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Manipulating directed networks for better synchronization

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Abstract. In this paper, we studied the strategies to enhance synchronization on directed networks by manipulating a fixed number of links. We proposed a centrality-based manipulating (CBM) method, where the node centrality is measured by the well-known PageRank algorithm. Extensive numerical simulation on many modeled networks demonstrated that the CBM method is more effective in facilitating synchronization than the degree-based manipulating method and the random manipulating method for adding or removing links. The reason is that the CBM method can effectively narrow the incoming degree distribution and reinforce the hierarchical structure of the network. Furthermore, we apply the CBM method to the links rewiring procedure where at each step one link is removed and one new link is added. The CBM method helps to decide which links should be removed or added. After several steps, the resulting networks are very close to the optimal structure from the theoretical analysis and the evolutionary optimization algorithm. The numerical simulations on the Kuramoto model further demonstrate that our method has an advantage in shortening the convergence time to synchronization on directed networks.

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Contents

1. Introduction

Synchronization is an important dynamical process in many systems. Understanding and controlling this collective dynamics is of both theoretical and practical significance [1, 2]. Many methods have been proposed to enhance the network synchronizability, including the redistribution of the coupling strengths [3–8], the modification of the network structure [9–13], the flipping of link directionality [14–17] and so on. Each group of methods has its specific range of applications since different systems are under different technical constraints.

As real systems are frequently manipulated by growing out new connections and eliminating redundant connections [18], we here focus on the link manipulating method for enhancing synchronizability. The word 'manipulating' stands for modification including adding, removing and rewiring links, and in each modification only one link is created or changed. The manipulating method for undirected networks has already been studied by using the information embedded in Laplacian eigenvectors [9]. However, the spectral method cannot be directly applied to directed networks, since the complex value emerges in eigenvectors when the Laplacian matrix is asymmetric. Until now, how manipulating methods affect the synchronization on directed networks has not been given a systematic consideration.

Under the framework of master stability analysis, the synchronizability of an undirected network can be quantified by the eigenvalue ratio of the corresponding Laplacian matrix of this network, namely $R = \lambda_N/\lambda_2$, where λ_N and λ_2 are, respectively, the largest and smallest non-zero eigenvalues of the Laplacian matrix [19–21]. The smaller the R, the stronger the network synchronizability will generally be. Previous works show that there are two important factors that mainly affect the synchronizability R on directed networks: the in-degree distribution [4] and the hierarchical structure [22–25]. Generally speaking, the more homogeneous the in-degree distribution in a directed network, the stronger the network synchronizability. In some cases, the synchronizability in directed networks can be approximately expressed by $R \approx k^{\text{in}}_{\max}/k^{\text{in}}_{\min}$ [3]. Smaller R indicates better synchronizability. Accordingly, to enhance synchronizability in directed networks, we can either decrease $k^{\text{in}}_{\max}$ or increase $k^{\text{in}}_{\min}$, which respectively correspond to removing the links that point to the nodes with maximum in-degree or adding links that point to the nodes with minimum in-degree. Besides the in-degree distribution, which plays a dominant role in determining the synchronizability of directed networks, the hierarchical structure may also have considerable effects [26]. If the reconstructing strategy only aims at the homogeneous in-degree distribution, an effective hierarchical structure cannot be formed and the resultant synchronizability may fall into local optimum. Therefore, how to choose the starting points for adding and removing links is very important, which may affect the overall hierarchical structure and thus further affect the synchronizability. In this paper, we employ the PageRank algorithm [27] to characterize the centralities of nodes on directed networks and design a centrality-based manipulating (CBM) method to enhance synchronizability accordingly. Generally, if a directed network is hierarchically organized, the nodes with high PageRank scores are more likely to be at the high layer of the network, while those with low PageRank scores are probably located at the low layer. The basic idea of the CBM method is that the newly added links should start from high-layer nodes (with high PageRank scores), while we should choose the links to remove starting from the low-layer nodes (with low PageRank scores).

Performing the linear stability analysis of synchronizability [19–21] in directed networks, we find that the CBM method is more effective in facilitating synchronization than the *degree-based manipulating* (DBM) method and the *random manipulating* (RM) method. Furthermore, we apply the CBM method to the links rewiring procedure. At each step we first remove one link from the network and then add a new one according to the removing and adding strategies of the CBM method. After several steps, we find that the resulting networks are very close to the optimal structure from the evolutionary optimization algorithm [15] and the theoretical analysis [16]. The numerical simulations on the Kuramoto model [28] further demonstrate that our method has an advantage in shortening the convergence time to synchronization on directed networks.

2. The centrality-based manipulating method

Consider a directed and unweighted network with N nodes and E links. Denote by A the adjacency matrix where the element $A_{ij} = 1$ if there is a directed link from node i to node j, otherwise 0. Specifically, i is the start and j is the end. The average degree of the network is $\overline{k} = \frac{E}{N}$. In the synchronization process, each node stands for an oscillator and each directed link represents the influence of one oscillator on another. The synchronization in heterogeneous directed networks is approximately formed by a centralized control mechanism [29]. The oscillators with higher dynamic centrality are supposed to be more influential in driving the whole system to synchronize. In directed networks, there are many different ways to measure the node's centrality [27, 30–33]. One prominent group of methods is based on the random walk process, such as PageRank [27], HITs [32] and LeaderRank [33] algorithms. In this paper, we apply the well-known PageRank algorithm to quantify the node's centrality in a directed network.

PageRank is a famous ranking algorithm which forms the basis of the Google™ search engine [27]. It has been applied to rank scientists in citation networks [34] and to detect community structure in directed networks [35]. In practice, PageRank assigns a score s_i to denote the attractiveness of the webpage i. Webpage i obtains a higher score if many other important webpages point to it. From the physics perspective, PageRank describes a random walk process on a directed network, where the score s_i is proportional to the frequency of visits to a particular node i by a random walker. In PageRank algorithm, a parameter c, called *return* *probability*, is introduced, which represents the probability for a random walker to jump to a random node, and $1-c$ is the probability for the random walker to continue walking through the directed links. Note that in the oscillator network the link from node i to node j indicates that node i has an influence on node j, and the nodes that have a larger influence on other nodes are more important for the network synchronization. Therefore, in our case the random walker should follow the opposite direction of links. In this way, the node i's centrality score at time t ($t \geqslant 1$) is given by

$$s_i(t) = c + (1-c)\sum_{j=1}^{N}\left[\frac{A_{ij}}{k_j^{\mathrm{in}}}(1-\delta_{k_j^{\mathrm{in}},0}) + \frac{1}{N}\delta_{k_j^{\mathrm{in}},0}\right]s_j(t-1), \qquad (1)$$

where $\delta_{a,b}=1$ if $a=b$, and $\delta_{a,b}=0$ otherwise. Initially, we assign to each node one random walker, namely $s_i(0)=1$ for $i=1,2,\ldots,N$. The typical value of return probability is about 0.15 [27]. The final score of each node is defined as the steady value after the convergence of $s_i(t)$.

Generally speaking, if a directed network is hierarchically organized, the nodes with high PageRank scores are more likely to be at the high layers of the network, while those with low PageRank scores are probably located at the low layers (see appendix A for a detailed discussion). With this in mind, we propose a CBM method to enhance the synchronizability on directed networks by manipulating a fixed number of links. Since the network synchronizability can be characterized by the indicator $R \approx k_{\mathrm{max}}^{\mathrm{in}}/k_{\mathrm{min}}^{\mathrm{in}}$: the smaller R, the higher the synchronizability. Therefore, we have two ways to enhance synchronizability: increasing $k_{\mathrm{min}}^{\mathrm{in}}$ by adding links pointing to the nodes with minimum in-degree and decreasing $k_{\mathrm{max}}^{\mathrm{in}}$ by removing links pointing to the nodes with maximum in-degree. The starting nodes for adding and removing links are selected according to the nodes' centrality scores given by equation (1). To add a link, we choose node i with minimum in-degree as the end, and node j with maximum centrality among all the nodes that have not yet pointed to i as the start. To remove a link, we first guarantee that the end is of maximum in-degree and then among all possible candidates of starts, we choose the one with minimum centrality. This strategy will help to generate more *receptors*, namely nodes without any outgoing link, which is a favorable structure for synchronization. For details, one can see the discussion in section 3.2. Note that, after adding or removing a link, the centrality score of each node will be recalculated.

We consider two other methods for comparison: the RM method and the DBM method. The strategies of choosing the ends of these two methods are the same as CBM, namely adding a new link that points to the node with minimum in-degree and removing a link that points to the node with maximum in-degree. The difference is how to choose the starts. When adding or removing links by the RM method, the starts of the links are randomly selected. For the DBM method, when adding a link, the node with maximum out-degree and not yet pointing to the end will be chosen as the start, while when removing a link, the link starting with a node of minimum out-degree is removed. In the following section, we will compare the CBM method with the RM and DBM methods on three directed network models based on the linear stability analysis of synchronizability and the numerical simulation on the Kuramoto model.

3. Results

The framework of master stability analysis allows us to use $R=\lambda_N/\lambda_2$ to measure the synchronizability of an undirected network [19–21]. In directed networks, since the Laplacian matrix, defined as $L_{ij} = k_i^{\mathrm{in}}\delta_{ij} - a_{ij}$, is asymmetric with zero row sum, it has complex eigenvalues. In order to achieve the synchronization condition, every eigenvalue should be entirely contained in the region of negative Lyapunov exponent for the particular master stability function. If the stability zone is bounded and the imaginary part of the complex eigenvalue is small enough, the network synchronizability can be approximately measured by the real part of the eigenvalue ratio $R = \lambda_N^{\mathrm{r}}/\lambda_2^{\mathrm{r}}$, where λ_N^{r} and λ_2^{r} are, respectively, the largest and second smallest real parts of eigenvalues [22, 23]. Generally speaking, given the same value of the imaginary part of the eigenvalues, the smaller the ratio R the stronger the network synchronizability. This synchronizability measurement can be considered as an extension of the eigenvalue ratio for undirected networks [19]. For undirected networks, the synchronizability should be defined according to different types of synchronized regions, in which all the Lyapunov exponents are negative. The synchronized regions are determined by the dynamical function and output function of each node and can be classified into four types: (i) bounded (α_1, α_2), where $0 < \alpha_1 < \alpha_2$; (ii) unbounded (α_1, ∞), where $0 < \alpha_1$; (iii) several disconnected regions; (iv) empty set. The synchonizability applied in this paper is suitable for case (i) [19]; for case (ii), the synchronizability is measured by $1/\lambda_2$ [36]; case (iii) is very complicated (see [37]); and the system cannot be synchronized in case (iv). We use the eigenratio because it is the most widely used metric and the synchronization of case (i) requires that the coupling strength must be in a proper range (not too small or too large) while for case (ii), if the network is connected, it is always synchronizable given a sufficiently large coupling strength. The situation is even more complicated for generally non-symmetrically weighted networks where the directed networks are special examples. See [38] for detailed information. Moreover, we have actually numerically checked that our method does not increase and, sometimes, can even reduce the imaginary part when manipulating links. Therefore, we employ the indicator R to evaluate the network synchronizability in the following analysis.

In this paper, we mainly consider three kinds of directed networks: (i) a directed regular network with identical degree $\bar{k}$ and clockwise links. Here $\bar{k}$ indicates either the average in-degree or the average out-degree since these two values are the same. For example, $\bar{k} = 1$ means that each node has one in-link and one out-link. (ii) A variant of Watts–Strogatz (WS) network [39] (directed WS network). Starting from a directed regular network, each link will be reconnected with two randomly selected nodes with probability $p \in (0, 1)$. (iii) A variant of the Barabási–Albert (BA) network [40] (directed BA network). Starting from a directed tree with N_0 nodes, a new node with m links (m is a random integer between 1 and $k_{\max}$) is added to the network in each step until the total number of nodes reaches N. Each new added link connects to an existing node i with the probability $q_i = \frac{k_i^{\mathrm{in}} + k_i^{\mathrm{out}}}{2E}$. The link direction is set to be from older nodes to younger nodes.

3.1. Adding

The results for adding links in three modeled networks are reported in figure 1. Generally speaking, CBM performs best among all three methods. Specifically, in directed regular networks (see figure 1(a)) all three methods can decrease R by adding links. The result implies that the enhancement of synchronizability in this case is due to the decreasing of the average shortest distance of networks [41, 42]. However, readers are warned that a smaller average shortest distance alone cannot guarantee better synchronizability [43]. As we can see, the DBM method and the CBM method outperform the RM method, especially when many links are

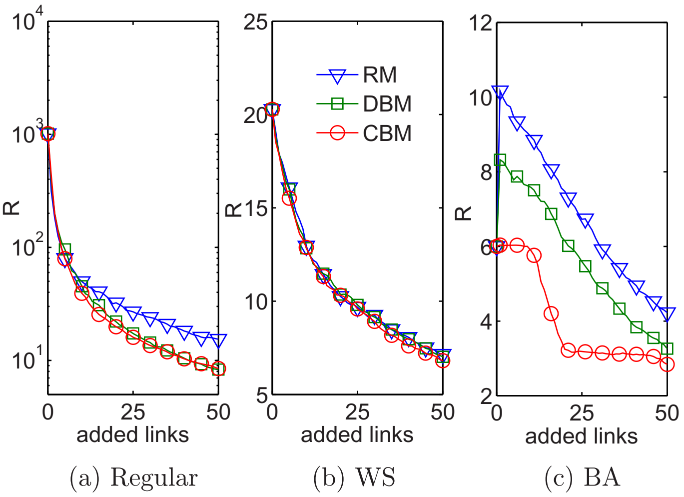


Figure 1. The performance of the RM, DBM and CBM methods on synchronizability when adding links to (a) directed regular networks ($N = 100$, $\bar{k} = 1$), (b) directed WS networks ($N = 100$, $\bar{k} = 3$, $p = 0.1$) and (c) directed BA networks ($N = 100$, $N_0 = 10$, $k_{\max} = 6$). The results are averaged over 100 independent realizations.

added. The reason is that the DBM method and the CBM method are capable of generating a network core during the adding process, which may involve one (when adding a small number of links) or several (when adding many links) nodes. The core node should have many outgoing links and mainly drives other nodes during the synchronizing process. In our experiments, the nodes whose out-degree is at least three times larger than the average degree are identified as core nodes. It has been pointed out that these core nodes (i.e. high-degree nodes) are favorable for the network synchronizability [15]. In contrast, the RM method is unable to induce such an effective core; thus its synchronizability enhancement is only from the decreasing of the average shortest distance. Two typical examples are shown in figures 2(a) and (b), which are obtained by adding 50 links to a directed regular network with RM and CBM methods, respectively. Clearly, there exists a center node as the core of the obtained CBM network yet there are no observable central nodes for the obtained RM network.

Figure 1(b) shows that the indicator R decreases with the increasing number of added links for all three methods and the difference between them is very small ($R_{\mathrm{CBM}} = 6.81$, $R_{\mathrm{DBM}} = 7.02$, $R_{\mathrm{RM}} = 7.16$). The enhancement mainly comes from narrowing the in-degree distribution. For the directed WS networks, even though the CBM and DBM methods can still form a core by adding a few links, the positive effect of the core is disrupted by the complicated structure of the initial network. Therefore, when adding a few links, like 50, compared with the RM method the synchronizability enhancements by CBM and DBM methods are very limited, respectively 4.9 and 2.0%. Note that, when we add more links, like 500, the improvements increase to 12.3 and 9.7% for the CBM and DBM methods ($R_{\mathrm{CBM}} = 1.71$, $R_{\mathrm{DBM}} = 1.76$, $R_{\mathrm{RM}} = 1.95$), respectively, since the effect of the initial network will be depressed. Additionally, the CBM and DBM methods can lead to shorter convergence time than the RM method due to the smaller core-distance (see section 3.4 for details of the Kuramoto model). Given a network, the core-distance is defined as the average shortest distance from the core node to all other nodes

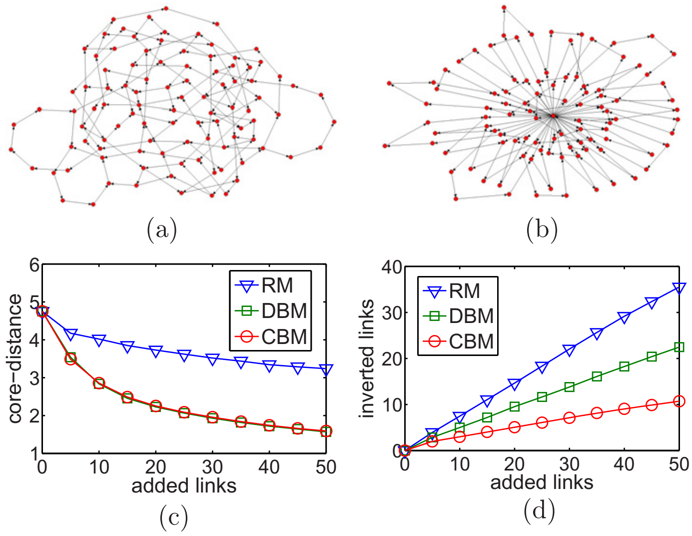
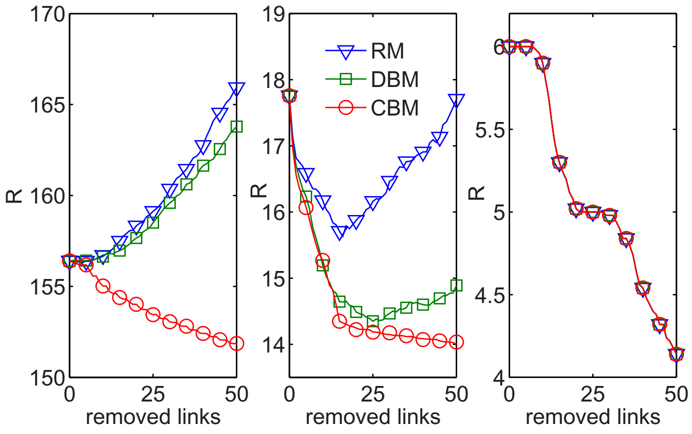


Figure 2. (a) The obtained network by adding 50 links to a directed regular network with the RM method. (b) The obtained network by adding 50 links to a directed regular network with the CBM method. (c) The dependence of core-distance on the number of added links in the directed WS networks. (d) The dependence of the number of inverted links on the number of added links in the directed BA networks. The parameters of the network models are the same as those in figure 1. The results in (c) and (d) are averaged over 100 independent realizations.

in this network. It was pointed out that the smaller the core-distance, the quicker the whole network converges to synchronization, since the core actually drives the whole network to the synchronized state [15]. The dependence of the core-distance on the number of added links in the directed WS networks is shown in figure 2(c). Note that, since there is no core in the RM network, we use the minimal distance from a node to all other nodes in the network (such a node is considered as a core). Clearly, the values of the core-distance of the CBM and DBM methods are much smaller than that of RM, and thus the CBM and DBM methods can result in shorter convergence time.

In directed BA models, as shown in figure 1(c) it is clear that the CBM method performs best. The directed BA model has an obvious hierarchical structure where the nodes with higher centrality scores tend to locate at the high layers. In the CBM method, the start of the new link is chosen as the node with the maximum centrality score; thus the generated core is actually the root node (in the highest layer) of the initial directed BA networks. In contrast, with the DBM method the core nodes are usually located at low layers. With starts in low layers many inverse links (i.e. links from low layers to high layers) will be formed, leading to a large number of loops. The situation is even worse with the RM method. The dependence of the number of inverse links on the number of added links of BA networks is shown in figure 2(d). We can see that the number of inverse links generated by the CBM method is fewer than for the DBM method and the RM method. The large number of loops is not beneficial to synchronization [22, 44], and thus in directed BA networks the CBM method can remarkably enhance the network synchronizability over the other two methods. The sudden jump of the



(a) Regular (b) WS (c) BA

Figure 3. The performance of the RM, DBM and CBM methods on synchronizability when removing links from (a) directed regular networks ($N = 100$, $\bar{k} = 3$), (b) directed WS networks ($N = 100$, $\bar{k} = 3$, $p = 0.1$) and (c) directed BA networks ($N = 100$, $N_0 = 10$, $k_{\max} = 6$). The results are averaged over 100 independent realizations.

indicator R for RM and DBM methods after adding one link is caused by the existence of a long loop that contains the root node. This loop breaks the leadership of the root node in driving the synchronizing process.

3.2. Removing

When removing links, the CBM method can enhance the synchronizability more effectively than the other two methods as shown in figure 3. In directed regular networks (see figure 3(a)), both the RM method and the DBM method weaken the synchronizability while the CBM method improves the synchronizability. By removing links, all three methods will destroy the uniform in-degree distribution in directed regular networks. However, the CBM method can generate a number of receptors (i.e. the nodes without any outgoing link) that are only affected by other nodes. This structure is favorable for synchronization since these receptors do not send back interruptive information to their upstream nodes. When removing the first link from the regular network, since the out-degree and the centrality score for all the nodes are the same, it is equivalent to a random selection of one link. After that, the node whose out-link was deleted will have the lowest centrality score. Therefore, in the next step a link starting from this node will again be removed, until all its out-links are removed. As a result, this node becomes a receptor. Figure 4(b) shows the number of generated receptors of the obtained networks when cutting 50 links by the three methods, respectively. The parameter $p = 0$ corresponds to regular networks, $p = 1$ to random networks and $0 < p < 1$ to WS networks. Clearly, the CBM method can generate more receptors than RM and DBM methods.

In directed WS networks, the CBM method also performs the best as shown in figure 3(b). At the beginning, the three methods can enhance the synchronizability by reducing the maximum in-degree in the networks. After the in-degree distribution becomes homogeneous, the situation will become similar to the directed regular networks. If we go on removing links

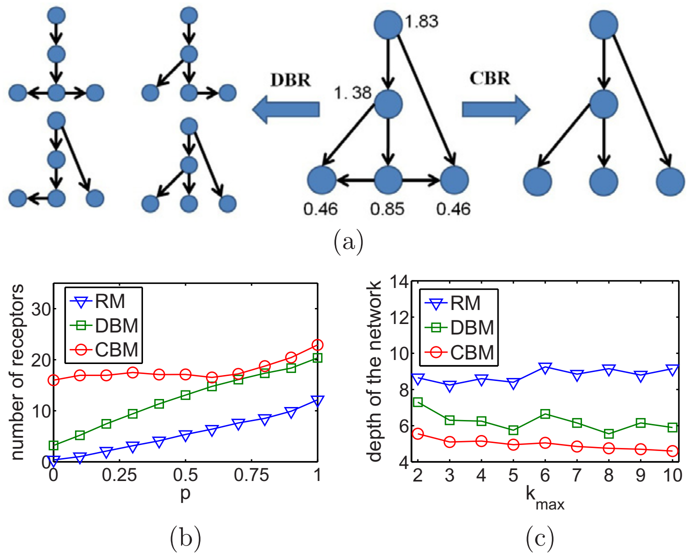


Figure 4. (a) A simple example to illustrate why the CBM method has an advantage in shortening the depth after removing links from directed BA networks. The nodes' centrality scores of the original network are labeled beside the nodes. (b) The number of generated receptors when cutting 50 links from directed WS networks by the three methods. The original networks are $N = 100$ and $\bar{k} = 3$ but with different p. (c) The depth of the obtained trees by three methods from directed BA networks. The original networks are $N = 100$ and $N_0 = 10$ but with different $k_{\max}$. The results in (b) and (c) are averaged over 100 independent realizations.

by the RM method or the DBM method, the synchronizability will be weakened since the homogeneous in-degree distributions are broken. By creating many receptors, the CBM method can further enhance the synchronizability and even the homogeneous in-degree distribution gets destroyed.

In directed BA models, the synchronizability is identical in the three methods since in acyclic networks the synchronizability is totally determined by the maximum and minimum in-degree. In figure 3(c), each stair corresponds to a typical maximum in-degree of the networks. Even though the three methods obtain the same synchronizability, the convergence time to synchronization is different. By removing the links from nodes in relatively lower layers, the obtained networks will converge faster to synchronization [24, 25]. Figure 4(a) gives a typical example to compare the DBM and CBM methods. By defining the *depth* of a tree as the maximum shortest path length from each node to the root node, we can see that after removing two links by the CBM method from the middle plot the depth of the obtained tree is 2. The DBM method can lead to four different trees with equal probability. Since three of them are of depth 3 and the other is of depth 2, the expected depth of the obtained tree by DBM is 2.75. The statistical results on the depth of the obtained trees after removing links from the directed BA models are shown in figure 4(c). Clearly, the CBM method can generate a tree with a shorter depth than the RM and DBM methods, and thus the networks obtained by the CBM method can converge faster to the synchronized state. See the Kuromoto model in section 3.4 for numerical evidence.

Table 1. The synchronizability $R = \lambda^{r}_{N}/\lambda^{r}_{2}$ and the largest imaginary parts of the eigenvalues Max(c) of the networks obtained by rewiring 300 links through RM, DBM and CBM methods. The network parameters are set as follows: $N = 100$ and $\bar{k} = 3$ for regular networks; $N = 100$, $\bar{k} = 3$ and $p = 0.1$ for WS networks; $N = 100$, $\bar{k} = 3$ and $p = 1$ for Erdös–Rényi (ER) networks [45]; $N = 100$, $N_0 = 10$, $k_{\max} = 6$ and $\bar{k} = 3$ for BA networks. The synchronizability of the original networks (R_0), the optimal cases from the evolutionary optimization algorithm (R-opt and R/c-opt) and theoretical analysis (R-theory) are shown for comparison.

	Regular		WS		ER		BA	
	$\lambda^{r}_{N}/\lambda^{r}_{2}$	Max(c)	$\lambda^{r}_{N}/\lambda^{r}_{2}$	Max(c)	$\lambda^{r}_{N}/\lambda^{r}_{2}$	Max(c)	$\lambda^{r}_{N}/\lambda^{r}_{2}$	Max(c)
R_0	156.43	2.49	18.38	2.19	239.49	1.27	6.00	0
R_{RM}	3.58	1.75	3.44	1.74	3.21	1.71	3.12	1.71
R_{DBM}	1.38	0.52	1.43	0.58	1.44	0.56	1.34	0.13
R_{CBM}	1.36	0.25	1.37	0.32	1.42	0.34	1.33	0.01
R-opt	1.17	1.0	1.17	1.0	1.17	1.0	1.17	1.0
R-opt	1.34	0	1.34	0	1.34	0	1.34	0
R-theory	1.33	0	1.33	0	1.33	0	1.33	0

3.3. Rewiring

An integrated way is to enhance the synchronizability by rewiring links while keeping the total number of links unchanged. In each step, we first remove a link from the network according to the strategy of removing links (see section 3.2) and then add a link according to the strategy of adding links (see section 3.1). Starting from different network models, we rewire 300 links via the RM, DBM and CBM methods, respectively. The synchronizability R of the obtained networks is shown in table 1.

The corresponding optimal synchronizability for such directed networks is studied by the evolutionary optimization algorithm [15] and the theoretical analysis [16]. In [15], the author considered two different indices as the 'fitness'. The author simply tries to minimize $R = \lambda^{r}_{N}/\lambda^{r}_{2}$ in the first type (denoted as R-opt). In the second type (denoted as R/c-opt), he minimizes R and makes sure that there is no imaginary part in all the eigenvalues. In [16], the authors provided the theoretical optimal synchronizability for a network with any given size and link density. Their objective function is to minimize R while keeping all eigenvalues without an imaginary part, so the theoretical optimal result is corresponding to and only comparable to the second case in the result from the evolutionary optimization algorithm. Here, we find that the synchronizability corresponding to the CBM method is very close to these optimal cases as shown in table 1. In addition, the topology of the obtained CBM network is very similar to the optimal structure, such as the emergence of the hierarchical structures and the existence of core nodes. These results indicate that the CBM method is effective in enhancing the synchronizability via link rewiring.

Note that the network size does not affect our main results. We have checked the link adding and link removing methods for different network sizes and the obtained results are consistent with those presented in figures 1 and 3. For the rewiring process, we report in figure 5

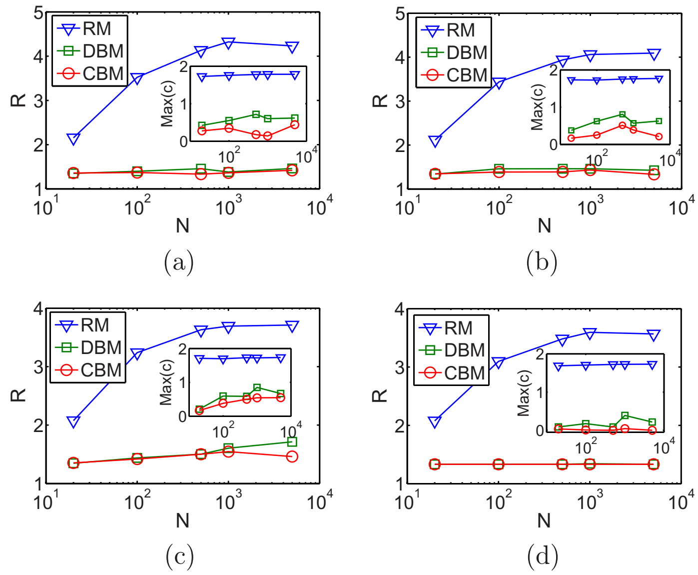


Figure 5. The dependence of the synchronizability R and the maximum imaginary parts of the eigenvalues (shown in the insets) on the network size in four different types of original networks after rewiring $N \cdot \overline{k}$ links on: (a) regular, (b) SW, (c) ER and (d) BA. In all these original networks, the average degree $\overline{k} = 3$.

how the synchronizability R and the largest imaginary parts of the eigenvalues change with the network size. As shown in figure 5, the network size indeed affects the results of the RM method, whereas the results of DBM and CBM methods are rather stable. More importantly, the CBM outperforms the DBM method in both R and the maximum imaginary part of the eigenvalue for different network sizes, indicating that our main conclusions are not sensitive to the network size.

3.4. The Kuramoto model

For the purpose of monitoring the effects of different rewiring methods on the convergence time to synchronization, we study the Kuramoto model [28] in the resulting networks. The dynamics of N coupled oscillators is described by the equation

$$\dot{\theta}_i = \omega_i + \frac{K}{\overline{k}} \sum_{j=1}^{N} A_{ji} \sin(\theta_j - \theta_i), \tag{2}$$

where ω_i and θ_i are the natural frequency and the phase of oscillator i, respectively. In this paper, ω follows a uniform distribution $(-1,\ 1)$, and the initial phase θ of the oscillators follows a uniform distribution $(-\pi, \pi)$. The coupling strength K is set to be a positive constant; here we fix $K = 10$ for convenience. The collective dynamics of the whole population is measured by the macroscopic complex order parameter

$$r(t)\mathrm{e}^{\mathrm{i}\phi(t)} = \frac{1}{N} \sum_{j=1}^{N} \mathrm{e}^{\mathrm{i}\theta_j(t)}, \tag{3}$$

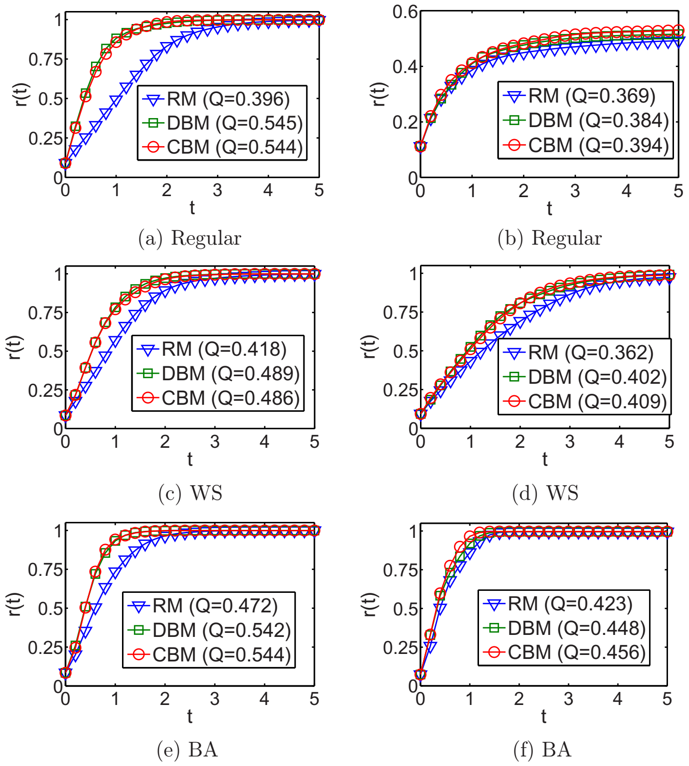


Figure 6. The order parameter of the Kuramoto model on (a) the obtained networks by adding 50 links to directed regular networks, (b) the obtained networks by removing 50 links from directed regular networks, (c) the obtained networks by adding 50 links to directed WS networks, (d) the obtained networks by removing 50 links from directed WS networks, (e) the obtained networks by adding 50 links to directed BA networks, (f) the obtained networks by removing links from directed BA networks. The network parameters are the same as in figure 1. The results are averaged over 100 implementations.

where the modulus $0 \leqslant r(t) \leqslant 1$ measures the phase coherence of the population and $\phi(t)$ is the average phase. $r(t) \simeq 1$ and $r(t) \simeq 0$ describe the limits in which all oscillators are, respectively, phase locked and moving incoherently. In order to monitor how fast the Kuramoto model reaches synchronization, we define a measure Q that reads

$$Q(T) = \frac{\sum_{i=1}^{T} r(t_i)\,(t_i)^{-1}}{\sum_{i=1}^{T} (t_i)^{-1}}, \tag{4}$$

where T is the number of observation points in the simulation (in our study $T = 500$ according to figure 6), and $t_i = i\Delta t$ $(i = 1, 2, \ldots, T)$ where Δt indicates the time interval of the Kuramoto model. Actually, Q is an average weighted parameter, which favors those cases where synchronization is reached more quickly. By using this measure, the results of the networks from different methods can be more easily distinguishable.

In figure 6, we compare the behavior of the Kuramoto model and the corresponding Q value on the networks obtained from (a) adding 50 links to directed regular networks, (b) removing 50 links from directed regular networks, (c) adding 50 links to directed WS networks, (d) removing 50 links from the directed WS model, (e) adding 50 links to directed BA networks and (f) the obtained tree by removing links from directed BA networks.

As we can see from figure 6, Q of both DBM and CBM networks are significantly larger than the Q of RM networks, indicating that, when manipulating the network to improve the network synchronization, consideration of the nodes' centrality can be really helpful. Moreover, the Q value suggests that CBM outperforms DBM in some networks since CBM can make use of hierarchical information.

As mentioned above, the emergence of the network core can greatly shorten the convergence time. The smaller the core-distance, the more quickly the whole network converges to synchronization, since the core actually drives the whole network to the synchronized state. In figures 6(a), (c) and (e), it is obvious that the CBM and DBM networks have a shorter convergence time than the RM method owing to the smaller core-distance.

In figure 6(b), the network cannot reach complete synchronization. However, it can be seen that the order parameter of CBM networks is higher than the RM and DBM networks, in accordance with the higher synchronizability predicted by the master stability analysis. Figure 6(d) shows that the networks from the CBM and DBM methods converge faster than those from the RM method. It is because RM is more likely to remove long-range links, resulting in an increase of the average distance of the network, which usually corresponds to a longer convergence time. In contrast, in the directed WS networks, the starts of the long-range links usually have relatively large out-degrees and high PageRank scores, and therefore are not likely to be removed according to the CBM or DBM methods. As shown in figure 6(f), Q of the CBM network is the largest, which indicates that the CBM method leads to the smallest convergence time among the three methods. Since the PageRank centrality score can help the CBM method to recognize the hierarchical structure of the directed BA network, the final spanning trees of resulting networks obtained by the CBM method are always of less depth than the DBM and RM methods (see also figure 4(c)), resulting in faster convergence.

4. Conclusion

In summary, we proposed a CBM method to facilitate synchronization in directed networks. The centrality is measured by the PageRank algorithm. Numerical analysis of three network models shows that the CBM method is more effective in enhancing network synchronizability than the DBM method and the RM method. Specifically, when adding links, the CBM method forms a wisely located core to drive the whole network to the synchronized state. When removing links, the CBM method generates a number of receptors which only receive information and do not disturb the upstream nodes. Furthermore, the CBM method can also be extended to deal with the link rewiring problem. Significantly, the network obtained through the CBM link rewiring method has very close synchronizability to the corresponding optimal case obtained by the evolutionary optimization algorithm. The result from the Kuramoto model also shows that the CBM method has an advantage in shortening the convergence time to synchronization.

This paper considers a general method for enhancing the synchronizability of networks, and investigates not only the synchronizability under the master stability analysis but also the Kuramoto model. Therefore, one would expect that this method is widely applicable to many real systems involving a synchronized process such as a power grid [14], a wireless communication system [46], opinion formation [47] and so on. In some specific systems such as ecosystems [48] and neuron systems [49], synchronization should be inhibited in some cases.

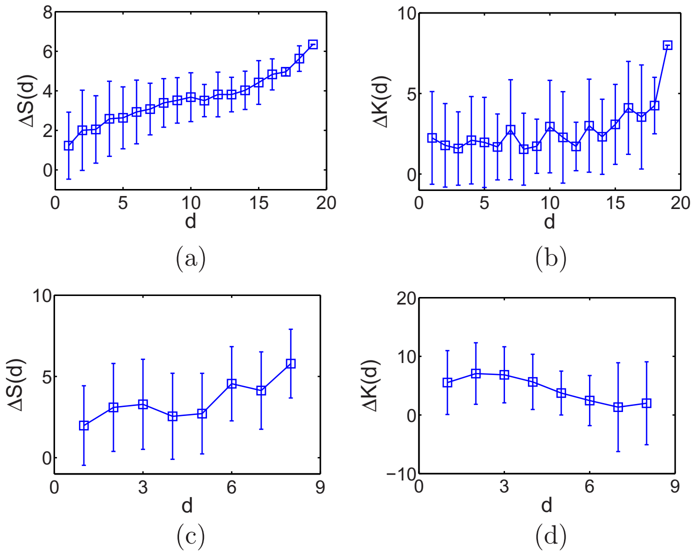


Figure A.1. The relation between $\Delta S(d)$ and d in tree networks (a) and directed BA networks (c). The relation between $\Delta K(d)$ and d in tree networks (b) and directed BA networks (d). The error bars are the standard deviations. In the tree networks, $N = 100$, depth $= 20$. In the BA networks, $N = 100$, $k_{\max} = 6$ and $\overline{k} = 3$. The results are averaged over 100 random samples.

In such a situation, the inverted CBM method can be applied to decrease the synchronizability, namely to add links starting from the nodes with low centrality scores to the nodes with high in-degrees and to remove the links whose starts have high centrality scores and whose ends have low in-degrees (see appendix B for the supporting results).

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Appendix A. The hierarchical structure reflected by the PageRank score

Let us consider two kinds of directed networks with an obvious hierarchical structure, namely the tree network and the directed BA model. Specifically, the tree network with N nodes and L layers is generated starting from a directed train with length L, in which each node represents a layer. Then the remaining $N - L$ nodes are added one by one. Each new added node is connected by a directed link starting from one of its ancestors that is not located in the layer L. When new links are added to these networks to enhance the synchronization, the new link should not start from one node to its upstream nodes (node x is an upstream node of node y if there exists at least one directed path from x to y and there is no directed path from y to x); otherwise loops will be generated and the synchronizability will be weakened. Suppose that we select one node i and denote its PageRank score and out-degree as s_i and k_i^{out}, respectively. Then we

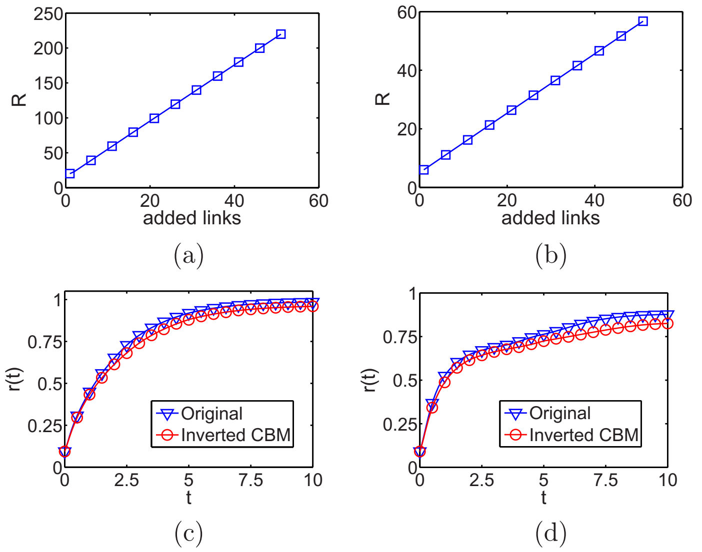

Figure B.1. The performance of the inverted CBM method on synchronizability when adding links to (a) directed SW networks and (b) directed BA networks. (c) and (d) are the order parameters of the Kuramoto model on original SW networks, BA networks and resulting networks after adding 50 links by the inverted CBM method. The network parameters are the same as those in figure 1 and the parameters for the Kuramoto are set the same as those in figure 6.

select one of its upstream nodes j with the shortest path length d to node i; the PageRank score and out-degree are s_j and k_j^{out}. In order to avoid the new link from the lower hierarchy to the higher hierarchy, s_j should be larger than s_i. Accordingly, we calculate $\Delta S(d) = s_j - s_i$ and $\Delta K(d) = k_j^{\text{out}} - k_i^{\text{out}}$ in the tree networks and directed BA networks. As we can see from figure A.1, $\Delta S(d)$ is generally larger than 0 and increases with d. Therefore, maximizing the PageRank centrality during adding links can guide the links from higher hierarchy to lower hierarchy. However, $\Delta K(d)$ is smaller than 0 in a large range and does not have a clear positive correlation with d. It indicates that out-degrees cannot reflect well the hierarchical structure of the network.

Appendix B. The inverted centrality-based manipulating method for inhibiting synchronization

In the inverted CBM method for adding links, at each step, we first select node i with the largest in-degree, and add a new link from the node with the smallest PageRank score to node i. Here, we considered the directed SW and BA models, and added some additional links based on the inverted CBM method. Note that we did not consider the regular network for experiments because it has been approved that the synchronizability can be generally enhanced by adding links to those regular networks (such as ring or lattice networks) [1]. The results (see figure B.1) from both the synchronizability R and the Kuramoto model suggest that the inverted CBM method can significantly inhibit synchronization. In the inverted CBM method for removing links, the link which points to the node with minimum in-degree will be removed first. As a result, some nodes will be immediately isolated and the network can never reach complete synchronization ($R \to \infty$). Finally, we remark that the strategy for inhibiting synchronization is a new topic for both directed and undirected networks. The inverted CBM method can be used to weaken the synchronization, but we believe that there will be some more effective strategies for this task, which call for further study in the future.

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