

Novel Dynamic Evolution Model Based on Improved Cellular Automata in Hierarchical Complex Networks

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Abstract—Modeling of network structures has been a popular issue in the study of complex networks. The use of complex network theory in modeling complex networks has gradually become a trend. In this study, the current research status of the modeling of complex networks was synthesized based on the BA scale-free network model. The advantages and disadvantages of most mainstream models were integrated, and a complex network model was established from the view of hierarchical community structures. Furthermore, a dynamic evolution network model was built by establishing a new evolution rule of cellular automata. Simulation experiments were conducted to validate the model. Results revealed that the network exhibits a power-law behavior and has a clear, controlled community structure. The model can suitably describe the characteristics of complex network topologies.

Index Terms—complex network, evolution model, community structure, cellular automata

I. INTRODUCTION

With the increased scale of modern networks, network structures have become increasingly complicated. The requirements of complex network design have become difficult to satisfy when the traditional network model is employed. The use of complex network theory to model complex networks has gradually become a research hot spot. The geometric properties, formation mechanisms, statistical law, and structural stability of the network as well as the combination of these elements within a specific system are the core issues in the research on complex networks. Network topology can effectively solve the problem of network transmission behavior. Thus, establishing an appropriate network topology model for different purposes, such as to predict and improve network performance is very important.

Since the emergence of complex network theory, modeling of complex networks has always been a hot topic, a lot of excellent and mature network model have been generated.

As shown in Fig. 1, the evolution of complex network models has passed through four stages: regular networks, random networks, small-world networks and scale-free networks.

In the early network theory, it is mainly through the regular networks to analyze network properties. In this model nodes must be connected to each other in accordance with the strict rules established in advance. In the 1960s, the random network model was proposed, which is obtained by starting with a set of n isolated nodes and adding successive edges between them at random. This model has small average path length, and has no clustering characteristics, which does not match with the reality; a real network usually has very obvious aggregation characteristics.

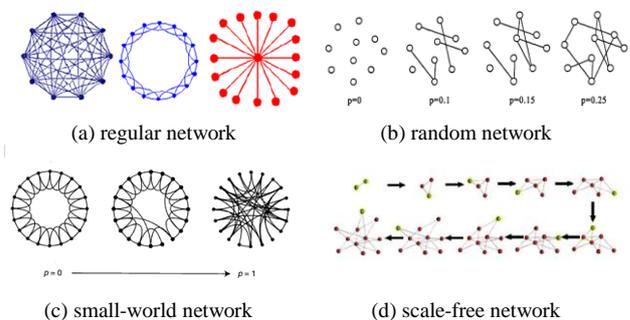


Fig. 1. Comparison of four classic network models

The small-world network is a type of mathematical graph in which most nodes are not neighbors of one another, but most nodes can be reached from every other by a small number of hops or steps. In 1998, Watts and Strogatz [1] proposed a type small-world network model, which is a random networks generation model that produces networks with small-world properties, including short average path lengths and high clustering coefficient.

Given the desired number of nodes N , the mean degree K (assumed to be an even integer), the model constructs an undirected graph with N nodes and $NK/2$ edges in the following way:

Construct a regular ring lattice, a graph with N nodes each connected to K neighbors, $K/2$ on each side. Randomly with probability p reconnecting each edge of the network, that is, one node on the edge remains unchanged, another is selected randomly in the network. When the probability p tends to 0, the network will tends to a rule network, when it tends to 1; the network will tends to a random network.

The major limitation of this model is that it produces an unrealistic degree distribution. In contrast, real

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networks are often scale-free networks inhomogeneous in degree, having hubs and a scale-free degree distribution. The Watts and Strogatz model also implies a fixed number of nodes and thus cannot be used to model the growth of network.

In 1998, Barabási and Albert proposed an algorithm for generating random scale-free networks using a preferential attachment mechanism [2], [3]. Scale-free networks are widely observed in natural and human-made systems, including the Internet, the world wide web, citation networks, and some social networks.

The network begins with an initial connected network of m_0 nodes.

New nodes are added to the network one at a time. Each new node is connected to $m(m \leq m_0)$ existing nodes with a probability that is proportional to the number of links that the existing nodes already have. Formally, the probability p_i that the new node is connected to node i is

$$p_i = \frac{k_i}{\sum_j k_j}$$

where k_i is the degree of node i and the sum is made over all pre-existing nodes j (i.e. the denominator results in the current number of edges in the network). Heavily linked nodes ("hubs") tend to quickly accumulate even more links, while nodes with only a few links are unlikely to be chosen as the destination for a new link. The new nodes have a "preference" to attach themselves to the already heavily linked nodes.

In recent years, academics believe the real network should also have three characteristics, namely small-world, community structure and scale-free. However, the small-world model does not reflect the scale-free characteristics, the scale-free model has short average path length, and has very low clustering coefficient. To this end, with the classic small-world and scale-free networks as the prototype, researchers made a lot of such as forecasts, cooperation, competition, absorption, elimination, the initial attractiveness, flow-driven and two-way selection features to generate network in order to improve and perfect the real network.

Research results starting from the scale-free network pose a series of questions about the microscopic generation mechanism of various macroscopic properties in an actual network system. The evolution of networks has become the focus of the academic community. The BA model reveals that the seemingly complex large-scale network is in fact characterized by very simple evolutionary dynamics; however, it also has many defects and cannot fully reflect the network structure. Thus, researchers proposed a series of improved BA models, such as the nonlinear preferential connection model proposed by Krapivsky *et al.* [4], the preferential linking model with initial attraction factor, and the model with

accelerating growth of communications proposed by Dorogovtsev *et al.* [5], [6]. Bianconi *et al.* [7] proposed the preferential connection model with fitness, and Peköz *et al.* [8] studied the model with both preferential and random attachments. Sen and Guan [9] proposed an evolving network model in the real world. Dargazany [10] proposed a purely micromechanical network evolution theory granting new insight into the damage mechanism and further formulated the network evolution model for implementation into finite element simulations. Liu *et al.* [11], [12] established a model based on the scale-free network by introducing coupling coefficients and attracting factors in the BA scale-free network. Wang and Chen [13] introduced dynamics equation into complex networks, through linear coupling diffusion, proposed a general dynamic scale-free network model. Chen [14] considered in scale-free networks, the priority connection usually occurs within the local world, which conducted a promotion for the BA model, and proposed a new type of local world evolving network model. This model is another progress of human knowledge in the real networks. According to the statistical properties of the Internet, Li *et al.* [15] proposed a new definition of scale-free networks and a concept of structural measure, using non-random connections to generate scale-free networks in line with the natural reality. These models are significant for the development of the modeling of complex networks.

This study aims to explore the relation between the network model and the communication that exists among communities and to reveal the intrinsic link between network topology and community structure in complex communication networks. The current research status of the modeling of complex networks was synthesized based on the BA scale-free network model. The advantages and disadvantages of most mainstream models were integrated. We focused on the node and link to join and dissolution, new internal connections within the network, and the conversion relationship between nodes. We also established a complex network model from the view of hierarchical community structures. Furthermore, a dynamic evolution network model was established through the establishment of a new evolution rule of cellular automata. The simulation experiments revealed that the network exhibits a power-law behavior and has a clear, controlled community structure. The degree distribution, average path length, and other major parameters of the model in the evolutionary process can suitably describe the characteristics of complex network topologies.

II. CELLULAR AUTOMATA

A cellular automata is a discrete model studied in many field. It has been widely applied in various fields of social, economic, military, and scientific research since their inception. The applications of cellular automata involve sociology, biology, ecology, information science,

computer science, mathematics, physics, chemistry, geography, military science and so on.

The concept [16] was originally discovered in the 1940s by Stanislaw Ulam and John von Neumann while they were contemporaries at Los Alamos National Laboratory. While studied by some throughout the 1950s and 1960s, it was not until the 1970s and Conway's Game of Life, a two-dimensional cellular automata, that interest in the subject expanded beyond academia. In the 1980s, Stephen Wolfram engaged in a systematic study of one-dimensional cellular automata, or what he calls elementary cellular automata; his research assistant Matthew Cook showed that one of these rules is Turing-complete. Wolfram [17] claiming that cellular automata have applications in many fields of science in 2002. These include computer processors and cryptography. Cellular automata can simulate a variety of real-world systems, including biological and chemical ones. There has been speculation that cellular automata may be able to model reality itself, i.e. that the universe could be viewed as a giant cellular automata.

A cellular automata is a dynamic system that is discrete in time dimension change, namely, time f is an integer with continuity straits and equal to the interval. If time interval $dt = 1$ and $t = 0$ at the initial time, then $t = 1$ for the succeeding moment. In the above conversion function, a cell's state at time $t+1$ (directly) depends only on its states and its neighbors' state at time t . However, the states of the cell and its neighbors at time $t-1$ indirectly affect the state of the cell at time $t+1$.

A standard cellular automata (A) is composed of the cell, its state, its neighbors, and the update rules of states, which are expressed as follows:

$$A = (L, d, S, N, f)$$

where L is the cellular space, d is the dimension of the cellular space in cellular automata, S is the finite and discrete state set of the cell, N is the set of all cells within a neighborhood, and f is the local mapping or local rules.

A cellular space is a set of spatial networks in which cells are distributed. Theoretically, a cellular space has unlimited extension in every dimension. Boundary conditions, including period type, reflection type, and constant value type, are defined for implementation on computers.

Cells are usually obtained from a state in a finite set at a time, such as $\{0, 1\}$; the cell's state can represent individual attitudes, traits, and behavior [18]. The cellular automata on the space-adjacent cells comprise a neighborhood.

Considering the adjacency matrix of the network, two states of cells exist depending on whether an edge is connected, i.e., 0 means no connection, and 1 denotes a connection. The black square in the Fig. 2 below represents the central cell, and the gray squares represent the neighbors of the central cell.

The neighbors of the central cell are defined as follows:

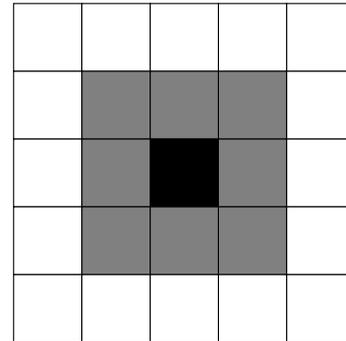


Fig. 2. Moore neighborhood

$$N_{Moore} = \{v_i = (v_{ix}, v_{iy}) \mid |v_{ix} - v_{ox}| \leq 1, |v_{iy} - v_{oy}| \leq 1, (v_{ix}, v_{iy}) \in Z^2\}$$

The definitions of v_{ix} , v_{iy} , and v_{ox} are the same as the previous. At this time, when the dimension is d , the number of one cell's neighbors is $(3^d - 1)$ for the square lattice.

III. DYNAMIC HIERARCHICAL COMMUNITY STRUCTURE EVOLUTION MODEL BASED ON CELLULAR AUTOMATA

The hierarchical community network was constructed first in the establishment of the model. The cellular automata rules were then introduced. The following is a specific algorithm of this model.

Only one edge exhibits agreement between nodes; each node cannot have edges connected to itself.

- 1) An initial network with m_0 backbone nodes and n_0 edges is given.
- 2) An operation is randomly performed in each time step as follows:
 - A backbone node is generated according to the probability of p and is connected to the existing backbone node i according to the probability of Π_i .

$$\Pi_i = \frac{k_i}{\sum_{l \in \Omega} (k_l)} \quad (1)$$

where Ω is a local network consisting of backbone nodes.

- An initial community network, including m_1 ordinary nodes and n_1 edges, is generated according to the probability of q . This network has the features of automatic dynamic growth and first connection. This network is connected to the existing backbone node i through m_2 edges in accordance with Formula (1).
- A community is randomly selected to establish m_2 edges according to the probability of s , and

m_3 edges are constructed between two communities that are randomly selected. One side of the edge is selected randomly, and the other edge is selected according to the probability of Formula (2).

$$\Pi_j = \frac{k_j}{\sum_l k_l} \quad (2)$$

where the denominator represents the sum of all ordinary nodes' degrees.

- The m_4 edges in a community are randomly demised according to the probability of $(1-s)$; the m_5 edges between two communities are also randomly demised. One side of the edges is selected randomly, and the other edges are selected according to Formula (3).

$$\Pi'_j = 1 - \frac{k_j}{\sum_l k_l}, \quad (3)$$

Isolated nodes that emerge in the process are removed.

- 3) Step 2 is repeated until the size of the network satisfies the requirement.

These parameters satisfy the conditions of $0 \leq p < q \leq 1$, $0.5 \leq s \leq 1$, and $p+q=1$. In step 2, the rate of growth of the generating community is random in each time step to ensure that all communities have different nodes and edges at time t .

After the above scale-free evolution, the adjacency matrix of the network is obtained. The adjacency matrix is modified as follows: the value of the edge whose one end is the backbone node is modified into 2. The cell is the data of the matrix, and the set of states includes $\{0, 1, 2\}$ as indicated in the definition of cellular automata. The cell has three states: 0 means no edge exists, 1 corresponds to an existing edge whose ends are ordinary nodes, and 2 corresponds to an existing edge, at least one end of which is the backbone node. A spatial network set in which cells are distributed is called cellular space. Cellular space is two dimensional, that is, the adjacency matrix of network nodes. Moore's selection method was employed in this study to select the cellular neighbors. The specific evolution rules are as follows:

- 1) As the number of connections or attraction factors increases, ordinary nodes can become backbone nodes and would thus require rules. Ordinary nodes can transform into backbone nodes, but the probability is generally low. The condition is that the state of the node is 1, the state of three or more neighbors is 2, and the next state of the node is 2.
- 2) The no-edge nodes may also be connected at a specific moment and would thus require rules; a connection may exist between ordinary nodes. The condition is that the state of the node is 0, the state of three or more neighbors is 1, and the next state of the node is 1.

- 3) Ordinary nodes may lose their connection because they do not update for a long time or their activity decreases and may thus require rules; a connection may exist between common nodes. The condition is that the state of the node is 1, the state of five or more neighbors is 0, and the next state of the node is 0.
- 4) For the same reason, backbone nodes can be reduced or even lose their connection although the probability is low. Thus, rules are needed. Backbone nodes can transform into ordinary nodes, but the probability is relatively low. The condition is that the state of the node is 2, the state of five or more neighbors is 0, and the next state of the node is 1.
- 5) Based on the adjacency matrix border, if a node is a left boundary node, the right boundary nodes of its corresponding row and column will become its left neighbor nodes. This rule also applies to the top and bottom nodes.

IV. ANALYSIS OF DEGREE DISTRIBUTION

The proposed model has two types of nodes; the evolution rules of these nodes are different. The mean field theory was employed to obtain the degree distribution of node i at time t . Below is the derivation process.

We assume that at time t , the network has N nodes and E edges without considering the isolated nodes. Then, $N = m_0 + pt + qt(m_1 + t)$, where the backbone nodes are $N_B = m_0 + pt$ and

$$E = n_0 + pt + qt(n_1 + mt + m_1) + st(m_2 + m_3 + m_4 + m_5) - t(m_4 + m_5)$$

- a) A backbone node is generated with probability p . Then,

$$\left(\frac{\partial k_i}{\partial t}\right)_{(i)} = p(m_0 + pt) \cdot \frac{k_i}{\sum_{l \in \Omega} (k_l)}$$

The right side of the equal sign shows the selection rules of the already existing backbone node i .

- b) An initial community network is generated with probability q . Then,

$$\left(\frac{\partial k_i}{\partial t}\right)_{(ii)} = qm_2(m_0 + pt) \cdot \frac{k_i}{\sum_{l \in \Omega} (k_l)}$$

The above equation describes a new community network associated with the network only through the backbone nodes.

- c) m_2 edges are established in one community network, and m_3 edges are randomly established between two random community networks with probability s . Then,

$$\left(\frac{\partial k_i}{\partial t}\right)_{(iii)} = \frac{sm_2}{m_0 + pt} \left[\frac{1}{N_\Omega(t)} + \left(1 - \frac{1}{N_\Omega(t)}\right) \frac{k_j}{\sum_l k_l} \right] + sm_3 \left[\frac{2}{(m_0 + pt)} - \frac{1}{(m_0 + pt)^2} \right] \frac{k_j}{\sum_l k_l}$$

The right side of the equal sign in the first part describes the selection of edges in one community network; the second part describes the selection of edges between two random community networks. One end of the edge is randomly selected; the other end is selected by the priority probability.

d) m_4 edges in one community network are removed, and m_5 edges between two random community networks are randomly removed with probability $(1-s)$. Then,

$$\left(\frac{\partial k_i}{\partial t}\right)_{(iv)} = \frac{(1-s)(m_4 + m_5)}{m_0 + pt} \left[\frac{1}{N_\Omega(t)} + \left(1 - \frac{1}{N_\Omega(t)}\right) \frac{1}{N_\Omega(t)-1} \left(1 - \frac{k_j}{\sum_l k_l}\right) \right]$$

$N_\Omega(t)$ represents the mean value of the ordinary nodes under backbone node Ω at time t . Then,

$$N_\Omega(t) = \frac{m_0 + pt + qt(m_1 + t)}{m_0 + pt}$$

When t is large,

$$\begin{aligned} \frac{\partial k_i}{\partial t} &= \frac{(m_0 - n_0)(qm_2 + p)k_i}{2pt} + \frac{sm_2}{m_0 + pt} \cdot \frac{p}{p + qt} \\ &+ \frac{sm_2}{m_0 + pt} \cdot \frac{p}{p + qt} \cdot \frac{qt}{p} \cdot \frac{k_j}{\sum_l k_l} + \frac{2sm_3}{(m_0 + pt)} \cdot \frac{k_j}{\sum_l k_l} \\ &- \frac{sm_3}{(m_0 + pt)^2} \cdot \frac{k_j}{\sum_l k_l} + \frac{(1-s)(m_4 + m_5)}{m_0 + pt} \cdot \frac{2p}{p + qt} \\ &- \frac{(1-s)(m_4 + m_5)}{m_0 + pt} \cdot \frac{p}{p + qt} \cdot \frac{k_j}{\sum_l k_l} \\ &= \left[\frac{sm_2q}{p(p + qt)} - \frac{(1-s)(m_4 + m_5)}{t(p + qt)} \right] \frac{pk_i}{2p + q(n_1 + mt + m_1) + s(m_2 + m_3 + m_4 + m_5) - (m_4 + m_5)} \\ &+ \frac{(m_0 - n_0)(qm_2 + p)k_i}{2pt} \\ &+ \frac{sm_2 + 2(1-s)(m_4 + m_5)}{t(p + qt)} \end{aligned}$$

If

$$\begin{aligned} \frac{sm_2q}{p} &= (1-s)(m_4 + m_5) \\ a &= \frac{[(m_0 - n_0)(qm_2 + p) - 2sm_3]}{2p} \\ b &= \frac{sm_2 + 2(1-s)(m_4 + m_5)}{q} \end{aligned}$$

Then,

$$\frac{\partial k_i}{\partial t} = \frac{1}{t^2} \cdot b + \frac{k_i}{t} \cdot a$$

When the above equation is solved and when $a \neq -1$,

$$k_i(t) = \frac{t^{a+1}(b/t + m + am)}{x^{a+1}(a+1)} - \frac{bt^a}{(a+1)t^{a+1}}$$

Considering $P(t_i) = \frac{1}{pt + qt^2}$,

$$\begin{aligned} P[k_i(t) < k] &= P[t_i > \left[\frac{k + b/t(a+1)}{m + b/t(a+1)} \right]^{-\frac{1}{a+1}} t] \\ &= 1 - \frac{1}{pt + qt^2} \cdot \left(\frac{k + b/t(a+1)}{m + b/t(a+1)} \right)^{-\frac{1}{a+1}} t \end{aligned}$$

We can then obtain the degree distribution as

$$\begin{aligned} P(k) &= \frac{\partial \{P[k_i(t) < k]\}}{\partial k} \\ &= \frac{1}{(a+1)(pt + qt^2)^{\frac{1}{a+1}}} \times \\ &\quad [m + b/t(a+1)]^{\frac{1}{a+1}} \cdot [k + b/t(a+1)]^{-r} \end{aligned}$$

where $r = \frac{1}{a+1} + 1$.

The above indicates that $P(k) \propto (k + b/t(a+1))^{-r}$, revealing that the network has the characteristics of power law but is different from the BA model. $b/t(a+1)$ illustrates that the generation rule of the local network significantly influences the global network.

The following is main steps of the algorithm:

```

for i=1:Base_Num
    Ordinary_Net(i)={SFNG(ceil(rand*Ordinary_scale),4,Ordinary_seed)};
    temp=cell2mat(Ordinary_Net(i));
    for j=1:length(temp)
        temp(j,j)=nan;
    end
    j=1;
    [a,b]=find(temp==1);
    for u=1:m1
        c=a(ceil(rand*size(a,2)));
        d=b(ceil(rand*size(b,2)));
        temp(c,d)=0;
        temp(d,c)=0;
        u=u+1;
    end
    u=1;
    [a,b]=find(temp==0);
    for v=1:m2
        c=a(ceil(rand*size(a,2)));
        d=b(ceil(rand*size(b,2)));
        temp(c,d)=1;
        temp(d,c)=1;
        v=v+1;
    end
    v=1;
    c=ceil(rand*size(temp,2));
    temp(:,c)=[];
    temp(c,:)=[];
    for k=1:length(temp)
        temp(k,k)=0;
    end
    k=1;
    Ordinary_Net(i)=mat2cell(temp);
    Ordinary_Length=Ordinary_Length+length(temp);
end
clear temp;
clear a,b;
temp=1;
Net=zeros(Ordinary_Length+Base_Num,Ordinary_Length+Base_Num);

Base_Net(Base_Net==1)=2;
Net(Ordinary_Length+1:Ordinary_Length+Base_Num,
Ordinary_Length+1:Ordinary_Length+Base_Num)=Base_Net;
for i=1:Base_Num
    t=length(cell2mat(Ordinary_Net(i)));
    Net(temp+1:t,temp+1:t)=cell2mat(Ordinary_Net(i));
    Net(Ordinary_Length+1,temp+1:temp+ceil(0.5*t))=2;
end
    
```

```

Net(temp:temp+ceil(0.5*t),Ordinary_Length+i)=2;
temp=temp+t;
end
temp=Net;
for j=1:length(temp)
temp(j,j)=nan;
end
[a,b]=find(temp==1);
for u=1:m3
c=a(ceil(rand*size(a,2)));
d=b(ceil(rand*size(b,2)));
temp(c,d)=0;
temp(d,c)=0;
u=u+1;
end
[a,b]=find(temp==0);
for v=1:m4
c=a(ceil(rand*size(a,2)));
d=b(ceil(rand*size(b,2)));
temp(c,d)=1;
temp(d,c)=1;
v=v+1;
end
for k=1:length(temp)
temp(k,k)=0;
end
Net=temp;

```

V. SIMULATIONS AND RESULTS

MATLAB was employed to verify the accuracy of the model. The specific evolution of the network was simulated by analyzing the degree distribution and average path length of the entire network.

A total of 200 randomly generated networks were compared in accordance with the following parameter values: $m_0 = 5$, $n_0 = 4$, $m_1 = 3$, $n_1 = 2$, $m_2 = 20$, $m_3 = 4$, $m_4 = 4$, $m_5 = 6$, $p = 0.8$, $q = 0.2$, and $s = 0.66$.

Fig. 3 shows the adjacency matrix of a complex network consisting of 10 hierarchical communities under different evolutionary t . As shown in Fig. 3, network evolution becomes more complex with the increase in t ; however, the community structure is always easily visible. The boundary of the communities blurs gradually, and small communities are derived aside from the large communities. Some randomly scattered connections emerge. However, these connections do not form a new community.

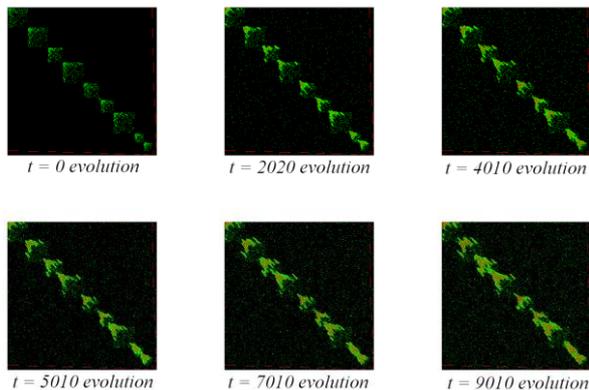


Fig. 3. Evolution of the network adjacency matrix consisting of 10 hierarchical communities.

TABLE I: THE AVERAGE DEGREE AND THE AVERAGE CLUSTERING COEFFICIENT OF THE EVOLUTION NETWORK IN FIG. 3.

t	Average Degree	Average Clustering Coefficient
0	7.716981132	0.475875163
2020	8.107692308	0.465025599
4010	8.199782845	0.433280963
5010	8.077922078	0.451432304
7010	8.031246807	0.450823219
9010	7.953179867	0.444285875

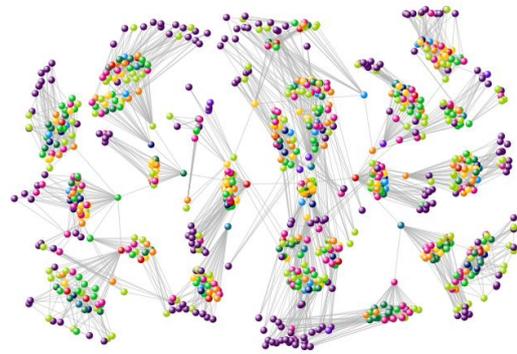


Fig. 4. The structure of the Evolution network when $t = 4010$.

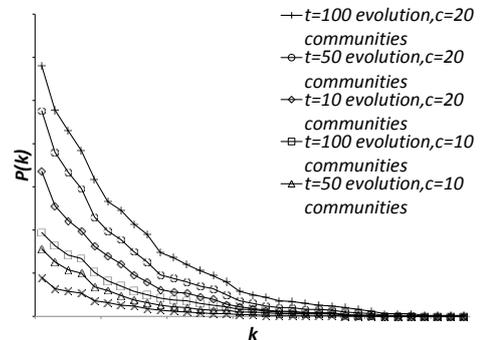


Fig. 5. Degree distribution of a complex network under different c and t .

Table I is the average degree and the average clustering coefficient of the Evolution network consisting of 10 hierarchical communities in Fig. 3.

As shown, the fluctuation range of both values is small, the average degree fluctuates around 8, the Average Clustering Coefficient fluctuates around 0.45, and the fluctuation range is associated with the initial state of the network.

Fig. 4 is the structure of the Evolution network consisting of 10 hierarchical communities when $t = 4010$. Therein the Maximum Degree is 39 and Minimum Degree is 2, the average Degree is 8.20, and the Average Clustering Coefficient is 0.433, after repeated evolutions, the community structure of the whole network is still definitely exists.

Fig. 5 shows the degree distribution of the above complex network under different c and t , where t represents the time number of evolution and c represents the number of communities in the network. According to the figure, the node degree distribution meets the power-law distribution. However, after a period of evolution, the curve trend slows and nodes with high connections gradually increase.

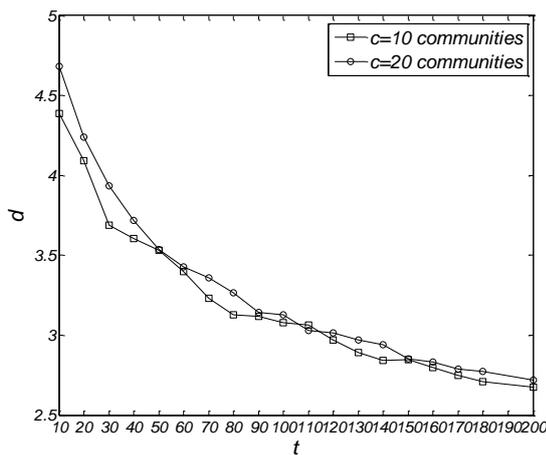


Fig. 6. Average path length variation trend of the network when $c = 10$ communities and 20 communities.

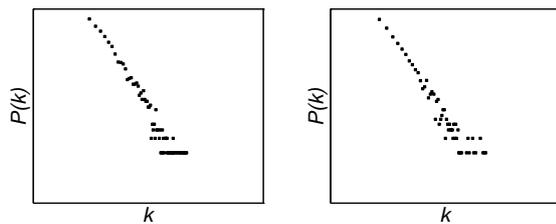


Fig. 7. Degree distribution comparison of our model on the left and Zheng's model on the right.

Fig. 6 shows the average path length variation trend of the network when $c = 10$ and 20. The evolutionary time is long, and the average path length of the network is short.

The network with more communities has a relatively larger average path length. After several tests, the average path length of the network stabilizes at approximately 1.9 when the number of evolutionary times is greater than 1000, indicating that the network has a stable average path length at this time.

Fig. 7 shows the Degree distribution comparison of our model and Zheng's model in [10], we can see that the distribution of the two models are independent of the network size and time asymptotic distribution.

From the above analysis, we know that our model conforms to the characteristics of small-world networks and scale-free networks. The results of several simulations revealed similar characteristics. The model has stability.

VI. CONCLUSION

The modeling of network structures is a problem long studied in the research on complex communication networks. A complex communication network model was established in this study based on the BA scale-free network model from the view of hierarchical community structures. A dynamic evolution network model was also established through the establishment of a new evolution rule of cellular automata. The simulation experiments revealed that the network exhibits power-law behavior

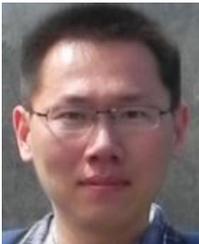
and has a clear, controlled community structure. The model can suitably describe the characteristics of complex network topologies. The proposed model extends the BA model and is consistent with actual abstraction and close to the evolution of the actual network. The model has certain stability and versatility and is easy to implement and extend.

In our future work, we will focus on how we can increase the weight of the edges and improve the efficiency of the model. In addition, more realistic constraint condition will be considered. The model is easy to implement and extend. We believe that the evolution model has tremendous potential on modelling the complex network based on hierarchical community structure. We hope that this new algorithm helps to uncover new interesting properties.

REFERENCES

- [1] D. J. Watts and S. H. Strogatz, "Collective dynamics of 'small-world' networks," *Nature*, vol. 393, no. 6684, pp. 440-442, 1998.
- [2] A-L. Barabási and R. Albert, "Emergence of scaling in random networks," *Science*, vol. 286, no. 5439, pp. 509-512, 1999.
- [3] R. Albert and A-L. Barabási, "Statistical mechanics of complex networks," *Reviews of modern physics*, vol. 74, no. 1, pp. 47-51, 2002.
- [4] P. L. Krapivsky, S. Redner, and F. Leyvraz, "Connectivity of growing random networks," *Physical review letters*, vol. 85, no. 21, pp. 4629-4632, 2000.
- [5] S. N. Dorogovtsev, P. L. Krapivsky, and J. F. F. Mendes, "Transition from small to large world in growing networks," *Europhysics Letters*, vol. 81, no. 3, pp. 30004, 2008.
- [6] S. N. Dorogovtsev, J. F. F. Mendes, A. M. Povolotsky, *et al.* "Organization of complex networks without multiple connections," *Physical review letters*, vol. 95, no. 19, pp. 195701, 2005.
- [7] G. Bianconi and A. L. Barabási, "Competition and multiscaling in evolving networks," *Europhysics Letters*, vol. 54, no. 4, pp. 436-442, 2001.
- [8] E. A. Peköz, A. Röllin, and N. Ross, "Degree asymptotics with rates for preferential attachment random graphs," *The Annals of Applied Probability*, vol. 23, no. 3, pp. 1188-1218, 2013.
- [9] Q. Sen and D. Guan-Zhong, "A new local-world evolving network model," *Chinese Physics B*, vol. 18, no. 2, pp. 383, 2009.
- [10] R. Dargazany, *et al.* "Network evolution model of anisotropic stress softening in filled rubber-like materials: Parameter identification and finite element implementation," *Journal of Mechanics of Materials and Structures*, vol. 7, no. 8, pp. 861-885, 2013.
- [11] Z. Meirong, L. Yuhua, X. Kaihua, and D. Wenwen, "Research on coupling coefficient of the scale-free network model," *Computer science in Chinese*, vol. 39, no. 5, pp. 66-68, 2012.
- [12] J. Jianzhi., L. Yuhua., L. T. Yang, N. Xiong, and F. Hu, "An efficient detecting communities algorithm with self-adapted fuzzy c-means clustering in complex networks," in *Proc. IEEE 11th International Conference on Trust, Security and Privacy in Computing and Communications*, Liverpool, 2012, pp. 1988-1993.
- [13] X. F. Wang and G. Chen, "Synchronization in scale-free dynamical networks: Robustness and fragility," *Circuits and Systems I: Fundamental Theory and Applications, IEEE Transactions on*, vol. 49, no. 1, pp. 54-62, 2002.

- [14] G. Chen, Z. P. Fan, and X. Li, "Modeling the complex Internet topology," in *Complex Dynamics in Communication Networks*, Springer Berlin Heidelberg, 2005, pp. 213-234.
- [15] L. Li, D. Alderson, J. C. Doyle, *et al.* "Towards a theory of scale-free graphs: Definition, properties, and implications," *Internet Mathematics*, vol. 2, no. 4, pp. 431-523, 2005.
- [16] WIKIPEDIA .The Free Encyclopedia: Cellular automaton. [Online]. Available: http://en.wikipedia.org/wiki/Cellular_automaton#wolfram
- [17] S. Wolfram, *A New Kind of Science*, Champaign: Wolfram Media, 2002.
- [18] Y. Kayama. (2010). Complex networks derived from cellular automata. *arXiv Preprint arXiv*. [Online]. Available: <http://arxiv.org/abs/1009.4509>



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