description of communities and how they are formed. Communities in social media are either explicit (emic) or implicit (etic). Community detection finds implicit communities in social media.

We reviewed member-based and group-based community detection algorithms. In member-based community detection, members can be grouped based on their degree, reachability, and similarity. For example, when using degrees, cliques are often considered as communities. Brute-force clique identification is used to identify cliques. In practice, due to the computational complexity of clique identifications, cliques are either relaxed or used as seeds of communities. k-Plex is an example of relaxed cliques, and the clique percolation algorithm is an example of methods that use cliques as community seeds. When performing member-based community detection based on reachability, three frequently used subgraphs are the k-clique, k-club, and k-clan. Finally, in member-based community detection based on node similarity, methods such as Jaccard and Cosine similarity help compute node similarity. In group-based community detection, we described methods that find balanced, robust, modular, dense, or hierarchical communities. When finding balanced communities, one can employ spectral clustering. Spectral clustering provides a relaxed solution to the normalized cut and ratio cut in graphs. For finding robust communities, we search for subgraphs that are hard to disconnect. k-edge and k-vertex graphs are two examples of these robust subgraphs. To find modular communities, one can use modularity maximization and for dense communities, we discussed quasi-cliques. Finally, we provided hierarchical clustering as a solution to finding hierarchical communities, with the Girvan-Newman algorithm as an example.

In community evolution, we discussed when networks and, on a lower level, communities evolve. We also discussed how communities can be detected in evolving networks using evolutionary clustering. Finally, we presented how communities are evaluated when ground truth exists and when it does not.

6.5 Bibliographic Notes

A general survey of community detection in social media can be found in [91] and a review of heterogeneous community detection in [278]. In related fields, [35, 305, 136] provide surveys of clustering algorithms and [294] provides a sociological perspective. Comparative analysis of community detection algorithms can be found in [162] and [168]. The description of explicit communities in this chapter is due to Kadushin [140].

For member-based algorithms based on node degree, refer to [158], which provides a systematic approach to finding clique-based communities with pruning. In algorithms based on node reachability, one can find communities by finding connected components in the network. For more information on finding connected components of a graph refer to [130]. In node similarity, we discussed structural equivalence, similarity measures, and regular equivalence. More information on structural equivalence can be found in [178, 166], on Jaccard similarity in [133], and on regular equivalence in [264].

In group-based methods that find balanced communities, we are often interested in solving the max-flow min-cut theorem. Linear programming and Ford-Fulkerson [61], Edmonds-Karp [80], and Push-Relabel [103] methods are some established techniques for solving the max-flow min-cut problem. We discussed quasi-cliques that help find dense communities. Finding the maximum quasi-clique is discussed in [231]. A well-known greedy algorithm for finding quasi-cliques is introduced by [2]. In their approach a local search with a pruning strategy is performed on the graph to enhance the speed of quasi-clique detection. They define a `peel` strategy, in which vertices that have some degree k along with their incident edges are recursively removed. There are a variety of algorithms to find dense subgraphs, such as the one discussed in [99] where the authors propose an algorithm that recursively fingerprints the graph (shingling algorithm) and creates dense subgraphs. In group-based methods that find hierarchical communities, we described hierarchical clustering. Hierarchical clustering algorithms are usually variants of single link, average link, or complete link algorithms [135]. In hierarchical clustering, COBWEB [88] and CHAMELEON [142] are two well-known algorithms.

In group-based community detection, latent space models [121, 129] are also very popular, but are not discussed in this chapter. In addition to the topics discussed in this chapter, community detection can also be per-

formed for networks with multiple types of interaction (edges) [279]; [280]. We also restricted our discussion to community detection algorithms that use graph information. One can also perform community detection based on the content that individuals share on social media. For instance, using tagging relations (i.e., individuals who shared the same tag) [292], instead of connections between users, one can discover overlapping communities, which provides a natural summarization of the interests of the identified communities.

In network evolution analysis, network segmentation is discussed in [157]. Segment-based clustering [269] is another method not covered in this chapter.

NMI was first introduced in [267] and in terms of clustering quality measures, the Davies-Bouldin [67] measure, Rand index [236], C-index [76], Silhouette index [241], and Goodman-Kruskal index [106] can be used.

6.6 Exercises

1. Provide an example to illustrate how community detection can be subjective.

Community Detection

2. Given a complete graph K_n, how many nodes will the clique percolation method generate for the clique graph for value k? How many edges will it generate?

3. Find all k-cliques, k-clubs, and k-clans in a complete graph of size 4.

4. For a complete graph of size n, is it m-connected? What possible values can m take?

5. Why is the smallest eigenvector meaningless when using an unnormalized laplacian matrix?

6. Modularity can be defined as

$$Q = \frac{1}{2m} \sum_{ij} \left[A_{ij} - \frac{d_i d_j}{2m} \right] \delta(c_i, c_j), \tag{6.52}$$

   where c_i and c_j are the communities for v_i and v_j, respectively.

   $\delta(c_i, c_j)$ (Kronecker delta) is 1 when v_i and v_j both belong to the same community ($c_i = c_j$), and 0 otherwise.

   - What is the range $[\alpha_1, \alpha_2]$ for Q values? Provide examples for both extreme values of the range and cases where modularity becomes zero.
   - What are the limitations for modularity? Provide an example where modularity maximization does not seem reasonable.
   - Find three communities in Figure 6.8 by performing modularity maximization.

7. For Figure 6.8:

- Compute Jaccard and Cosine similarity between nodes v_4 and v_8, assuming that the neighborhood of a node excludes the node itself.
- Compute Jaccard and Cosine similarity when the node is included in the neighborhood.

Community Evolution

8. What is the upper bound on densification factor α? Explain.

Community Evaluation

9. Normalized mutual information (NMI) is used to evaluate community detection results when the actual communities (labels) are known beforehand.
   - What are the maximum and minimum values for the NMI? Provide details.
   - Explain how NMI works (describe the intuition behind it).
10. Compute NMI for Figure 6.15.
11. Why is high precision not enough? Provide an example to show that both precision and recall are important.
12. Discuss situations where purity does not make sense.
13. Compute the following for Figure 6.17:

Figure 6.17: Community Evaluation Example.

- precision and recall
- F-measure
- NMI
- purity