

# A cluster-growing dimension of complex networks: From the view of node closeness centrality

Bo Wei<sup>a,b</sup>, Yong Deng<sup>a,\*</sup>

<sup>a</sup> Institute of Fundamental and Frontier Science, University of Electronic Science and Technology of China, Chengdu, 610054, China

<sup>b</sup> School of Control and Computer Engineering, North China Electric Power University, Beijing, 102206, China

## HIGHLIGHTS

- The classical cluster-growing method chooses a sufficient number of seed nodes to measure the dimension of complex networks.
- A modified cluster-growing method is proposed to prevent choosing the seed nodes located at the periphery of networks.
- The dimension of complex networks can be better obtained by the proposed method, especially for the heterogeneous networks.

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## ABSTRACT

The cluster-growing method has been widely used to measure the fractal dimension of complex networks. In this method, a seed node is chosen at random and the number of nodes centered at the seed node is calculated. The procedure is then repeated by choosing many seed nodes at random and the total number of nodes within the same fixed length is averaged over the number of seed nodes. In order to improve the statistics, one has to repeat the calculations for sufficient number of seed nodes. However, most real world networks are featured with heterogeneous properties and it is possible that some of the seed nodes are located at the periphery of the networks. In this paper, a modified cluster-growing dimension of complex networks based on closeness centrality of nodes is proposed. By observing and comparing the distinction dimension by choosing the seeds via the proposed method, the original method, the hubs-based method and the CI-based method in a number of networks, we conclude that the dimension of complex networks can be better obtained by choosing the seeds located in the center of complex networks.

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## 1. Introduction

Complex networks have attracted increasing interest of scientists from many fields of research owing to their relevance to many real systems such as world-wide web, transportation, biological and social systems [1–6]. A large number of real networks show the well-known small world [7,8] or scale-free [9] properties. In the pioneering work [10], Song et al. revealed that a variety of real complex networks have fractal and self-similarity properties, where the box-counting method was used to calculate the fractal dimension of complex networks. In [11,12], Shanker first used the cluster-growing method to study the fractal problem of complex networks. Subsequently, the fractal and self-similarity properties were extensively studied in network science (see e.g., [13–18]). The dimension is a crucial parameter to characterize the complex networks. Two independent methods, the box-covering method [19–23] and cluster-growing method [16,24,25] are widely used for

\* Corresponding author.

E-mail addresses: [wb0218@126.com](mailto:wb0218@126.com) (B. Wei), [dengentropy@uestc.edu.cn](mailto:dengentropy@uestc.edu.cn) (Y. Deng).

calculating the dimension of complex networks. Recently, the multifractal characterization of complex networks has been analyzed by the extension of these two methods [26]. Due to the uncertainty in real complex world [27–31], the fuzzy set theory was also introduced to model the fractal dimension of complex networks [32]. In addition, based on entropy function [33–37], the information fractal of complex network was developed in [38,39].

In this paper, we focus on the study of cluster-growing method. The idea of cluster-growing method is that a seed is chosen randomly and the number of nodes  $M(r)$  within a hypersphere of radius  $r$  from the seed is calculated [11,12]. In order to improve the statistics, one has to repeat the calculations for many seed nodes, and then average the sum of  $M(r)$  with the same length over the number of seed nodes [16,26,40]. In some other works, all the nodes are set as the seeds in turn and average the sum of  $M(r)$  over the total number of complex networks [11,12,24,25,41,42]. The estimated value of the dimension of complex networks is obtained by linear regression of the log–log scale of statistical data. A natural problem is raised up: can we choose one node as the seed to measure the dimension of complex networks? It is interesting and necessary to address this issue. In recent years, identifying the node influence in networks has attracted great attention and many centralities of nodes have been proposed, see e.g., the hubs centrality and collective influence (CI) centrality [43–45]. In this paper, we pay attention to the selection of the seed by its location at the center of the whole network and proposed a closeness-based method to measure the fractal dimension of complex networks. Based on the proposed method, the dimension of real world networks and the NW small-world networks can be observed by choosing the most important node as the seed. Through the comparison with the original method, the hubs-based method and the CI-based method, we show that the dimension of the complex networks can be better obtained by the closeness-based method.

The rest of this paper is organized as follows. In Section 2, some basic concepts of complex networks and the proposed method are introduced. Some applications of the proposed method are illustrated in Section 3. Finally, conclusions are drawn in Section 4.

## 2. Method

For a complex network, it is conveniently denoted by a graph,  $G = (V, E)$  with  $V = (1, 2, \dots, N)$  and  $E = (1, 2, \dots, M)$ , where  $N$  is the total number of the nodes and  $M$  is the total number of the edges. The cell  $e_{ij}$  ( $i, j = 1, 2, \dots, N$ ) of the edges equals to 1 if node  $i$  is connected to node  $j$ , and 0 otherwise. The distance between two nodes  $i$  and  $j$  is equal to the total number of edges that connect them through shortest linkages. Denote the distance by  $d_{ij}$ . The distance  $d_{ij}$  is different from the Euclidean distance and  $d_{ij}$  is also called topological distance between  $i$  and  $j$  [46].

Most real world networks are featured with heterogeneous topologies. In [19,20,47], the authors have studied the fractal structure for the skeleton and the boundary nodes of networks based on the box-covering method. To investigate the fractal and self-similarity properties of complex networks, the cluster-growing method is another successful analytical technique [11,12,16]. To the best of our knowledge, the influence of the boundary nodes of networks has not been studied in the cluster-growing method. It is intuitively plausible that if a node is located in the periphery of complex networks, the number of nodes  $M(r)$  will increase slowly and then increase very fast when the  $r$  increases to a fixed point. Thus, the linear regression of the log–log scale of  $M(r)$  vs  $r$  may not follow a power law and results in the failure of characterizing the fractal property of complex networks. However, if we choose the seed whose location is at the center of the whole network, the above mentioned phenomenon may not occur. Motivated by this observation, we propose a modified cluster-growing dimension of complex networks based on closeness centrality of nodes.

Closeness centrality relies on the length of the paths from a node to the rest of all other nodes in the network, and is defined as the inverse of the total lengths [43,48]. Closeness centrality can be formalized as follows:

For a node  $i$ , the closeness centrality, denoted by  $C_i$ , is defined as

$$C_i = \left[ \sum_{j=1, j \neq i}^N (d_{ij}) \right]^{-1}, \quad (1)$$

where  $d_{ij}$  is the topological distance between node  $i$  and  $j$ .

Closeness centrality is a basic indicator of complex networks. It plays a very important role in the study of complex networks, especially in identifying the importance of the nodes in the networks [5,47]. With an efficient information fusion tool, namely evidence theory [49–51], closeness centrality measure is combined with other parameters, such as betweenness, to obtain the rank of the influential nodes [52,53]. Based on the closeness centrality, we set the node with the highest value of closeness centrality as the seed node. Then the fractal dimension of complex network  $G$  can be obtained through choosing this seed node and carrying out the following steps:

**Step 1:** Calculate closeness centrality of each node using (1) and sort the nodes according to their centralities in an increasing order.

**Step 2:** Choose the node with the highest value of closeness centrality as the seed. Let the initial radius  $r_1 = 1$ . Count the number of nodes  $M(r_1)$  within a hypersphere of radius  $r_1 = 1$  from the seed.

**Step 3:** Repeat Step 2 by replacing  $r_1$  with  $r_2 = r_1 + 1$ ,  $r_3 = r_2 + 1 \dots$ , until all the nodes are covered by some radius  $r$ .

**Table 1**

General characteristics, fractal dimension and fitness comparison of four real word complex networks.

Network	$N$	$M$	Closeness-based method		Original method	
			$d_f$	$mse$	$d_f$	$mse$
E. coli	2859	6890	1.1814	0.0032	3.2433	0.0482
Dolphins	62	159	1.9534	0.0034	1.4989	0.0037
Yeast	2361	7182	2.7553	0.0094	3.4560	0.0163
Petster	1858	12533	1.7072	0.0033	3.1037	0.0310

**Step 4:** Plot the log–log of  $M(r)$  versus radius  $r$ . The fractal dimension of the network is obtained by the slop of the fitting line.

Note that  $M(r)$  is regarded as a function of  $r$  to obtain the following scaling

$$M(r) \sim r^{d_f}, \quad (2)$$

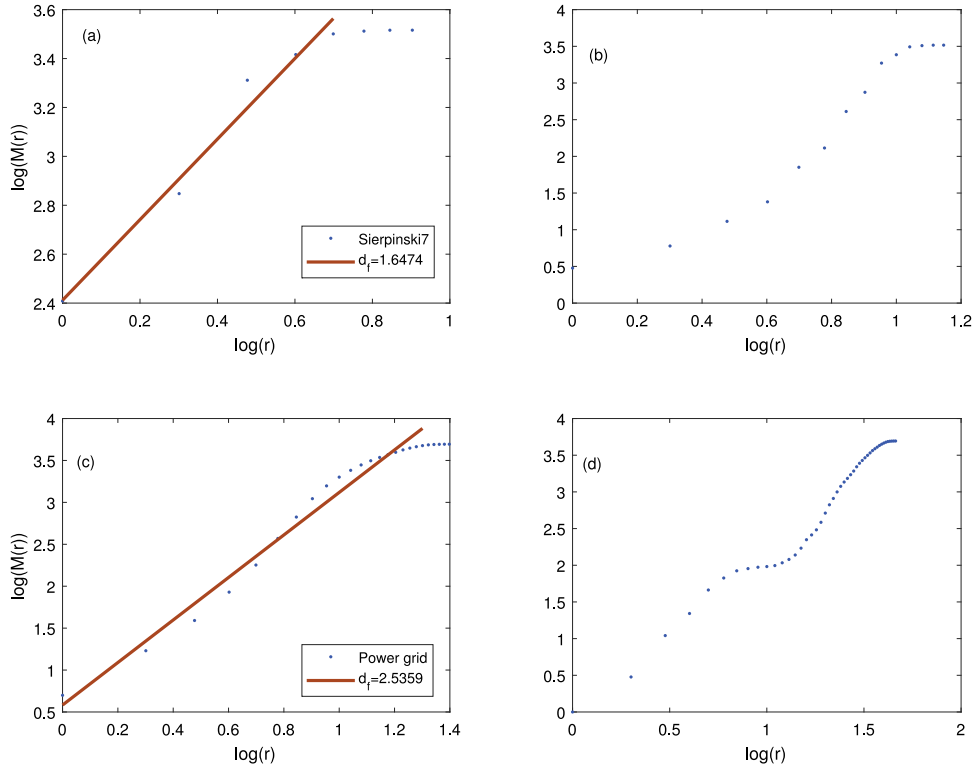
where  $M(r)$  is number of nodes within a distance  $r$  from the seed node and  $d_f$  is the eliminated fractal dimension of complex networks. Since the fractal dimension is obtained by using the closeness centrality of nodes, we call the proposed method as closeness-based method. One can also use other centralities to measure the fractal dimension of complex networks, such as the hubs-based method and CI-based method. In the next section, we will verify the effectiveness of the closeness-based method and apply this method to measure some real complex networks and NW small-world networks [8]. Meanwhile, some comparisons with the original method, degree-based method and CI-based method are presented.

### 3. Applications and discussions

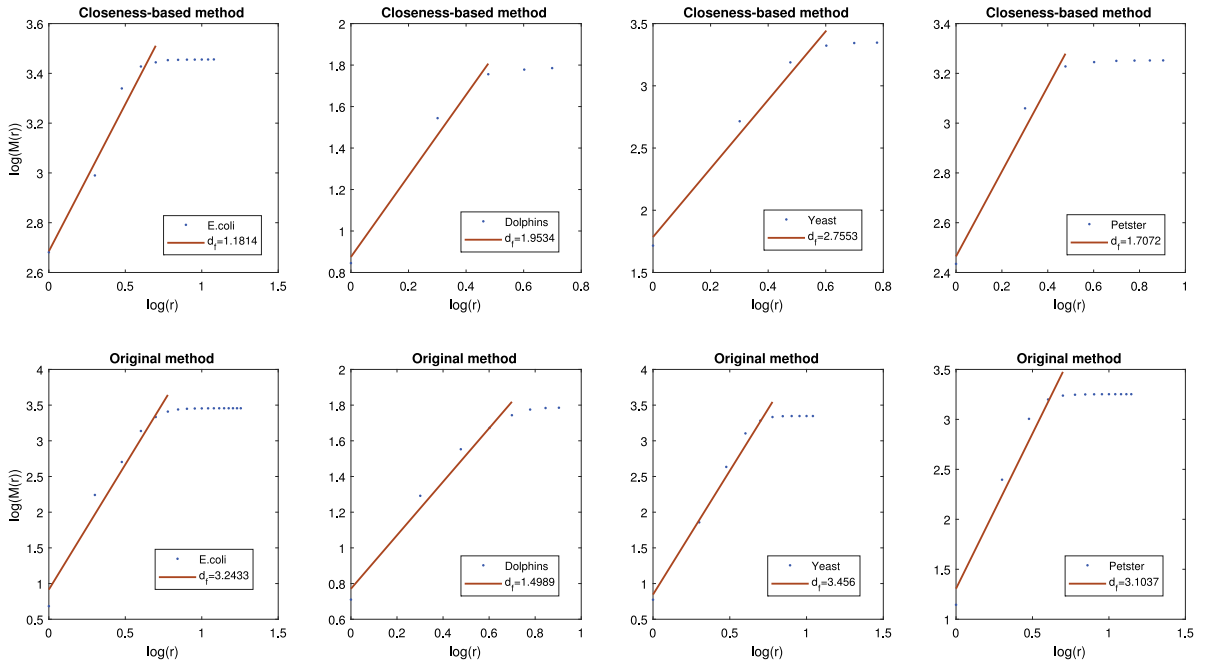
In this section, we first show that the seeds we choose play an important role on whether the fractal properties of complex network can be observed. A artificial “Sierpinski” networks [15] and a technological network, the western states high-voltage power grid of United States [7] are considered by applying the proposed method to measure the fractal dimension. The “Sierpinski” networks are classical fractal networks and are built by Iterated Function Systems [54], whose Hausdorff dimension is completely characterized by the number of copies  $s$  and the scaling factor  $f$ . Here, we consider “Sierpinski” network with  $s = 7$  and  $f = 1$ . Denote this network by “Sierpinski7”. This network is composed of 3282 nodes and 6561 edges. For the power grid network, the transformers, substations and generators are considered as nodes, and the links are high-voltage transmission lines. The network is composed of 4941 nodes and 6549 edges.

For the above networks, we analyze fractal properties by choosing one node as the seed node. Fractal scaling analysis of these networks is shown in Fig. 1. In Fig. 1(a) and (c), the number of nodes  $M(r)$  evolves as a function of the metric distance  $r$  by choosing the center node as the seed based on the closeness centrality. In Fig. 1(b) and (d), the number of nodes  $M(r)$  evolves as a function of the metric distance  $r$  by choosing the periphery as the seed node measured by the closeness centrality. As Fig. 1 shows, for these two networks, the fractal properties can be well revealed by choosing the center node as the seed. Fig. 1(a) and (c) illustrate that the number of nodes  $M(r)$  within a distance  $r$  scales in a power-law form; that is,  $M(r) \sim r^{d_f}$ . The fractal dimension of the “Sierpinski” network and power grid network are 1.6474 and 2.5359, respectively. While the fractal properties of this two networks cannot be found if we choose the periphery node as the seed node (see Fig. 1(b) and (d)) because the number of nodes  $M(r)$  increases slowly at initial phase and then increase very fast when the  $r$  increases to some value. The log–log scale of  $M(r)$  vs  $r$  may not follow a power law and the seed nodes chosen from the periphery of complex networks may have negative influence on the fractal characterization of networks.

In the following, we carry out more fractal analysis of real networks by the proposed method and compare this method with the original one studied in [11,12,24,25,41,42]. We apply these two methods to measure the fractal dimension for the chemical biology networks such as the protein–protein interaction network (PIN) in budding yeast [55] and *E. coli* network [56], the social networks such as the frequent associations between 62 dolphins in a community living off Doubtful Sound dolphin [56], i.e., dolphin social network, and the friendships between users of the website hamsterster.com, i.e., Petster Hamsterster friendships network. Some basic information of these networks are shown in Table 1, where we list the number of nodes  $N$ , the number of edges  $M$  and the fractal dimension  $d_f$  obtained by the proposed method and the original method. In Fig. 2, the first panel displays the evolution of  $M(r)$  as a function of  $r$  based on the proposed method, which shows that  $M(r)$  evolves as a scaling function of  $r$  with some exponent  $d_f$  in a certain range of scaling. The second panel in Fig. 2 shows the scaling property obtained by the original method. Note that number of the effective data obtained by these two methods may be different. Thus, for the comparison of the proposed method and the original one, we use the mean squared error  $mse$  to evaluate the performance of the corresponding fitting. The mean squared error is given by  $mse = \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2$ , where  $y_i$  is the original data,  $\hat{y}_i$  is the value in the fitting curve corresponding to  $y_i$ , and  $n$  is the number of effective data used in the fitting. Obviously, the smaller the mean squared error  $mse$  is, the better the fitting. The mean squared errors of these two methods have been shown in Table 1, from which one can see that the proposed method outperforms the original method.



**Fig. 1.** The  $M(r)$  vs.  $r$  of “Sierpinski7” network and power grid network obtained in a log–log scale. (a), (c) show the number of nodes  $M(r)$  as a function of the metric distance  $r$  by choosing the center seeds with the highest score given by closeness centrality measure and (b), (d) show the number of nodes  $M(r)$  as a function of the metric distance  $r$  by choosing the periphery seeds with the lowest score given by closeness centrality measure.



**Fig. 2.** Scaling for E. coli, dolphin social network, protein–protein interaction network (PIN) in budding yeast and Petster Hamsterster friendships. The first panel shows the log–log plot of  $M(r)$  vs.  $r$  obtained by the proposed method and the second panel shows the corresponding results obtained by the original method.

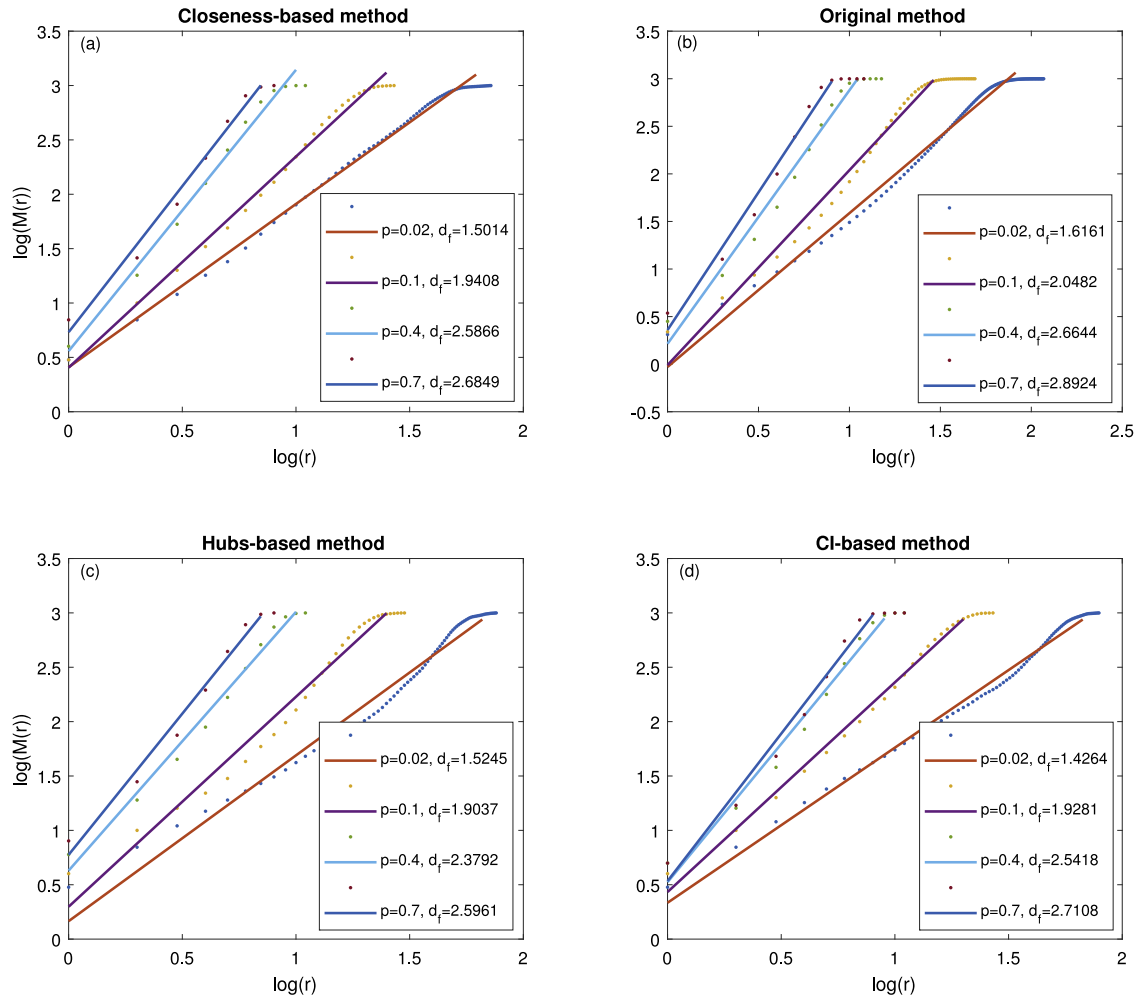


Fig. 3. Scaling for the NW small-world networks with varying shortcut density  $p$ .

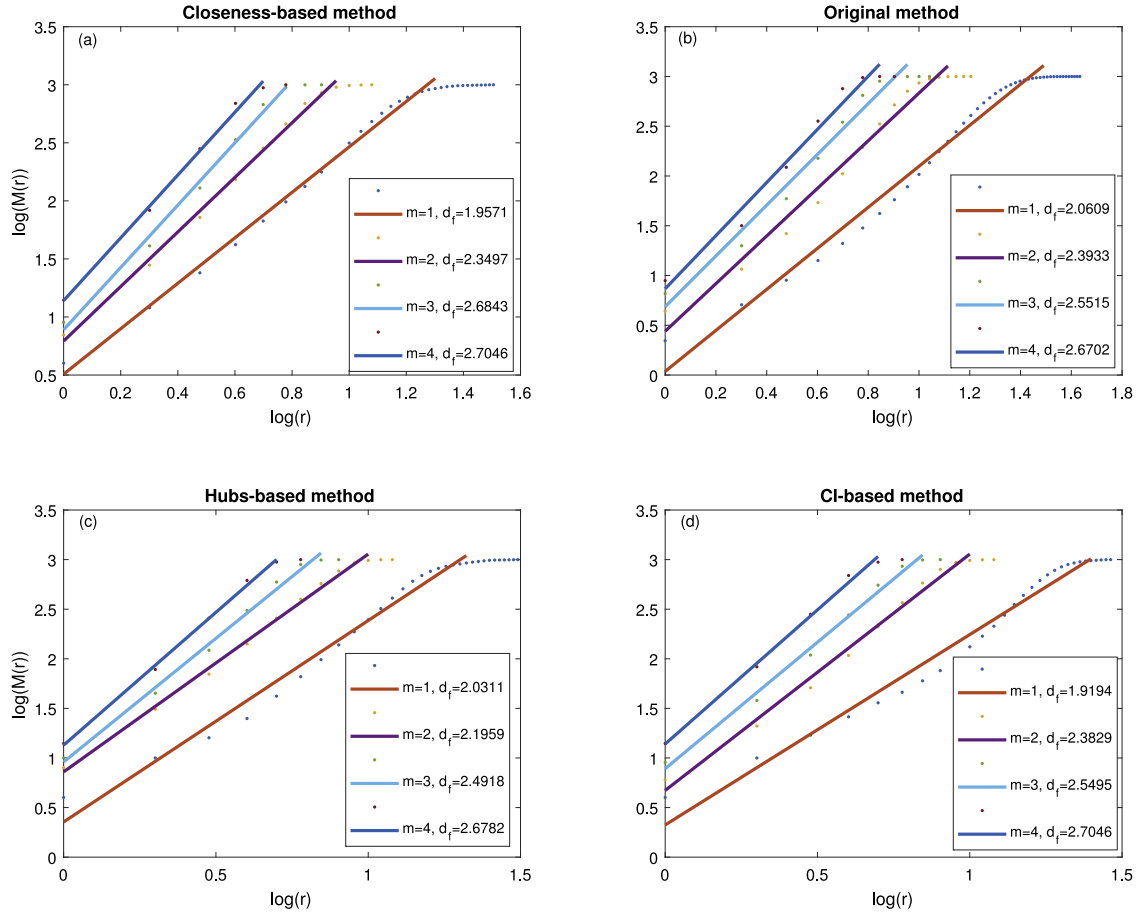
The above results have shown that identifying the importance of nodes is also vital in computing the dimension of complex networks. The hubs and collective influence of each node are two effective indicators in the identification of the influential nodes [44,45]. The scaling property may be obtained by replacing the closeness centrality by hubs centrality or CI centrality in Steps 1 and 2 of the proposed method. In the following, the performance of the proposed method, the original method, the hubs-based method and the CI-based method in the fractal analysis for the NW small-world networks is presented. The network is constructed from a lattice consisting of  $N = 1000$  nodes arranged in a ring, where each node has  $2m$  neighbors initially. For each pair of originally unconnected nodes, an edge is added with probability  $p$  (also called shortcut density) to connect these two nodes. In this process, the multiple edges and self-loops are excluded. We employ this model to construct networks with different adding edge probability  $p$  and initial degree  $2m$ . The fractal structure of the networks is shown in Figs. 3 and 4 measured by the proposed method, the original method, the hubs-based method and the CI-based method. From Figs. 3 and 4, one can see that the fitting curves agree with the statistic data well and the dimension can be obtained by the closeness-based method. The mean squared errors of the four methods have been shown in Tables 2 and 3, from which one can see that the closeness-based method outperforms the other methods for almost all the considered NW small-world networks. The results also show that dimension of the networks is closely related to the network structure, such as the shortcut density and the initial degree; that is, the dimension will increase as the increasing of the shortcut density  $p$  and the initial degree  $2m$ .

#### 4. Conclusions

In the classical cluster-growing method, one needs to choose many seeds to reduce the statistical errors when measuring the dimension of complex networks. Most real world networks are featured with heterogeneous topologies and it is more

**Table 2**Fractal dimension and fitting comparison for the NW small-world networks with varying shortcut density  $p$ .

NW network	Closeness-based method		Original method		Hubs-based method		CI-based method	
	$d_f$	$mse$	$d_f$	$mse$	$d_f$	$mse$	$d_f$	$mse$
$p = 0.02$	1.532	<b>0.0016</b>	1.55	0.0051	1.525	0.0101	1.43	0.0034
$p = 0.1$	1.941	0.0036	1.863	0.0116	1.91	0.0136	1.9	<b>0.0035</b>
$p = 0.4$	2.587	<b>0.0060</b>	2.637	0.0152	2.379	0.0074	2.516	0.0110
$p = 0.7$	2.685	<b>0.0073</b>	2.84	0.0134	2.596	0.0089	2.711	0.0119

**Fig. 4.** Scaling for the NW small-world networks with varying initial degree  $2m$ .**Table 3**Fractal dimension and fitness comparison for the NW small-world networks with varying initial degree  $2m$ .

NW network	Closeness-based method		Original method		Hubs-based method		CI-based method	
	$d_f$	$mse$	$d_f$	$mse$	$d_f$	$mse$	$d_f$	$mse$
$m = 1$	1.9571	<b>0.0027</b>	2.0609	0.0230	2.0311	0.0097	1.9194	0.0126
$m = 2$	2.3497	<b>0.0020</b>	2.3933	0.0585	2.1959	0.0023	2.3829	0.0050
$m = 3$	2.6843	<b>0.0032</b>	2.5515	0.0193	2.4918	0.0032	2.5495	0.0037
$m = 4$	2.7046	0.0020	2.6702	0.0169	2.6782	<b>0.0010</b>	2.7046	0.0020

likely to choose the periphery nodes of networks as the seed nodes. Thus, it is not possible to get a reasonable result in this case. When the center node of the network is chosen as the only seed, there will be no cluster with too few nodes. In this situation, the scaling properties of networks can be well observed. In this paper, we take the closeness centrality into consideration when deciding which node should be chosen as the seed node. Our results show that the proposed method is effective when dealing with the fractal dimension problem of complex networks. One should be warned that, however, the fractal of the complex networks can only be observed in a certain scaling range. By the proposed method in this paper, the



dimension of the NW small-world networks can be easily obtained. Moreover, our results also show that the identifying the importance of each node is also vital in computing the dimension of complex networks. However, this paper only considered fractal properties of unweighed networks. The extensions of this work to weighed complex networks and to the multifractal analysis are also meaningful and interesting.

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