
Dynamic diffusion in evolutionary optimised networks

Takanori Komatsu* and Akira Namatame

Department of Computer Science,
National Defense Academy,
Hashirimizu 1-10-20, Yokosuka-shi, Kanagawa-Pref, 239-8686, Japan
Fax: +81-46-8445911
E-mail: ed10004@nda.ac.jp
E-mail: nama@nda.ac.jp
*Corresponding author

Abstract: Diffusion is the process by which new products and practices are invented and successfully introduced into a society. This paper presents a possible explanation of this phenomenon in terms of a network of interacting agents whose decisions are determined by the action of their neighbours according to a probabilistic model. It is known that the maximum eigenvalue of the network decides a tipping point of a diffusion process by probabilistic model. The network with large maximum eigenvalue is susceptible to a diffusion process. Evolutionary optimisation is used to make the network in which the diffusion process will start more early than in other networks. Two properties are identified in which the network is suitable for fast diffusion. These are a power law of degree distribution and the phenomena in which hub nodes are connected very densely, it is called a rich-club phenomena. Finally, the results of numerical diffusion simulation are compared with other network topology to verify the performance of evolutionary optimised networks.

Keywords: diffusion of innovations; threshold of diffusion; evolutionary design.

Reference to this paper should be made as follows: Komatsu, T. and Namatame, A. (2011) 'Dynamic diffusion in evolutionary optimised networks', *Int. J. Bio-Inspired Computation*, Vol. 3, No. 6, pp.384–392.

Biographical notes: Takanori Komatsu holds a Bachelor of Science in Electrical and Electronic Engineering at Tokyo University of Agriculture and Technology in Japan and Master of Science in Computer Science and Engineering at National Defense Academy of Japan. Currently, he is doing his PhD in Computer Science at National Defense Academy of Japan. His research interests include network design, network security and multi-agents.

Akira Namatame is a Professor of Department of Computer Science National Defense Academy of Japan. He holds a degree of Engineering in Applied Physics from National Defense Academy, Master of Science in Operations Research and PhD in Engineering-Economic System from Stanford University. His research interests include multi-agents, game theory, evolution and learning, complex networks, economic sciences with interaction agents and a science of collectives. He is a member of the AAI, IEEE, and SICE.

1 Introduction

For decades, social scientists, economists and physicists have been interested in the fundamental and widespread question of how infectious diseases, new technological practices, or the latest trends spread into a society (Arthur, 1989).

The main study on the diffusion process is based on the Bass (1969) model. The Bass diffusion model describes the process by which new products are adopted as an interaction between users and potential users, who do not adopt yet. More specifically, the Bass model formalises the aggregate level of penetration of a new product, emphasising two processes: external influence via advertising and mass media and internal influence via word-of-mouth. The

decision of a consumer is described as the probability of the consumer adopting the new product at a specific time, and it is assumed to depend on both external and internal influences. The Bass model displays a cumulative S curve of adopters: when the number of users of a new product is plotted against time. The resulting curve shows an S-shaped distribution, which means adoption proceeds slowly at first, accelerates as it spreads throughout the potential adopting population, and then slows down as the relevant population becomes saturated.

The S-shape is a natural implication of the observation that adoption is usually an absorbing state. The fast growth of diffusion is generated by the interaction between early adopters and late adopters. The Bass model, however, does

not specify the consumer decision-making process or how consumers communicate with, and influence others at the micro level. The Bass model also assumes the population of consumers to be homogeneous. Therefore, such diffusion models are referred to as aggregate models.

Rosenberg and Nathan (1972) observed two dominant characteristics of the diffusion process: the overall slowness of the process, on one hand, and the wide variations in the rates of acceptance of different inventions on the other hand. Empirical measurement and study have since confirmed his view. Why is diffusion sometimes slow? Why is it faster in some regions than others? Why do rates of diffusion differ among different types of innovations? What factors govern the wide variation in diffusion rates? Hall (2004) provides a comparative historical perspective on diffusion that looks at the broad economic, social, and institutional determinants.

Our recent paper shows one solution to design a network which has a low threshold for early diffusion by using evolutionary optimisation (Yamamoto et al., 2010). The aim of this paper is to evaluate how our solution works well quantitatively by being compared with other network topology and simulating diffusion process on those networks. Topological analysis is also done to understand how evolutionary optimised network is formed because it is essential, in the further work, to make a network model which enables us to make optimised networks more efficiently.

In the modern world, markets occasionally accept innovations very slowly, despite many technological advances (Chakravorti, 2003). In recent years, the progress of study in complex network expands our knowledge about the property of existing social networks (Barabasi and Albert, 1999). Some social networks show that few agents have chances to communicate with many other agents. However, many agents are directly connected with a small number of other neighbours, colleague, friends, or family. This type of heterogeneity between agents suggests the difference of diffusion speed in each region over networks, resulting in the slow pace of diffusion at the macro-level.

Important processes that take place within social networks, such as the spreading of opinions and innovations, are influenced by the topological properties. Here, each node of the network represents a dynamical system. Individual systems are coupled according to the network topology. Thus, the topology of the network remains static while the states of the nodes change dynamically. Important processes studied within this framework include synchronisation of the individual dynamical systems and contact processes, such as opinion formation and information diffusion. These studies have clarified that certain topological properties have strong impacts on the diffusion process on networks (Ball, 2004).

In recent years, motivated by applications to marketing, the result of diffusion study is not only used for predicting how well the new product or innovation will be adopted, but also is used for creating optimised network for diffusion. For example, many corporations make special portal site or fun site to make good communication network when they

produce new products. Such websites make word-of-mouth community, consisting of people who are adopters for same products regardless of their real-life location. For long times, consciously or unconsciously, people try to find optimal network topologies for diffusion of products or information. As a result, in our life, there are many types of network topologies such as hierarchical or scale-free networks. We are motivated by this demand to get good network for diffusion. This paper investigates what kind of networks is good for diffusion based on the contact process by many agents. In many studies about diffusion process, agents are represented by nodes (or vertices) and communications between nodes are represented by links (or edges). And any graph (or network) G can be represented by its adjacency matrix, $A(G)$, which is a real symmetric matrix. The element of a matrix $A(G)$ in the i^{th} row and the j^{th} column is expressed as a_{ij} . If $a_{ij} = 1$ node i and node j are connected, and $a_{ij} = 0$, if these two nodes are not connected. Adjacency matrix is often used as a good tool to manipulate and investigate the networks. The spectrum of a graph is the set of eigenvalues of $A(G)$. Wang et al. (2003) suggest the maximum eigenvalue of the adjacency matrix is closely related to the spreading power on networks. The network with a larger maximum eigenvalue helps faster spreading on the network. However, the spectrum of network does not decide network topology, thus we should know optimised network topology for diffusion.

In this paper, using an evolutionary algorithm, we obtain the optimised network for diffusion with a large maximum eigenvalue and a low average degree. Maximum eigenvalue means ease of diffusion. The aim of this paper is also to understand how the network topology determines the diffusion dynamics occurring on various network topologies. We evaluate the diffusion performance of the optimised network by comparing with Erdos and Reny (ER) random network and Barabasi and Albert (BA) scale-free network.

The network on ER model is symmetric network, so there is no centre and end node in the network. The distribution of number of links on each node (also called the degree) obeys a Poisson distribution. It means consumers on ER model can communicate with others randomly over the network. The network on BA model is very asymmetric, and the degree distribution obeys power law. It means consumers on BA model can communicate with other nodes via hub nodes, nodes with many links.

2 Diffusion models

Among research concerning various diffusion processes, the diffusion of diseases has received the most attention (Colizza et al., 2006). The information diffusion process can be viewed as like the viral propagation in which virus spreads on contact process between individuals (Dodds and Watts, 2004).

In the study of viral propagation, two major diffusion models are well studied. These are SIR model and SIS

model. In SIR model, the population is classified into three categories, susceptible (S), infected (I) and removed (R). The difference between SIR model and SIS model is infected (or informed) people is removed from the population with the probability δ in the SIR model. The removed people do not communicate with other people after that.

In the SIS model, the population is classified into two categories, susceptible (S) and infective (I). A susceptible person is changed into an infected person by other infected persons with some probability β . The infected person becomes susceptible again with the probability δ .

The SIR model can be represented as

$$\begin{aligned} \frac{dS}{dt} &= -\beta IS \\ \frac{dI}{dt} &= \beta IS - \delta I \\ \frac{dR}{dt} &= \delta I \end{aligned} \tag{1}$$

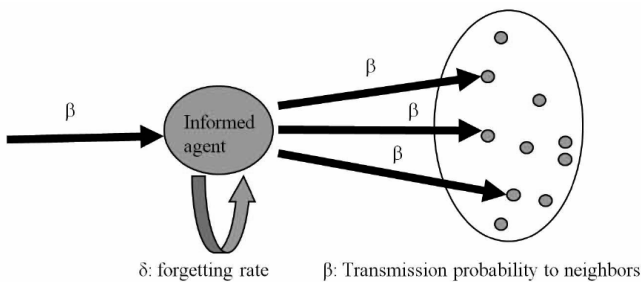
On the other hand, the SIS model can be represented as

$$\begin{aligned} \frac{dS}{dt} &= -\beta IS + \delta I \\ \frac{dI}{dt} &= \beta IS - \delta I \end{aligned} \tag{2}$$

The network with high link density and small variance between populations meets the homogeneous assumption. However, many real network does not meets the homogeneous model assumption. In many networks, the number of contactable nodes of each node is restricted to some extent by the network regulation, and we should consider the effect of the network topology on the diffusion process.

In this paper, we view the information propagation as a dynamical birth-death process with self-recovery using the SIS model, as shown in Figure 1. An informed agent propagate the information to adjacent agent j in a single step with probability β , while at the same time an informed agent may forget or lose interest with probability δ . The ratio of the two factors β / δ is defined as the relative diffusion rate of the contact process.

Figure 1 Diffusion on networks



3 Evolutionary optimised networks

Network topologies are often not static. The creation of link between new added node and existed node makes global law like power law behaviour in the internet (Barabasi et al., 2000). The application on networks also changes and evolves network topology. We can observe some aspects of network optimisation in transport network, power grid network, the internet and so on. In this paper, we obtain an optimised network for information diffusion, which has a large maximum eigenvalue, as a result of accumulation of little improvement under pressure to reduce the number of links, by using genetic algorithm (GA).

3.1 Modelling of diffusion process

Any graph (network) G can be represented by its adjacency matrix $A(G)$, which is a real symmetric matrix, $a_{ij} = a_{ji} = 1$, if nodes i and j are connected, or 0, if these two nodes are not connected.

The diffusion process by probabilistic model is we denote the probability that agent i aware the information at time t as $p_i(t)$. The column vector $p(t) = (p_1(t), p_2(t), \dots, p_N(t))$ represents the set of awareness probabilities of the whole agents in the population. The transition of the awareness probabilities are described as

$$p(t+1) = (\beta A + (1 - \delta)I) p(t) \tag{3}$$

where I is a $N \times N$ identity matrix. The long-run behaviour of the above system is determined by the structure of the system matrix, $S = \beta A + (1 - \delta)I$. Wang et al. (2003) proved that the spectral of the system matrix S (the distribution of eigenvalue of S) is closely related to the spectral of the adjacency matrix A , and we have equation (4).

$$\lambda_i(S) = \beta \lambda_i(A) + 1 - \delta \quad i = 1, 2, \dots, N \tag{4}$$

where $\lambda_i(S)$ is the i^{th} maximum eigenvalue of the system matrix S . The maximum eigenvalue is denoted as $\lambda_1(S)$ which is also called the principal eigenvalue of the system matrix. The eigenvalue of the system matrix S can be explained by the eigenvalue of adjacency matrix A . If the $\lambda_1(S)$ satisfies of equation (5), $p(t)$ in equation (3) converges to the zero vector.

$$\lambda_1(S) < 1 \tag{5}$$

From equation (4) and equation (5), we obtain a relational expression in equation (6) that is if the inverse of $\lambda_1(A)$ is greater than the relative diffusion rate β / δ , then $p(t)$ converges to the zero vector.

$$\frac{\beta}{\delta} < \frac{1}{\lambda_1(A)} \tag{6}$$

From equation (6), the diffusion process is characterised as the threshold phenomenon, and the diffusion process start if the relative diffusion rate β / δ is greater than the threshold $1 / \lambda_1(A)$.

Therefore, there are two strategies to accelerate diffusion through a society. One is exploiting the network topology G to increase maximum eigenvalue. Another one is promoting the information to have the relative high diffusion ratio β / δ .

3.2 Definition of the fitness function

We take two factors into consideration to design an optimal networks. One is the maximum eigenvalue of the associated adjacency matrix. This factor determines a threshold for diffusion on the network. The diffusion process will start at lower relative diffusion rate (β / δ) on the network with large maximum eigenvalue. The other factor is the number of link. In many cases, the network with a lot of links has a good performance. For example, in the case of the airway network, if every airport is directly connected by an airline, travel time will be reduced drastically. In the case of the computer network, if every host is connected directly by a communication link, the congestion may not happen.

However, these situations are not realistic, since the resources for network is usually finite in many situations. The number of links usually represents the link cost for designing an optimal network.

Therefore, we evaluate a given network by maximum eigenvalue $\lambda_1(A)$ with average degree $\langle k \rangle$, which is associated with the number of links L ($\langle k \rangle = 2L / N$, where N denotes the number of nodes.).

We define the fitness function to minimise as follows:

$$E = \omega \frac{1}{\lambda_1(A)} + (1 - \omega) \frac{\langle k \rangle}{N - 1} \quad (7)$$

where $\omega(0 \leq \omega \leq 1)$ is a parameter controlling the linear combination of the inverse of $\lambda_1(A)$ and $\langle k \rangle / (N - 1)$. The minimisation of E means the maximisation of the largest eigenvalue as well as the average degree. Here, we are interested in only the connected graph, the average degree of the network $\langle k \rangle$ has a value from $2(N - 1) / N$ to $N - 1$. To make a balance of the range of value between two terms in equation (7), the average degree is normalised by $N - 1$.

4 Effects of network topologies for better diffusion

It is very simple question, ‘What kind of the network topology is best for diffusion process?’. The simple answer is complete graph with the largest eigenvalue $\lambda_1(A) = N - 1$, in which each node is connected to every other node. However, it is not realistic to make complete graph as the size of network grows. It takes a lot of costs to set and keep links between nodes. Therefore, many networks in our life, for example, social network, railway network and neuron network adjust balance between the performance of the network and the number of links.

Let G be a connected graph on N nodes with L links. The maximum degree and spectral radius are denoted by

d_{\max} and $\rho(G) = \max | \lambda |$ respectively. The simplest bound for $\rho(G)$, is

$$\rho(G) \leq d_{\max} \quad (8)$$

A bound in terms of the numbers of nodes and links only is found by Hong (1988).

$$\rho(G) \leq \sqrt{2L - N + 1} \quad (9)$$

From equation (9), large number of links is necessary to design network with large maximum eigenvalue.

We obtain an optimised network by using GA MGG (Sato et al., 1997). The object of our design is to make the network which has large maximum eigenvalue with small number of links which we regard as costs to make network. In other words, we want to discover a new network topology, which has larger maximum eigenvalue comparing to other network topologies which have same the number of links.

The GA is a meta-heuristic algorithm. We use the adjacency matrix of the network as chromosome. The parameter on GA MGG is shown in Table 1. In this way, we design optimised network for diffusion process by varying parameter $\omega(0 \leq \omega \leq 1)$ on equation (7).

Table 1 Parameters for GA

Genetic algorithm model	Minimum generation gap model (Sato et al., 1997)
Initial population size	100
‘Child’ population size	100
Objective function	$E = \omega \frac{1}{\lambda_1(A)} + (1 - \omega) \frac{\langle k \rangle}{N - 1}$
Crossover	Uniform crossover
Mutation	Not used
Selection	An elite selection strategy
The number of evaluations	Over 600,000

If we have infinite resource to make network, we need not to care the number of links. Then we set $\omega = 1$ in equation (7). Then fitness function in this case becomes the following equation.

$$E = \frac{1}{\lambda_1(A)} \quad (10)$$

The optimal network with the fitness function equation (10) has a largest maximum eigenvalue $N - 1$ with the average degree $N - 1$.

By setting $\omega = 0$ in equation (7), the fitness function becomes as follows:

$$E = \frac{\langle k \rangle}{N - 1} \quad (11)$$

The network optimised under the fitness function equation (11) has a tree structure with average degree close to $2(N - 1) / N \approx 2$.

5 Topological properties of evolutionary optimised networks

Figure 2 shows the comparison of the maximum eigenvalue between optimised networks using GA by changing ω in equation (7) (We plot the average value over 10 run.), random networks and scale-free network with same and similar average degree, and optimised network has much larger eigenvalue compared with those of random networks and scale-free networks.

Let T be the ratio of maximum eigenvalue of optimised network $\lambda_{\text{optimised}}$ to that of random network λ_{random} which has same average degree, as shown in equation (12).

$$T = \frac{\lambda_{\text{optimised}}}{\lambda_{\text{random}}} \tag{12}$$

Figure 2 Maximum eigenvalue vs. average degree for GA-constructed networks, $\omega = (0.1, 0.2, \dots, 0.9)$, for random network with the same average degree, and for a scale-free network (average degree 5.96)

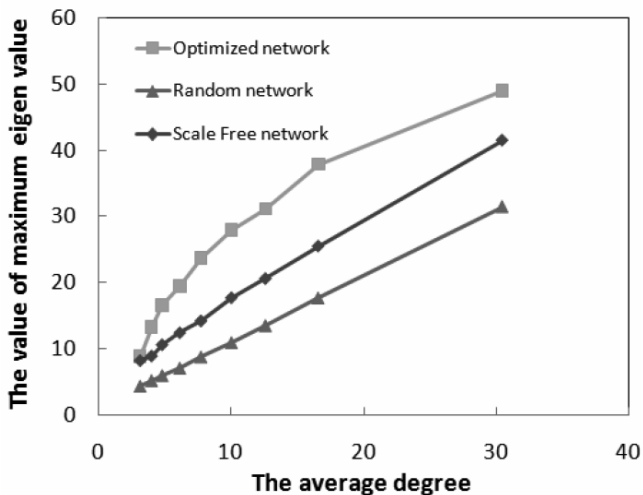
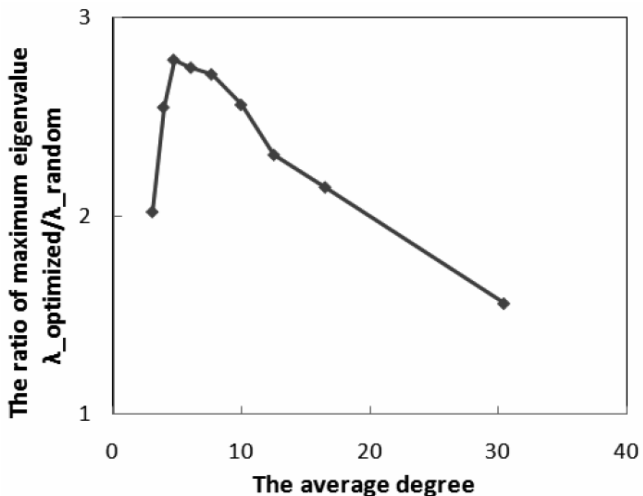


Figure 3 Ratio T of maximum eigenvalue of optimised network to random network with the same average degree



Note: At average degree $\langle k \rangle = 4.8$ ($\omega = 0.3$), the ratio T has most high value (= 2.8).

At $\omega = 0.3$ in equation (7), the optimised network has 4.8 average degree and the highest ratio $T = 2.8$, as shown in Figure 3. It means at $\omega = 0.3$, our GA method provided most meaningful result compared with at other conditions in terms of a network with larger maximum eigenvalue.

Now we have new question, ‘What a kind of topology does our GA method produce as best?’. In other words, the question is ‘How nodes in optimised network are connected by links?’. We show some insights to answer this question.

Figure 4 shows a visualisation of the optimised network topology at $\omega = 0.3$ in equation (7). It is basic method to understand how nodes are connected by links. However, we cannot see the structure of the network from Figure 4, since there is very dense core in optimised network.

Figure 4 The snapshot of optimised network (300 nodes, 716 links)

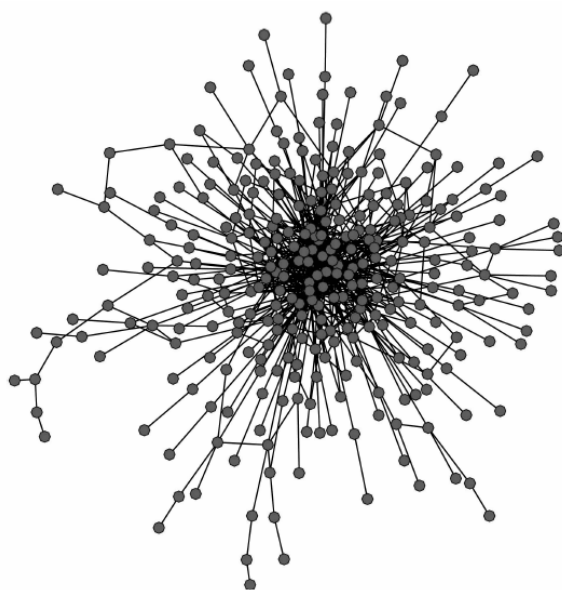


Figure 5 Fraction of nodes vs. hop distance from a node with largest degree for a GA-constructed network ($\omega = 0.3$) (300 nodes, 716 links), for a random network with the same average degree and for a scale-free network (300 nodes, 894 links)

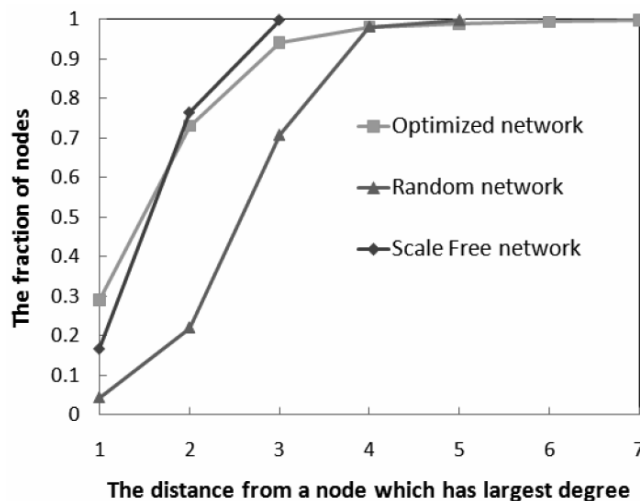


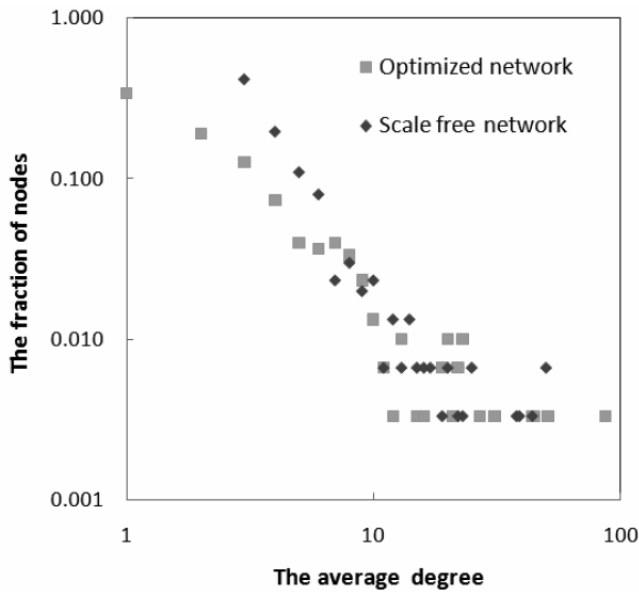
Figure 5 shows where nodes are distributed on each networks of Table 2. As shown, on optimised network and scale-free network, the over 90% nodes are within three hop distance from a hub node which contains most number of links.

Figure 6 shows the degree distribution of optimised network seems to be power law like a scale-free network. This means the optimised network is heterogeneous and has hub nodes in it.

Table 2 The property of network property 1

	Optimised network at ($\omega = 0.3$) in equation (11)	Scale- free network	Random network
The number of node	300	300	300
The number of link	716	894	716
The average distance	3.6	3.0	3.8
The number of average degree	4.8	6.0	4.8
The maximum eigenvalue of adjacency matrix	17	12	6

Figure 6 The degree distribution for a GA constructed network ($\omega = 0.3$) (300 nodes, 716 links) and for a scale-free network (300 nodes, 894 links)

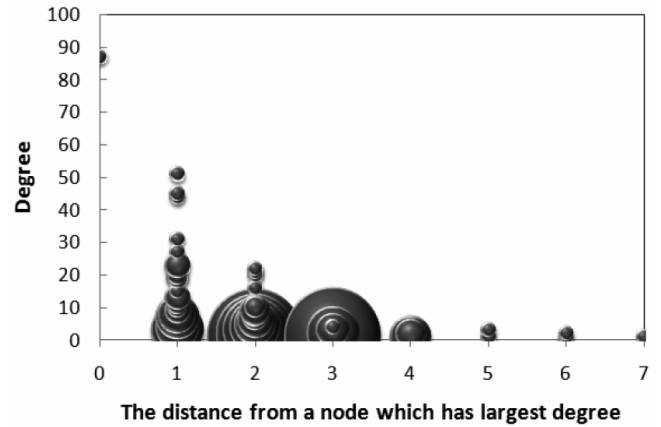


Figures 7 to 9 show degree of nodes vs. the location of nodes (the hop distance from a largest hub node) on the each network of Table 2. Although optimisation process started from random networks in which the location of hub nodes is homogeneous, hub nodes in optimised network are located around the largest hub node like scale-free network.

Figure 10 shows the rich-club connectivity (Zhou and Mondragón, 2004). The rich-club connectivity is characterised by the interconnection between hub nodes. It gives us good insights to understand network topology. In this paper, we obtained rich-club connectivity as follows. In the paper (Zhou and Mondragón, 2004), nodes are divided

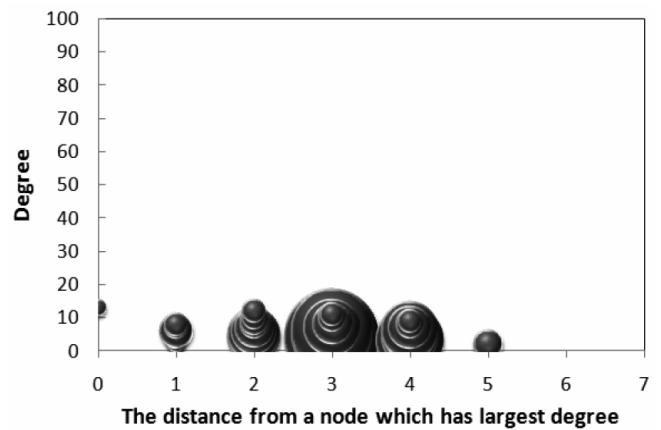
to groups by same number of links and look at interconnectivity between groups. However, in this paper, nodes in the network are sorted by decreasing number of links that each node contains and look at interconnectivity between nodes. The node rank r denotes the position of a node on this ordered list. r is normalised by the total number of nodes N .

Figure 7 Degree vs. the number of nodes against hop distance from a node with largest degree for a GA-constructed ($\omega = 0.3$) (300 nodes, 716 links)



Notes: The size of each circle is in proportion to the number of nodes. The size of circle at 0 distance means there is one node with about 90 degrees.

Figure 8 Degree vs. the number of nodes against hop distance from a node with largest degree for a random network (300 nodes, 716 links)



Notes: The size of each circle is in proportion to the number of nodes. The size of circle at 0 distance means there is one node with 13 degrees.

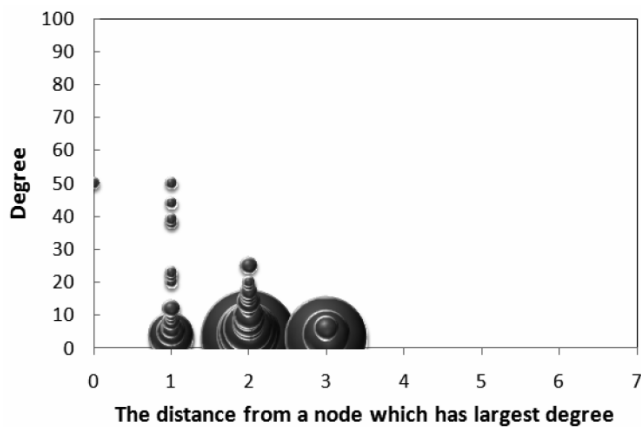
The rich-club connectivity $\phi(r)$ is defined as the ratio of the total actual number of links $L(r)$ to the maximum possible number of links between members of the rich-club ($n(r)$ nodes), as shown in equation (13).

$$\phi(r) = \frac{L(r)}{n(r)C_2} \quad (13)$$

As an example, we obtained the rich-club connectivity $\phi(r)$ of optimised network at $\omega = 0.3$ in equation (11) and

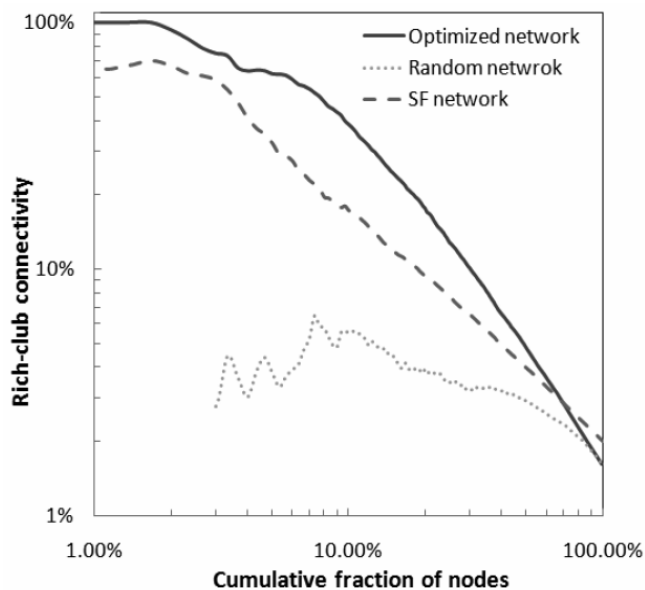
compared it to both scale-free network and random network in Table 2.

Figure 9 Degree vs. the number of nodes against hop distance from a node with largest degree for a scale-free network (300 nodes, 894 links)



Notes: The size of each circle is in proportion to the number of nodes. The size of circle at 0 distance means there is one node with 50 degrees.

Figure 10 Rich club connectivity of networks in Table 2



Note: We have plotted rich club connectivity (link density) against cumulation fraction of nodes, which are sorted by decreasing number of links that each node contains.

Figure 10 shows the rich-club connectivity $\phi(r)$ against cumulative fraction of nodes r on a log-log scale. As shown, rich nodes of the optimised network by GA are very well connected between each other. The top 10% rich nodes in optimised network have 38.6% of the maximum possible number of links, compared with $\phi(r = 10\%) = 17.2\%$ in scale-free network, although scale-free network has more 178 links than other network, and only $\phi(r = 10\%) = 5.5\%$ of random network.

Table 3 Table of network property 2

	Optimised network at ($\omega = 0.4$) in equation (11)	Scale-free network	Random network
The number of node	300	300	300
The number of link	917	894	917
The average distance	3.3	3.0	3.3
The number of average degree	6.11	6.0	6.1
The maximum eigenvalue of adjacency matrix	19	12	7

Table 4 Comparison between diffusion thresholds of networks in Table 2

Network topology	Threshold expression	Threshold transmission rate β at $\delta = 0.1$	Score = $\frac{\beta}{\delta} / \frac{1}{\lambda_1(A_{\text{optimised}})}$
Optimised network at ($\omega = 0.3$) in equation (11)	$\frac{1}{\lambda_1(A_{\text{optimised}})}$	0.0060	1
Scale-free network	$\frac{\langle k \rangle}{\langle k^2 \rangle}$	0.0079	1.3
Random network	$\frac{1}{\lambda_1(A_{SF})}$	0.0085	1.4
Random network	$\frac{1}{\langle k \rangle}$	0.021	3.5
Random network	$\frac{1}{\lambda_1(A_{\text{random}})}$	0.0168	2.8

Table 5 Comparison between diffusion thresholds of networks in Table 3

Network topology	Threshold expression	Threshold transmission rate β at $\delta = 0.1$	Score = $\frac{\beta}{\delta} / \frac{1}{\lambda_1(A_{\text{optimised}})}$
Optimised network at ($\omega = 0.3$) in equation (11)	$\frac{1}{\lambda_1(A_{\text{optimised}})}$	0.0051	1
Scale-free network	$\frac{\langle k \rangle}{\langle k^2 \rangle}$	0.0079	1.5
Random network	$\frac{1}{\lambda_1(A_{SF})}$	0.0085	1.7
Random network	$\frac{1}{\langle k \rangle}$	0.0160	3.2
Random network	$\frac{1}{\lambda_1(A_{\text{random}})}$	0.0140	2.8

From results as above mentioned, several network properties of the optimised network by GA and a scale-free network seems to be similar. However, in only an optimised network, we can observe rich-club phenomena. The results of networks in Table 3 are also very similar (these are not included in this paper).

6 Simulated diffusion in optimised networks

In this section, we present a set of simulation results. The simulations are conducted to confirm the diffusion process will start more easily on our optimised network by GA, compared with scale-free network and random network.

6.1 Simulation settings

Scale-free networks used in this study are generated by Barabasi-Albert model. Random graphs are generated by Erdos-Reny model. The details of our network settings are shown in Tables 2 and 3.

We begin each simulation with a node which contains most number of links on a given network topology. Simulation proceeds in steps of one time unit. During each step, an informed node attempts to infect each of its neighbours with probability β . In addition, every informed node is changed to susceptible condition with probability δ . An infection attempt on an already informed node has no effect. Each simulation proceeds until diffusion process becomes steady state $\frac{dI(t)}{dt} \approx 0$. Unless otherwise specified, each simulation plot is averaged over 100 individual runs.

In each simulation, we set transmission rate β and forgetting rate δ as follows:

$$\beta = \text{Score} \times \frac{\delta}{\lambda_1(A)} \quad (14)$$

$$\delta = 0.1 \quad (15)$$

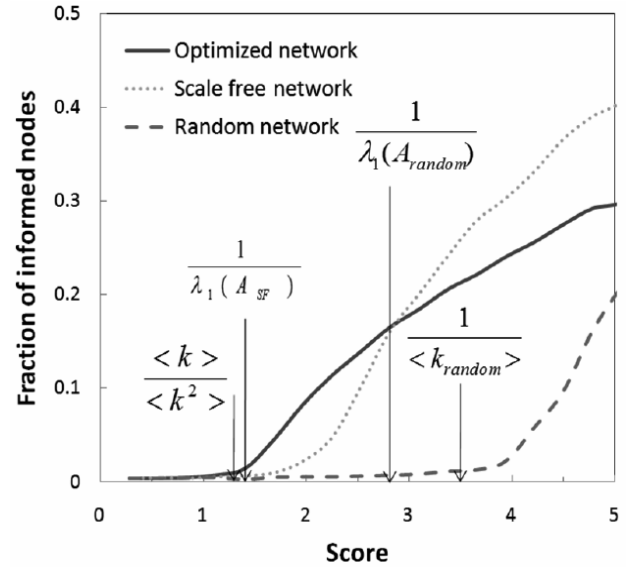
where the *Score* is a scaling parameter to control the relative diffusion rate. We vary score parameter from 0.1 to 5.

6.2 Simulation results

Figures 11 and 12 show time evolution of the fraction of informed nodes on the optimised network by GA, scale-free network and random network. As shown, the diffusion process start at lower score on optimised network, compared with scale-free network and random network. The fraction of informed nodes at *score* = 2 on optimised network is more than 10%, though less than 3% on scale-free network and random network. And the maximum eigenvalue of adjacency matrix shows diffusion thresholds which are well fitted to the simulation results, compared to $\langle k \rangle / \langle k^2 \rangle$ and $1 / \langle k \rangle$, which are proposed as diffusion thresholds of scale-free network and random network respectively (Pastor-Satorras and Vespignani, 2002; Kephart and White, 1991).

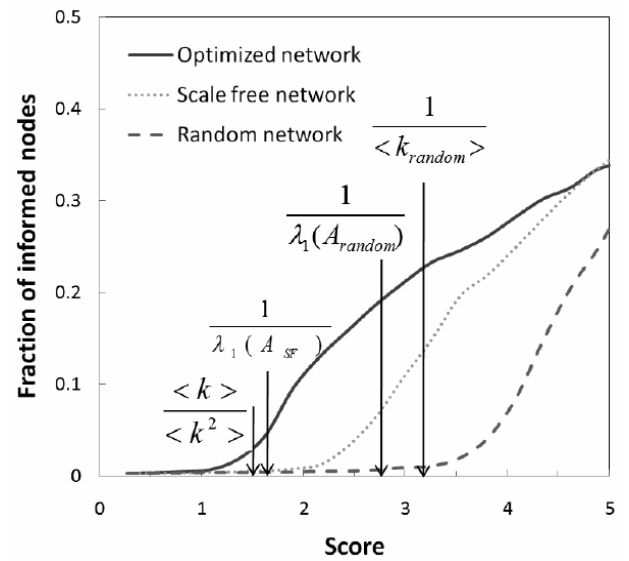
Figures 11 and 12 also show the number of the fraction of informed nodes at *score* = 5 on scale-free network and random network is larger than those on optimised network, and this can be taken to mean that although the maximum eigenvalue $\lambda_1(A)$ decides whether new products or information will diffuse through our society when the value of the relative transitivity β / δ is similar to the threshold $1 / \lambda_1(A)$, however we need another discussion to explain about the diffusion when the value of β / δ is sufficiently larger than $1 / \lambda_1(A)$.

Figure 11 Comparison between diffusion process on each network in Table 2



Note: For each network we have plotted the fraction of informed nodes in steady state at each *Score* = $\beta / \delta * \lambda_1(A)$ and diffusion threshold $\langle k \rangle / \langle k^2 \rangle$ and $1 / \langle k \rangle$, where β , δ , $\langle k \rangle / \langle k^2 \rangle$ and $1 / \langle k \rangle$ are given in Sections 2 and 6.2, respectively.

Figure 12 Comparison between diffusion process on each network in Table 3



Note: Other setting is same in Figure 11.

7 Conclusions

In this paper, we investigated diffusion processes based on the epidemiological model that describes information spread in terms of transmissibility and forgetting at the individual level. Our model is an extended diffusion model that explicitly includes decision influenced by social situations and word-of-mouth processes. We evolutionary designed network with a larger maximum eigenvalue in which the networks low threshold for diffusion process.

By topological analysis, we showed the degree distribution of optimised network obeys power law and there are hub nodes which are interconnected very well (rich club phenomena). As a result, many nodes are located with in three hop distance from a node which contains most number of links.

By diffusion simulation, we showed the optimised network by GA has better performance with the early start of diffusion (diffusion process start at low relative transmission rate) compared to random network and scale-free network.

Our simulations in this paper are done under a variety of very simple conditions. However, these results give us good insights for diffusion process. Interconnectivity between hub nodes seems to be very important role to early start for diffusion process. We hope this paper will serve for the study of promoting the diffusion process at early stage.

References

- Arthur, W.B. (1989) 'Competing technologies, increasing returns, and lock-in by historical events', *The Economic Journal*, Vol. 99, No. 394, pp.116–131.
- Ball, P. (2004) *Critical Mass: How One Thing Leads to Another*, 1st ed., 1 June, Farrar, Straus and Giroux, New York, USA.
- Barabasi, A.L. and Albert, R. (1999) 'Emergence of scaling in random networks', *Science*, Vol. 286, No. 5439, pp.509–512.
- Barabasi, A-L., Albert, R. and Jeong, H. (2000) 'Scale-free characteristics of random networks: the topology of the world-wide web', *Physica A*, Vol. 281, Nos. 1–4, pp.69–77.
- Bass, F.M. (1969) 'A new product growth for model consumer durables', *Management Science*, January, Vol. 15, No. 5, pp.215–227.
- Chakravorti, B. (2003) *The Slow Pace of Fast Change: Bringing Innovations to Market in a Connected World*, June, Harvard Business Press, Boston, MA., USA.
- Colizza, V., Barrat, A., Barthelemy, M. and Vespignani, A. (2006) 'The role of the airline transportation network in the prediction and predictability of global epidemics', *Proceedings of the National Academy of Sciences of the United States of America*, February, Vol. 103, No. 7, pp.2015–2020.
- Dodds, P.S. and Watts, D.J. (2004) 'Universal behavior in a generalized model of contagion', *Physical Review Letters*, March, Vol. 92, No. 21, pp.218701+.
- Hall, B.H. (2004) *Innovation and Diffusion*, January, National Bureau of Economic Research, Cambridge, Massachusetts, USA.
- Hong, Y. (1988) 'A bound on the spectral radius of graphs', *Linear Algebra and its Applications*, September, Vol. 108, pp.135–139.
- Kephart, J.O. and White, S.R. (1991) 'Directed-graph epidemiological models of computer viruses', *Research in Security and Privacy, Proceedings*, pp.343–359.
- Pastor-Satorras, R. and Vespignani, A. (2002) 'Epidemic dynamics in finite size scale-free networks', *Physical Review E*, March, Vol. 65, No. 3, pp.035108+.
- Rosenberg and Nathan (1972) 'Factors affecting the diffusion of technology', *Explorations in Economic History*, Vol. 10, No. 1, pp.3–33, Elsevier.
- Sato, H., Isao, O. and Shigenobu, K. (1997) 'A new generation alternation model of genetic algorithms and its assessment', *Journal of Japanese Society for Artificial Intelligence*, Vol. 12, No. 5, pp.734–744.
- Wang, Y., Chakrabarti, D., Wang, C. and Faloutsos, C. (2003) 'Epidemic spreading in real networks: an eigenvalue viewpoint', *International Symposium on Reliable Distributed Systems (SRDS'03)*, pp.25–34.
- Yamamoto, T., Komatsu, T. and Namatame, A. (2010) 'Networks of genetic algorithm optimization', *Computer Software*, in Japanese, Vol. 28, No. 1, pp.26–33.
- Zhou, S. and Mondragón, R.J. (2004) 'The rich-club phenomenon in the internet topology', *Communications Letters*, March, Vol. 8, No. 3, pp.180–182.