Multiple-predators-based capture process on complex networks*

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The predator/prey (capture) problem is a prototype of many network-related applications. We study the capture process on complex networks by considering multiple predators from multiple sources. In our model, some lions start from multiple sources simultaneously to capture the lamb by biased random walks, which are controlled with a free parameter α. We derive the distribution of the lamb's lifetime and the expected lifetime $\langle T \rangle$. Through simulation, we find that the expected lifetime drops substantially with the increasing number of lions. Moreover, we study how the underlying topological structure affects the capture process, and obtain that locating on small-degree nodes is better than on large-degree nodes to prolong the lifetime of the lamb. The dense or homogeneous network structures are against the survival of the lamb. We also discuss how to improve the capture efficiency in our model.

Keywords: capture process, random walk, scale-free networks

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1. Introduction

Complex network modeling has been used in many natural and artificial systems, where nodes represent individuals, and edges represent interactions between the individuals. Over the past decade, researchers have made great efforts to study the structural properties of complex networks,[1–3] the dynamical processes existing in complex networks,[4] and the interaction among them.[5,6] For instance, it was found that a variety of complex networks have similar statistical structural properties, such as small-world,[7,8] scale-free,[9,10] high clustering,[11] and so on. Moreover, these general network properties were demonstrated to have great impacts on the network-based problems, such as traffic,[12–16] epidemic spreading,[17–21] network attacks,[22–28] synchronization,[29,30] and control,[31–36] link prediction,[37–39] etc. For example, one of the great findings is that the scale-free networks are robust to random attacks, but very fragile to target attacks.[40] Another breakthrough is that the scale-free networks are proved to have very low (even zero) epidemic thresholds.[41] Also, the results[42,43] show that the combination of short average distance and small standard deviation of degree distribution ensures strong network synchronizability.

Random walk is a basic process related to many of these network problems.[44,45] In graph theory, random walk has been studied for decades, and thus the random walk characteristics like arrival time, meet time, commuting time, cover time, etc.[46,47] have been thoroughly discussed. In recent studies, the random walk theory is used to explore the structures of complex networks such as network sampling,[48] calculating node centrality,[49] detecting cluster structures,[50,51] predicting missing links,[52] etc. Furthermore, random walk has wide applications in communication networks for locating resources,[53] detecting replication attacks,[54] and designing navigation[55,56] or routing protocols.[57] The predator–prey (lion–lamb) model is a common random walk model.[58] In the past, this model was used to illustrate the processes of energy transfer in ecological systems.[59,60] Recently, Sungmin *et al.*[61] studied the predator–prey model on complex networks, and they particularly focused on how the network structures affect the lamb survival probability. Wang *et al.*[62] further utilized the predator–prey model in the search problems in point-to-point (P2P) networks. However, in both of their works, there is only one start point of the predator.

In this paper, we generalize the predator–prey model by considering multiple start points of the predators with biased random walks. We first derive the lifetime distribution as well as the expected lifetime of the lamb. Then, we study how the control parameter of the biased random walks and the number of the lions affect the expected lifetime of the lamb. Next, we investigate how the underlying network structure affects the expected lifetime. Finally, we study how to improve the capture efficiency of our model.

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2. Model

We use the Price model[63] to generate the underlying scale-free networks. This model contains two steps. (i) Growth: Initially, there are m_0 isolated nodes in the network. Then, each time we add a new node to the network with m links going from the new node and pointing to the old ones, where $m \leq m_0$. (ii) Cumulative advantage: A new node points to an old node i with probability Φ_i,

$$\Phi_i = \frac{k_i^{\text{in}} + a}{\sum_j (k_j^{\text{in}} + a)}, \tag{1}$$

where k_i^{in} is the degree of node i, and a is a given constant. Multiple connections from the new node to an old node are not allowed. The process goes $N - m_0$ steps, where N is the desired network size. We ignore the directions of links and obtain the undirected scale-free network. The average node degree is $\langle k \rangle = 2m$, and the power-law parameter is $\gamma = 2 + a/m$.

In our capture model, initially some lions start from distinct source nodes to capture a lamb at the destination node. At each time step, every lion steps onto a neighbor node through biased random walk. For instance, a lion at node u steps onto a neighbor node i of u with the transition probability[64,65]

$$\phi_{ui} = \frac{k_i^{\alpha}}{\sum_j k_j^{\alpha}}, \tag{2}$$

where k_j is the degree of j, and the sum runs over all the neighbor nodes of u. α is a control parameter; when $\alpha > 0$, the random walk is biased to large-degree nodes, while when $\alpha < 0$, the random walk is biased to small-degree nodes. When $\alpha = 0$, the biased random walk is degenerated to simple random walk. The capture process will end when the lamb is captured by the lion which first arrives at the destination node.

3. Analytical results

Assume a graph $G(N, M)$, where N and M represent the sets of nodes and edges, respectively. The adjacency relationship of G can be represented by a matrix $\boldsymbol{A}$. If there is a link between nodes i and j, then $A_{ij} = k_j^{\alpha}$. Here A_{ij} can be taken as the directed weight of the link so that A_{ij} is generally not equal to A_{ji}. When $\alpha = 0$, $A_{ij} = A_{ji} = 1$, which is the same as the general adjacency matrix. If there is no link between nodes i and j, $A_{ij} = A_{ji} = 0$, which is also the same as the general adjacency matrix. Then, the strength of node i is $s_i = \sum A_{ij}$. Furthermore, the transition probability matrix is $\boldsymbol{P} = \boldsymbol{K}^{-1}\boldsymbol{A}$, where $\boldsymbol{K} = \text{diag}(s_1, s_2, \ldots, s_N)$. Assuming that at time $t = 0$, a lion on node u begins to perform the biased random walk, then the probability of reaching node v after t steps of walks can be described as

$$p_{uv}(t) = (\boldsymbol{P}^t)_{uv} = \sum_{j_1 \ldots j_{t-1}} \frac{A_{uj_1}}{s_u} \cdot \frac{A_{j_1 j_2}}{s_{j_1}} \cdots \frac{A_{j_{t-1} v}}{s_{j_{t-1}}} = \phi_{uj_1}\phi_{j_1 j_2} \cdots \phi_{j_{t-1} v}, \tag{3}$$

where j_i is the intermediate node the lion visits at time i. Note that the lion may visit v many times in t steps. According to our model, the capture process ends when the destination node (the location of the lamb) is first visited by the lion. To compute the first arrival time, we set the v-th column of $\boldsymbol{P}$ to be zero, and obtain the new transition probability matrix as

$$\boldsymbol{Q}(v) = (\boldsymbol{p}_1, \ldots, \boldsymbol{p}_{v-1}, 0, \boldsymbol{p}_{v+1}, \ldots, \boldsymbol{p}_N). \tag{4}$$

We can infer through the new transition probability matrix that the probability the lion leaves v after first arriving is zero. Then, we can compute the probability that v has not been visited in the t steps, or in other words, the probability that the lifetime of the lamb is larger than t, which is as follows:

$$\text{Prob}\{T_{uv} > t\}) = \sum_{j=1}^{N} (\boldsymbol{Q}(v)^t)_{uj}, \; t = 0, 1, 2, \ldots, \tag{5}$$

where T_{uv} is the time when a lion starting from node u arrives at node v for the first time, which is also the lifetime of the lamb on node v. Next, we assume that initially there are many lions starting from multiple source nodes, which are marked as $1, 2, \ldots, z$ ($z < N - 1$), and the lamb is still on node v. Note that v is not among the z source nodes. The numbers of lions on the z source nodes are $n_1, n_2, \ldots, n_z$, respectively. We define T_{iv}^j as the time when the j-th lion on source node i first arrives at node v. Then, the lifetime of the lamb T_v is the smallest first arrival time of all the lions, which can be described as follows:

$$T_v = \min\{T_{1v}^1, T_{1v}^2, \ldots, T_{1v}^{n_1}, \ldots, T_{zv}^1, T_{zv}^2, \ldots, T_{zv}^{n_z}\}. \tag{6}$$

The probability that the lifetime of the lamb is larger than t is

$$\begin{aligned} &\text{Prob}\{T_v > t\} \\ &= \text{Prob}\{\min\{T_{1v}^1, T_{1v}^2, \ldots, T_{1v}^{n_1}, \ldots, T_{zv}^1, T_{zv}^2, \ldots, T_{zv}^{n_z}\} > t\} \\ &= \left(\prod_{i=1}^{n_1} \text{Prob}\{T_{1v}^i > t\}\right) \cdots \left(\prod_{i=1}^{n_z} \text{Prob}\{T_{zv}^i > t\}\right). \end{aligned} \tag{7}$$

Since each lion performs independent biased random walks, we have

$$\text{Prob}\{T_v > t\} = \prod_{i=1}^{z} (\text{Prob}\{T_{iv} > t\})^{n_i}. \tag{8}$$

Combining Eqs. (5) and (8), we have

$$\text{Prob}\{T_v > t\} = \prod_{i=1}^{z} \left(\sum_{j=1}^{N} (\boldsymbol{Q}(v)^t)_{ij}\right)^{n_i}, \quad t = 0, 1, 2, \ldots. \tag{9}$$

Then, the distribution of the lamb's lifetime can be calculated as follows

$$\begin{aligned} \text{Prob}\{T_v = t\} &= \text{Prob}\{T_v > t - 1\} - \text{Prob}\{T_v > t\} \\ &= \prod_{i=1}^{z} \left(\sum_{j=1}^{N} (\boldsymbol{Q}(v)^{t-1})_{ij}\right)^{n_i} \end{aligned}$$

$$-\prod_{i=1}^{z}\left(\sum_{j=1}^{N}(\boldsymbol{Q}(v)^t)_{ij}\right)^{n_i},\quad t=1,2,\ldots \quad (10)$$

Finally, the expected lifetime of the lamb is calculated as below:

$$\begin{aligned}\langle T_v\rangle &= \sum_{t=1}^{\infty} t\cdot \mathrm{Prob}\{T_v=t\}\\ &= \sum_{t=0}^{\infty}\mathrm{Prob}\{T_v>t\}\\ &= \sum_{t=0}^{\infty}\prod_{i=1}^{z}\left(\sum_{j=1}^{N}(\boldsymbol{Q}(v)^t)_{ij}\right)^{n_i}. \end{aligned}\quad (11)$$

The above derivation provides a general method for calculating the expected lifetime for all types of graphs and we have more, simpler calculation methods for special graphs.

3.1. Fully connected graph

Let us consider a fully connected graph, in which each node is connected to every other node with an edge, and thus the degrees of all nodes are identical and equal $N-1$. We assume that there are n lions and a lamb randomly distributed in the fully connected graph. Note that, initially, the lions' sites may be overlapping or not, and the only constraint is that the lamb's site is not occupied by any lion at the beginning. For this case, we have $\mathrm{Prob}\{T>0\}=1$, $\mathrm{Prob}\{T>1\}=(1-\frac{1}{N-1})^n$, and $\mathrm{Prob}\{T>t\}=(1-\frac{1}{N-1})^{tn}$. Furthermore, we calculate the expected lifetime as follows:

$$\langle T\rangle = \sum_{t=1}^{\infty} t\,[\mathrm{Prob}(T>t-1)-\mathrm{Prob}(T>t)] \quad (12)$$

$$= \sum_{t=1}^{\infty} t\left[\left(1-\frac{1}{N-1}\right)^{(t-1)n}-\left(1-\frac{1}{N-1}\right)^{tn}\right] \quad (13)$$

$$\begin{aligned}&= \left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]\\ &\quad+\sum_{t=1}^{\infty}(t+1)\left[\left(1-\frac{1}{N-1}\right)^{tn}-\left(1-\frac{1}{N-1}\right)^{(t+1)n}\right].\end{aligned} \quad (14)$$

Based on Eq. (13), we have

$$\begin{aligned}&\left(1-\frac{1}{N-1}\right)^{n}\langle T\rangle\\ &= \sum_{t=1}^{\infty} t\left[\left(1-\frac{1}{N-1}\right)^{tn}-\left(1-\frac{1}{N-1}\right)^{(t+1)n}\right].\end{aligned} \quad (15)$$

Subtracting Eq. (15) from Eq. (14) yields

$$\begin{aligned}&\left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]\langle T\rangle\\ &= \left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]\\ &\quad+\sum_{t=1}^{\infty}\left[\left(1-\frac{1}{N-1}\right)^{tn}-\left(1-\frac{1}{N-1}\right)^{(t+1)n}\right]\\ &= \left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]+\sum_{t=1}^{\infty}\left(1-\frac{1}{N-1}\right)^{tn}\\ &\quad-\sum_{t=2}^{\infty}\left(1-\frac{1}{N-1}\right)^{tn}\\ &= \left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]+\frac{\left(1-\frac{1}{N-1}\right)^{n}}{1-\left(1-\frac{1}{N-1}\right)^{n}}\\ &\quad-\frac{\left(1-\frac{1}{N-1}\right)^{2n}}{1-\left(1-\frac{1}{N-1}\right)^{n}}\\ &= \left[1-\left(1-\frac{1}{N-1}\right)^{n}\right]+\left(1-\frac{1}{N-1}\right)^{n}=1.\end{aligned} \quad (16)$$

Then, we obtain

$$\langle T\rangle = \frac{1}{1-\left(1-\frac{1}{N-1}\right)^{n}}. \quad (17)$$

According to Eq. (17), when $n=1$, $\langle T\rangle = N-1$, while when n is very large, we have

$$\langle T\rangle \approx \frac{1}{1-\left(1-\frac{n}{N-1}\right)} = \frac{N-1}{n}. \quad (18)$$

From Eq. (18), we can see that the expected lifetime is approximately proportional to the network size and inversely proportional to the number of lions.

3.2. ER random graph

For the ER random graph,[66] the degree distribution obeys the Poisson distribution. We assume that the degrees of all nodes are $\langle k\rangle$. We know that for the ER random graph, the probability for any two nodes being connected with an edge is

$$p \approx \frac{N\langle k\rangle/2}{N(N-1)/2} = \frac{\langle k\rangle}{N-1}. \quad (19)$$

Then, we have $\mathrm{Prob}\{T>0\}=1$, $\mathrm{Prob}\{T>1\}=\left(1-\frac{\langle k\rangle}{N-1}\frac{1}{\langle k\rangle}\right)^n=\left(1-\frac{1}{N-1}\right)^n$, and $\mathrm{Prob}\{T>t\}=\left(1-\frac{1}{N-1}\right)^{tn}$, which are all the same as the fully connected graph. Thus, equations (17) and (18) are also applicable to the ER random graph when $\langle k\rangle$ is large. When $\langle k\rangle$ is small, approximating $1/k_i$ (the degree of node i) with $1/\langle k\rangle$ is not suitable in the calculation. Thus, equations (17) and (18) are not applicable to the ER random graph when $\langle k\rangle$ is small.

4. Simulation results

In this section, we mainly study how the lamb's expected lifetime is affected by the factors in our model such as the control parameter of the biased random walks, the number of the lions, as well as the degree of the node where the lamb

locates on. In addition, we investigate how the average node degree and the degree distribution of the underlying networks influence the expected lifetime. Moreover, we discuss the improvement of our capture model with applications to the P2P networks.

First, we study the control parameter α of the biased random walks, and at the same time testify the analytical results by simulation. We use the Price model to generate the underlying scale-free network which contains 100 nodes with an average degree of 4 and a power-law parameter of 2.5, as shown in Fig. 1. Then, we set node 40 as the destination node where the lamb is located, nodes 10 and 90 as the lions' starting points, on which the numbers of lions are 1 and 2, respectively. We let the lions perform the biased random walks to capture the lamb, and record the lamb's lifetime. We perform the simulation 10^4 times and calculate the average (expected) lifetime $\langle T \rangle$. The analytical and simulation results are given in Fig. 2. We see that $\langle T \rangle$ decreases first and then increases with α, and there is an optimal α (around 0 in Fig. 2) corresponding to the minimum $\langle T \rangle$. Moreover, the analytical and simulation results agree very well with each other.

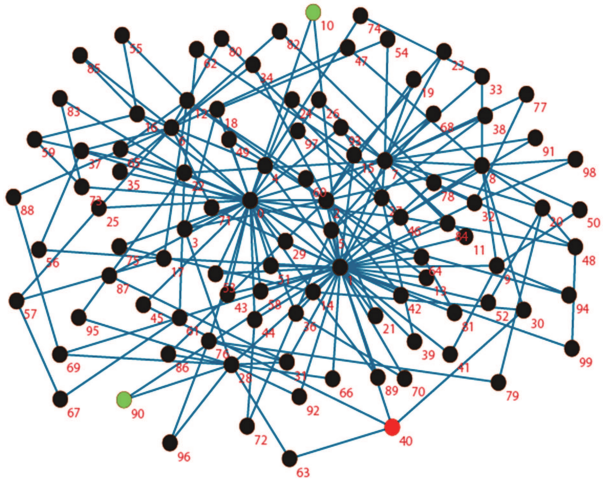


Fig. 1. (color online) A small network generated by the Price model, where $N = 100$, $\langle k \rangle = 4$, and $\gamma = 2.5$. The lamb's site is node 40, and the lions' sites are nodes 10 and 90 with one lion on each site.

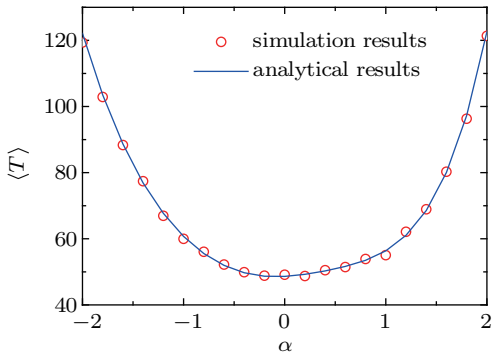


Fig. 2. (color online) The lamb's expected lifetime $\langle T \rangle$ vs. the parameter α of the biased random walks. The underlying network is shown in Fig. 1. Each data point is the average of 10^4 independent runs.

Then, we investigate how the number of the lions affects the expected lifetime. In the simulation, we randomly select a node as the lamb's site and another n lions' sites with one lion on each site. Under this condition, we perform the capture simulation and calculate the expected lifetime, which is given in Fig. 3(a). Clearly, we can see that $\langle T \rangle$ decreases with n abruptly and then converges. Through the above derivation of the lamb's expected lifetime, we know that the lifetime of the lamb equals the first arrival time of the luckiest lion among all the lions. Generally, the more lions, the smaller the lamb's lifetime, which agrees with the analytical results of the fully connected graph and the ER random graph (Eq. (18)). Next, we discuss the influence of the degree of the lamb's site, denoted by k_{lamb}. In the simulation, we select the lamb's site based on its degree, and then randomly select another 10 sites with one lion on each site. The control parameter α is set to be zero. In this case, we calculate the expected lifetime as a function of the degree of the lamb's site, which is shown in Fig. 3(b). Obviously, we can see that $\langle T \rangle$ decreases with increasing k_{lamb}, which means that locating on large-degree sites is adverse to the survival of the lamb. In other words, large-degree nodes are easier to visit for random walkers than small-degree nodes, which is also obtained in Ref. [67].

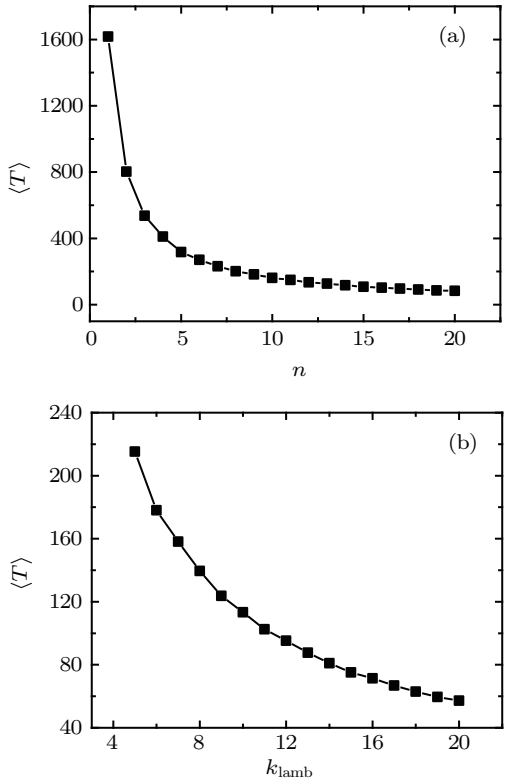


Fig. 3. The lamb's expected lifetime $\langle T \rangle$ vs. (a) the number of lions n and (b) the degree of the lamb's site k_{lamb}. The underlying network is generated by the Price model. The network parameters are the same for panels (a) and (b), which are $N = 1000$, $\langle k \rangle = 10$, and $\gamma = 2.5$. The random walk parameter α equals 0 for both panels. In panel (b), the number of lions n is 10. The details about the sites' selection for the lamb and lions are illustrated in the text. Each data point is the average of 10^4 independent runs.

Next, we discuss how the network structure affects the lifetime of the lamb. We focus on the average node degree and the degree distribution, and study one network parameter by fixing the others. In the simulation, we randomly select a node as the lamb's site, and another 10 nodes as the lions' sites with one lion on each site. The biased random walk parameter α is set be zero. The simulation results are given in Fig. 4, in which each data point is the average of 10^4 independent runs. We see a similar trend of the curves of $\langle T\rangle$, which go down quickly and then tend to be stable with increasing $\langle k\rangle$ in Fig. 4(a) and γ in Fig. 4(b). When the network becomes more dense, the network diameter becomes smaller, which means that the lions and the lamb get closer to each other, and this leads to the decrease of the lamb's lifetime. When the network is very dense, $\langle k\rangle$ does not have a significant influence on $\langle T\rangle$, which can also be predicted by Eq. (18). Furthermore, from Fig. 3(b) we know that random walkers are prone to visit large-degree nodes. If the lamb locates on one of the small-degree nodes, which constitute the largest part of the scale-free networks, it is relatively hard for the lions to catch the lamb. Thus, when the network becomes more homogeneous (by increasing γ), the random walkers will visit all nodes more fairly, which increases the capture efficiency or decreases the lamb's lifetime.

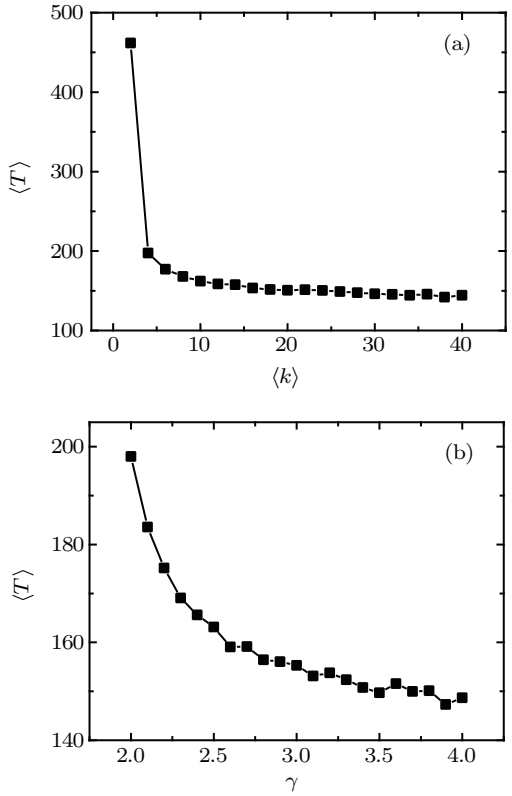


Fig. 4. The lamb's expected lifetime $\langle T\rangle$ vs. (a) the average node degree $\langle k\rangle$ and (b) the power-law parameter γ. The underlying networks are generated by the Price model. The parameters are $N = 1000$, $\alpha = 0$, and $n = 10$, with $\gamma = 2.5$ for panel (a), and $\langle k\rangle = 10$ for panel (b). The details about the sites' selection for the lamb and lions are illustrated in the text. Each data point is the average of 10^4 independent runs.

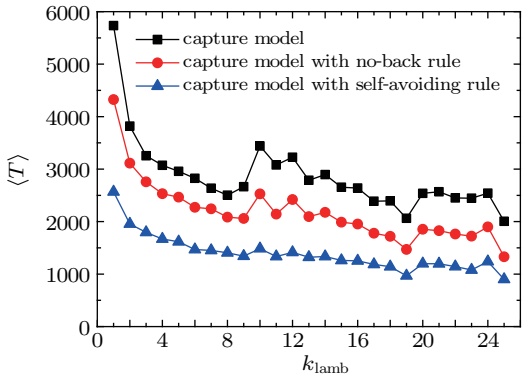


Fig. 5. (color online) The lamb's expected lifetime $\langle T\rangle$ vs. the degree of the lamb's site $k_{\rm lamb}$ on the P2P network, which has 6299 nodes and 20776 edges. In each run, the lions are initially located at the four largest-degree nodes with one lion at each node, and we randomly select a node of degree $k_{\rm lamb}$ as the site of the lamb with the constraint that the site of the lamb and the sites of the lions cannot be overlapped, and then we conduct the capture simulation. The biased random walk parameter α is -1 for all three models. For each degree $k_{\rm lamb}$, the results are the average of 10^4 independent runs.

In our capture model, the lions perform the biased random walks to find the lamb on the network. In fact, the biased random walk mechanism is a basic type, and there are many other random walk mechanisms,[68] such as no-back walk, self-avoiding walk, etc. We can also consider these random walk mechanisms in the capture process. Here we integrate the no-back rule and the self-avoiding rule into our capture model to further improve the capture efficiency. In the improved models, the lions perform biased random walks simultaneously, and obey no-back and self-avoiding rules as well. When considering the no-back rule, a lion will avoid visiting the node which is the last visited node at the next time step unless there is no other choice. When considering the self-avoiding rule, the lion will avoid visiting the nodes which have been visited before at the next time step unless there is no other choice. We compare our original capture model with the modified capture models with the two rules on the P2P network,[69] since the capture model is one of the prototypes of the search problems in P2P networks. The P2P network used in the experiment originally has 6301 nodes and 20777 edges. We process the P2P network by ignoring the directions of the edges and deleting the smaller isolated cluster (which consists of two connected nodes), and finally obtain a connected network with 6299 nodes and 20776 edges. In each run, the lions are located at the four largest-degree nodes with one lion at each node, the site of the lamb is selected among the nodes of degree $k_{\rm lamb}$. The biased random walk parameter α is fixed to be -1. For each $k_{\rm lamb}$, the models run 10^4 times and the average lamb's lifetime $\langle T\rangle$ is calculated. In Fig. 5, we can see that T decreases with $k_{\rm lamb}$ for all the three models. Both the no-back rule and self-avoiding rule improve the capture efficiency since they result in a smaller lifetime of the lamb compared to that of our original capture model, and the

self-avoiding rule is better than the no-back rule in terms of the capture efficiency.

5. Discussion and conclusion

In summary, we study a new kind of capture process, in which there are many lions starting from different source nodes. In detail, we derive the distribution of the lamb's lifetime as well as the expected lifetime. For the fully connected graph and the ER random graph, we provide a simple approximate calculation of the expected lifetime, and find that the expected lifetime is proportional to the network size and inversely proportional to the number of lions. Next, we study how the factors in our model affect the capture process on scale-free networks by simulation. We find that different values of the biased random walk parameter lead to different capture efficiencies. Generally, given the source and destination nodes, there is always an optimal parameter corresponding to the smallest lifetime, or the highest capture efficiency. Furthermore, we obtain that the more lions, the faster to capture the lamb; especially when the number of lions is small, a few more lions results in a large improvement of the capture efficiency. We also find that the larger the degree of the lamb's site, the smaller the expected lifetime. Then, we study how the network structure affects the capture process by simulation. We find that the more dense or the more homogeneous the underlying network is, the smaller the lifetime of the lamb is. Finally, we improve our model by considering the no-back rule and the self-avoiding rule with applications to the P2P networks. It is worth mentioning that our model has the potential to be used in many other scenarios, such as the identification of disease genes.[70] We can set the source nodes of lions as the known disease genes associated with a hereditary disorder, then the destination node where the lamb has the smallest lifetime can be another unknown disease gene with large probability.

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