

Abnormal Synchronization in Complex Clustered Networks

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Recent research has revealed that complex networks with a smaller average distance and more homogeneous degree distribution are more synchronizable. We find, however, that synchronization in complex, clustered networks tends to obey a different set of rules. In particular, the synchronizability of such a network is determined by the interplay between intercluster and intracluster links. The network is most synchronizable when the numbers of the two types of links are approximately equal. In the presence of a mismatch, increasing the number of intracluster links, while making the network distance smaller, can counterintuitively suppress or even destroy the synchronization. We provide theory and numerical evidence to establish this phenomenon.

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There has been a growing interest in the synchronizability of complex networks [1–3]. Earlier works [1] suggest that small-world [4] and scale-free [5] networks are generally more synchronizable than regular networks. While heterogeneous degree distributions can inhibit synchronization [2], adding suitable weights to the network elements can enhance their chances to synchronize with each other [3]. In general, given a complex network with a fixed number of nodes, its synchronizability can be improved by increasing the number of links. This is intuitive as a denser linkage makes the network more tightly coupled or “smaller,” thereby facilitating synchronization.

In this Letter, we present a counterintuitive finding about the synchronizability of clustered networks. A clustered network consists of a number of groups, where nodes within each group are densely connected, but the linkage among the groups is sparse [6]. These networks have recently been discovered in important areas of biological physics [7,8]. A complex clustered network is typically small world so that its average distance is small. Moreover, its degree distribution can be made quite homogeneous. The surprising phenomenon is that more edges (links), which make the network smaller, do not necessarily lead to stronger synchronizability. There can be situations where more edges can even suppress synchronization if placed improperly. In particular, we find that the synchronizability of a clustered network is determined by the interplay between the interconnections (links among clusters) and intraconnections (links within clusters) of the network. Strong synchronizability requires that the numbers of the interlinks and intralinks be approximately matched. In this case, increasing the number of links can indeed enhance the synchronizability. However, if the

matching is deteriorated, synchronization can be severely suppressed or even totally destroyed.

Our finding can have potential impacts on real network dynamics. In particular, there is mounting evidence that several types of biological networks possess a clustered structure, such as the metabolic networks [7] and the protein interaction graphs [8]. In biology, synchronization is fundamental, on which many biological functions rely. Our result implies that, in order to achieve robust synchronization for a clustered biological network, the characteristics of the links are more important than the number of links. Simply counting the number of links may not be enough to determine its synchronizability. Instead, links should be distinguished and classified to predict synchronization-based functions of the network. Clustered structure has also been identified in technological networks such as electronic circuit and computer networks [9]. Suppose a large-scale, parallel computational task is to be accomplished by a computer network, for which synchronous timing is of paramount importance. Our result can provide clues as to how to design the network to achieve the best possible synchronization and consequently optimal computational efficiency.

Our approach is to introduce nonlinear dynamics on each node in the network and then perform stability and eigenvalue analyses [10,11]. The theoretical derivation yields the stability regions for synchronization in the two-dimensional parameter space defined by the numbers of the two types of links. The analytic predictions are verified by numerical simulations.

We consider a random clustered network model: N nodes are classified into M groups, where each group has $n = N/M$ nodes. In a group, a pair of nodes is connected

with probability p_s , and nodes belonging to different groups are connected with probability p_l . For a clustered network, the number of interconnections is typically far less than the number of intraconnections. As a result, the parameter region of small p_l values is more relevant. To be concrete, we first study the following general class of coupled-map networks: $\mathbf{x}_{m+1}^i = \mathbf{f}(\mathbf{x}_m^i) - \varepsilon \sum_j G_{ij} \mathbf{H}[\mathbf{f}(\mathbf{x}_m^j)]$, where $\mathbf{x}_{m+1} = \mathbf{f}(\mathbf{x}_m)$ is a d -dimensional map, ε is a global coupling parameter, \mathbf{G} is the Laplacian matrix, and \mathbf{H} is a coupling function. For convenience we choose $G_{ij} = -A_{ij}/k_i$ for $j \neq i$ and $G_{ii} = 1$, where k_i is the degree of node i and A_{ij} is an element of the adjacent matrix \mathbf{A} of the network. Since the rows of the coupling matrix \mathbf{G} have zero sum, the system permits an exact synchronized solution: $\mathbf{x}_m^1 = \mathbf{x}_m^2 = \dots = \mathbf{x}_m^N = \mathbf{s}_m$, where $\mathbf{s}_{m+1} = \mathbf{f}(\mathbf{s}_m)$. To gain insight, we set $\mathbf{f}(\mathbf{x})$ to be the logistic map $f(x) = 1 - ax^2$ ($0 < a \leq 2$) and choose $\mathbf{H}(\mathbf{x}) = x$. If the system is synchronizable, starting from a random initial condition, it will approach the synchronization state. In the simulation, synchronization is defined as $\langle |x_i - \langle x_i \rangle| \rangle < 10^{-10}$, where $\langle \cdot \rangle$ denotes the average over the network. The average time T required for the system to become synchronized can be used to characterize the ability of the system to synchronize. If the system is unsynchronizable, T is infinite. Figure 1 shows the behavior of T in the two-dimensional parameter space (p_l, p_s) for networks with 2 clusters (a) and 10 clusters (b). This gives the synchronizable region (gray regions in Fig. 1) in the parameter space that the system is able to synchronize within a certain time, and the unsynchronizable region (white regions in Fig. 1). The shape of the figure depends on the coupling strength ε and on the contour lines of λ_2 and λ_N (see Fig. 2). For 2-cluster networks, if $\varepsilon = 1$, the shape appears to be symmetric, while if $\varepsilon < 1$, the boundary is asymmetric. Figure 1(a) demonstrates that for a given p_l (e.g., 0.2), as p_s is increased from 0.2, synchronization time T is also increased. At a certain point (about 0.75 in this case), the system becomes unsynchronizable. That is, too many intra-links tend to destroy the global synchronization [12].

For the coupled-map network, the variational equations are

$$\delta \mathbf{x}_{m+1}^i = \mathbf{Df}(\mathbf{s}_m) \cdot \delta \mathbf{x}_m^i - \varepsilon \sum_j G_{ij} \mathbf{DH}[\mathbf{f}(\mathbf{s}_m)] \cdot \mathbf{Df}(\mathbf{s}_m) \cdot \delta \mathbf{x}_m^j, \quad (1)$$

where $\delta \mathbf{x}^i \equiv \mathbf{x}^i - \mathbf{s}$, and \mathbf{Df} and \mathbf{DH} are the Jacobian matrices of the corresponding vector functions. Diagonalizing the Laplacian matrix G yields a set of eigenvalues $\{\lambda_i, i = 1, \dots, N\}$, which are real and non-negative [11]. Thus we can sort the eigenvalues as $0 = \lambda_1 \leq \lambda_2 \leq \dots \leq \lambda_N$ and denote the corresponding normalized eigenvectors by $\mathbf{e}_1, \mathbf{e}_2, \dots, \mathbf{e}_N$. The smaller the ratio λ_N/λ_2 , the stronger the synchronizability of the network [1–3]. The transform $\delta \mathbf{y} = \mathbf{O}^{-1} \cdot \delta \mathbf{x}$, where \mathbf{O} is a matrix whose columns are the set of eigenvectors, leads to the block-diagonally decoupled form of Eq. (1),

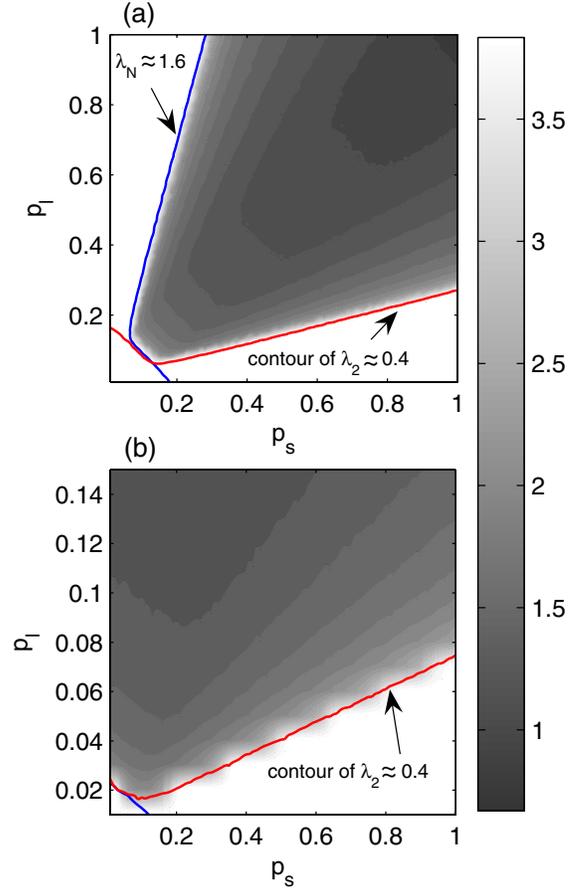


FIG. 1 (color online). Contour plot of the synchronization time T (on a logarithmic scale $\log_{10} T$) in (p_l, p_s) space for coupled logistic-map network with (a) $N = 100, M = 2$, and (b) $N = 500, M = 10$. $\varepsilon = 1, a = 1.9$. The line segments defining the boundaries between the synchronizable and unsynchronizable regions are determined by theory. Each data point is the result of averaging over 100 network realizations.

$\delta \mathbf{y}_{m+1}^i = \{\mathbf{I} - \varepsilon \lambda_i \mathbf{DH}[\mathbf{f}(\mathbf{s}_m)]\} \cdot \mathbf{Df}(\mathbf{s}_m) \cdot \delta \mathbf{y}_m^i$. The system is stable if for any $i, 2 \leq i \leq N$, the following holds: $\lim_{m \rightarrow \infty} (1/m) \ln(|\delta \mathbf{y}_m^i|/|\delta \mathbf{y}_0^i|) = \lim_{m \rightarrow \infty} (1/m) \times \ln \prod_{j=0}^{m-1} (|\delta \mathbf{y}_{j+1}^i|/|\delta \mathbf{y}_j^i|) < 0$. For a linear coupling function \mathbf{H} , \mathbf{DH} is a constant matrix. If the system is one dimensional, \mathbf{DH} is simply a constant, say, γ . We obtain $\ln|1 - \varepsilon \lambda_i \gamma| + \lim_{m \rightarrow \infty} (1/m) \ln \prod_{j=0}^{m-1} |f'(s_j)| < 0$, where the second term is the Lyapunov exponent μ of a single map. We have $|e^\mu(1 - \varepsilon \lambda_i \gamma)| < 1$ for $i = 2, \dots, N$. For the coupled logistic-map network, we have [11] $\gamma = 1$ and $|e^\mu(1 - \varepsilon \lambda_i)| < 1, i = 2, \dots, N$. Because of the ordering of the eigenvalues, this condition becomes $\lambda_2 > (1 - e^{-\mu})/\varepsilon$ and $\lambda_N < (1 + e^{-\mu})/\varepsilon$. The boundaries of the synchronization regions in the parameter space can be determined by setting $\lambda_2 = (1 - e^{-\mu})/\varepsilon$ and $\lambda_N = (1 + e^{-\mu})/\varepsilon$. In our simulations, we have used $a = 1.9$ ($\mu \approx 0.55$). Thus we have $\lambda_2 \approx 0.4$ and $\lambda_N \approx 1.6$ for $\varepsilon = 1$, the contour lines of which are shown in Fig. 1. There is a good agreement between the theory and numerics. If the cou-

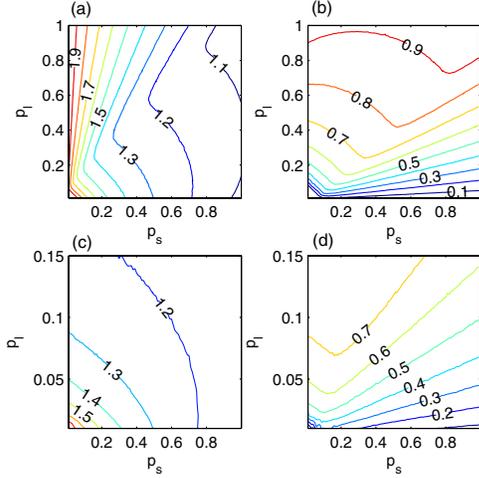


FIG. 2 (color online). Contour plot of λ_N (a), (c) and λ_2 (b), (d) in the (p_l, p_s) plane, for $N = 100$ and $M = 2$ (a), (b) and $N = 500$ and $M = 10$ (c), (d).

pling function \mathbf{H} is nonlinear, $\mathbf{DH}[\mathbf{f}(\mathbf{s}_m)]$ will depend on the value of $\mathbf{f}(\mathbf{s}_m)$ and it is difficult to obtain explicit boundaries for λ_2 and λ_N .

To better understand the abnormal behavior of the dependence of synchronizability on p_s , we analyze the eigenvalues of the Laplacian matrix of a general clustered network. Figure 2 shows the contour plots of the λ_N and λ_2 in the parameter space, for 2 [2(a) and 2(b)] and 10 [2(c) and 2(d)] clusters. There is an apparent similarity between some of the contour lines and the stability boundaries in Fig. 1. From Fig. 2 we can see that, for a given value of p_l , λ_N decreases as p_s increases, so it is easier to synchronize the network. However, for large values of p_s , λ_2 decreases as p_s increases, thus synchronization becomes more difficult. We see that the behavior of λ_2 accounts for the abnormal synchronizability behavior shown in Fig. 1. In the following, we shall derive a theoretical formula to understand the dependence of λ_2 on p_l and p_s for small values of p_l (typical parameter regime of clustered networks).

For a clustered network, the components of the eigenvector \mathbf{e}_2 have approximately the same value within any cluster, while they can vary among clusters, as demonstrated in Fig. 3. Thus, we can write $\mathbf{e}_2 \approx [\tilde{e}_1, \tilde{e}_1, \dots, \tilde{e}_1, \tilde{e}_2, \dots, \tilde{e}_2, \tilde{e}_3, \dots, \tilde{e}_3]^T$, where $[\ast]^T$ denotes the transpose, and for each I , $1 \leq I \leq M$, there are $n \tilde{e}_I$'s in \mathbf{e}_2 . By definition, $\mathbf{G} \cdot \mathbf{e}_2 = \lambda_2 \mathbf{e}_2$ and $\mathbf{e}_2 \cdot \mathbf{e}_2 = 1$, we have $\lambda_2 = \mathbf{e}_2^T \cdot \mathbf{G} \cdot \mathbf{e}_2 = \sum_{i,j=1}^N e_{2i} G_{ij} e_{2j}$, where e_{2i} is the i th component of \mathbf{e}_2 . Expanding the summation in j yields $\lambda_2 = \sum_{i=1}^N e_{2i} \{G_{i1} \tilde{e}_1 + G_{i2} \tilde{e}_1 + \dots + G_{in} \tilde{e}_1 + G_{i(n+1)} \tilde{e}_2 + \dots + G_{iN} \tilde{e}_M\}$. If i and j belong to the same cluster, G_{ij} equals $-1/k_i$ with probability p_s and 0 with probability $1 - p_s$; while if i and j belong to different clusters, G_{ij} equals $-1/k_i$ with probability p_l and 0 with probability $1 - p_l$. We thus have $\lambda_2 = \sum_{i=1}^N e_{2i} [N(p_l/k_i) \tilde{e}_1 - n(p_l/k_i) \sum_{j=1}^M \tilde{e}_j]$, where \tilde{e}_I is the component associated with the cluster that contains node i ,

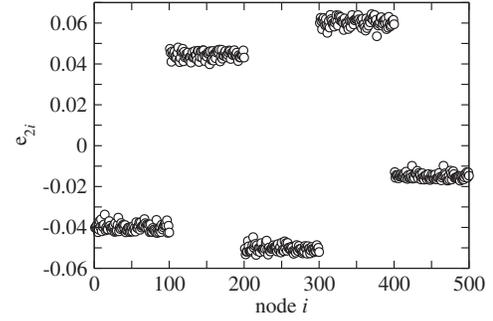


FIG. 3. A typical profile of components of the eigenvector \mathbf{e}_2 . Parameters are $N = 500$, $M = 5$, $p_l = 0.01$, and $p_s = 0.8$.

and the equality $1 - np_s/k_i = (N - n)p_l/k_i$ has been used. For a randomly clustered network, the degree distribution has a narrow peak centered at $k = np_s + (N - n)p_l$, implying $k_i \approx k$. This allows us to carry out the summation over i . We obtain $\lambda_2 \approx N(\sum_{I=1}^M n \tilde{e}_I^2) p_l/k - (n \sum_{j=1}^M \tilde{e}_j)^2 p_l/k$. Since $\sum_{I=1}^M n \tilde{e}_I^2 \approx \sum_{i=1}^N e_{2i}^2 = 1$, and $n \sum_{j=1}^M \tilde{e}_j = \sum_{i=1}^N e_{2i}$, we have

$$\lambda_2 = \frac{N p_l}{n p_s + (N - n) p_l} - \left(\sum_{i=1}^N e_{2i} \right)^2 \frac{p_l}{k}. \quad (2)$$

As the normalized eigenvector \mathbf{e}_1 associated with λ_1 describes the synchronized state, its components are identical: $\mathbf{e}_1 = [1/\sqrt{N}, \dots, 1/\sqrt{N}]^T$. If \mathbf{G} is symmetric, its eigenvectors are orthogonal to each other: $\mathbf{e}_i \cdot \mathbf{e}_j = \delta_{ij}$, where $\delta_{ij} = 1$ for $i = j$ and 0 else. Taking $i = 1, j = 2$ we have $\sum_{i=1}^N e_{2i} = 0$. If \mathbf{G} is slightly asymmetric (as for a weighted network), $\sum_{i=1}^N e_{2i}$ is nonzero but small, and the second term in Eq. (2) can be neglected. These approximations lead to

$$\lambda_2 \approx \frac{N p_l}{n p_s + (N - n) p_l}. \quad (3)$$

For $p_l \ll p_s$, the above equation agrees well with the numerics. This provides an analytic explanation for the observed abnormal behavior. Furthermore, the fact that λ_2 depends only on the ratio of p_l/p_s explains the straightline patterns in Fig. 1 and in Fig. 2(b) and 2(d) for $p_s > p_l$.

The above analysis can be extended to more general clustered networks, i.e., those with different cluster sizes or heterogeneous degree distributions in each cluster, by replacing n with n_I —the size of the I th cluster—for each I , and using the degree distribution $P_I(k)$ in the summation over $1/k$. In this case, p_s and p_l can be regarded as effective parameters, and may vary for different clusters. A formula similar to Eq. (3) can be obtained, because even in such a case, the contribution of the second term in Eq. (2) is small.

To assess the generality of the abnormal synchronization behavior, we have considered clustered networks of continuous-time oscillators, e.g., $d\mathbf{x}_i/dt = \mathbf{F}(\mathbf{x}_i) - \epsilon \sum_{j=1}^N G_{ij} \mathbf{H}(\mathbf{x}_j)$, where $\mathbf{x} = [x, y, z]^T$, $\mathbf{F}(\mathbf{x}) = [-(y + z), x + 0.2y, 0.2 + z(x - 9)]^T$ (the Rössler oscilla-

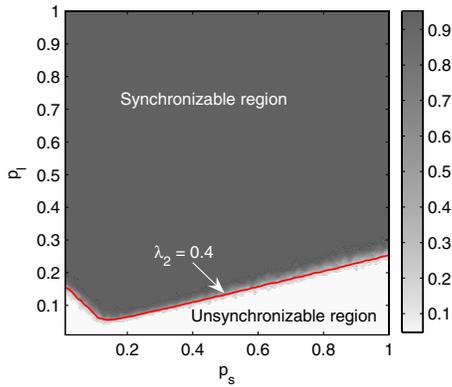


FIG. 4 (color online). Contour plot of synchronization probability of a clustered network of Rössler oscillators with $N = 100$ and $M = 2$. $T_0 = 10^4$ and $\epsilon = 0.5$. Each datum is the result of averaging over 1000 network realizations. The boundary is obtained by theoretical analysis.

tor), and $\mathbf{H}(\mathbf{x}) = [x, 0, 0]^T$ is a linear coupling function, and \mathbf{G} is the Laplacian matrix describing the network topology. The master stability function $\Psi(K)$ is negative in the interval $[K_1, K_2]$, and the system is stable if $K_1 < \epsilon\lambda_2 \leq \dots \leq \epsilon\lambda_N < K_2$ [10]. For the parameters given above, $K_1 \approx 0.2$, $K_2 \approx 4.62$. Thus the stable condition becomes $\lambda_2 > K_1/\epsilon$ and $\lambda_N < K_2/\epsilon$. Figure 4 shows the boundary from the above analysis with $\epsilon = 0.5$, and the synchronization probability [the probability that $\langle |x_i - \langle x_i \rangle| \rangle < 0.01$ in a time interval of $T_0 = 10^4$]. We see that the matching condition of the number of inter- and intra-links plays the same role in shaping the synchronizability of the continuous-time network system.

In conclusion, we have uncovered a phenomenon in the synchronization of complex clustered networks, namely, the balance between the numbers of the intercluster and intracluster links plays a key role in the global synchronizability of the network [13]. The network has the strongest synchronizability only when these numbers match. Mismatch can weaken and even destroy the synchronizability. Clustered networks have been increasingly recognized to be important for real network systems. Our work may provide fresh insight into the functionings of such networks.

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- [12] Our result does not depend on the details of the synchronized states. Consider two clustered networks where (A) the two types of links are approximately matched and (B) there is a substantial mismatch. Our theory would predict that network A is more synchronizable than network B. This statement is meaningful in a probabilistic sense, as whether or not a specific system may achieve synchronization is also determined by many other factors such as the choice of the initial condition, possible existence of multiple synchronized states, and noise, etc. Our result means that, under the influence of these random factors, there is a higher probability for network A to be synchronized than network B.
- [13] A recent work [14] showed that statistical properties of a complex network are not sufficient to determine its synchronizability. In particular, it has been proved rigorously that degree distribution of a network does not suffice to characterize its synchronizability. Our result indicates that nonstatistical properties of a network can have a significant effect on its ability to synchronize. This is consistent with the result in [14].
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