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# Research On Dual Evolution Pattern Mining Model For Time-Varying Community Detection In Dynamic Networks

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## Abstract

Nowadays, more and more groups are studying community detection. Community detection also has many practical applications in real life, such as: modeling the brain in the field of neuroscience, effectively inferring relationships and preferences between users in social networks, etc. At present, most teams use time snapshots to simulate the dynamic community network, which ignores the small error caused by the change of time between each time snapshot. Therefore, in order to simulate the influence of time on this clique network, we add two time evolution matrices corresponding to both the sum matrix and the system matrix, and propose our new evolution model: double evolutionary pattern mining model for time-varying community detection in dynamic networks. At the same time we find that finally, the experimental results on the actual network show that the proposed algorithm has higher prediction accuracy in dynamic networks compared with other algorithms.

## Keywords

Community testing; Non-negative matrix factorization; Time evolution matrix; Dual evolution

## 1. Introduction

Since its inception, complex network research has evolved into a focal point in network relationship studies. Community discovery, as a key analytical tool for complex networks, plays a vital role in extracting critical information, revealing structural characteristics, and controlling or predicting network evolution. In real-world contexts, whether it's social interactions, interpersonal connections, or metabolic processes in biological networks, these phenomena can be abstracted into complex networks. Through such networks, we can uncover the relationships and interactions among individuals.

In recent years, as research on complex networks has deepened, community discovery has found increasingly widespread applications across various fields. [1]For instance, in biology, community discovery is used to analyze functional modules in metabolic networks, revealing key information related to cycles and pathways[2,3]. In protein complex analysis, scientists can more accurately identify protein interactions and functional compositions through community discovery[4]. In sociology, community discovery is applied to analyze criminal groups, helping law enforcement uncover the organizational structures of crime networks and providing robust support for combating crime[5].

In complex networks, static and dynamic networks represent two fundamental types. Static networks primarily focus on community structures at individual time snapshots, while dynamic networks better capture the evolutionary characteristics of real-world systems. As research progresses, dynamic community mining in dynamic networks has emerged as a key research focus. Compared to static complex networks, dynamic ones typically evolve more slowly, with community structures between adjacent snapshots exhibiting certain similarities. This makes historical information particularly crucial for understanding current community structures. In dynamic complex networks, temporal topology serves as a critical basis for designing similarity functions between entities.

In early research, Hopcroft et al. proposed a snapshot-based independent matching method [8]. The approach consists of two steps: first, analyzing community structures on each snapshot using existing static community detection methods, then designing a series of similarity metrics for community matching between snapshots to track community evolution. Subsequently, Palla et al. [9] applied the Community Permeability Method (CPM) [10] to detect each network snapshot and proposed a method based on historical structural dependencies. This method avoids redundant calculation of identical historical structures across snapshots, significantly improving computational efficiency.

To gain deeper insights into the generation rules and properties of network underlying structures, researchers have proposed an evolutionary modeling approach. The Xing-led research team developed the Mixed Membership Stochastic Block Model (MMSB). Additionally, a dynamic network community detection method based on Non-negative Matrix Factorization (NMF) has been introduced. This method constructs matrix factors with key network characteristics and demonstrates the convergence and correctness of the NMF algorithm. The model is applicable to weighted/unweighted and directed/undirected networks, capable of identifying both non-overlapping and overlapping community structures. By integrating temporal and structural information, experimental results on real-world networks show that this algorithm delivers superior prediction quality in dynamic networks compared to other methods.

However, conventional approaches to dynamic networks often overlook errors

caused by gradual matrix changes over time. To address this, we enhanced the original model by introducing a regularization term to correct such errors. Furthermore, we carefully evaluated the impact of each regularization term on the overall model and made corresponding adjustments to further improve its accuracy and stability.

## 2. Background

With the advancement of complex networks, community detection has emerged as a prominent research focus. Through continuous global scholarly efforts, various community detection approaches have been developed, including spectral clustering-based methods, modularity optimization-based approaches, label propagation-based techniques, and deep learning-based solutions. Among these, spectral clustering-based methods have garnered widespread attention due to their simplicity and strong adaptability.

### 2.1. Two-step Strategy

First, the two-step strategy is a method designed for static network analysis to detect community structures in each snapshot and analyze community evolution between adjacent time snapshots [11,12]. The core principle involves dividing the network into discrete time steps and applying static symmetric NMF (SNMF) [13] to each snapshot individually. This straightforward approach treats each network snapshot as an independent static entity, facilitating in-depth exploration of gradual community shifts and interactions across consecutive snapshots. While excelling in static community detection, the method has limitations when processing connections between successive snapshots. It may overlook dynamic information embedded in these connections, potentially missing critical trends in community evolution and vital insights into dynamic changes. Therefore, analyzing community structures and evolution requires further consideration of continuity between consecutive snapshots to fully capture the network's dynamic evolution process.

### 2.2. Dynamic Community Detection Based on Incremental Clustering

In the field of dynamic community discovery, Huang Yongfeng et al. [14] proposed a unique community discovery method based on the periodic evolution of social features. They recognized that in certain scenarios, community structures in networks exhibit relative stability, which provides strong support for designing network routing and forwarding strategies. To capture this stability, they developed an algorithm capable of identifying and tracking periodic changes in community structures, thereby enabling effective community discovery without significant network topology changes. On the other hand, Shanbo et al. [15] proposed the Incremental IC algorithm, a community discovery method for dynamic networks. This approach avoids the high computational cost of global community discovery during each network structure change through incremental updates. The

Incremental IC algorithm effectively handles local network changes while maintaining community structure consistency and improving discovery efficiency. Xiao Jiebin et al. [16] introduced a stochastic walk incremental processing method for related nodes. This method captures dynamic network changes by simulating random node walks, enhancing algorithm applicability while reducing computational complexity to improve efficiency. In the context of dynamic network changes, Chakrabarti et al. [17] first proposed an evolutionary clustering analysis framework. This method aims to minimize historical costs while ensuring consistency in static network topology results. This approach enables community discovery while preserving structural stability through optimal utilization of historical information. By maintaining the fundamental structure of previous time snapshots, it achieves community identification in dynamic networks. To further enhance accuracy, Thang et al. [18] proposed an adaptive evolutionary clustering method for community discovery. This approach not only considers network modularity and distribution characteristics but also dynamically adapts to network changes. Through this method, they successfully improved discovery accuracy and achieved more refined community classification results.

These researchers have conducted in-depth explorations in the field of dynamic community discovery, proposing multiple effective community discovery methods. These methods not only consider the static characteristics of networks but also fully account for their dynamic changes, thereby achieving more accurate and efficient community discovery. The introduction of these methods has not only advanced the development of dynamic community discovery but also provided valuable references for research in other related fields.

## 2.3. Non-negative Matrix Factorization

With the continuous advancement of community discovery techniques, dynamic community discovery presents greater challenges compared to static community discovery. Dynamic community discovery aims to capture the evolving community structures within networks over time, which is crucial for understanding the dynamic behaviors of complex systems. Rossetti et al. [19] conducted in-depth research on this issue and proposed a series of methods, among which the NMF (Non-negative Matrix Factorization) approach has garnered significant attention due to its outstanding performance in community detection.

The NMF method has become an ideal community detection model primarily due to its high interpretability, simplicity, flexibility, and versatility. By representing networks as matrices, NMF can reveal hidden structural information within the matrix, thereby identifying community structures in networks. Additionally, NMF demonstrates excellent scalability, enabling it to process large-scale network data.

Beyond its applications in community discovery, the Non-negative Matrix Factorization (NMF) method demonstrates extensive potential in diverse domains

including image representation [20], dimensionality reduction [21], and recommendation systems [22]. By transforming images into matrix form, NMF extracts essential features to enable effective image representation and classification. In dimensionality reduction, NMF decomposes matrices to reduce data dimensions, simplifying structures and boosting computational efficiency. For recommendation systems, NMF identifies latent features within user-item rating matrices to deliver personalized recommendations.

However, a key challenge in dynamic community discovery lies in effectively mitigating the impact of anomalous nodes on community structure. To address this, Baingana and Giannakis [23] proposed a dynamic factor model based on sparse outlier matrices. By identifying and removing anomalous nodes, this model enhances the accuracy of dynamic community discovery. This research provides innovative approaches and methodologies for the field.

In the field of dynamic community discovery, measuring community robustness and consistency remains a critical challenge. To address this, Du et al. [24] introduced a novel metric called community strength, which quantifies both the cohesion among nodes within a community and its stability during dynamic evolution. Building upon the NMF model, the researchers further developed a dynamic community discovery framework that tracks changes in community strength, thereby revealing the community's evolutionary trajectory.

To better address challenges in dynamic community research, Ma et al. proposed an evolutionary non-negative matrix factorization (ENMF) model [25]. By incorporating a temporal dimension, this model enables modeling and evolutionary analysis of dynamic community structures. The ENMF model not only captures static community structures in networks but also reveals their dynamic evolution. Additionally, it demonstrates strong generalization capabilities, adapting to dynamic network data of various types and scales.

Inspired by the Gaussian Non-negative Matrix Factorization (GNMF) [23], Ma et al. extended the Ensemble Non-negative Matrix Factorization (ENMF) to the Graph Rule Evolutionary Non-negative Matrix Factorization (GrENMF) [26]. By incorporating graph rule constraints, this model significantly improves the accuracy of dynamic community discovery. Moreover, GrENMF maintains the stability and consistency of community structures throughout the evolutionary process, thereby better revealing the evolutionary patterns of dynamic community structures.

To better demonstrate the temporal characteristics of dynamic community discovery and smooth its evolutionary process, we propose a dual-evolution pattern mining model for time-varying community discovery. By simultaneously considering both static and dynamic features of community structures, this model enables comprehensive analysis and mining of time-varying community structures. The dual-evolution pattern mining model not only reveals the static and dynamic characteristics of community structures but also identifies key nodes and events

during their evolution, thereby providing robust support for in-depth understanding of dynamic community discovery.

## 3. DE-NMF Method

### 3.1. Community Detection

Since network links between nodes are always non-negative (i.e., edge weights are non-negative), non-negative matrix factorization (NMF) is particularly suitable for community detection [27,28,29,30,31]. We represent a given dynamic network using a set of undirected binary graphs, where network nodes W(VU) are ∈ (n, n). NMF is defined as decomposing the community discovery result into a base vector matrix Ŵ by finding the largest low-rank factor matrix Ŵ that approximates the original network data. After dimensionality reduction, the sparse and linearly independent community feature matrix H represents the membership degree of corresponding nodes and communities. The Euclidean distance minimization method is generally adopted. The symmetric matrix At0, At1...AT denotes the adjacency network matrix Wt0, Wt1...WT. In dynamic networks, link prediction aims to predict future link occurrences at time T, where T is the time interval.

**Table 3-1.** Physical Meaning Table

| Index | Notation | Physical Meaning |
|---|---|---|
| **1** | A | Adjacency Matrix |
| **2** | W | Custom Weight Matrix |
| **3** | U | Latent Space Matrix |
| **4** | T\V | Coefficient Matrix |
| **5** | T | Time Interval |
| **6** | Zu | Community Transition Matrix for Latent Space |
| **7** | Zv | Community Transition Matrix for Coefficient |
| **8** | z | Evolution Parameter |
| **9** | α | Balance Parameter (alpha) |
| **10** | β | Balance Parameter (beta) |
| **11** | λ | Temporal Decay Coefficient |
| **12** | n,k | Matrix Dimensions |

### 3.2. Non-negative Matrix Factorization

When we identify these two adjacent non-negative matrices, the matrix U and the basis matrix V, their product approaches the non-negative matrix A infinitely closely. The non-negative matrix A represents the adjacency matrix of the community structure:

$$A \approx U \star V^{T} \tag{3-1}$$

As illustrated in Figure 1-1, this model diagram demonstrates the method of transforming the real network model into a matrix, along with the state of the

generated matrix across different time snapshots. It also clarifies the role of the regularization matrix we introduced during this process. The selected common time snapshots help the paper clearly present the entire evolutionary process.

The matrix factorization problem can be modeled as an optimization problem of the following Frobenius norm:

community structure:

$$\min \| A - UV^T \|_F^2, U > 0, V > 0 \tag{3-2}$$

Here, $\|.\|_F^2$ denotes the Frobenius norm. The similarity between nodes I and j in the potential space can be represented by the similarity between the Ith and jth rows of the matrix v. Given that communities in dynamic networks evolve slowly over time, we define ($At_0$, $At_1$,..., $At_t$) as the adjacency matrix of the dynamic network at time t ($t \in [1, T]$).

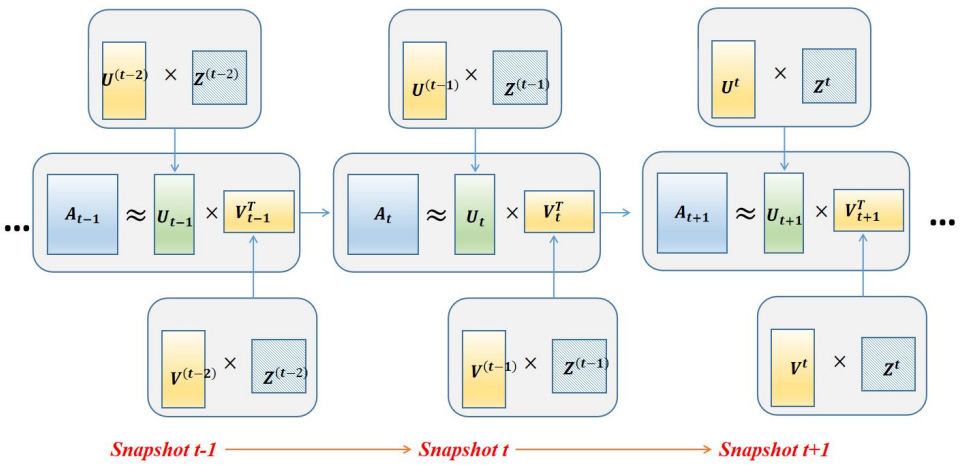



**Figure 3-1.** Illustraton of Model

The dynamics of society constitute a complex and ever-evolving phenomenon that continuously transforms over time. These temporal changes create disparities in community proportions across different periods, thereby altering their status and role within networked societies. To better capture and describe such transitions, we must incorporate the time-dependent damping coefficient λ into relevant equations, enabling a more comprehensive consideration of the distributional weight of cluster topological structures. The rapid development of networked societies provides us with vast amounts of information and data that continuously circulate and become available online. Over time, outdated information gradually gets replaced by newer content, while emerging information gradually gains public attention and becomes focal points. Consequently, the distribution of information within online communities exhibits evolving trends across different time periods. To integrate this evolutionary process into our research framework, we need to introduce the time decay coefficient λ. This coefficient quantifies how the importance and influence of

information within communities diminish over time. During each iteration, community weights are reduced through the decay coefficient, reflecting the gradual waning of information's significance and impact.

We can determine the specific value of the time decay coefficient λ by statistically analyzing community information and applying it to real-world scenarios. For instance, through studying the speed and reach of information dissemination within communities, as well as analyzing factors like the frequency of information sharing and forwarding, we can establish the appropriate range for λ. Such analysis and computation enable us to more accurately grasp the evolving trends of communities in the digital society. Therefore, understanding the dynamic characteristics of social dynamics that lead to variations in community proportions is crucial. The introduction of the time decay coefficient λ provides us with a more effective tool to describe and predict these changes. In future research, we will further explore methods for determining λ's value and its practical applications, aiming to better comprehend and address the complex transformations in the digital society.

In the study of dynamic changes in community structures, we face a key challenge: how to quantify structural losses between adjacent communities while maintaining inter-community connections and achieving effective matrix dimensionality integration. To address this issue, we introduce two innovative matrix tools—the regularization consensus U* space matrix and the potential coefficient matrix V*.

In social networks, a community structure refers to a collection of interconnected nodes that form relatively independent subnetworks. However, over time, these structures may undergo changes due to various factors such as shifts in node connections, the addition of new nodes, or the departure of existing ones. Such transformations can lead to structural degradation within communities or the emergence of new configurations, potentially causing previously tightly-knit groups to become loosely connected or even disintegrate entirely.

To effectively address this issue, we introduce the regularization consensus U* space matrix. This matrix functions by adjusting connection weights between nodes when community structures change, thereby strengthening connections between adjacent communities. Specifically, the regularization consensus U* space matrix balances intra-community and inter-community connections, making inter-community connection weights more reasonable and reducing structural loss caused by dynamic changes. However, simply adjusting connection weights is not sufficient to fully resolve community structure loss. Therefore, we also need to introduce the potential coefficient matrix V*. This matrix assigns a potential value to each community based on the strength and closeness of inter-community connections. The potential value reflects a community's status and influence within the network. By adjusting potential coefficients, we can ensure that communities with higher potential values are more likely to attract others during dynamic changes, thereby reducing structural loss.

Through the regularization consensus U* space matrix and potential energy coefficient matrix V* introduced above, we can effectively address structural degradation in dynamic social network evolution. These matrix tools not only enable us to adjust inter-community connection weights but also assign potential energy values to each community, ensuring greater stability and order during dynamic changes. This approach will provide more efficient and reliable methodologies for studying social networks, biological networks, and related fields.

$$\begin{cases} U* = \dfrac{\sum_{t=1}^{T} U_t}{T} \\ V* = \dfrac{\sum_{t=1}^{T} V_t}{T} \end{cases}$$

(3-3)

To better understand the dynamic relationships between time snapshots and clarify the impact of historical structural information, we introduce a new variable: the community evolution matrix Z. This matrix captures the transition trends of nodes from time t-1 to time t. Additionally, we incorporate two evolution matrices, Zu and Zv, derived from the differences between the coefficient matrix and the base matrix.

$$\begin{cases} Z_u = \dfrac{\sum_{t=1}^{T} U_t}{TU_{t-1}} \\ Z_v = \dfrac{\sum_{t=1}^{T} V_t}{TV_{t-1}} \end{cases}$$

(3-4)

To address the issues arising from the coefficient matrix and error basis matrix, we integrated the two equilibrium parameters α and β with minor adjustments, ultimately deriving our objective function:

$$f = \sum_{t=1}^{T} \lambda^{T-t} \| A - U_t V_t^T \|_F^2 + \alpha \sum_{t=1}^{T} \lambda^{T-t} \| U_t - Z_u U_{t-1} \|_F^2 + \beta \sum_{t=1}^{T} \lambda^{T-t} \| V_t - Z_v V_{t-1} \|_F^2$$

(3-5)

## 3.3. Rule of iteration

Given the four variables t, Vt, Zu, and Zv in the U equation, we propose a new iterative rule:

The entire process consists of four steps, where you use three fixed variables to determine the value of one variable, which serves as the optimal minimization objective function.

Step 1: Update Ut by repair x matrices Vt, Zu and Zv.

Step 2: Update Vt by fixing x matrices Zv, Ut, Zu.

Step 3: Update Zu by fixing x matrices Vt, Zv, Ut.

Step 4: Update Zv by fixing x matrices Vt, Ut, Zu.

Step 1: Update Ut

By fixing x matrices Vt, Zv, Zu and updating Ut, we aim to minimize f;

$$f(U_t) = \lambda^{T-t} \| A_t - U_t V_t^T \|_F^2 + \beta \lambda^{T-t} \| V_t - Z_v V_t - 1 \|_F^2$$

(3-6)

From:

$$\frac{\partial f(U_t)}{\partial U_t} = -\lambda^{T-t}\left[-2\beta A_t V_t + \alpha U_t \beta V_t^T V_t + \alpha U_t - 2Z_u U_{t-1}\right]$$

(3-7)

According to the Karush-Kuhn-Tucker (KKT) conditions, we know that:

$$-2\beta A_t V_t + \alpha U_t \beta V_t^T V_t + \alpha U_t - 2Z_u U_{t-1} = 0$$

(3-8)

This gives us:

$$U_t \leftarrow U_t \frac{\beta A_t V_t + Z_u U_{t-1}}{\alpha U_t \beta V_t^T V_t + \alpha U_t}$$

(3-9)

Step 2: Update Vt

By modifying the x matrix Zv, Ut, Zu, and updating Vt to minimize f;

$$f(V_t) = \lambda^{T-t} \|A_t - U_t V_t^T\|_F^2 + \alpha \lambda^{T-t} \|U_t - Z_u U_{t-1}\|_F^2$$

(3-10)

From:

$$\frac{\partial f(V_t)}{\partial v_t} = -\lambda^{T-t}\left[2\alpha U_t^T U_t V_t - \alpha U_t^T A_t + 2\beta V_t - 2Z_v V_{t-1}\right]$$

(3-11)

According to the Karush-Kuhn-Tucker (KKT) conditions, we know that:

$$2\alpha U_t^T U_t V_t - \alpha U_t^T A_t + 2\beta V_t - 2Z_v V_{t-1} = 0$$

(3-12)

This gives us:

$$V_t \leftarrow V_t \frac{\left(\alpha U_t^T A_t\right)^T + Z_v V_{t-1}}{\left(\alpha U_t^T U_t V_t\right)^T + \beta V_t}$$

(3-13)

Step 3: Update Zu

By modifying the x matrix Vt, Zv, and Ut, and updating Zu to minimize f;

$$f(Z_u) = \sum_{t=1}^{T} \lambda^{T-t} \|A_t - U_t V_t^T\|_F^2 + \alpha \sum_{t=1}^{T} \lambda^{T-t} \|U_t - Z_u U_{t-1}\|_F^2$$

(3-14)

From:

$$\frac{\partial f(Z_u)}{\partial Z_u} = \frac{\partial}{\partial Z_u} \alpha \sum_{t=1}^{T} \|U_t - Z_u U_{t-1}\|_F^2 = \sum_{t=1}^{T} 2\lambda^{T-t} \alpha (U_t - Z_u U_{t-1})$$

(3-15)

According to the Karush-Kuhn-Tucker (KKT) conditions, we know that:

$$\lambda^{T-t} \alpha (U_t - Z_u U_{t-1}) = 0$$

(3-16)

This gives us:

$$Z_u = \frac{1}{\sum_{t=1}^{T} \lambda^{T-t} U_{t-1}} \sum_{t=1}^{T} \lambda^{T-t} U_t$$

(3-17)

Step 4: Update Zv

By modifying the x matrix Vt, Ut, Zu, and updating Zv to minimize f;

$$f(Z_v) = \sum_{t=1}^{T} \lambda^{T-t} \|A_t - U_t V_t^T\|_F^2 + \beta \sum_{t=1}^{T} \lambda^{T-t} \|V_t - Z_v V_{t-1}\|_F^2$$

(3-18)

From:

$$\frac{\partial f(Z_v)}{\partial Z_v} = \frac{\partial}{\partial Z_v} \alpha \sum_{t=1}^{T} \|V_t - Z_v V_{t-1}\|_F^2 = \sum_{t=1}^{T} 2\lambda^{T-t} \alpha (V_t - Z_v V_{t-1})$$

(3-19)

According to the Karush-Kuhn-Tucker (KKT) conditions, we know that:

$$\lambda^{T-t}\alpha\left(V_t - Z_v V_{t-1}\right) = 0 \tag{3-20}$$

This gives us:

$$Z_v = \frac{1}{\sum_{t=1}^{T}\lambda^{T-t}V_{t-1}}\sum_{t=1}^{T}\lambda^{T-t}V_t \tag{3-21}$$

The above outlines all processes and formula evolution for the four iteration types. Figure 2-1, a pseudocode diagram, clearly illustrates the matrix transformation and time slice process of real communities, which also summarizes the aforementioned procedures.

**Algorithm 1** Framework of ensemble learning for our system.

**Input:**
adjacent matrices of the dynamic: $\mathbf{A}_{t0},\mathbf{A}_{t1}...\mathbf{A}_T$;
network in times 1...T ;
The dampin factor:$\lambda$;
balance parameter:$\alpha,\beta$;

**Output:**
latent space matrices:$\mathbf{U}_{t0},\mathbf{U}_{t1}...\mathbf{U}_T$;
coefficient matrices:$\mathbf{V}_{t0},\mathbf{V}_{t1}...\mathbf{V}_T$;

Initialize the matrices $\mathbf{V}_t,Z_v,\mathbf{U}_t,Z_u$
for iter=300
for t=1...T;
$U_t \leftarrow U_t\frac{\beta A_t V_t + U*}{\alpha U_t \beta V_t^T V_t + \alpha U_t}$
$V_t \leftarrow V_t\frac{(\alpha U_t^T A_t)^T + V*}{(\alpha U_t^T U_t V_t)^T + \beta V_t}$
$Z_u = \frac{1}{\sum_{t=1}^{T}\lambda^{T-t}U_{t-1}}\sum_{t=1}^{T}\lambda^{T-t}U_t$;
$Z_v = \frac{1}{\sum_{t=1}^{T}\lambda^{T-t}V_{t-1}}\sum_{t=1}^{T}\lambda^{T-t}V_t$;
**return** $V;U$;

**Figure 3-2.** Pseudo-code

## 4. Convergence and Comparative Experiments

### 4.1. Evaluating Indicator

For dynamic community discovery experiments, this chapter employs two standard metrics: normalized mutual information (NMI) and community accuracy (CA). NMI quantifies the discrepancy between detected community structures and known community structures, with higher NMI values indicating closer alignment between partition results and known community configurations. The CA error rate (CA) measures the deviation between algorithm-generated community results and actual

community structures, with values ranging from 0 to 1. Notably, unlike NMI, higher CA values correspond to lower detection accuracy. In subsequent experiments, this paper will utilize these two comparative methods to evaluate our approach against existing techniques from multiple perspectives.

### 4.2. Comparative Approach

- SNMF[32]: The classical static NMF model treats each snapshot of a dynamic network as an independent static network, ignoring the correlation between dynamic evolution information and snapshots. This represents a typical two-step strategy approach.
- FaceNet[33]: An evolutionary clustering-based extension of the Non-negative Matrix Factorization (NMF) model, this algorithm employs Hidden Markov Model (HMM) assumptions. As a classical dynamic complex network community discovery approach, it minimizes errors through the use of relative entropy from information theory.
- DYNMOGA[34]: A classical dynamic multi-objective genetic algorithm for dynamic community discovery. It transforms the balance problem between snapshot structure loss and time-varying loss in evolutionary clustering into a multi-objective problem. The algorithm features a multi-objective method for automatically determining balance parameters, as well as a genetic representation method for determining the number of communities in each snapshot.
- FVI-NMF: An extended evolutionary clustering framework that not only introduces evolutionary smoothing constraints but also quantitatively characterizes dynamic community evolution, while incorporating constraints on inconsistent node transfer trends. It demonstrates strong scalability.
- MSSC: A dynamic community discovery algorithm based on multi-similarity spectrum clustering. It introduces multiple similarity metrics into the evolutionary spectrum clustering and learns time-varying balance parameters through an adaptive strategy. This method is a parameter-adaptive approach.

### 4.3. Parameter Sensitivity and Algorithm Convergence Analysis

To validate the proposed method's effectiveness and reliability, this chapter presents experimental designs conducted on both artificial and real-world networks, yielding robust conclusions. Our tests employed a widow size parameter ( $\lambda$ =0.7) and balanced parameters ( $\alpha$ =0.3, $\beta$ =0.7) selected through parameter sensitivity analysis. The event-driven dynamics encompass emergence, disappearance, expansion, contraction, merging, and splitting. Two representative event-driven network types were used to generate datasets: • Birth-Death networks, where community emergence and disappearance probabilities were controlled by adjusting parameters P1 and P2. The network-generation parameter configurations

are as follows: Birth-Death-1 (p1=0.2, p2=0.1); Birth-Death-2 (p1=0.3, p2=0.1); and Birth-Death-3 (p1=0.3, p2=0.2).

To validate the convergence of DE-NMF, convergence experiments were conducted on both artificial and real networks. As the number of iterations increased, the corresponding values of the objective function were displayed. The x-axis represents the iteration count, while the y-axis shows the objective function values. The two subplots demonstrate that when the iteration count reaches 10-20, the objective function of each snapshot DE-NMF model converges.

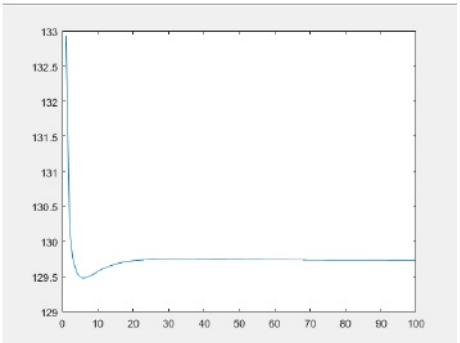



**Figure 4-1.** Real Network

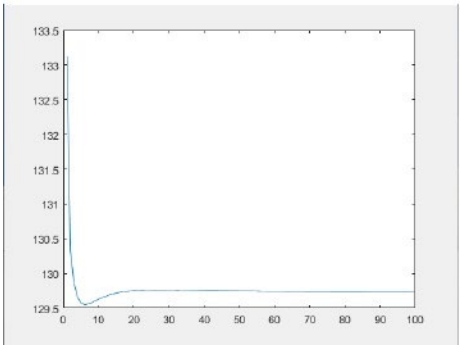



**Figure 4-2.** Artificial Network

## 5. Analysis of the experimental results

For dynamic networks where the number of communities remains constant over time, the figure below presents comparative results of dynamic community discovery. The x-axis represents the network snapshot label t, while the y-axis displays the corresponding NMI and CA values.

1) T-gn[35]: This dataset represents a dynamically generated network based on the Girvan-Newman benchmark. During generation, the network parameters were configured as follows: snapshot count T = 10, node count N = 128, and community count K = 4. The hybrid parameter Z (controlling neighborhood noise level) was set to 3, with node d and Y averaging 16 and 20 respectively. Additionally, the community migration parameter nc (controlling node migration dynamics) was set to 10% and 30%.

2) T-lfr[36]: A classical artificial generation of complex networks, primarily considering the evolution of specific communities within the network to describe its dynamism. Evolutionary events include emergence, disappearance, expansion, contraction, merging, and segmentation. Here, we selected two typical event-driven networks to generate the dataset:

a) birth-death, where different probabilities P1 and P2 are set during network generation to control the occurrence and disappearance rates of communities. The generated network corresponds to the parameter settings as follows:

Birthday-1, p1= 0.2, p2 = 0.1;

Birthday-2, p1= 0.3, p2 = 0.1;

Birthday-3, p1= 0.3, p2 = 0.2;

b) Merge and split. Set different probabilities P1 and P2 during network generation to control the probability of community merging and splitting. The relationship between the generated network and parameter settings is as follows:

Mergesplit-1, p1 = 0.2, p2 = 0.1; Mergesplit-2, p1 = 0.3, p2 = 0.1;

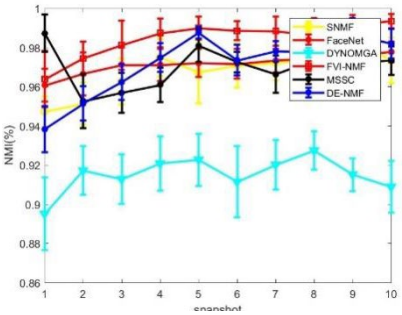



**Figure 5-1.** Real Society

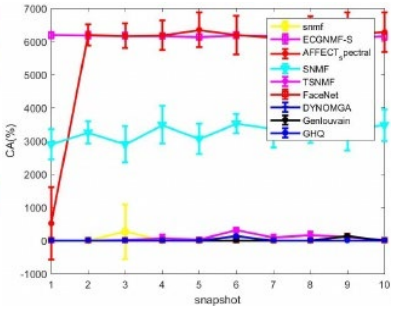



**Figure 5-2.** Real Society

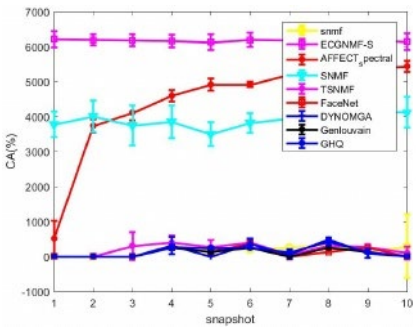



**Figure 5-3.** Artificial Community

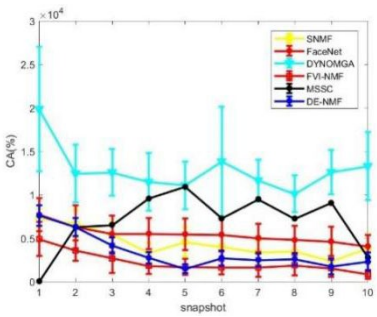



**Figure 5-4.** Artificial Community

## 6. Conclusion

This paper proposes a novel dynamic network community detection method. DE-NMF can handle dynamic networks with evolving structures over time. By iteratively updating matrices, DE-NMF captures and adapts to the dynamic evolution of network architectures. The introduction of a regularization consensus matrix and potential coefficient matrix helps stabilize community structures, ensuring relative stability during network changes. Through this approach, we develop a non-negative matrix factorization algorithm that achieves better link prediction results. The algorithm learns latent features from both dynamic and topological graph structures, demonstrating superior predictive performance compared to similarity-based methods. Additionally, the time-decay coefficient allows flexible adjustment of information importance over time, enabling the algorithm to adapt to network feature variations across different time points. For constructing NMF factors, we propose new iteration rules with proven convergence and correctness. Our experiments show that the similarity index based on NMF

weighted representations outperforms static representation-based methods. Real-world network experiments validate DE-NMF as a versatile approach applicable to dynamic network analysis in diverse domains such as social networks and biological networks.

Compared to other algorithms, this method delivers superior prediction quality in dynamic networks. Going forward, we will prioritize diverse regularization techniques to achieve faster and more accurate iterations and detection. Our model is also designed to adapt to a wider range of data types while maintaining high prediction accuracy.

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