Mean trapping time for an arbitrary node on regular hyperbranched polymers

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Abstract. The regular hyperbranched polymers (RHPs), also known as Vicsek fractals, are an important family of hyperbranched structures which have attracted widespread attention during the past several years. In this paper, we study the first-passage properties for random walks on the RHPs. Firstly, we propose a way to label all the different nodes of the RHPs and derive exact formulas to calculate the mean first-passage time (MFPT) between any two nodes and the mean trapping time (MTT) for any trap node. Then, we compare the trapping efficiency between any two nodes of the RHPs by using the MTT as the measures of trapping efficiency. We find that the central node of the RHPs is the best trapping site and the nodes which are the farthest nodes from the central node are the worst trapping sites. Furthermore, we find that the maximum of the MTT is about 4 times more than the minimum of the MTT. The result is similar to the results in the recursive fractal scale-free trees and T-fractal, but it is quite different from that in the recursive non-fractal scale-free trees. These results can help in understanding the influences of the topological properties and trap location on the trapping efficiency.

Keywords: rigorous results in statistical mechanics, polymer dynamics, transport properties (theory), network dynamics
1. Introduction

In the last few decades, polymer physics has attracted considerable attention within the scientific community, with various polymer networks proposed to describe the structures of macromolecules [1]. Among numerous polymer networks, the regular hyperbranched polymers (RHPs), also known as Vicsek fractals, are important models of the hyperbranched polymers [2], which have wide applications in coatings [3, 4], conjugated functional materials [5, 6], modifiers and additives [7], drug and gene delivery [8–10] etc.

In view of the wide applications of the Vicsek fractals, interest in Vicsek fractals is growing rapidly. Jayanthi and Wu [11–13] succeeded in determining the eigenvalues of connectivity matrix $A$ of the original Vicsek fractals by determining the roots of iteratively constructed polynomials. Blumen et al. [14, 15] determined the eigenvalue spectrum of general Vicsek fractals for any generation $t$ through an algebraic iterative
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procedure. From these works, one can determine the eigenvalue spectrum of very large Vicsek fractals to a very high accuracy, and then calculate many other dynamical quantities of them [16–20].

Among a plethora of fundamental dynamical processes, random walks are crucial to a lot of branches of science and engineering and have attracted much interest [21–28]. A large variety of other dynamical processes occurring in complex systems can be analyzed and understood in terms of random walks. Examples of these dynamics include energy or exciton transport in polymer systems [29], reaction kinetics [30], and so on. A basic quantity relevant to random walks is the mean first-passage time (MFPT) \( F(x, y) \), which represents the expected number of steps for a walker starting from the source node \( x \) to arrive at the trap node \( y \) for the first time. One can also define the mean trapping time (MTT) for the trap node \( y \) by

\[
T_y = \frac{1}{N-1} \sum_{x \in \Omega, x \neq y} F(x, y),
\]

where \( \Omega \) denotes the node set and \( N \) is the total number of nodes.

As is well known, the topological properties of complex systems have nontrivial influences on the MTT. Therefore, considerable endeavor has been devoted to uncover the MTT for different topological structures [31–43]. It is also well known that the trap location has great effect on the MTT and the MTT can be used as the measure of trapping efficiency for different trap nodes. One should analyze the MTT for an arbitrary trap node and compare the trapping efficiency among all the different traps. The locations which have the minimum MTT can be seen as the best trapping sites and the locations which have the maximum MTT can be seen as the worst trapping sites. These results have wide applications in physical and chemical societies. For example, the best trap sites can be used as the best data collection sites for energy or exciton transport in polymer [29] and geometry-controlled kinetics [30].

In order to analyze the MTT to an arbitrary trap node, one must propose a way to label all the different nodes and then derive formulas to calculate the MTT for the different nodes. For the Cayley trees, Zhang [44] labeled the nodes by their levels and derived the exact analytic formula of the MTT for an arbitrary trap node. For the recursive fractal scale free trees, non-fractal scale-free trees and T-fractal, we labeled the nodes through their edge replacing structure (i.e. the network of generation \( k \), which is denoted by \( G(k) \), is obtained by replacing every edge of \( G(k-1) \) by a special structure) [45–47]. Results shows that the ratio between the maximum and minimum of the MTT is almost a constant in the recursive fractal scale-free trees and T-fractal, whereas it grows logarithmically with network order in the recursive non-fractal scale-free trees. Therefore the effect of trap location on the MTT varies with the topological structures of the complex systems.

As for the Vicsek fractals, they have self-similar treelike structure which can be constructed iteratively by node replacing (i.e. the Vicsek fractals of generation \( k \), which is denoted by \( G(k) \), are obtained by replacing every node of \( G(k-1) \) with a star) [15,48]. The exact analytical solution of the MTT for the central node was obtained in [49]; the exact analytical solution of the MTT for the peripheral node and the global MFPT (i.e. the average of MFPTs over all pairs of nodes) were obtained in [44], but the MTT for any trap node is still unresolved and one cannot completely uncover the effect of trap location on the MTT in the RHPs.
Although we have proposed a method to derive the exact analytic formula of the
MTT for an arbitrary trap node in the recursive fractal scale-free trees and the recursive
non-fractal scale-free trees [45,47], and the method works well on the iterative structures
obtained by edge replacing such as the recursive fractal and non-fractal scale-free trees,
tree like fractal, (u,v) flower, etc it does not work on the iterative structures obtained by
node replacing, such as Vicsek fractals.

In this paper, we first propose a new way to label all the different nodes of the RHPs
and derive exact formulas to calculate the MTT for any node. Then, we compare the
trapping efficiency between any two nodes of the RHPs and find the best and worst
trapping sites by using the MTT as the measure of trapping efficiency. Our results show
that the central node of the RHPs is the best trapping site and the nodes which are the
farthest nodes from the central node are the worst trapping sites. Finally, we find
that the maximum of the MTT is almost $3m^2+3m-2$ times the minimum of the MTT. The
result is similar to the result in the recursive fractal scale-free trees and T-fractal, but it
is quite different from that in the recursive non-fractal scale-free trees. These results can
help in understanding the influences of the topological properties and trap location on
the trapping efficiency.

2. The network model

The RHPs (or Vicsek fractals) [14,15,48] of generation $t$, denoted by $G(t)$ ($t \geq 0$),
are constructed in the following iterative way. For $t = 0$, $G(0)$ consists of an isolated
node without any edge. For $t = 1$, $m$ ($m \geq 2$) new nodes are generated with each being
connected to the node of $G(0)$ to form $G(1)$, which is exactly a star. For $t \geq 2$, $G(t)$ is
obtained from $G(t-1)$. The detailed process is as follows. We introduce $m$ new identical
copies of $G(t-1)$ and arrange them around the periphery of the original $G(t-1)$, and
add $m$ new edges, each of them connecting a peripheral node in one of the $m$ corner copy
structures and a peripheral node of the original central structure, where a peripheral node
is a node farthest from the central node. The first three generations of the Vicsek fractals
for the case $m = 4$ are shown in figure 1. The Vicsek fractals $G(t)$ can also be constructed
by another method, i.e. $G(t)$ is obtained from $G(t-1)$ by replacing every node of $G(t-1)$
with a star as shown in figure 2.

According to its construction, at each generation the total number of the nodes
increases by a factor $m+1$; therefore, the total number of nodes of $G(t)$ is $N_t = (m+1)^t$,
and the total number of edges of $G(t)$ is $E_t = N_t - 1 = (m+1)^t - 1$.

3. The MTT for random walks on Vicsek fractals

3.1. Simplification of the expressions for the MTT

For any two nodes $x$ and $y$ of Vicsek fractals $G(t)$, $F(x,y)$ is the MFPT from $x$ to $y$, the sum

$$k(x,y) = F(x,y) + F(y,x)$$

Figure 1. The first three generations of the Vicsek fractals for the case $m = 4$.

Figure 2. Iterative construction method of the the Vicsek fractals, i.e. $G(t)$ is obtained from $G(t-1)$ by replacing every node of $G(t-1)$ with a star on the right-hand side of the arrow.

is called the commute time and the MFPT can be expressed in terms of commute times [50]:

$$F(x, y) = \frac{1}{2} \left\{ k(x, y) + \sum_{u \in G(t)} \pi(u)[k(y, u) - k(x, u)] \right\},$$ (2)

where ‘$u \in G(t)$’ means that $u$ belongs to the node set of $G(t)$, $\pi(u) = \frac{du}{2E_t}$ is the stationary distribution for random walks on Vicsek fractals and $du$ is the degree of node $u$.

If we view the networks under consideration as electrical networks by considering each edge to be a unit resistor and let $\Psi_{xy}$ denote the effective resistance between two nodes $x$ and $y$ in the electrical networks, we have [50]

$$k(x, y) = 2E_t \Psi_{xy},$$ (3)

where $E_t$ is the total numbers of edges of $G(t)$. Since the Vicsek fractals we study are trees, the effective resistance between any two nodes is just the shortest-path length between the two nodes. Hence

$$\Psi_{xy} = L_{xy},$$ (4)

where $L_{xy}$ denotes the shortest path length between node $x$ to node $y$. Thus

$$k(x, y) = 2E_t L_{xy}.$$ (5)

Replacing $k(x, y)$ from equation (5) in equation (2), and defining

$$S_x = \sum_{y \in G(t)} L_{xy},$$ (6)

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Figure 3. Construction of subunit $\Gamma_{0,i_1,i_2,...,i_{k-1}}$ and the way we label its subunits. It is represented by the biggest dashed circle and is composed of $m + 1$ subunits $\Gamma_{0,i_1,i_2,...,i_k}$ ($i_k = 0, 1, 2, ..., m$) represented by solid circles. It connects with other parts of $G(t)$ (i.e. $SG_{0,i_1,i_2,...,i_{k-1}}$, $i_k = 1, 2, ..., m$) at its $m$ corners. Each subunit $\Gamma_{0,i_1,i_2,...,i_k}$ is also composed of $m + 1$ subunits $\Gamma_{0,i_1,i_2,...,i_k+1}$ represented by small dashed circles. The value of $i_k$ (or the numbers in every small dashed circle) shows the relation between $i_k$ (or $i_k+1$) and the locations of the corresponding subunits in subunit $\Gamma_{0,i_1,i_2,...,i_{k-1}}$.

$$W_x = \sum_{u \in G(t)} \pi(u) L_{xu} = \frac{1}{2E_t} \sum_{u \in G(t)} (L_{xu} \cdot d_u),$$ (7)

$$\Sigma = \sum_{u \in G(t)} \left( \pi(u) \sum_{x \in G(t)} L_{xu} \right),$$ (8)

we obtain

$$F(x, y) = E_t (L_{xy} + W_y - W_x).$$ (9)

Substituting $F(x, y)$ from equation (9) in equations (1), one gets

$$T_y = S_y + N_t \cdot W_y - \Sigma.$$ (10)

Hence, if we can calculate $\Sigma$ and $S_y, W_y$ for any node $y$, we can calculate $F(x, y)$ for any two nodes $(x, y)$ and the MTT for any node $y$. In this paper, we calculate these quantities of the RHPs based on its self-similar structure.

3.2. General methods of calculating the MTT

According to the construction of Vicsek fractals, $G(t)$ is composed of $m + 1$ copies, called the subunit, of $G(t - 1)$ which are connected with each other by their peripheral nodes. For convenience, we classify the subunits of $G(t)$ into different levels and let $\Lambda_k$ denote...
the subunit of level \( k \) \((k \geq 0)\). In this paper, \( G(t) \) is said to be the subunit of level 0. For any \( k \geq 0 \), the \( m + 1 \) subunits of \( \Lambda_k \) are said to be the subunits of level \( k + 1 \). Thus, any node of \( G(t) \) is a subunit of level \( t \) and \( \Lambda_k \) is a copy of the Vicsek fractals with generation \( t - k \). Similarly, we classify all the nodes of \( G(t) \) into different levels and the node which is the central node of a certain subunit \( \Lambda_k \) \((k \geq 0)\) is said to belong to level \( k \). The reason that we only assign level \( k \) to the central node of subunit \( \Lambda_k \) is so we can use the same labels to label the subunit \( \Lambda_k \) and its central node.

In order to distinguish the subunits of different locations, inspired by the method of [34], we label the subunit \( \Lambda_k \) \((0 \leq k \leq t)\) by a sequence \(\{0, i_1, i_2, \ldots, i_k\}\) and denote it by \(\Gamma_{0,i_1,i_2,\ldots,i_k}\), where \(i_j = 0, 1, 2, \ldots, m\) \((1 \leq j \leq k)\) labels its location in its parent subunit \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\). In particular, \(\{0\}\) represents the Vicsek fractal \(G(t)\) itself. Figure 3 shows the construction of \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) and the way we label its subunits. As shown in figure 3, \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) \((k > 0)\), which is represented by the biggest dashed circle, is composed of \(m + 1\) subunits \(\Gamma_{0,i_1,i_2,\ldots,i_k}\) \((i_k = 0, 1, 2, \ldots, m)\) represented by solid circles. It also connects with other parts of \(G(t)\) \((\text{i.e.} \ SG_{0,i_1,i_2,\ldots,i_k}^{i_k} = 1, 2, \ldots, m)\) at its \(m\) corners. Each subunit \(\Gamma_{0,i_1,i_2,\ldots,i_k}\) is also composed of \(m + 1\) subunits \(\Gamma_{0,i_1,i_2,\ldots,i_{k+1}}\) represented by small dashed circles. We label the subunit at the center of \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) by \(i_k = 0\) and the \(m\) peripheral subunits surround the central one by \(i_k = 1, 2, \cdots, m\). The value of \(i_k\) shows the relation between \(i_k\) and the location of subunit \(\Gamma_{0,i_1,i_2,\ldots,i_k}\) in subunit \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\). The numbers in each of the small dashed circles, which are the corresponding values of \(i_{k+1}\), show the relation between \(i_{k+1}\) and the location of subunit \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\). If \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) is the central subunit of \(G(t)\) \((\text{i.e.} \ i_j = 0 \text{ for } j = 1, 2, \cdots, k - 1)\), the dashed circle near the center of \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) should be labeled by \(i_{k+1} = 1\), and the other one should be labeled by \(i_{k+1} = 2\); otherwise, the labels for the two subunits should be exchanged. According to the way we label the subunits, for any subunit \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}\) \((k \geq 1)\), we find

\[
N_{0,i_1,i_2,\ldots,i_{k-1}}^1 \geq N_{0,i_1,i_2,\ldots,i_{k-1}}^2 \geq \cdots \geq N_{0,i_1,i_2,\ldots,i_{k-1}}^m, \tag{11}
\]

where \(N_{0,i_1,i_2,\ldots,i_{k-1}}^m\) denote the total numbers of nodes of \(\text{SG}_{0,i_1,i_2,\ldots,i_k}^{i_k}\) \((i_k = 1, 2, \cdots, m)\). The calculation of \(N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_k}\) and the proof of equation (11) are presented in appendices A and B respectively.

For any node \(x \in G(t)\), it must be a central node of a certain subunit \(\Gamma_{0,i_1,i_2,\ldots,i_k}\) (note: for any terminal node of \(G(t)\), it can be viewed as a subunit of level \(t\) which has only one node, then it can also be regarded as the central node of this subunit). For convenience, we also label the node \(x\) by the same sequence \(\{0, i_1, i_2, \ldots, i_k\}\). Therefore we can use this label to represent \(\text{‘}x\text{’}\) in symbol \(\text{‘}S_x\text{’}, \text{‘}W_x\text{’}, \text{‘}T_x\text{’}\) and \(\text{‘}D_x\text{’}\). As derived in appendix C, for any \(k \geq 1\),

\[
S_{0,i_1,i_2,\ldots,i_k} = S_{0,i_1,i_2,\ldots,i_{k-1}} + 3^{t-k} \left( (m + 1)^t - 2(m + 1)^{t-k} - 2N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_k} \right), \tag{12}
\]

and

\[
W_{0,i_1,i_2,\ldots,i_k} = W_{0,i_1,i_2,\ldots,i_{k-1}} + 3^{t-k} \left( \frac{(m + 1)^t}{E_t} \right) \left( (m + 1)^t - 2(m + 1)^{t-k} - 2N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_k} \right), \tag{13}
\]

where

\[
N_{0,i_1,i_2,\ldots,i_{k-1}}^0 = \left( (m + 1)^t - 2(m + 1)^{t-k} \right)/2, \tag{14}
\]

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and \(N_{0,i_1,i_2,...,i_{k-1}}^{i_k}\) \((i_k = 1, 2, \cdots, m)\), which denote the total numbers of nodes of \(SG_{0,i_1,i_2,...,i_{k-1}}^{i_k}\) \((i_k = 1, 2, \cdots, m)\), are calculated in appendix A.

Replacing \(S_x\) and \(W_x\) with the right-hand side of equations (12) and (13) in equations (10), we obtain the MTT for the node labeled as \\{0, i_1, i_2, ..., i_k\}:

\[
T_{\{0, i_1, i_2, ..., i_k\}} = T_{\{0, i_1, i_2, ..., i_{k-1}\}} + 3^{t-k} \frac{2E_t + 1}{E_t} \left[ (m+1)^t - 2(m+1)^{t-k} - 2N_{0,i_1,i_2,...,i_{k-1}}^{i_k} \right].
\] (15)

Using equation (15) repeatedly, we obtain

\[
T_{\{0, i_1, i_2, ..., i_k\}} = T_{\{0\}} + \frac{2E_t + 1}{E_t} \left[ (m+1)^t \sum_{j=1}^{k} 3^{t-j} - 2 \sum_{j=1}^{k} (3m+3)^{t-j} - 2 \sum_{j=1}^{k} 3^{t-j} N_{0,i_1,i_2,...,i_{j-1}}^{i_j} \right]
\]  

\[
= T_{\{0\}} + \frac{2E_t + 1}{2E_t} \left[ (m+1)^t (3^t - 3^{t-k}) - \frac{4}{3m+2} \right.
\]

\[
\times \left[ (3m+3)^t - (3m+3)^{t-k} - 4 \sum_{j=1}^{k} 3^{t-j} N_{0,i_1,i_2,...,i_{j-1}}^{i_j} \right].
\] (16)

As for \(T_{\{0\}}\), we have calculated them as examples in section 3.3. Therefore, we can calculate the MTT for any node.

### 3.3. Examples

In order to explain our methods, we calculate the MTT for the node labeled as \{0\} and nodes denoted by \(P_k\) \((1 \leq k \leq t)\) with labels \(\{0, i_1, i_2, ..., i_k\} = \{0, m, m, \cdots, m\}\). They are the farthest nodes from the central node \{0\} among all nodes of level \(k\).

For the node labeled as \{0\}, inserting equations (D.4), (D.5) and (E.4) into equations (10), we obtain

\[
T_{\{0\}} = \frac{1}{[(m+1)^t - 1] \ast (6m + 4)} \left\{ 4m3^t(m+1)^{2t-1} - (m+1)^{t-1}(m^23^{t+1} - 3m^2 + 8m + 4) + 4 \right\}.
\] (17)

The result is consistent with that derived in [49].

For any nodes \(P_k\) \((1 \leq k \leq t)\), note that \(N_{0,m,m,\cdots,m}^{m} = 0\) and \(E_t = (m+1)^t - 1\).

Let \(\{0, i_1, i_2, ..., i_k\} = \{0, m, m, \cdots, m\}\), replace \(T_{\{0\}}\) from equations (17) in equations (16), one gets

\[
T_{P_k} = \frac{1}{[(m+1)^t - 1] \ast (6m + 4)} \left\{ (m+1)^{2t-1}[(6m^2 + 6m - 4) \right.
\]

\[
\times 3^t - (6m^2 + 10m + 4)3^{t-k}] + 8 \times 3^{t-k}(m+1)^{2t-k}
\]

\[
- (m+1)^{t-1}[(6m^2 + m - 2)3^t - (3m^2 + 5m + 2)3^{t-k}]
\]

\[
- 3m^2 + 8m + 4\right]\times (3m+3)^{t-k} + 4 \right\}.
\] (18)

These results are consistent with those obtained by the simulation we have just done. The comparison between the simulation results and the derived results for nodes \(P_k\) \((k = 0, 1, 2, 3, 4)\) in Vicsek fractals with \(m = 4\), \(t = 4\) are shown in figure 4. The horizontal
Figure 4. The MTT for nodes $P_k$ ($k = 0, 1, 2, 3, 4$).

axis stands for the different times, the vertical axis is the MTT, the lines with different shape and color stand for the derived results, and the scattered dots with the same color represent the corresponding results obtained at different time’s simulation. Averaging the 100 times’ results and comparing them with the derived results, we find the relative error is less than $10^{-3}$.

4. Effect of trap location on trapping efficiency in Vicsek fractals

In this section, we compare the trapping efficiency among all the nodes of Vicsek fractals by using the MTT as the measures of trapping efficiency, and then find the best and the worst trapping sites. Because any node of $G(t)$ is in one to one correspondence with a sequence $\{0, i_1, \cdots, i_t\}$, we can find from equations (16) that the difference of the MTT for different nodes depends on $\sum_{j=1}^{t} 3^{-j} N^{i_j}_{0,i_1,i_2,\cdots,i_{j-1}}$, and that nodes with maximum MTT must have the minimum $\sum_{j=1}^{t} 3^{-j} N^{i_j}_{0,i_1,i_2,\cdots,i_{j-1}}$, whereas nodes with minimum MTT must have the maximum $\sum_{j=1}^{t} 3^{-j} N^{i_j}_{0,i_1,i_2,\cdots,i_{j-1}}$.

In order to find the maximum and minimum $\sum_{j=1}^{t} 3^{-j} N^{i_j}_{0,i_1,i_2,\cdots,i_{j-1}}$ among all nodes of $G(t)$, we compare $N^{i_k}_{0,i_1,i_2,\cdots,i_{k-1}}$ ($i_k = 0, 1, 2, \cdots, t$) in any fixed subunit $\Gamma_{0,i_1,i_2,\cdots,i_{k-1}}$ ($k = 1, 2, \cdots, t$), the results can be divided into two cases.

Case I: If $\Gamma_{0,i_1,i_2,\cdots,i_{k-1}}$ is the central subunit of $G(t)$ (i.e. $\{i_1, i_2, \cdots, i_{k-1}\} = \{0, 0, \cdots, 0\}$), we obtain

$$\begin{cases} N^0_{0,i_1,\cdots,i_{k-1}} > N^1_{0,i_1,\cdots,i_{k-1}} \\ N^1_{0,i_1,\cdots,i_{k-1}} = N^2_{0,i_1,\cdots,i_{k-1}} = \cdots = N^m_{0,i_1,\cdots,i_{k-1}} \end{cases}$$

by comparing equation (14) with equation (A.6). Case II: If $\{i_1, i_2, \cdots, i_{k-1}\} \neq \{0, 0, \cdots, 0\}$, as derived in appendix B,

$$N^1_{0,i_1,\cdots,i_{k-1}} \geq N^2_{0,i_1,\cdots,i_{k-1}} \geq \cdots \geq N^m_{0,i_1,\cdots,i_{k-1}}.$$
Therefore, the central node of $G(t)$ must be a node of $SG^1_{0,i_1,\ldots,i_{k-1}}$ which have the maximum number of nodes among all the subgraphs $SG^1_{0,i_1,\ldots,i_{k-1}} (i_k = 1,2,\ldots,m)$. Hence,

$$N^1_{0,i_1,\ldots,i_{k-1}} > \frac{(m+1)^t}{2} > N^0_{0,i_1,\ldots,i_{k-1}}. \quad (21)$$

Note that $\sum_{k=1}^{m} N^0_{0,i_1,\ldots,i_{k-1}} = (m+1)^t - (m+1)^{t-k-1}$. We obtain

$$N^1_{0,i_1,\ldots,i_{k-1}} > N^0_{0,i_1,\ldots,i_{k-1}} > N^2_{0,i_1,\ldots,i_{k-1}}. \quad (22)$$

Therefore, for nodes with label $\{0, i_1, \ldots, i_{t}\}$, let $i_1 = i_2 = \cdots = i_t = m$ (i.e. the node $P_t$ of section 3.3). We find from equations (19), (20) and (22) that it has the minimum $\sum_{j=1}^{t} 3^{t-j} N^j_{0,i_1,i_2,\ldots,i_{j-1}}$ among all nodes of $G(t)$. Thus,

$$T_{\{0,m,\ldots,m\}} = \max\{T_x : x \in G(t)\}. \quad (23)$$

Note that any node of $G(t)$ (except the central node with label $\{0\}$) can be labeled by $\{0,0,\ldots,0,i_k,i_{k+1},\ldots,i_{t}\}$ ($i_k \neq 0, k = 1,2,\ldots,t$), let $i_{k+1} = i_{k+2} = \cdots = i_t = 1$. We find from equations (19), (20) and (22) that it has the maximum $\sum_{j=1}^{t} 3^{t-j} N^j_{0,i_1,i_2,\ldots,i_{j-1}}$ among all these kind of nodes. That is to say, for any $i_k \neq 0 (k = 1,2,\ldots,t)$ and $i_j = 0,1,2,\ldots,m$ ($t \geq j > k$),

$$T_{\{0,0,\ldots,0,i_k,1,\ldots,1\}} \leq T_{\{0,0,\ldots,0,i_k,i_{k+1},\ldots,i_t\}}. \quad (24)$$

As proved in appendix F, for any $k = 1,2,\ldots,t$ and $i_k \neq 0$,

$$T_{\{0\}} < T_{\{0,0,\ldots,0,i_k,1,\ldots,1\}}. \quad (25)$$

Equations (24) and (25) imply

$$T_{\{0\}} = \min\{T_x : x \in G(t)\}. \quad (26)$$

Let $k = t$ in equation (18) and compare it with $T_0$ shown in equation (17), while $t \to \infty$,

$$T_{\{0,m,m,\ldots,m\}} \approx \frac{3m^2 + 3m - 2}{2m} > 4. \quad (27)$$

Comparing the result with that in the recursive fractal or non-fractal scale-free trees [45,47], we find that the effect of the trap location on the MTT in the RHPs is similar to the result in the recursive fractal scale-free trees, but it is quite different from that in the recursive non-fractal scale-free trees.

### 5. Conclusion

Firstly, a way to label the nodes of the RHPs is proposed in this paper. It is inspired by the method of [34]. Although the method of [34] has broad applications and works well on the iterative structures obtained by edge replacing, such as tree like fractal, $(u, v)$ flower, etc it does not work on the iterative structures obtained by node replacing, such
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as Vicsek fractals. Our method works well on Vicsek fractals and it is also suitable for other iterative structures obtained by node replacing.

Then, we derive formulas to calculate the MTT for any node and compare the trapping efficiency for any two nodes of the RHPs by using the MTT as the measure of trapping efficiency. Our results show that the central node of the RHPs is the best trapping site and the nodes which are the farthest nodes from the central node are the worst trapping sites. One can find the direct applications of the results, e.g. if we study energy or exciton transport on the RHPs, our results show that the central node is the best data collection site.

Finally, we find that the ratio between the maximum and minimum of the MTT in RHPs is almost a constant. The result is similar to the result in the recursive fractal scale-free trees and T-fractal, but it is quite different from that in the recursive non-fractal scale-free trees which grows logarithmically with network order. What are the reasons for the difference and what are the results for other networks? They are still interesting unresolved problems.

Having the MFPT and the MTT for unbiased random walks on unweighted RHPs, some further works might be the MFPT and the MTT for biased random walks on weighted (or unweighted) RHPs [51–53]. Although the method with which we calculate the MFPT and MTT does not work directly on this case, the method in which we label the nodes of RHPs is still suitable for this case and the relation between the commute time and effective resistance is also a useful bridge.

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Appendix A. Calculation of $N_{0,i_1,i_2,...,i_{k-1}}^{i_k}$

For any subunit $\Gamma_{0,i_1,i_2,...,i_{k-1}}$ ($k \geq 1$), $N_{0,i_1,i_2,...,i_{k-1}}^{i_k}$ ($i_k = 1, 2, \ldots, m$) denote the total numbers of nodes of subgraph $SG_{i_k}$ which is connected with $\Gamma_{0,i_1,i_2,...,i_{k}}$, as shown in figure 3. For $k = 1$, note that $\Gamma_0$ is $G(t)$ itself and there is no node surround $\Gamma_0$, therefore,

$$N_{0}^{i_1} = 0, \quad i_1 = 1, 2, \cdots, m.$$ 

Assuming that $N_{0,i_1,i_2,...,i_{k-1}}^{i_k}$ ($i_k = 1, 2, \cdots, m$, $k \geq 1$) are known, we now analyze $N_{0,i_1,i_2,...,i_{k}}^{i_k+1}$. Note that the total number of nodes for subunit $\Gamma_{0,i_1,i_2,...,i_{k}}$ is $(m + 1)^{t-k}$, if $i_k = 0$ (see the central red solid circle in figure 3), for any $i_{k+1} = 1, 2, \cdots, m$,

$$N_{0,i_1,i_2,...,i_{k-1},0}^{i_k+1} = N_{0,i_1,i_2,...,i_{k-1}}^{i_k+1} + (m + 1)^{t-k}. \quad \text{(A.1)}$$

If $i_k \neq 0$ (see the green solid circles in figure 3), the calculation is divided into two cases.
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Case I: $\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}$ is the central subunit of $G(t)$ (i.e. $i_j = 0$ for $j = 1, 2, \ldots, k - 1$), for any $i_k = 1, 2, \ldots, m$ and $i_{k+1} = 1, 2, \ldots, m$,

$$\begin{align*}
N_{0,i_1,i_2,\ldots,i_{k-1},i_k}^{i_{k+1}} &= \begin{cases} 
(m+1)^t - (m+1)^{t-k} - N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 1 \\
N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 2 \\
0 & i_{k+1} > 2
\end{cases}.
\end{align*}$$

(A.2)

Case II: If $\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}$ is not the central subunit of $G(t)$, for any $i_{k+1} = 1, 2, \ldots, m$,

$$\begin{align*}
N_{0,i_1,i_2,\ldots,i_{k-1},i_k}^{i_{k+1}} &= \begin{cases} 
(m+1)^t - (m+1)^{t-k} - N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 1 \\
N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 2 \\
0 & i_{k+1} > 2
\end{cases}
\end{align*}$$

(A.3)

and for $i_k = 2, 3, \ldots, m$ , $i_{k+1} = 1, 2, \ldots, m$,

$$\begin{align*}
N_{0,i_1,i_2,\ldots,i_{k-1},i_k}^{i_{k+1}} &= \begin{cases} 
(m+1)^t - (m+1)^{t-k} - N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 1 \\
N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}} & i_{k+1} = 2 \\
0 & i_{k+1} > 2
\end{cases}
\end{align*}$$

(A.4)

Therefore, we can calculate $N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_{k+1}}$ for any subunit $\Gamma_{0,i_1,i_2,\ldots,i_{k-1}}$ ($k \geq 1$).

For example, if $\{0,i_1,i_2,\ldots,i_t\} = \{0,m,m,\ldots,m\}$,

$$\begin{align*}
N_{0,m,m,\ldots,m}^m &= 0, \quad k = 0, 1, \ldots, t - 1.
\end{align*}$$

(A.5)

If $\{0,i_1,i_2,\ldots,i_t\} = \{0,0,\ldots,0,i_k,1,1,\ldots,1\}$ ($k \geq 1$, $i_k \neq 0$), using equation (A.1) repeatedly, we obtain

$$\begin{align*}
N_{0,0,\ldots,0}^m &= \frac{(m+1)^t - (m+1)^{t-k+1}}{m}
\end{align*}$$

(A.6)

Let $i_{k+1} = 1$ in equation (A.2), we get

$$\begin{align*}
N_{0,0,\ldots,0}^1 &= (m+1)^t - (m+1)^{t-k} - N_{0,0,\ldots,0}^1 \\
&= \frac{(m-1)(m+1)^t + (m+1)^{t-k}}{m}
\end{align*}$$

(A.7)

We can also obtain from equation (A.3) that, for any $j$ ($j = 1, 2, \ldots, t - k - 1$),

$$\begin{align*}
N_{0,0,\ldots,0}^1 &= N_{0,0,\ldots,0}^1
\end{align*}$$

(A.8)

Appendix B. Proof of equation (11)

We prove equation (11) by mathematical induction.

Step 1: For $k = 1$, equation (11) is true for subunit $\Gamma_0$, since $N_{0}^{i_1} = 0$ for any $i_1 = 1, 2, \ldots, m$.

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Step 2: Suppose equation (11) is true for any subunit $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}}$ with some $(k \geq 1)$. Then we prove it also hold for $k + 1$, that is to say,

$$N^1_{0, i_1, i_2, \ldots, i_k} \geq N^2_{0, i_1, i_2, \ldots, i_k} \geq \cdots \geq N^m_{0, i_1, i_2, \ldots, i_k} \tag{B.1}$$

is also true for any subunit $\Gamma_{0, i_1, i_2, \ldots, i_k}$ ($i_k = 0, 1, 2, \ldots, m$). If $i_k = 0$, we obtain equation (B.1) from equation (A.1) and the induction hypothesis.

If $i_k \neq 0$, the proof is divided into two cases.

Case I: $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}}$ is the central subunit of $G(t)$ (i.e. $i_j = 0$ for $j = 1, 2, \ldots, k - 1$), according to equation (A.2), we find, for any $i_k = 1, 2, \ldots, m$,

$$N^1_{0, i_1, i_2, \ldots, i_k} = 0, \quad i_{k+1} = 3, \ldots, m, \tag{B.2}$$

and

$$N^2_{0, i_1, i_2, \ldots, i_k} - i_k = N^1_{0, i_1, i_2, \ldots, i_k} < \frac{N_t}{2}.$$

Note that $SG^1_{0, i_1, i_2, \ldots, i_k}$ is the subgraph containing the central node of $G(t)$ (see figure 3). Therefore,

$$N^1_{0, i_1, i_2, \ldots, i_{k-1}, i_k} > \frac{N_t}{2}.$$

Hence, equation (B.1) holds for any $i_k = 1, 2, \ldots, m$.

Case II: $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}}$ is not the central subunit of $G(t)$. $SG^1_{0, i_1, i_2, \ldots, i_{k-1}}$ must be the subgraph containing the central node of $G(t)$ (see figure 3). Therefore, for any $i_k = 1, 2, \ldots, m$,

$$N^1_{0, i_1, i_2, \ldots, i_{k-1}, i_k} > \frac{N_t}{2}.$$

Hence,

$$N^1_{0, i_1, i_2, \ldots, i_{k-1}} \geq N^1_{0, i_1, i_2, \ldots, i_{k-1}} > \frac{N_t}{2}.$$

But for any $i_k = 1, 2, \ldots, m$,

$$N^1_{0, i_1, i_2, \ldots, i_k} = 0, \quad i_{k+1} = 3, \ldots, m. \tag{B.3}$$

Thus, equation (B.1) holds for any $i_k = 1, 2, \ldots, m$.

### Appendix C. Derivation of equations (12) and (13)

For any node $x$ of Vicsek fractals labeled by $\{0, i_1, i_2, \ldots, i_k\}$, $0 \leq i_j \leq m$, $j = 1, 2, \ldots, k$, $k \geq 1$, it is the central node of subunit $\Gamma_{0, i_1, i_2, \ldots, i_k}$. If $i_k = 0$, $\Gamma_{0, i_1, i_2, \ldots, i_k}$ and $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}}$ have the same central node. Thus,

$$S_{\{0, i_1, i_2, \ldots, i_{k-1}, 0\}} = S_{\{0, i_1, i_2, \ldots, i_{k-1}\}}, \tag{C.1}$$

$$W_{\{0, i_1, i_2, \ldots, i_{k-1}, 0\}} = W_{\{0, i_1, i_2, \ldots, i_{k-1}\}}. \tag{C.2}$$

If we denote $N^1_{0, i_1, i_2, \ldots, i_{k-1}} = [(m + 1)^t - 2(m + 1)^{t-k}] / 2$, it is straightforward that equations (12) and (13) hold for $i_k = 0$.

If $i_k = 1$, as shown in figure 3, $\Gamma_{i_1, i_2, \ldots, i_{k-1}}$ connects with $SG^1_{0, i_1, i_2, \ldots, i_{k-1}}$ by an edge and connects with other part of Vicsek fractals by $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}, 0}$. Both $\Gamma_{0, i_1, i_2, \ldots, i_{k-1}, 0}$ and
By symmetry, we have
\[
\sum_{y \in G_0} L_{xy} = \sum_{y \in G_1} L_{py}, \tag{C.3}
\]
and
\[
\sum_{y \in G_1} L_{xy} = \sum_{y \in G_0} L_{py}, \tag{C.4}
\]
and
\[
\sum_{y \in G_0, G_1} \pi(y)L_{xy} = \sum_{y \in G_0, G_1} \pi(y)L_{py} + (m - 1)\frac{3^{t-k}}{2E_t}.
\]
where \(G_0\), \(G_1\) are the simplifications of \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1},0}\) and \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1},1}\) respectively. Let \(G_{\text{others}}\) denote the rest part of Vicsek fractals except for \(SG_{0,i_1,i_2,\ldots,i_{k-1},1}\), \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1},0}\) and \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1},1}\), the total numbers of nodes of \(G_{\text{others}}\) is \((m+1)^t - 2(m+1)^{t-k} - N_{0,i_1,i_2,\ldots,i_{k-1}}\). We find that for any node \(y \in G_{\text{others}}\), \(L_{xy} = L_{py} + L_{px}\) and that for any node \(y \in SG_{0,i_1,\ldots,i_{k-1},1}\), \(L_{xy} = L_{py} - L_{px}\). Hence,
\[
S_{0,i_1,i_2,\ldots,i_{k-1},1} = S_x = \sum_{y \in G(t)} L_{xy}
\]
\[
= \sum_{y \in G_0} L_{xy} + \sum_{y \in G_1} L_{xy} + \sum_{y \in G_0} L_{xy} + \sum_{y \in G_{\text{others}}} L_{xy}
\]
\[
= \sum_{y \in G_0} (L_{py} - L_{xp}) + \sum_{y \in G_0} L_{py} + \sum_{y \in G_1} L_{py} + \sum_{y \in G_{\text{others}}} (L_{py} + L_{xp})
\]
\[
= \sum_{y \in G(t)} L_{py} + L_{xp} \left[ (m+1)^t - 2(m+1)^{t-k} - 2N_{0,i_1,i_2,\ldots,i_{k-1}} \right]
\]
\[
= S_p + 3^{t-k} \left[ (m+1)^t - 2(m+1)^{t-k} - 2N_{0,i_1,i_2,\ldots,i_{k-1}} \right]. \tag{C.5}
\]
where \(N_{0,i_1,i_2,\ldots,i_{k-1}}\) and \(SG_{0,i_1,\ldots,i_{k-1}}\) are the simplifications of \(N_{0,i_1,i_2,\ldots,i_{k-1}}\) and \(SG_{0,i_1,\ldots,i_{k-1}}\) respectively.

Therefore, equation (12) holds for \(i_k = 1\).

Similarly,
\[
W_{0,i_1,i_2,\ldots,i_{k-1},1} = W_x = \sum_{y \in G(t)} \pi(y)L_{xy}
\]
\[
= \sum_{y \in G_1} \pi(y)L_{xy} + \sum_{y \in G_0, G_1} \pi(y)L_{xy} + \sum_{y \in G_{\text{others}}} \pi(y)L_{xy}
\]
\[
= \sum_{y \in G_1} \pi(y)(L_{py} - L_{xp}) + \sum_{y \in G_{\text{others}}} \pi(y)(L_{py} + L_{xp})
\]
\[
+ \sum_{y \in G_0, G_1} \pi(y)L_{py} + (m - 1)\frac{3^{t-k}}{2E_t}
\]
\[
= W_p + \frac{3^{t-k}}{E_t} \left[ (m+1)^t - 2(m+1)^{t-k} - 2N_{0,i_1,i_2,\ldots,i_{k-1}} \right]. \tag{C.6}
\]
Therefore, equation (13) holds for \(i_k = 1\).

By symmetry, we can also verify that equations (12) and (13) hold for \(i_k = 2, 3, \ldots, m\).

\(\Gamma_{i_1,i_2,\ldots,i_{k-1},1}\) are copies of Vicsek fractals of generation \(t-k\). We denote by \(p\), the node which is labeled by \(\{0, i_1, i_2, \ldots, i_{k-1}\}\). Node \(p\) is also the central node of subunit \(\Gamma_{0,i_1,i_2,\ldots,i_{k-1},0}\).
Appendix D. Derivation of $S_{\{0\}}$ and $W_{\{0\}}$

In this section, we derive $S_x$ and $W_x$ for node $x$ labeled by $\{0\}$, which is the central node of $G(t)$. But it is difficult to calculate them directly. We first calculate $S_x$ and $W_x$ for the node denoted by $P$, which is the farthest node from the central node $\{0\}$. Then we calculate $S_{\{0\}}$ and $W_{\{0\}}$ from equations (12) and (13). In order to tell the difference of $S_P$ and $W_P$ for Vicsek fractals of different generation $t$ ($0 \leq t$), we denote by $S_P^t$, $W_P^t$ the $S_P$ and $W_P$ in Vicsek fractals of generation $t$ respectively. It is straightforward that $S_P^0 = 0$ and $W_P^0 = 0$. For $t > 0$, according to the self-similar structure, $S_P^t$ satisfies the following recursion relation:

$$S_P^t = S_{P}^{t-1} + \left[S_{P}^{t-1} + N_{t-1}3^{t-1}\right] + (m - 1) \cdot \left[S_{P}^{t-1} + 2N_{t-1}3^{t-1}\right] = (m + 1)S_{P}^{t-1} + (2m - 1)(m + 1)^{t-1}3^{t-1}. \quad \text{(D.1)}$$

Using equation (D.1) repeatedly, we obtain

$$S_P^t = (m + 1)^tS_{P}^{0} + (2m - 1)(m + 1)^{t-1}3^{t-1} = (m + 1)^tS_{P}^{0} + (2m - 1)(m + 1)^{t-1}(1 + 3^{t-1} + \cdots + 3^{t-1}) = (2m - 1)(m + 1)^{t-1}\frac{3^t - 1}{2} \quad \text{for Vicsek fractals of different generation} \quad t \quad \text{(D.2)}$$

Similarly,

$$W_P^t = \frac{(m + 1)^t - 1}{(m + 1)^t - 1}(m + 1)W_{P}^{t-1} - \frac{m}{2[(m + 1)^t - 1]} + 3^{t-1}(2m - 1)\frac{(m + 1)^t - 1}{(m + 1)^t - 1} = \cdots = \frac{m}{2[(m + 1)^t - 1]}[1 + (m + 1)^t + \cdots + (m + 1)^t] = \frac{1}{2[(m + 1)^t - 1]} \cdot \left[(m + 1)^t - (2m - 1)3^{t-1} - 3m + 1\right]. \quad \text{(D.3)}$$

Let $P_k$ ($0 \leq k \leq t$) denote the node whose label satisfies $\{0, i_1, i_2, \cdots, i_k\} = \{0, m, m, \cdots, m\}$. We have $P_t \equiv P$ and $P_0 \equiv \{0\}$. Note that $N_{0,m,m,\cdots,m}^{m} = 0$, for any $k$ ($1 \leq k \leq t$). Therefore, we can obtain from equations (12) and (13) that

$$S_{P_{k-1}} = S_{P_k} - 3^k \left[(m + 1)^t - 2(m + 1)^{t-k}\right], \quad W_{P_{k-1}} = W_{P_k} - \frac{3^k}{2[(m + 1)^t - 1]} \left[2(m + 1)^t - 4(m + 1)^{t-k}\right].$$

Thus

$$S_{\{0\}} = S_{P_0} = S_{P_1} - 3^{t-1} \left[(m + 1)^t - 2(m + 1)^{t-1}\right] = S_{P_1} - (m + 1)^t[1 + 3^1 + \cdots + 3^{t-1}] + 2[1 + (3m + 3)^1 + \cdots + (3m + 3)^{t-1}] = (m - 2)(m + 1)^{t-1}\frac{3^t - 1}{2} + 2 \cdot \frac{(3m + 3)^{t-1} - 1}{3m + 2}, \quad \text{(D.4)}$$

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and

\[ W_{\{0\}} = W_{P_0} = W_{P_t} \frac{2(m+1)^t}{2[(m+1)^t - 1]} (1 + 3^1 + \cdots + 3^{t-1}) \]
\[ + \frac{4}{2[(m+1)^t - 1]} [1 + (3m+3)^1 + \cdots + (3m+3)^{t-1}] \]
\[ = \frac{1}{2[(m+1)^t - 1]} \left\{ (m+1)^{t-1} [((m-2)3^t - 2m + 1] \right. \]
\[ + 1 + 4 \cdot \frac{(3m+3)^t - 1}{3m+2} \} \]. (D.5)

Appendix E. Exact calculation of \( \Sigma \)

We find that

\[ \Sigma = \sum_{u \in G(t)} (\pi(u) \sum_{x \in G(t)} L_{xu}) = \sum_{u \in G(t)} W_u. \]

Because any node of \( G(t) \) is in one to one correspondence with a sequence \( \{0, i_1, \ldots, i_t\} \), thus

\[ \Sigma = \sum_{i_1, \ldots, i_t} W_{\{0, i_1, \ldots, i_t\}}. \] (E.1)

where the summation runs over all the possible values of \( i_k = 0, 1, 2, \ldots, m \) \((1 \leq k \leq t)\). For any \( k \) \((0 \leq k \leq t)\), let

\[ \Sigma_k = \sum_{i_1, \ldots, i_{k-1}} W_{\{0, i_1, \ldots, i_k\}}. \] (E.2)

Therefore \( \Sigma_0 = W_{\{0\}} \). Note that

\[ \sum_{i_k=0}^m N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_k} = \frac{3}{2} (m+1)^t - (m+1)^{t-k+1} + (m+1)^{t-k}. \]

For any \( k \) \((1 \leq k \leq t)\), replacing \( W_{\{0,i_1,\ldots,i_k\}} \) from equation (13) in equation (E.2), we obtain

\[ \Sigma_k = \sum_{i_1, \ldots, i_{k-1}} \sum_{i_k=0}^m W_{\{0, i_1, \ldots, i_k\}} \]
\[ = \sum_{i_1, \ldots, i_{k-1}} \sum_{i_k=0}^m \left\{ W_{\{0, i_1, i_2, \ldots, i_{k-1}\}} + \frac{3^{t-k}}{E_t} \right. \]
\[ \times \left[ (m+1)^t - 2(m+1)^{t-k} - 2 N_{0,i_1,i_2,\ldots,i_{k-1}}^{i_k} \right] \}
\[ = (m+1) \Sigma_{k-1} + (m+1)^{k-1} \frac{3^{t-k}}{E_t} \times [(m-2)(m+1)^t + 2(m+1)^{t-k}]. \] (E.3)
Using equation (E.3) repeatedly and replacing $\Sigma_0$ with $W_0$ (see equation (D.5)), we obtain

$$
\Sigma \equiv \Sigma_t = (m+1)^t \Sigma_{t-1} + (m+1)^{t-1} \frac{3^0}{E_t} \times [(m-2)(m+1)^t + 2(m+1)^0]
$$

$$
= (m+1)^t \Sigma_0 + \frac{(m+1)^{2t-1}}{E_t} \frac{E_t}{(m-2)[1 + 3^1 + \cdots + 3^{t-1}]}
$$

$$
+ \frac{2(m+1)^{t-1}}{E_t} \frac{E_t}{[1 + (3m+3)^1 + \cdots + (3m+3)^{t-1}]}
$$

$$
= \frac{1}{2E_t} \left\{ (m+1)^{2t-1} \left[ 2(m-2)3^t - 3m - 3 \right] + (m+1)^t \right. 
$$

$$
\left. + \frac{(3m+3)^t - 1}{3m+2} (4m+8)(m+1)^{t-1} \right\}, \quad (E.4)
$$

where $E_t = (m+1)^t - 1$.

### Appendix F. Proof of equation (24)

For any node with label $\{0, i_1, i_2, \ldots, i_t\}$. Let $k = t$ in equation (16), we can obtain

$$
T_{\{0, i_1, i_2, \ldots, i_t\}} - T_0 = \frac{2E_t+1}{2E_t} \Phi(i_1, i_2, \ldots, i_t), \quad (F.1)
$$

where

$$
\Phi(i_1, i_2, \ldots, i_t) = (m+1)^t (3^t - 1) - \frac{4}{3m+2} [(3m+3)^t - 1] - 4 \sum_{j=1}^t 3^{t-j} N_{i_1, i_2, \ldots, i_{t-1}}. \quad (F.2)
$$

Let $\{i_1, i_2, \ldots, i_t\} = \{0, 0, \cdots, 0, 1, 1, \ldots, 1\}$ ($i_k \neq 0$) in equation (F.2) and replace $N_{i_1, i_2, \ldots, i_{t-1}}$ from equations (A.6)–(A.8), we get

$$
\Phi(0, 0, \cdots, 0, i_k, 1, 1, \ldots, 1)_{k-1}^{t-k} = (m+1)^t (3^{t-k+1} - 1) - \frac{4}{3m+2} [(3m+3)^{t-k+1} - 1]
$$

$$
- \frac{4}{m} 3^t [ (m+1)^t - (m+1)^{t-k+1} ] - 2 \frac{(m-1)(m+1)^t + (m+1)^{t-k}}{m} (3^{t-k} - 1)
$$

$$
= (m+1)^t (3^{t-k+1} + 1 - \frac{2}{m}) + (3m+3)^{t-k}
$$

$$
\times \frac{2m+4}{m(3m+2)} + \frac{2}{m} (m+1)^{t-k} + \frac{4}{3m+2}
$$

$$
> 0. \quad (F.3)
$$

Therefore, $T_{\{0, 0, \cdots, 0, i_k, 1, 1, \ldots, 1\}_{k}^{t-k}} - T_0 > 0$.

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References

[1] Gurtovenko A A and Blumen A 2005 Adv. Polym. Sci. 182 171
[2] Gao C and Yan D 2004 Prog. Polym. Sci. 29 183
[3] Johansson M, Malmström E, Jansson A and Hult A 2000 J. Coat. Technol. 72 49
[4] Lange J, Stenroos E, Johansson M and Malmström E 2001 Polymer 42 7403
[5] Bai F, Zheng M, Lin T, Yang J, He Q, Li Y and Zhu D 2001 Synth. Met. 119 179
[6] Duan L, Qiu Y, He Q, Bai F, Wang L and Hong X 2001 Synth. Met. 124 373
[7] Mezzenga R, Plummer C J G, Boogh L and Manson J-A E 2001 Polymer 42 305
[8] Gao C, Xu Y M, Yan D Y and Chen W 2003 Biomacromolecules 4 704
[9] Uhrich K 1997 Trends Polym. Sci. 5 388
[10] Esfand R and Tomalia D A 2001 Drug Discov. Today 6 427
[11] Jayanthi C S, Wu S Y and Cocks J 1992 Phys. Rev. Lett. 69 1955
[12] Jayanthi C S and Wu S Y 1993 Phys. Rev. B 48 10199
[13] Jayanthi C S and Wu S Y 1993 Phys. Rev. B 50 897
[14] Blumen A, Jurjiu A, Koslowski T and Ferber C V 2003 Phys. Rev. E 67 061103
[15] Blumen A, Ferber C V, Jurjiu A and Koslowski T 2004 Macromolecules 37 638
[16] Blumen A, Volta A, Jurjiu A and Koslowski T 2005 Physica A 356 12
[17] Blumen A, Volta A, Jurjiu A and Koslowski T 2005 J. Lumin. 111 327
[18] Volta A, Galiceanu M and Jurjiu A 2010 J. Phys. A: Math. Theor. 43 105205
[19] F¨urstenberg F, Dolgushev M and Blumen A 2013 J. Chem. Phys. 138 034904
[20] Jurjiu A, Volta A and Beu T 2011 Phys. Rev. E 84 011801
[21] Havlin S and ben-Avraham D 1987 Adv. Phys. 36 695
[22] Chepizhko O and Peruani F 2013 Phys. Rev. E 86 031143
[23] Bentz J L and Kozak J J 2006 J. Chem. Phys. 125 034905
[24] Bentz J L, Turner J W and Kozak J J 2010 Phys. Rev. E 82 011137
[25] Meyer B, Agliari E, Bénichou O and Voituriez R 2012 Phys. Rev. E 85 026113
[26] Zhang Z Z, Guan J H, Xie W L, Qi Y and Zhou S G 2009 Europhys. Lett. 86 10006
[27] Agliari E and Burioni R 2009 Phys. Rev. E 80 031125
[28] Agliari E, Burioni R and Manzotti A 2010 Phys. Rev. E 82 011118
[29] Wu S Q, Zhang Z Z and Chen G R 2011 Eur. Phys. J. B 82 91
[30] Cornellas F and Miralles A 2010 Phys. Rev. E 81 061103
[31] Zhang Z Z, Qi Y, Zhou S G, Gao S Y and Guan J H 2010 Phys. Rev. E 81 061103
[32] Zhang Z Z, Wu B, Zhang H J, Zhou S G, Guan J H and Wang Z G 2010 Phys. Rev. E 81 051118
[33] Zhang Z Z, Li X T, Lin Y and Chen G R 2011 J. Stat. Mech. P08013
[34] Agliari E 2008 Phys. Rev. E 77 051128
[35] Lin Y and Zhang Z Z 2013 J. Chem. Phys. 138 094905
[36] Peng J H and Xu G 2014 J. Stat. Mech. P04032
[37] Peng J H and Xu G 2014 J. Chem. Phys. 40 134102
[38] Peng J H, Xiong J and Xu G 2014 Physica A 407 231–44
[39] Vicsek T 1983 J. Phys. A: Math. Gen. 16 L647
[40] Wu B, Lin Y, Zhang Z Z and Chen G R 2012 J. Chem. Phys. 137 044903
[41] Tetali P 1991 J. Theor. Probab. 4 101
[42] Lin Y and Zhang Z Z 2014 Sci. Rep. 4 5365
[43] Peng X and Zhang Z Z 2014 J. Chem. Phys. 140 234104
[44] Lin Y and Zhang Z Z 2014 Sci. Rep. 4 6274

doi:10.1088/1742-5468/2014/12/P12018 18