Information propagation in a novel hierarchical network

Feng Fu, Lianghuan Liu, Long Wang
Laboratory for Intelligent Control, Center for Systems and Control,
Department of Mechanics and Engineering Science,
Peking University, Beijing 100871, P. R. China

Abstract
A novel hierarchical model of complex network is proposed, and information propagation process taking place on top of the network is investigated. Our model is demonstrated to have small world property. We found that the frequency distribution of refractory elements number is bimodal and the location of initially chosen seed infection affects the spreading range of the information.

Keywords: complex networks, hierarchy, small world, SIR model, information propagation

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1 Introduction

The research in the realm of complex networks has been boosted spectacularly these years. The beauty of complex networks fascinates many scientists from different background to contribute to this issue [1, 2, 3, 4, 5]. Since the existence of random graph theory has been the important transition from regular lattices to irregular networks, the small-world (Watts-Strogatz) model and scale-free (Barbási-Albert) model have been the catalyst for the rise of interest of the whole scientific world. Meanwhile, the dynamical evolution of the networks (i.e. epidemic spreading in the networks, cascading failure of the power grid, cooperation in the networks and etc) has been also investigated. To our best knowledge, although the Watts-Strogatz (WS) and Barbási-Albert (BA) model could reflect some properties of real complex networks, both of them are not sufficient to elucidate the real networks. Recently, the generic features of hierarchical structure and self-similarity of complex networks shed light on development of novel models [6].

The literature related to networks is like booming mushroom after rain these years. Based upon Erdős and Rényi’s prominent work of random graph theory [7, 8], Watts and Strogatz first published their results about small-world phenomenon [9], which is first discovered by the sociologist Milgram [10]. And almost at the next year, Barabási and Albert unravelled the twist of real complex networks, such as World Wide Web, internet, scientific collaboration networks and etc. They discovered the scale-free topology of the real networks, namely, the degree distribution has power law tail—\( p(k) \sim k^{-\gamma} \). They also
Fig. 1: Hierarchical organizations in World Wide Web, which denote communities of web pages with common interests.

proposed an algorithm to generate such scale-free networks which composed of two factors: growth and preferential attachment [11]. After Barabási’s work, Krapivsky studied a class of growing random networks and found that a power law distribution of degree arises only for linear connection kernel [12]. Dynamical evolving processes in networks such as age, fitness, epidemic spreading, rumor, cooperation and so forth have also been investigated and some important results are obtained [13, 14, 15, 16].

Fundamental characteristics of real complex networks—small worlds and scale-invariant topology, are essential to existent network models. However, real networks are deviated from smooth simulation results obtained from these ideal models. For instance, the degree distribution of BA model obeys power law strictly, whereas most of real networks only have power law tails. Therefore, such discrepancy between models and empirical measurements is attributable to previously disregarded, yet generic feature of many real networks: their hierarchical topology. Along with hierarchy, most networks are modular: many small modules of highly connected nodes combine in a hierarchical manner into larger, less cohesive units, and modules build up into larger blocks and so on. In this way, modules are self-organized into hierarchical structures. Indeed, in the World Wide Web, web pages most link to the ones shared their common interests, and these interdependent communities develop into larger groups focusing on more general topics. In this sense, the WWW has its “core” which is composed of the most influential web sites, and this core generates plenty of subdivisions and so on (see Fig. 1). Accordingly, the WWW develops into the most huge networks in the world with hierarchical structures.

Although hierarchical structures of complex networks are investigated by many researchers, existent models which account for hierarchy are very few [17]. Barabási and his collaborators constructed a model of network which has hierarchical structure by iteration [18, 19]. Cellular metabolic networks are also demonstrated to have hierarchical organizations [20, 21]. However, hierarchical organizations are ubiquitous in real complex networks, for instance, social organizations or departments, the Internet at the domain level, hierarchical architecture of web pages, and etc. Recently, real networks are revealed that they commonly have fractal geometry patterns corresponding to tree and snowflakes, namely, self-similarity [22]. Consequently, it is necessary and meaningful to depict the complex networks from their hierarchical organization. Thus, this paper mainly deals with hierarchy, and proposes an alternative generating approach of complex networks.
Fig. 2: Illustration of typical hierarchical structures in complex networks, and the red lines are the long-range connections between nodes at different/same layers.

Research on epidemic in networks has received increasing attention since the inspiring work of Sudbury in random graph [23]. The problem of epidemic deals with whether an initially localized seed infection can spread to a substantial part of the network. The discoveries of small-world and scale-free networks model boost the studies of epidemic in these complex networks. The pioneering work of Pastor-Satorras and Vespignani found that there does not exist intrinsic spreading threshold for scale-free networks [24]. By contrast, there exits nonzero spreading threshold for the homogeneous and small world networks [25, 26]. The susceptible-infected-refractory(SIR) model has been widely used to understand the spreading process of virus (for example, transmission of influenza), rumor spreading and so forth [27, 28, 29, 30, 31]. Nevertheless, sometimes it is desirable to spread the “epidemic” quickly and effectively. Some typical examples are rumor-based protocols for data dissemination and resource discovery on the Internet and marketing campaigns using rumor-like strategies (viral marketing) [32]. Epidemic spreading process is also investigated under the different hierarchical network topologies [33, 34, 35].

In this paper, the information (rumor, news and facts) propagation on top of our hierarchical network is investigated by using SIR model. Once the ignorant gets a piece of information, there is a high possibility that he/she would like to spread the information to his/her neighbors in the network. By convenience, the spreading rate is set to be unit, which is the possibility that a susceptible individual is infected when contacted.

Our paper is organized as follows. Section II proposes the hierarchical network model and construction procedure; Section III discusses the SIR dynamics of information propagation on top of the network; Section IV gives out the simulation results, and some important conclusions are made in Section V.

2 Hierarchical Network Model and Construction Procedure

Considering the undirected graph, we start with $m_0$ nodes at the first layer, and each node connects to his distinct sons (not more than $m$) which belong to the next layer and repeat this procedure $l$ times, we obtain the skeleton. Such tree-like web is hierarchical, hub-cascading and not sufficient to reflect the complexity of real networks. However, despite the local links, additional long-range direct connections (shortcuts) between nodes should be necessary in order to make the average path short (see Fig. 2). So for nodes belonging to the same layer, connect to each other with possibility $p_{ij} = c_1 e^{-\alpha x_{ij}}$, where $\alpha > 0$ is tunable parameter and a measure of homophily—the tendency of like to associate with like and
$c_1 > 0$ is a normalizing constant. $x_{ij}$ is “social distance” of node $i, j$, i.e. the lowest height of their common ancestor. When $e^{-\alpha} \ll 1$, individuals will connect only to those most similar to themselves. Besides, nodes of lower layer would prefer to link to nodes of upper layers. Define the height of layers from top to bottom as $l_j, j = 1, 2, \ldots, l$ respectively. Node $k$ of $i$th layer links to node $n$ of $j$th layer with possibility $p_{kn} = \frac{l_j}{\sum_k l_k} e^{-\alpha x_{kn}}, (l_j > l_i)$. Given such connection kernel, individuals prefer to link to the nodes of higher layers and most similar to themselves. After addition of these shortcuts, a hierarchical network topology is obtained.

3 Dynamics of Information Propagation

Considering the information propagation process taking place on our hierarchical social networks, assume each node has three different states, analogously to SIR model in epidemiology: susceptible (S), infected (I), refractory (R). Node $i$ could only be in one of the three possible states at each time step of evolution. At the beginning, only one individual randomly chosen as seed obtains a piece of information and becomes infected. And all the remnant population is susceptible. The evolution rules act as follows [36]. At each time step, an individual $i$ is chosen at random from the infected population. This individual contacts one of his/her neighbors $j$. If $j$ is in the susceptible state, and it becomes infected. Otherwise, if $j$ is already infected or refractory, then $i$ becomes refractory. This progress continues until there are no longer infected individuals in the population. The time the whole process takes is the information lifetime $T$. For $t \geq T$, the number of refractory nodes $N_R$ represents the number of nodes that are infected in the network and acquire the information finally.

Qualitatively speaking, the dynamical process of information propagation could be summarized as follows. In the early stage of the evolution, the number of infected nodes increases and with lower rate, the refractory population grows as well. Consequently, the increasing contacts of infected nodes between themselves and with refractory ones results in the decline of infected population. At the end, the infected individuals vanish, and the population consists of a group of $N_R$ refractory individuals, who have been infected during the evolution and a group of susceptible ones who have never heard the information. In practice, the distribution $f(N_R)$ of the number $N_R$ of refractory nodes is usually investigated over a large number of realizations of the system evolution. Thus the average fraction $r$ of the refractory population could be calculated as $r = \langle N_R \rangle / N = N^{-1} \sum_{N_R=0}^{N} N_R f(N_R)$. This could be measurement of the influence of the information propagation on top of complex networks.

For homogenous networks (e.g. random networks), the analytical mathematical theory of SIR dynamics with unit spread rate suggests that the fraction $r$ approaches to a limit $r^*$ as the system size $N \to \infty$, where $r^*$ is the nontrivial solution of the transcendental equation: $r^* = 1 - e^{-2r^*}$, i.e. $r^* \approx 0.796$[23]. In other words, about 20% of the population would never have the chances to receive the information. For more complex networks, we have to rely on the numerical simulations to investigate the temporal behavior of the information propagation process.
4 Simulation Results

Statistical quantities of such hierarchical network are computed, namely, degree distribution, clustering coefficient and average path length.

In our simulations, $c_1 = 0.2$, $\alpha = 0.5$, $m = 6$, and the number of layers depends upon generating process, different numbers of nodes $N = 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000$ are computed respectively.

Our algorithm is as follows:

- step 1: $n_1$ nodes are selected as members of the first layer, where $n_1$ is a random number not more than $\frac{1}{100}N$;

- step 2: generate a random number $r$, which is the number of nodes of next layer. If $r > n_i^m$ or $r > N_{\text{left}}$, let $r = \min\{n_i^m, N_{\text{left}}\}$, where $n_i$ is the number of node of upper layer $i$, and $N_{\text{left}}$ is the number of unallocated nodes. And then stochastically find these $r$ nodes’ father in upper layer until every node finds their father, and every father has no more than $m$ sons;

- step 3: repeat this procedure until all nodes are allocated to corresponding layers;

- step 4: for nodes belonging to the same layer, each pair of individuals connect to each other with possibility $p_{ij} = c_1 e^{-\alpha x_{ij}}$;

- step 5: begin with nodes of the lowest layer, generate connections to nodes of upper layers with possibility $p_{kn} = \frac{l_i}{\sum l_i} e^{-\alpha x_{kn}}$ until nodes of every two layers have been linked with the possibility function.

Clustering coefficient $C(N)$ is defined as the average clustering coefficient $C_i$ of each node $i$, and $C_i = \frac{2E_i}{k_i(k_i-1)}$, where $k_i$ is the degree of node $i$, and $E_i$ is the number of existent links between its $k_i$ nearest neighbors. Average path length is the average length of all existent connections between pairs of nodes. Diameter of the graph is the maximum path length of pairs of connected nodes. The following table is the summary of simulation results.

| Number of Nodes | Clustering Coefficient | Average Path Length | Diameter |
|-----------------|------------------------|---------------------|----------|
| 1000            | 0.297                  | 4.2                 | 11       |
| 2000            | 0.180                  | 3.1                 | 11       |
| 3000            | 0.191                  | 4.3                 | 12       |
| 4000            | 0.153                  | 3.5                 | 9        |
| 5000            | 0.131                  | 3.6                 | 12       |
| 6000            | 0.130                  | 3.4                 | 10       |
| 7000            | 0.137                  | 3.4                 | 18       |
| 8000            | 0.116                  | 2.9                 | 12       |
| 9000            | 0.145                  | 2.7                 | 15       |
| 10000           | 0.135                  | 3.2                 | 16       |
| 15000           | 0.100                  | 3.5                 | 15       |
| 20000           | 0.137                  | 3.9                 | 17       |
| 25000           | 0.079                  | 3.0                 | 11       |
| 30000           | 0.083                  | 2.7                 | 11       |
Our simulation results demonstrate that our hierarchical network has small world property, as the average path length is considerably short, compared to the same size of random graph. Furthermore, the clustering coefficient is also relatively high, which means that such network has small worlds phenomenon. Meanwhile, the long-range connections between nodes are essential to make the network searchable, i.e. short average path length. Equivalently, our hierarchy network has good searchability.

From the Fig. 3, our simulation results indicate that the clustering coefficient depends on the system size as $C(N) \sim N^{-0.32}$, which is significantly larger for large $N$ than the random network prediction $C(N) \sim N^{-1}$. Indeed, many real networks have the same property as our model. Yet, degree distribution of our model does not follow the power law.

Concerning the information propagation process on top of our hierarchical network, we make some slight variations of the simulated network model in order to reveal more new phenomena because of the hierarchical topology, other than singularity of the structure. Firstly, the node number of the first layer is not more than $1/1000$ of the total population. Secondly, exception for the nodes of the lowest layer, every node has constant $m$ sons which belong to the next layer. And also the situation that $m$ is subject to a uniform gaussian distribution is considered. Thirdly, node $i$ connects to the other node $j$ belonging to the same layer with probability $p_{ij} = c_1 e^{-\alpha x_{ij}}$, and links to his ancestor $j$ in upper layers with probability $p_{ij} = \frac{i_j}{\sum_k i_k}$. 

The information propagation process was performed by using SIR model as above instructions. The initial condition was that randomly chosen individual got a piece of information and became “infected” (spreader). He/she would spread the information to his/her “susceptible” (ignorant) neighbors until he/she became “refractory” (stiffer). Fig. 5 shows the information propagation process with population $N = 1000$. The fraction of infected individuals $i(t)$ increases faster than the fraction of refractory individuals $r(t)$ in the beginning. Then $i(t)$ decreases to zero at the end of evolution. The fraction of refractory population is 79.4% when the information propagation process terminates. Accordingly, there are still 20.6% of the total population who never acquire the information through their neighbors.

One of the important practical aspects of information propagation is whether or not it could reach a high number of individuals. Hence, we have studied the distribution of the number $N_R$ of R elements at the end of evolution. Fig. 6 shows the normalized frequency $f(N_R)$ obtained from series of $10^4$ realizations for large $N_R$ with system size $N = 10000$, $m = 32$. Most of the $N_R$ falls into the large-$N_R$ structure, whereas very few $N_R$ is in the neighborhood of zero. In Fig. 6 only one point is adjacent to zero. Therefore, we could conjecture that this particular distribution $f(N_R)$ is attributable to the network’s hierarchical topology. To investigate more details about the effect of the network topology on information propagation, different initial conditions are considered. Different groups of realizations corresponding to the layers are conducted as follows: for each group of realizations, the initially selected at random infected individual always belongs to the
same layer. Figure 6 shows the distribution $f(N_R)$ over $10^4$ realizations with the initially infected node in the first layer. Obviously, here the distribution $f(N_R)$ is bimodal, with a maximum close to $N_R = 0$ and an additional bump for larger $N_R$. For small $N_R$ near zero, the frequency follows a power law, $f(N_R) \sim N_R^{-\alpha}$ ($\alpha \approx 3$). Contributions to this zone of the distribution result from realizations where propagation ceases before a shortcut is reached. Howbeit, $f(N_R)$ approximately obeys gaussian distribution for large $N_R$. In a typical realization contributing to this area of the distribution, large quantity of contacts occur through shortcuts and a finite portion of the population becomes infected.

Our simulation results show that the positions of initially randomly selected individual significantly affect the spreading range of information. When chosen individual belongs the lower layer, the distribution $f(N_R)$ has more points falling into the large-$N_R$ structure (see Fig. 7, for the initial individuals lying in the third layer, almost all of the points consist of the gaussian distribution). The average fraction of refractory individuals $r$ over large number of realizations is computed. With system size $N = 10000$, $m = 8$, the hierarchical network realization has 5 layers. The fractions $r$ corresponding to each layer are 77.21%, 77.91%, 78.34%, 78.27%, 78.28% respectively. We found that the discrepancies of the spreading range are remarkable when initially selected nodes belong to different layers. Thereby, the hierarchical topology intrinsically affects the shape of distribution function $f(N_R)$ (see Fig. 6, 7 for comparison).

Additionally, taking account for slight variation of the hierarchical topology, i.e. $m$ is not constant for each node, but subject to a uniform gaussian distribution. The reason why this regime is adapted is to investigate whether or not irregularity of the hierarchy would affect the information propagation. Fig. 8 shows that the frequency distribution of $N_R$ by using the initial condition that the randomly chosen node to be infected lies in the first layer (In this realization, there are total 8 layers). The distribution is similar to the case where $m$ is constant. The distribution of small $N_R$ near zero also follows power law (see Fig. 8 $\alpha \approx 2.86$), whereas the large-$N_R$ structure approximately obeys gaussian distribution. As well as the situation that $m$ is constant, along with the initially infected individual falling into the lower layers, the number of data points near the zero decreases.

In other words, the spreading range of the information increases as the initially selected node lies in the lower layers. In this case, the average fractions according to each layer are 67.52%, 70.17%, 74.99%, 78.24%, 78.94%, 78.98%, 78.98%, 75.23% respectively.

Our simulations results also demonstrate that the possible maximum fraction of $R$
Fig. 5: The insert shows frequency distribution $f(N_R)$ of $N_R$ over $10^4$ realizations. System size is $N = 10000$, $m = 32$. Gaussian fit of the data shows that for large $N_R$, $f(N_R)$ approximately follows a gaussian distribution.

Fig. 6: The frequency distribution $f(N_R)$ over $10^4$ realizations with initially infected individual belonging to the first layer. System size $N = 10000,m = 8$. The lower insert shows the $N_R$’s distribution near zero and the upper insert is the corresponding plot on logarithmic scale, where the red line is linear fit.

Fig. 7: The large-$N_R$ structure. The insert shows the frequency distribution $f(N_R)$ over $10^4$ realizations with initially infected individuals belonging to the third layer. System size $N = 10000,m = 8$. 
Fig. 8: The plot of the situation that $m$ is subject to gaussian distribution over $10^4$ realizations. The left insert shows the detailed plot of the distribution near the zero on logarithmic scale. The red line is linear fit of which slope is about -2.86. And the right shows the large-$N_R$ structure which is approximately a gaussian distribution. The system size is $N = 20000$. The mean value $\mu$ of $m$ is 8, and the standard deviation $\delta$ is 2.

Figure 9: Plot of the $N_R$ distribution with the initial infection lying in the 6th layer. The other initial conditions are the same as Fig. 8.

individuals in the end of evolution depends upon the position of the initially infected individual in the hierarchical network. When the initially selected individual belongs to a certain intermediate layer, the maximum spreading range of the information would be achieved.

5 Conclusion

In conclusion, the top layer of our model could be illustrated as the core of real networks, for instance, the most popular web sites. The model we propose in this paper has nontrivial properties: it has short average path length and high clustering coefficient, i.e. small world property; average clustering coefficient depends on system size. From these two respects, our preliminary model might be enlightening to reveal mechanism of complex networks, and reflects characteristics of real networks. Besides, the information propagation on top of our hierarchical network is investigated by using SIR model. It is observed that distribution $f(N_R)$ is bimodal: for small $N_R$ near the zero, it follows power
law whereas for large \( N_R \), it is approximately a gaussian distribution. We also found that the spreading range approaches to maximum when the initially chosen individual is in a certain intermediate layer. Our simulation results indicate that the optimal strategy to spread the information efficiently is to make the individuals belonging to the intermediate layers obtain the information and would like to spread it to her/his neighbors. It is also helpful to develop methods to control the information propagation in networks. For example, to prevent the rumor from mongering. Besides, our results demonstrate for a generic realization, the fraction of population who obtain the information is less than the limit of fraction of \( R \) individuals. Namely, there are always ignorant individuals who are not aware of the information. As a result, it is also significant to develop novel propagandistic strategy to make almost everyone acquire the information.

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