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Predicting Stability of Community Members in Complex Networks using profile closeness

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Abstract

This work introduces profile closeness, a novel variant of closeness centrality, to analyze and predict community evolution in complex networks. By prioritizing influential nodes within communities, profile closeness serves as a reliable indica- tor of community dynamics in both static and dynamic networks. This metric can predict node addition and departure, offering valuable insights into how commu- nities evolve over time. Furthermore, integrating profile closeness with established research on epidemic spread reveals its potential in identifying key individuals for targeted interventions and predicting outbreaks. Our findings underscore the importance of understanding the nuanced interplay between community struc- ture and individual node characteristics for effectively modeling and mitigating the spread of diseases in complex networks.

Keywords: Small world networks, Centrality, Community, Closeness, Clustering, Profile closeness

1 Introduction

The most promising characteristic of a real-world complex network is the small world nature it exhibits irrespective of its size [1–3]. A small-world network has minimal characteristic path length, owing to its significant local clustering capabilities [4, 5].

In such networks, nodes tend to form densely connected regions or communities [6]. While the nodes exhibit high connectivity within their community, they have very few connections to reach out to the nodes in other communities. Robustness of a community depends on the extent of interactions between its members[7]. High level of intra-community interactions and existence of inter-community relations lead to small path lengths. Thus, the relative importance of a community member depends on their influence on other community members and the network as a whole[8].

Modeling the structural changes in a network is an important problem that nat- urally accommodates an extra time component. Adding or removing nodes or edges from communities can alter their structure, which has drawn the interest of numer- ous academics. Preferential attachment is a key idea that is at play here. According to Barabasi[9], this phenomenon controls the evolution of the network. i.e., Rich gets richer. He added that a scale-free power low is observed in the degree distribution of the majority of the large network. The idea is analytically proved in [10]. i.e., the existence of hubs or influencers. Here, we tried to tackle whether the behavior of an influencer can affect the structure of a community.

In evolving networks, communities are also evolving. Some members might choose to remain in the community for a long time, while others might decide to move out. A member's ability to remain stable in a community is directly influenced by how they connect with other members of the group. This community change of a member will happen when its intra-communication is low and its inter-communication with another community is high. Quantifying the stability of members in a community is a challenging task.

In this paper, we try to investigate the above-addressed limitations. In order to understand the behavior of a member of a community, we need to quantify it. The main aim of this study is to give a clear answer to provide a measure to predict whether a member will remain in the same community for an extended period of time or not. Real networks are very different in their properties. If quantifying such a metric is possible, we also look at the common characteristics of these networks that result in the prediction. We have validated the suggested strategy through several experiments on a wide range of real-world datasets.

One of the most important applications of this work is epidemic spreading. There are many studies involving the effect of community structure evolution on epidemic spreading[11–13]. Communities, representing clusters of individuals with frequent interactions, act as transmission hubs, with the disease spreading rapidly within and slower between them. The strength and permeability of community boundaries significantly influence the rate of spread. Furthermore, certain individuals within com- munities can act as super-spreaders, accelerating transmission. Understanding the dynamic nature of communities, which change due to behavioral shifts or interven- tions, is crucial for an effective epidemic response. By analyzing these changes, public health officials can identify vulnerable communities, implement targeted interventions, and develop early warning systems, ultimately controlling and mitigating the spread of the disease.

Research suggests that understanding the mesoscopic structure of communities, rather than focusing solely on individual communities, is crucial for predicting and controlling disease outbreaks. Community profiling, which highlights key members like the core and bridge nodes, can refine this understanding. By monitoring changes in community profiles, such as the closeness of these key nodes, we can predict potential outbreaks, identify vulnerable communities, and develop targeted interventions. This approach can guide vaccination strategies, inform educational campaigns, and even personalize treatment plans for chronic diseases. Combining community profiling with other network metrics and machine learning techniques could further enhance our ability to understand and control further epidemic spread.

This is how the rest of the paper is structured. Basic definitions and related works were explained in Section 2, 3. Sections 4 and 5 are devoted to the proposed strategy. The algorithms and evidence based on empirical networks with ground truth commu- nities are proposed in Section 6. The findings of the experiments and observations on dynamic networks are presented in Section 7. Section 8 concludes with a summary.

2 Related Works

Guimerá and Amaral (2005) [14] studied the pattern of intra-community connections in metabolic networks. They analyzed the degrees of nodes within the community (within-module degree) and participation coefficient to understand if it is centralized or decentralized. A community is centralized if its members have different within- module degrees. They found that 80% of nodes only had connections to other nodes in their same community.

Wang et al. (2011) [15] proposed two kinds of significant nodes in communities: *community cores and bridges*. Community cores are the most central nodes within the community, whereas bridges act as connectors between communities. Han et al. (2004) [16] have also given a similar characterization of nodes important in a com- munity as *party hubs and date hubs* where party hubs are like community cores, and date hubs are like bridges.

Apart from the classical techniques, identifying these cores and hubs in accordance with the community structure helps in forecasting the stability of a member of the community. Several community-based centrality measures have been introduced in recent years. We have only considered the important papers from 2016. Gupta et al. (2016) [17] proposed a community-based centrality known as *Comm Centrality* to find the influential nodes in a network. The computation of this centrality does not require the entire global information about the network but only the intra- and inter-community links of a node. More specifically, comm centrality comes in handy when processing data about a huge network is extremely challenging or when limited information is available about the entire network. Without considering the complete network, this centrality can identify the most significant nodes at the community level. Recently, in 2020, Zhao et al. [18] proposed a method for finding the influential nodes that combine node closeness and community structure. The method is known as identifying influential nodes considering closeness and the community structure (ICC).

Also, ICC of a node depends on the community's size and its neighbors' closeness. This method is most effective in identifying the information spreaders in social networks.

A metric called community membership consistency was proposed by Kuppevelt et al. (2020) [19] to identify the core community of a network. It provides a thorough understanding of a community's strengths. Additionally, it provided details regarding the reliability of putting a node in that community. This method uses consensus clustering, and the consistency metric can distinguish between the core and non-core nodes with a high degree. To measure a node's community membership consistency, the threshold method is presented. This method considers the percentage of edges that have consistency scores higher than a selected threshold. To obtain relevant results, the threshold value should be carefully chosen, taking into account the distribution of edge consistencies. Also, the edge consistency(node pair metric) value can be defined as a dispersion metric of the consensus values, identical to the mean absolute difference. Third laplacian energy centrality(LC) was a novel concept in 2022 that Zhao and Sun[20] presented. It was based on Laplacian graph energy notions. Although they define centrality globally, they also reduce it to a local formula that can understand both characteristics. Here, for computing LC, they use the information of a node and its neighbors by measuring the energy change by removing that node from the network.

Rajeh et al., in 2022[21], have done a comparative analysis of community-aware centrality measures. They correlated the effectiveness of these measures with many real-world datasets. They have considered the *Participation coefficient (2005)* by Guimera and Amaral[14], *Community-based centrality (2015)* by Zhao et al.[22], *K- shell with Community (2016)* introduced by Luo et al.[23], *Comm centrality (2016)* by Gupta et al.[17], *Community-based Mediator (2018)* by Tulu et al.[24], *Commu- nity Hub-Bridge (2019)* by Ghalmane et al.[25], and *Modularity Vitality (2021)* by Magelinski et al[26]. The results of their experiments indicate that correlations range from negative to positive. Modularity Vitality, being a signed centrality that explic- itly targets hubs, shows low negative correlations with other measures. In contrast, other centrality measures, targeting bridges or hubs and bridges simultaneously, ex- hibit positive correlations ranging from weak to medium. The correlation pattern is influenced by the strength of the community structure, where weaker structures are related to higher correlations and stronger structures to lower correlations.

Curado et al. (2023)[27] proposed a novel community-aware centrality metric that employs effective distance gravity models and the return random walk to identify the influential nodes. This model's primary benefit is its ability to identify the essential nodes that play a crucial role in the community at the local level. The three methods used to calculate the measure are the effective distance, the gravity model, and the return random walk. To capture the static and dynamic information of a network's topology, it first employs effective distances. In addition, a gravity model is employed to quantify a node's power of attraction inside the network. To assess the true strength of every node within a cluster, both local and global data are considered, and return random walks are employed for this purpose.

Lv et al.(2023)[28] presented a combined form of centrality measure known as the Community-Based Centrality Measure (CBCM) that can identify the influential nodes in multilayer networks. They develop a fourth-order tensor-based multilayer network model with interlayer edges. Based on this tensor, a centrality metric called PR_BIS is created to assess the significance of network layers and vertices in multilayer networks simultaneously. The PR_BIS is a PageRank centrality based on the interlayer similarity metric. Three factors are taken into account by CBCM when evaluating a vertex's significance in each network layer: the vertex's PageRank centrality score, the importance of the community in which it is located, and the vertex's influence on other vertices in different communities within the community.

In November 2023, Heru et al.[29] proposed novel community consideration-based variants of degree, closeness, and betweenness centralities. The method also includes a parameter known as *weight of consideration* α, lies between 0 and 1. This parameter is used to balance its importance at the community level or the network-wide level. Their algorithms include computation of classic degree, closeness, and betweenness centralities with considering the community information and α. They noted that the new techniques are sufficient for identifying the key players in every community. They tested it on the Dolphin social network and the Zachary Karate dataset. They observed the centralities of datasets related to lung cancer, and the outcomes were superior.

Research on epidemic spreading on complex networks increasingly recognizes the importance of community structure evolution. Studies like Yang et al.(2020)[11] and Stegehuis et al.(2016)[12] have shown that changes in community structure, such as the formation, dissolution, or merging of communities, significantly impact disease trans- mission dynamics. These findings emphasize the need for incorporating community evolution into epidemic models and control strategies. Identifying key nodes within these dynamic communities, particularly core and bridge nodes as highlighted by the concept of community profiling, can offer crucial insights. Core nodes, with their high degree and centrality, are potential super-spreaders, while bridge nodes connect differ- ent communities and can act as gateways for disease spread. Monitoring the changing roles and influence of these nodes through metrics like profile closeness can provide early warning signals for outbreaks and inform targeted interventions.

The above works indicate that the communities, especially the relative importance of their members, influence the overall behavior of the network considerably. In this study, we attempt to predict the stability of a community based on profile closeness, a variant of closeness centrality. Profile closeness was introduced in [30][31] as a measure to detect secondary targets in a backup attack plan. We use the same concept here to analyze the fragility of members in a community.

3 Prelimnaries

Dynamic Networks: Dynamic networks are the networks that consider an ex- tra dimension - time. These networks are continuously evolving. There are many representations for dynamic networks. Here, we considered network snapshots[32].

Let $\{1, 2, ..., T\}$ be a finite set of time steps and $G^{(k)}$ represents a slice of the network G where k varies from 0 to T. The network G can be represent as a sequence of snapshots $G = \{G^{(1)}, G^{(2)}, ..., G^{(T)}\}$ where each $G^{(k)}$ is a tuple $(V^{(k)}, E^{(k)})$. Here, $V^{(k)}$ is the set of vertices and $E^{(k)}$ is the set of edges in the k^{th} snapshot.

Closeness Centrality: In general centrality in a network is a function from an admissible network with n vertices to a real number $f : G(n) \to \mathrm{R}$. It can quantify the significance of a node in a network. There are many variants of centralities. Here we consider closeness centrality in detail.

Closeness centrality can be defined as the reciprocal of the farness[33][34]. But we consider the normalized version rather than the unnormalized form. Closeness centrality ($c_C(v)$) of a vertex v is the inverse of the average total shortest distance of
v to all other nodes.

$$\underline{n-1\ d(v,u)}$$

$$c_C(v) = \sum_u$$

where $d(v, u)$ is the shortest distance between u and v and n is the nodes in the network. In other words, a node's average proximity to every other node in a graph is expressed as its closeness centrality. It measures how well a node can communicate within the network with other nodes. On average, nodes with high closeness centrality are thought to be more central. The values of closeness centrality fall between 0 and 1. In graphs that lack connectivity, certain nodes or groups of nodes cannot be reached from one another. In such cases, closeness centrality might not be defined for those nodes. Closeness extends degree centrality by considering its neighborhoods of all radii. A non-linear correlation exists between degree and closeness. The logarithm of degree has a linear relationship with the inverse of closeness[35].

Furthermore, we have considered community-aware centralities. They are the spe- cial centralities that can be computed on the community level. We have noticed that community-aware centralities are crucial in a variety of applications. We have already mentioned some of them in 2.

Community detection: Communities are the partitions in a network in which intra-connections are high and inter-connections are low. In order to understand the network's modular structure, it is crucial to recognize these divisions. The quality of communities is analyzed by quality functions. One of the main quality functions is modularity. Let G be the network with n nodes, m edges and $C = \{C_1, C_2, ..., C_k\}$ are the k communities. Modularity can be defined as

$$Q \quad 2m$$

$$\underline{1} \qquad = \qquad \sum$$

$\sum$ A_{uv} $-\frac{d_u d_v}{2m}$

$C_i \in C \;\; u, v \in C_i$

where A is the adjacency matrix and d_u, d_v are the degrees of vertices u and v.

We used the Louvain[36] method to detect communities. It is a community detection method that uses a greedy heuristic strategy to optimize modularity. Later they gave an analysis and generalization to Louvain algorithm[37].

Dynamic communities are communities within dynamic networks. They are changing as the network is changing. Some of the communities may *disappear*, and others may *remain* as such. Certain communities *expand* consistently, drawing new members. Some may *shrink* as a result of having nodes removed from them. Some communities *merge* to form a new one, while some are *split* into more. These are known as community events[38]. These changes are driven by various factors, such as the behavior of individual nodes, external events, the overall network structure, and the characteristics of the community itself. Understanding the dynamic nature of communities is crucial in various fields.

4 Computing profile closeness

Consider a large network N with n nodes and m links. Then, a profile π[39], is a weighted subset of nodes.

$\pi = \{(u, r(u)) | u \in N\}$

where u is an arbitrary node of N and $r(u)$ is the rank of u in π based on its priority. N may contain disconnected components. When two nodes are unconnected and belong to separate disconnected components, then we have taken the distance between them as infinity. Given a node v, the total distance of v with respect to π is

$$D_\pi(v) = \sum_{u \in \pi, u \neq v} d(u, v) \times r(u)$$

Note that if v and any $u \in \pi$ are in disconnected components, then $D_\pi(v)$ will be ∞.
Now, we define the profile closeness $c_\pi(v)$ as the normalized inverse of $D_\pi(v)$.

$$c_\pi(v) = \frac{n-1}{D_\pi(v)}.$$

When v and any node in π are disconnected, c_π becomes zero. As in the case of a normal closeness centrality, nodes with higher c_π values are the ones with better access to profile nodes.

4.1 Choosing rank function

Degree (δ) of a node refers to the number of edges incident on it. A high-degree node has a direct influence on a larger part of the network (See Opsahl et al. [40]). Therefore, it is a potentially important decision-maker in the consensus problem. Such nodes should be given a higher priority. We can do this by assigning $r(u) \rightarrow \delta(u)$.

However, the choice of the rank function depends on the problem. An excellent candidate for the rank function is the degree (δ) itself. In network analysis, degree (δ), the number of connections a node has, serves as a simple yet effective measure of influence. High-degree nodes, often referred to as hubs, are considered influential due to their direct impact on a larger portion of the network. Assigning rank ($r(u)$) proportionally to degree prioritizes these hubs for analysis or intervention. However, this ranking method may be domain-specific. While degree is a useful starting point, the optimal ranking function may vary depending on the nature of the network and the research question at hand. For instance, social network analysis might consider the quality or type of connections, while biological networks might prioritize the strength of interactions or specific pathways involved. Therefore, while degree centrality offers a valuable foundation for understanding node influence, it should be considered alongside other domain-specific factors when determining node rankings.

4.2 Choosing a profile

The relevance of a profile depends on the proportion of high-rank nodes included in it. If π consists of prominent nodes (say, hubs) from different disconnected components

in N , then it follows that c_π effectively captures the relative closeness of a node to the critical nodes in N . A high $c_\pi(v)$ indicates that v can act as a crucial access point to the vital areas of the network. There are several ways to identify a set of critical nodes in a network. Refer [41] for a state-of-art review of critical-node identification. In the context of community evolution and epidemic spread, profile closeness pro- vides a valuable lens to assess node significance and community dynamics. A node's high profile closeness within its community signifies strong connections with influen- tial members and a high likelihood of continued membership. Conversely, low profile closeness suggests weak ties and a potential for departure. This understanding can be leveraged to predict community evolution, identify vulnerable members, and at- tract new ones, ultimately contributing to a more comprehensive understanding of disease transmission. For instance, tracking changes in profile closeness could serve as an early warning system for potential outbreaks, guiding targeted interventions like prioritizing vaccinations for core members or implementing contact tracing measures focused on bridge nodes. This approach aligns with the concept that influential nodes play a disproportionate role in disease propagation, as highlighted by the empha- sis on mesoscopic community structures in the literature (Stegehuis et al., 2016[12]). By integrating profile closeness analysis with existing network models, we can gain deeper insights into the complex interplay between community dynamics and disease
transmission, paving the way for more effective prevention and control strategies.

5 Closeness and profile closeness

As discussed in the introduction, the profile closeness of a node v measures its closeness centrality when the profile is the entire node set and rank of the nodes is unity. i.e.

$$c_\pi(v) = c_C(v)$$

when $\pi = V(N) \times \{1\}$.

In 1979, Freeman [42] introduced the concept of centralization of a graph or net- work to compare the relative importance of its nodes. Centralization is also a way to compare different network based on their respective centrality scores.
In order to find the centralization scores, we need to determine the maximum possible value of centrality (c^*) and the deviation of the centrality of different nodes $(c_\pi(v))$ from c^*. The centralization index C_c^π is the ratio of this deviation to the maximum possible value for a network containing the same number of nodes.

Freeman [42] showed that for both the center of a star graph and the complete graph of the same size, the closest centrality achieves the highest score. This was proven later by Everett et al. [43]. Also, the minimum value is attained when the graph is a cycle.
The profile closeness c_π attains the maximum value in a connected network when π is the entire set of the network nodes. In this case, $c_\pi(v) = c_C(v)$ for any node v. Therefore, the centralization of the profile closeness coincides with the closeness centrality.

However, we need to compare the performance of c_C and c_π for the intended applications of c_π. As c_C is a global measure, whereas c_π is highly localized to the

$\delta_{average}$	**50**	**100**	**500**	**1000**
2	0.516 [0.864-0.124]	0.617 [0.879-0.272]	0.782 [0.944-0.605]	0.833 [0.935-0.658]
5	0.522 [0.793-0.128]	0.628 [0.816-0.247]	0.805 [0.900-0.684]	0.857 [0.924-0.710]
7	0.480 [0.732-0.054]	0.617 [0.803-0.312]	0.817 [0.900-0.660]	0.872 [0.930-0.692]

Table 1: Correlation between closeness and profile closeness

profile π, the comparisons need to be done locally as well. So, two comparisons need to be done - one with the global closeness centrality c_C, and the other with a local closeness measure known as cluster closeness, $c_{cluster}$. Note that the only difference here is that $c_{cluster}$ does not have the priority ranking of group members, which is an essential feature of c_π.

$$D_{cluster}(v) = \sum_{u \in cluster, u \neq v} d(u, v) \times r(u), \quad r(u) = 1$$

$$c_{cluster}(v) = \frac{n - 1}{D_{cluster}(v)}.$$

We generate some random scale-free networks and identify their clusters. Subse- quently, we calculate the global closeness c_C for each node. We calculate the $c_{cluster}$ of a node as its closeness to its parent cluster. Besides, we construct a profile with these clusters. Here, the rank of a node v, $r(v)$, is $\delta_{cluster}(v)$(the number of neighbors of v within the cluster). Thus, if a node has a large number of connections within its cluster, then it is considered as having higher priority in the profile. We compute c_π with these profiles and compare them with c_C and $c_{cluster}$ over all the generated networks. For comparing these measures, we use the correlation between them.

Simulating correlation in Synthetic networks

To Analyze the correlation between c_C and $c_{cluster}$, we have simulated some synthetic networks and identified their clusters. We have generated the scale-free networks with the Barabasi-Albert model (BA model) available in the Networkx package in Python. Subsequently, we calculate the global closeness c_C for each node. We determined the clusters in each network using the Louvain algorithm. Then, We calculate the $c_{cluster}$ of each network. We construct a profile with these clusters, calling it cluster closeness. Here, the rank of a node v, $r(v)$, is $\delta_{cluster}(v)$(the number of neighbors of v within the cluster). The experiment is conducted on Barabasi-Albert network with 50, 100, 500, and 1000 nodes with average degrees 2, 5, and 7. The cluster is determined, and the $c_{cluster}$ and c_π are calculated for each network with profile π as the clusters. This process is repeated 100 times to obtain the average; then, the correlation is computed with the original global closeness c_C and the cluster closeness $c_{cluster}$ with the profile closeness c_π.

The correlation results are shown in tables 1 and 2. The values in each cell are the average correlation between the measures. The range of correlation (max-min) when experimented with 100 iterations is shown below each value in brackets.

$\delta_{average}$	**50**	**100**	**500**	**1000**
2	0.953 [1.0-0.595]	0.960 [0.997-0.734]	0.962 [0.999-0.049]	0.980 [0.999-0.923]
5	0.947 [0.999-0.514]	0.948 [1.0-0.653]	0.965 [0.999-0.646]	0.970 [0.999-0.752]
7	0.957 [0.999-0.748]	0.949 [1.0-0.537]	0.953 [0.999-0.595]	0.968 [1.0-0.706]

Table 2: Correlation between cluster closeness and profile close- ness

Table 1 shows the correlation between the closeness centrality and profile closeness for the generated random networks. Both are positively correlated, and the rela- tionship is reasonably good enough. An important point here is that the closeness centrality in large networks is highly correlated with its profile closeness. This fact seems interesting because the computation of profile closeness is less data-consuming when compared to the calculation of closeness centrality. Assume that both measures give the same ranking of nodes in a large network N . Then, we can use the low- computational profile closeness for the closeness ranking of nodes in N . However, more investigations need to be done in this regard. We need to perform the analysis of the simulation on vast network to ensure this capability of profile closeness.

Table 2 shows the correlation between cluster closeness and profile closeness for the generated random networks. We observed that the average correlations are high, which indicates a strong relationship between $c_{cluster}$ and c_{π}. Another interesting observation is that the average correlation increases steadily with network size for sparse as well as dense networks.

6 Predicting community stability

When the profile under consideration is a community, we call it a *community profile*. A community profile captures the relative importance of the community members. Here, all the nodes are not considered homogenous and we prioritize nodes like community cores and bridges. The application of a community profile is two-fold.

- *Assessing Global Network Accessibility*: The community cores and bridges are prior- itized in all the communities as a profile. Then, the profile closeness determines the accessibility of these vital nodes from every nook and corner of the network. This first application, the details of which are outside the scope of this work, provides a means to measure the global accessibility of the network.
- *Predicting Community Evolution*: The community profile is constructed from a single community; with priority given to vital members. Then, the profile closeness predicts the new nodes who may join the community and members who may be on the verge of leaving the community. This second application, which will be discussed in detail in the next section, is associated with the local accessibility to a community. Focusing on a single community, community profiling constructs a blueprint of the group's internal social structure and interaction patterns. It utilizes the concept of profile closeness to gauge the level of integration and influence of each individual within the community. Nodes with high profile closeness, indicating strong con- nections and active participation, are more likely to remain loyal members, while those with low profile closeness may be on the periphery and potentially depart. By analyzing profile closeness across the community, we can anticipate membership changes, identify individuals who might join or leave, and ultimately understand the community's evolution over time. These insights are invaluable for designing strategies to strengthen communities, foster engagement, and mitigate risks, such as the loss of key members.

6.1 Construction of community profile

The first step in constructing a community profile is the identification of communities in the network. Once we have detected the communities, we need to rank the members in each community. The ranking is based on the intra-modular degree (δ_{comm}). We can also use other relevant community-based measures like *Comm centrality* ([17]) for ranking. $r(v)$ denotes the rank of a node v. Now, we define the community profile π as

$$\pi = \{(v, r(v)) | v \in C,\ C \text{ is a Community}\}$$

The construction of a community profile is devised in algorithm 1, Gen_π.

```
Algorithm 1 Gen_$\pi$: Constructing community profile Require: Community $comm = (V_{comm}, E_{comm})$
Ensure: $\pi$
for $v \in V_{comm}$ do
    $\delta_{comm}(v) = |Neighbor_{comm}(v)|$
    $\pi \leftarrow \pi \cup \{(v, \delta_{comm}(v))\}$
end for
return $\pi$
```

6.2 Computing community closeness

Algorithm 2 computes the community closeness of the entire network $cc_{\pi}[.]$

6.3 Predicting community members

Given a node u and profile π in N , algorithm 2 correctly computes the closeness of the node to the community corresponding to π. A community is stable when every node in that community has low variance in its closeness values. In other words, the community is unstable when the intra-community closeness of its nodes show drastic variations. Nodes with higher values are likely to continue in the community, whereas those with minimal values may leave the community in the future. We conducted experiments on networks with first-hand information on their ground-truth communities. Empirical evidence shows that the above observation is correct. Another interesting observation was that the nodes that exhibit more closeness towards an external community tend to join that community in future. Thus, profile closeness is an adequate indicator of how communities evolve in a network. The efficiency of this prediction depends on the design of the community profile.

Algorithm 2 CC: Finding community closeness

```
Require: Network $N$, profile $\pi$
Ensure: $c_\pi[.]$
for $u \in V(N)$ do
    $du[.] \leftarrow SSSP(N, u)$ {SSSP - Single Source Shortest Path}
    $D_\pi(u) = 0$
    for $(v, r(v)) \in \pi$ do
        if $(u /= v$ and $du[v] /= \infty)$ then
            $D_\pi(u) = D_\pi(u) + [du[v] \times r(v)]$
        end if
    end for
    $c_\pi[u] \leftarrow \frac{n-1}{D_\pi[u]}$
end for
return $c_\pi[.]$
```

6.4 Empirical evidence - Networks with ground-truth communities

Research on community detection has been very active for the past two decades. Many community detection techniques were devised. The Girvan-Newman method of community detection [6], based on edge betweenness, was a novel approach. Later, the same team came up with the *modularity* concept, a qualitative attribute of a community. See [44]. Modularity is defined as the difference between the fraction of the edges in a community and the expected fraction in a random network. Girvan and Newman observed that, for a robust community, this attribute falls between 0.3 and 0.7. Therefore, modularity optimization can lead to better community detection. However, this is an NP-complete problem [45]. Different approximation techniques based on modularity optimization produce community structures of high quality, that too with little time requirements of the order of network size. A very recent survey by Zhao et al. [46] gives a clear picture of the state-of-art in this regard.

In this study, we used the Louvain method [36] of modularity optimization for detecting communities. It is an agglomerative technique with each node initially as- signed as a unique community. The algorithm works in multiple passes until the best partitions are achieved. Each pass consists of two phases; in phase 1 the nodes are moved to the neighbouring community if it can make a higher gain in modularity and in stage 2 a new network is created from the communities detected in pass 1.

First, we simulated our results using two real-world networks in which the com- munity structure is evident. The networks are Zachary's karate club network [47], the American college football network [6] and the Dolphin's network. See table 3.

Network	**Nodes**	**Edges**	**Communities**	**Density**
Karate Club	34	78	2	0.2781
College Football	115	613	12	0.0935164
Dolphin	62	159	2	0.0840825

Table 3: Networks with ground-truth communities

Community	**Member nodes**								
I	1	2	3	4	5	6	7	8	9
	11	12	13	14	17	18	20	22	
II	10	15	16	19	21	23	24	25	26
	27	28	29	30	31	32	33	34	

Table 4: Ground-truth communities in Karate network

Comm.	**Member nodes**										
I	1	2	3	4	8	12	13	14	18	20	22
II	5	6	7	11	17						
III	9	10	15	16	19	21	23	27	30	31	33
	34										
IV	24	25	26	28	29	32					

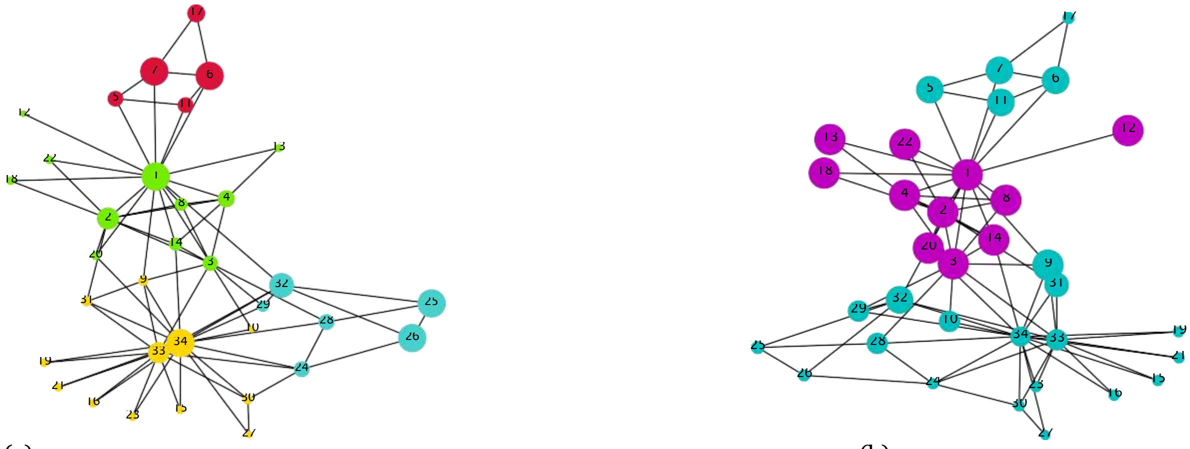
Table 5: Communities detected in Karate network

We identified 4 communities in the network (using the Louvain method). See table 5.

6.4.1 Zachary's karate club network

We conducted our primary survey on the famous karate club network data collected and studied by Zachary [47] in 1977. In his study, Zachary closely observed the in- ternal conflicts in a 34-member group (a university-based karate club) over a period of 3 years. The conflicts led to a fission of the club into two groups. See table 4. He modeled the fission process as a network. The nodes of the network represented the club members and edges represented their interactions outside the club. Zachary pre- dicted this fission with greater than 97% accuracy and argues that his observations are applicable to any bounded social groups. Many researchers used this network as a primary testbed for their studies on community formation in complex networks.

We used the intra-module degree ($\delta_{community}$) of nodes for constructing the pro- file. The nodes in the profile were prioritized based on their $\delta_{community}$ value. Nodes
having higher value were given higher priority. Subsequently, the profile closeness was computed for each community member. See figure 1a. Different colors represent the members of different communities. The relative size of the nodes represent their profile closeness with respect to their own community.
The profile closeness of node 9 in its community ($cc_{Community_{III}}(9)$) is very low.
From this, we can interpret that 9 has a higher tendency to leave its community. Also, we compared the profile closeness of all nodes with respect to *Community I* ($cc_{Community_I}$). See figure 1b. Nodes external to *Community I* are colored blue.



(a) (b)

Figure 1: (a) Community closeness in Karate club network. (b) Profile closeness of external nodes to the community *I*.

Among them, *Node 9* has a higher value for $cc_{Community_I}$. This high value of $cc_{Community_I}(9)$ and the low value of $cc_{Community_{III}}(9)$ indicates that 9 has more affinity towards *Community I* than its community, *Community III*.

This observation is relevant since node 9 originally belonged to *Community I* as noted by Zachary. Furthermore, Zachary had even observed that member 9 is a weak supporter of the second faction (*II*); but joined the first faction (*I*) after the fission. Our method also reproduced the same fact.

6.4.2 American college football network

The second network chosen for our study was the American college football network, from the dataset collected by Newman [6]. The nodes in this network represent the college football teams in the U.S., and the edges represent the games between them in the year 2000. About 8-12 teams were grouped into a conference. Altogether 12 conferences were identified. Most of the matches were between the teams belonging to the same conference. Therefore, the inherent community structure in this network corresponds to these conferences. These ground-truth communities are given in table 6.

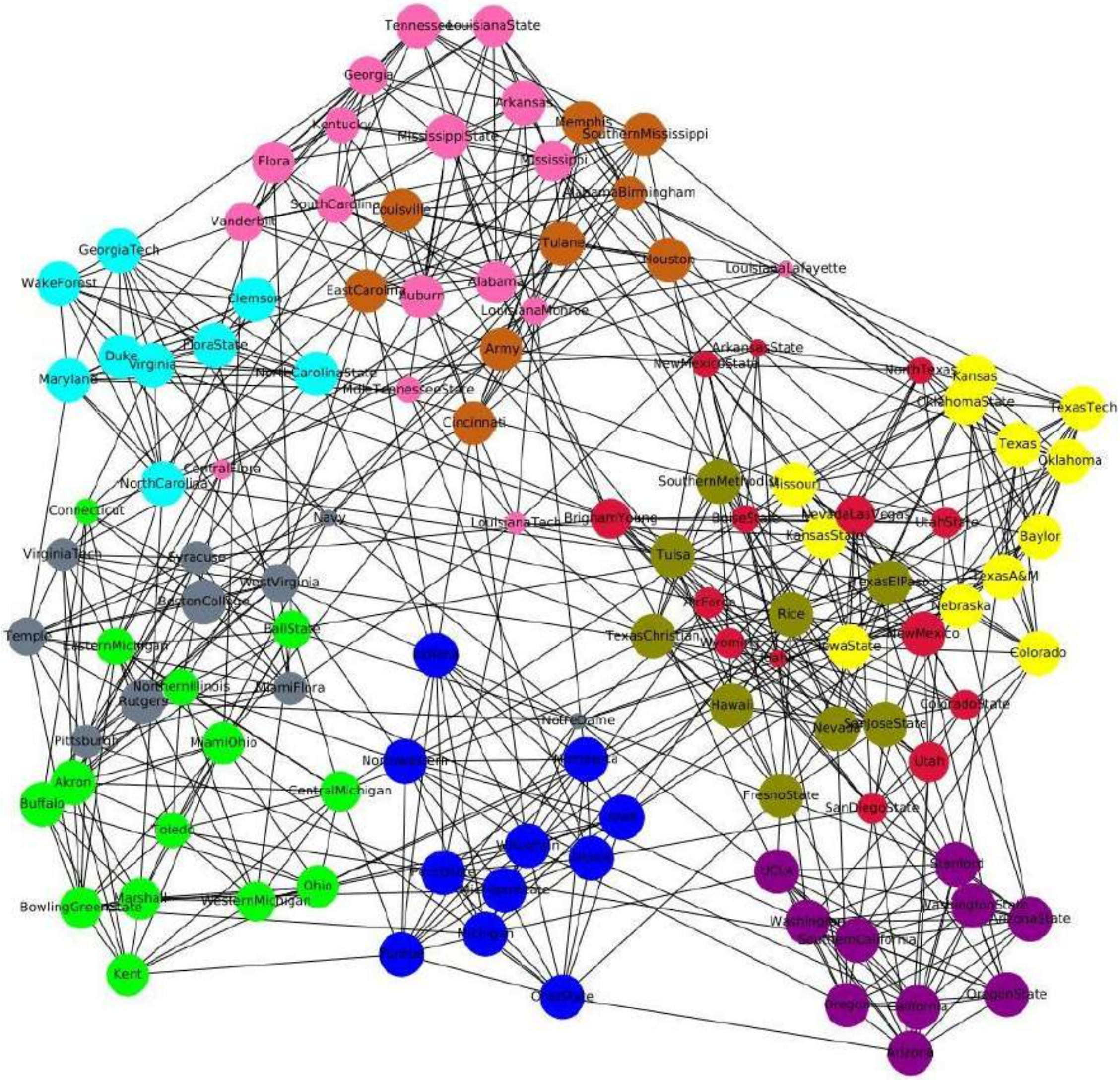


Figure 2: Community closeness in American college football network.

In the community detection step, we identified ten communities (See table 7). Four among them (I, VII, IX and X) correspond to the ground-truth communities (*AtlanticCoast, Pac 10, Big 10 and Big 12* respectively.) Community $VIII$ is a combination of two actual communities, *Mountain West* and *Sun Belt*. We computed the community closeness of nodes. See figure 2.

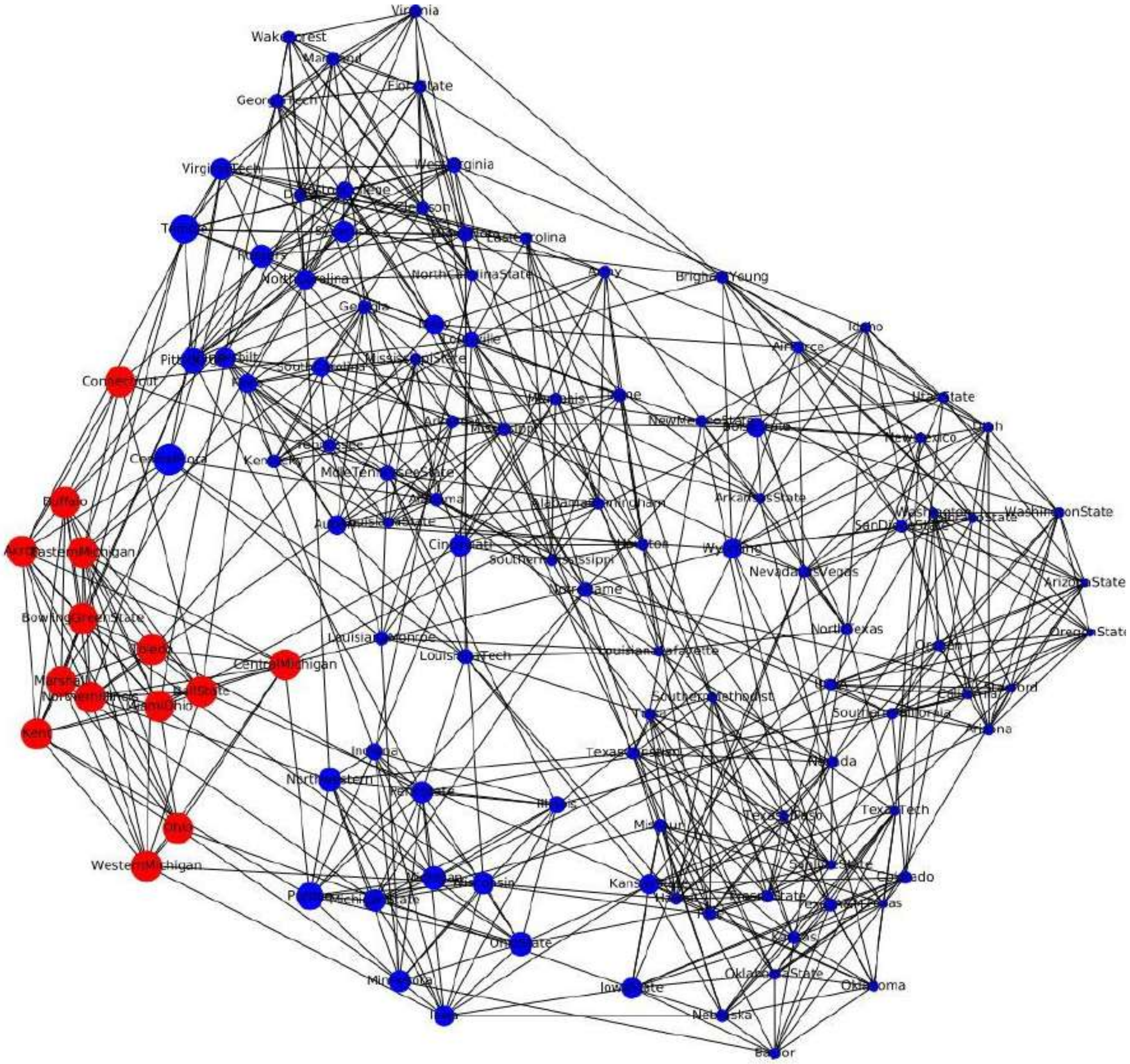


Figure 3: Profile closeness of external nodes to community *II* of American college football network.

We then examined the profile closeness of all the nodes to community *II*. See figure 3. We observed that *Central Florida* has a greater closeness to *II*. This obser- vation conforms to the ground truth that *Central Florida* team played with teams like *Connecticut* in many matches.

Table 6: US Football Network: Ground truth communities

Conference	College teams			
tlantic Coast	ora. St. Duke Wake Forest	N. Caro. St. N. Caro.	Virginia Clemson	eorg. Tech Maryland
IA Independents	Cent. Flora Utah St.	Connecticut	Navy	Notre Dame
Mid American	Akron Miami Ohio W. Michigan E. Michigan	Bowl. Green St. Marshall Ball St.	Buffalo Ohio C. Michigan	Kent N. Illin. Toledo
Big East	Virg. Tech Pittsburg	Boston Coll. Temple	W. Virg. Miami Flora	Syracuse Rutgers
Conference USA	Alabama Birm. Houston Army	E. Caro. Louisville T. Christ.	S. Missis. Tulane	Memphis Cincinnati
SEC	Vanderbilt Georgia Alabama	Florida Tennessee Missis. St.	Kentucky Arkansas Louis. St.	S. Caro. Auburn Missis.
W. Athletic	Louis. Tech Nevada Hawaii	Fresno St. an Jose St. Boise St.	Rice T. El Paso	S. Method. Tulsa
Sun Belt	Louis. Monroe Arkansas St.	Louis. Lafay. Idaho	Mid. Tenn. St. New Mex. St.	N. Texas
Pac 10	Oreg. St. Calif. Washing. St.	S. Calif. Ariz. St. Oregon	UCLA Ariz.	Stanford Washing.
Mountain West	Brigh. Y. Utah	New Mex. Colorado St.	San Diego St. Nev. Las Vegas	Wyoming Air Force
Big 10	Illin. Penn St. Purdue	Nwestern Mich. Indiana	Mich. St. Ohio St. Minnesota	Iowa Wisconsin
Big 12	Oklah. st. Kansas Texas Tech	Texas Iowa St. Texas A & M	Baylor Missouri Oklahoma	Colorado Nebraska Kansas St.

Table 7: US Football Network: Detected communities

Community	Member teams			
I	Flora St. Duke Wake Forest	N. Caro. St. N. Caro.	Virginia Clemson	eorg. Tech Maryland
II	Connecticut Buffalo Ohio C. Mich.	Toledo Kent N. Illin. E. Mich.	Akron Miami Ohio W. Mich.	Bowl. Green St. Marshall Ball St.
III	Virg. Tech ttsburg Navy	Boston Coll. Temple Notre Dame	W. Virg. Miami Flora	Syracuse Rutgers
IV	Alabama Birm. Houston Army	E. Caro. Louisville	S. Missis. Tulane	Memphis Cincinnati
V	Vanderbilt Georgia Alabama Louis. Monroe C. Flora	Flora Tennessee Missis. St. Mid. Tennes. St.	Kentucky Arkansas Louis. St. Louis.Lafay.	S. Caro. Auburn Missis. Louis. Tech
VI	Rice T. El Paso T. Christ.	S. Method. Tulsa	Nevada Hawaii	San Jose St. Fresno St.
VII	Oregon St. Calif. Washing. St.	S. Calif. izona St. Oregon	UCLA Arizona	Stanford Washing.
VIII	Brigham Y. Utah Boise St. Utah St.	New Mex. Colorado St. . Texas Idaho	San Diego St. N Las Vegas Arkansas St.	Wyoming Air Force New Mex. St.
IX	Illinois enn St. Purdue	Nwestern ichigan Indiana	Mich. St. Ohio St. Minnesota	Iowa Wisconsin
X	Oklah. st. Kansas Texas Tech	Texas Iowa St. Texas A & M	Baylor Missouri Oklahoma	Colorado Nebraska Kansas St.

6.4.3 Dolphins network

Another chosen network with the ground-truth community is the dolphins network, which is from the dataset collected by Lusseau et al., in the University of Otago- Marine Mammal Research Group [48] (2003). Lusseau along with Newman [49] (2004) used this data to study social networks of bottlenose dolphins. In their study, they

Group	Member dolphins						
I	Beak	Bumper	CCL	Cross	Double	Fish	Five MN105
	Fork	Grin	Haecksel	Hook	Jonah	Kringel	Shmuddel
	MN60	MN83	Oscar SN4	Patchback	PL SN63	Scabs	SN96
	SMN5	SN100	Topless		SN89	SN9	TSN103
	Stripes	Thumper	Whitetip	TR120	TR77	Trigger	
	TSN83	Vau		Zap	Zipfel		
II	Beescratch	DN16 Knit	DN21	DN63	Feather	Gallatin	Jet
		MN23	Mus TR88	Notch	Number1	Quasi	Ripplefluke
	SN90	TR82		TR99	Upbang	Wave	Web
	Zig						

Table 8: Ground-truth groups in dolphin network

Group	Member dolphins						
I	Beak	Bumper	Fish	Knit	DN63	PL	SN96
	TR77						
II	CCL	Double	Oscar	SN100	SN89	Zap	
III	Cross	Five	Haecksel	Jonah	MN105	MN60	MN83
	Patchback	SMN5	Topless	Trigger	Vau		
IV	Fork	Grin	Hook	Kringel	Scabs	Shmuddel	SN4
	SN63	SN9	Stripes	Thumper	TR120	TSN103	TSN83
	Whitetip	Zipfel	TR99	TR88			
V	Beescratch	DN16 Mus	DN21	Feather	Gallatin	Jet	MN23
		Notch	Number1	Quasi Zig	Ripplefluke	SN90	TR82
	Upbang	Wave	Web				

Table 9: Communities detected in dolphin network observed fission in the network to two groups with one individual (*SN100*) temporarily leaving the place. These communities are shown in table 8.

We detected 5 communities. See figure 4. The communities are shown in table 9. We checked the closeness to community V . See figure 5. It is clearly visible that *DN63* and *Knit* are having higher chances of grouping with community V. This conforms to the observation made by Lusseau and Newman.

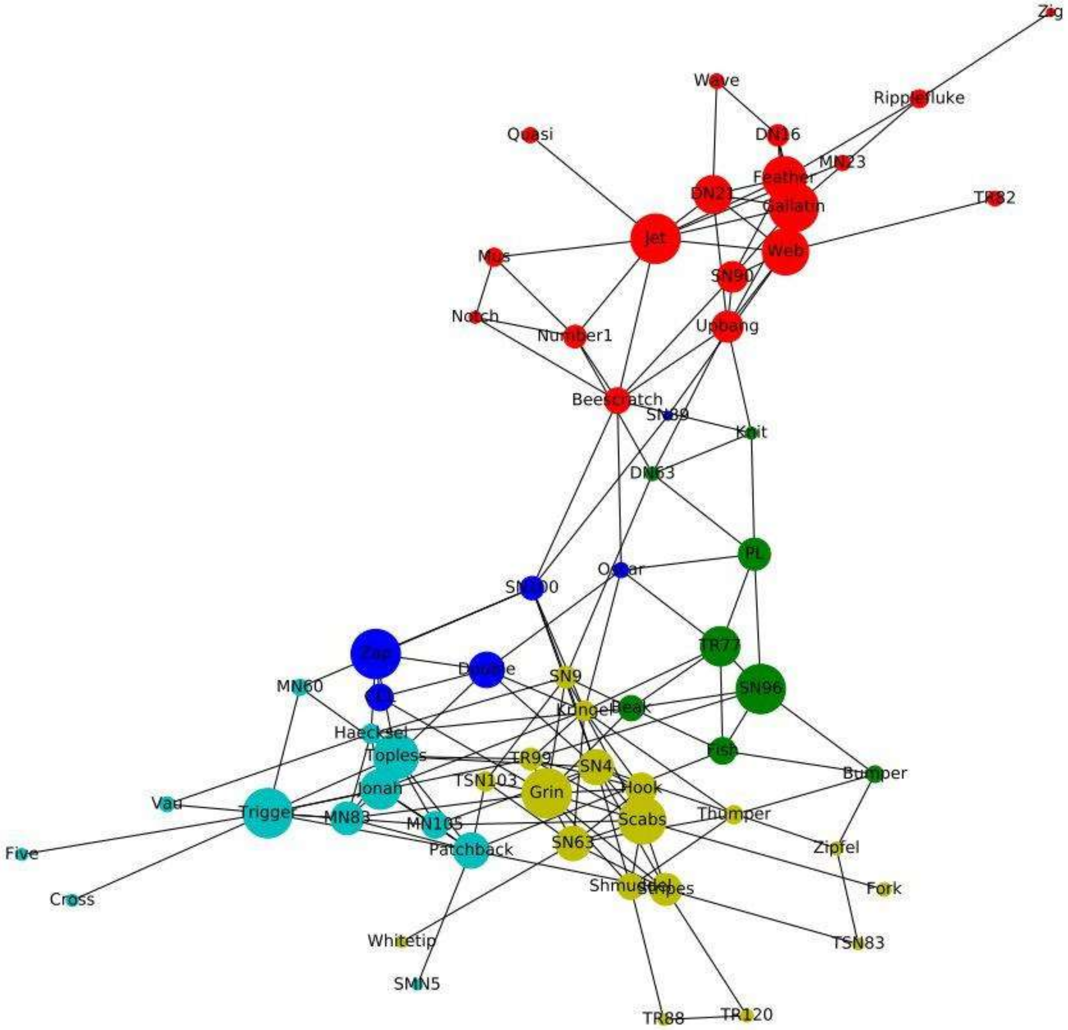


Figure 4: Community closeness in Dolphins network.

7 Empirical evidence - Dynamic networks

We experimented on seven dynamic real-world networks as well. Verifying the impact of community closeness in dynamic networks is crucial to confirming its strength. Networks that change over time are called dynamic networks. Real-world networks are mostly dynamic. In this case, our dynamic networks are presented as a sequence of snapshots. The original graph $G(V, E)$ can be modeled as a sequence $\{G1, G2, \ldots, Gn\}$, where G_i are the snapshots at time t. There might be variations in the number of nodes and edges in each $G_i(V_i, E_i)$. Now, when discussing community closeness in a

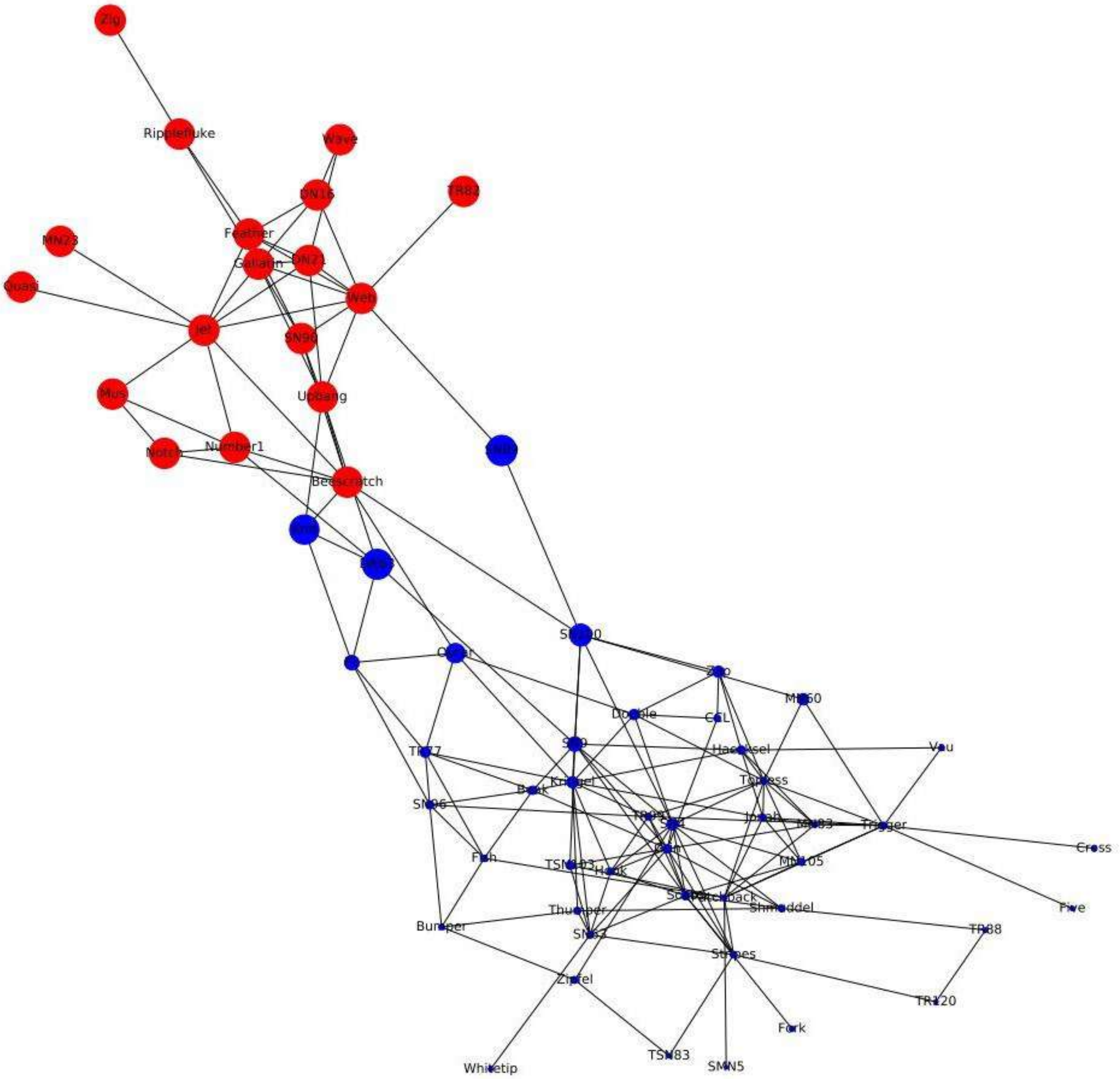


Figure 5: Community closeness in Dolphins network.

dynamic setting, it is important to define dynamic communities. The communities that are defined in each snapshot are called dynamic communities. If a snapshot G_t has (C_1^t, C_2^t, ..., C_m^t) communities, we denote $C_i^t = (v_1, v_2, ..., v_k)$ be the i^{th} community of G_t at time t where $v_i \in V_t$. Using the Louvain algorithm, we calculate the communities in each snapshot of the selected dynamic networks.

For computing the community closeness of a node we use the above-mentioned algorithms1 and 2. After that, we selected those nodes within the community with low community closeness and moved to other communities in the subsequent snapshots. Similarly, we highlighted those nodes outside the community with high community closeness and will move to this community later in the following snapshots. We have taken into consideration these two categories of nodes and determined their respective percentages across all snapshots.

Dutch school friendship network(2003) [50]: It is a friendship network at a secondary school in the Netherlands in 2003–2004. It is unweighted temporal data. There are four snapshots available on the network. In the first two snapshots, we had four communities. Then it changed to 2, then to 3. For every snapshot, we have traced those nodes within the community with a low affinity to stay back and those nodes outside the community with a high affinity to move to the community. We have observed that in this network, 52.20% of the nodes within the community with low community closeness are removed from the community and 31.10% of outside nodes with high community closeness are added to the community in the very next snapshots.

Jakarta terrorist network(2009) [51]: This network is a communication net- work involved in the 2009 Jakarta bombing. Nodes are the individuals, and edges are the communication between them. It is a weighted temporal network. The weights on the edges are the number of operations they worked together. We are not considering the weights. There are four instances of graphs. We got good results for the inside nodes removed from communities as 50% but outside nodes with high community closeness attracted to the communities are only 4%.

Australian Embassy bombing(2004) [52]: It is also a bombing network that represents the Australian Embassy bombing in Indonesia in 2004. Nodes denote the individuals or terrorists and edges the communication between them. There are 15 snapshots. The performance of community closeness is also not satisfactory here, similar to the Jakarta network. The terrorist network's vague community structure is the main reason for this. Terrorist networks are only active in the moments preceding the associated operation. This led us to conclude that only networks with excellent community structures exhibit the qualities of community closeness. Here, we got 19.3% nodes removed, which has low intra-community closeness, and only 5% of outside nodes were added, which has high community closeness.

Enron email network(2011) [53]: The Enron email network is between em- ployees of Enron Company from 1999–2001, released in 2011. We have only considered the data in 2001 alone. When preprocessing, we divide the whole network according to the months. So there are 12 months altogether. It has an average of 789 nodes and 2702 edges. Snapshots have an average of 13 communities with the Louvain algorithm, avoiding isolated nodes. This network performs well with community closeness due to its good community structure.

Autonomous Systems AS-733 Network(2001) [54]: AS-733 is an au- tonomous systems network. It consists of routers and their communications. The data was collected from the University of Oregon Route Views Project from 1997 to 2000.

It has 14 timestamps with an average node of 6086 and an edge of 11862. The result we obtained is very convincing here. We got around 43% of community nodes with low community closeness going out of the community and 48% of outside nodes with high affinity joining the community in the near future.

College messaging network(2009) [55]: This dataset involves private messages sent in an online social network at the University of California, Irvine. The users can log in, search for other individuals, and start a conversation. The nodes are the individuals and the edges are formed if they have a conversation. Edges are of the form (*u, v, t*), where *u* and *v* are the individuals and *t* is the time of the conversation. The dataset has an email with a total span of 193 days. We have considered six complete months of data. So we have a total of 6 snapshots with averages of node 704 and edge 2605. The prediction results here are also above satisfactory, with nodes with low intra-community closeness removed at 51%.

Oregon 2 Autonomous systems network(2001) [54]: It is a collection of 9 autonomous system networks. These networks modeled Oregon 2 route views collected from their routing registry from March 31 to May 26, 2001. It has nine snapshots with a high node average of 11150 and edges of 31559. We observed good results in this network. 50% of outside community nodes with high affinity is attracted to the community, and 51% of intra-community nodes with low affinity is removed in the preceding snapshots.

All the networks here mentioned are taken from public repositories: - The Col- orado Index of Complex Networks (ICON) and Stanford Network Analysis Platform (SNAP). The details of these networks are given in 10.

We analyzed how the evolution of communities in these networks is effected by the profile closeness of its members. Table 11 shows results of these experiments.

Network	**Percentage of nodes with high inter-community closeness added**	**Percentage of nodes with low intra-community closeness removed**
Dutch school friendships	35.10%	52.20%
Jakarta terrorists	4%	50%
Australian Embassy bombing	5%	19.30%
Enron email network	12.90%	53.25%
Autonomous systems AS-733 network	47.66%	43.16%
College messaging network	25.62%	51.47%
Oregon 2 Autonomous systems network	49.50%	50.45%

Table 11: Analysis of community evolution in temporal networks based on community closeness

The results presented provide compelling evidence for the predictive power of profile closeness in understanding community evolution across diverse real-world networks. In most networks, approximately half of the nodes that left a community exhibited low intra-community closeness, underscoring the metric's ability to identify individuals at risk of departure. However, the percentage of nodes with high inter-community closeness that subsequently joined a community varied widely, suggesting that factors influencing node addition are more complex and network-specific.

Notably, social networks (Enron email, College messaging) showed the highest rates of new member addition based on high inter-community closeness, indicating their relative openness compared to other network types. Larger networks (AS-733, Oregon 2) displayed high rates of both node addition and removal, reflecting their dynamic nature. Smaller networks, like the Australian Embassy bombing network, showed less consistent results, possibly due to their limited size and less defined community structures.

Overall, these findings demonstrate that profile closeness can effectively predict community evolution, particularly in larger and more open networks. While smaller networks may exhibit more variability, the consistent patterns observed across diverse datasets underscore the potential of profile closeness as a valuable tool for under- standing the complex dynamics of community membership and its impact on network structure and function. The comparison of results obtained are shown in the figure 6. We ignored the *splitting/merging* event of community evolution here since commu- nity splitting and changing the membership of a small fraction of nodes are different scenarios. We are considering this as an immediate follow-up to this work.

8 Summary

The most noteworthy finding of this work is that the relative importance of the com- munity members plays a crucial role in attracting new nodes or repelling existing nodes. This finding can be useful in assessing the dynamically changing degree of participation of a node to different communities.

Here, we used the concept of profile closeness centrality for predicting the stability of network communities. Some of the salient features of profile closeness are the following.

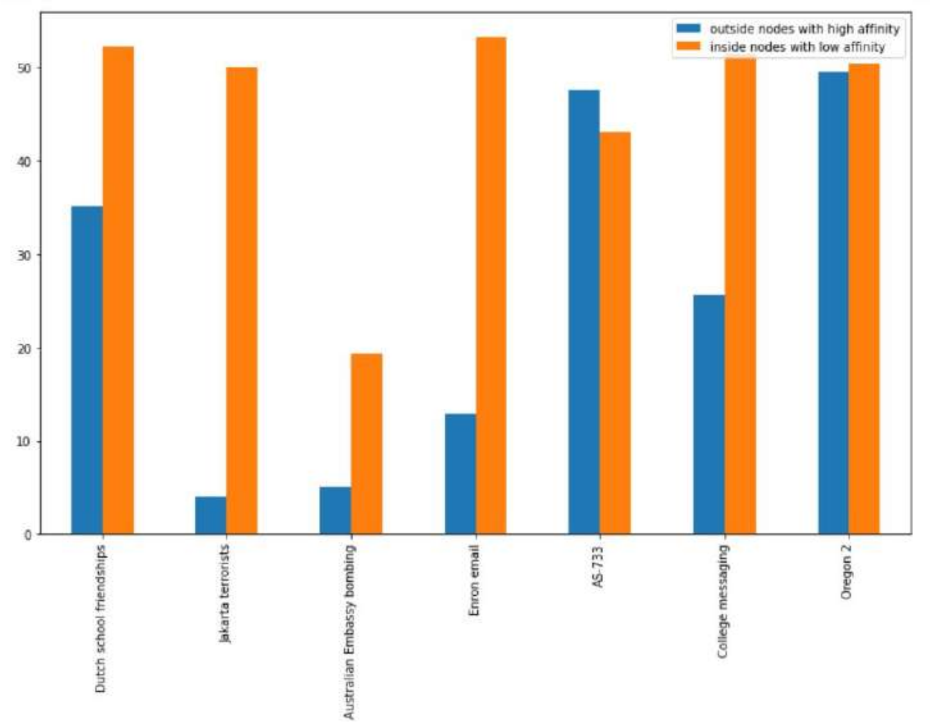


Figure 6: Barplot for the comparison of nodes added or removed in Dynamic networks

- The rank assigned to a profile node depends on the extent of the influence that it has on the network. For example, high-degree nodes, which directly influence a large part of the network, are ranked high.
- Choice of the rank function depends on the network domain.
- We can use this measure for Community membership prediction.
- It closely correlates with the global closeness centrality for large networks. There- fore, profile closeness offers a low computational complexity approximation of closeness ranking.
- It can aid in predicting community evolution.

We have also analyzed the role of community closeness in understanding the re- pulsion of a node to its community and its affinity towards another community in temporal networks. We have concluded that, on average, half of the nodes removed from a community are those with low intra-community closeness. Also, in very large networks, half of the new nodes added to a community are those with high community closeness.

In conclusion, our work demonstrates the significant potential of profile closeness as a tool for understanding and predicting community evolution in complex networks. By prioritizing influential nodes within communities, we can gain insights into the dynamic processes of node addition and departure, as well as the overall accessibility of vital network hubs. Additionally, exploring alternative ranking methods and incorporating the complexities of overlapping, splitting, and merging communities would further enhance the applicability of this framework. Nevertheless, our research pro- vides a valuable foundation for understanding the intricate dynamics of community evolution, with implications for diverse fields ranging from social network analysis to epidemic modeling and beyond.

However, we need more investigations to develop alternative techniques to as- sign member priorities. One of the major limitations of this work is that small networks with relatively little community structure are anomalies for the prediction issue. In that instance, more research is required. We simply employed the Louvain algorithm for community detection. We can compare the outcomes using various com- munity detection algorithms. Furthermore, the overlapping, splitting, and merging of communities are not taken into account.

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