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Synchronization propensity in networks of dynamical systems: A purely topological indicator

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Chapter 1

Synchronization propensity in networks of dynamical systems: a purely topological indicator

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Abstract

Synchronization in networks of identical dynamical systems is enhanced by the number of manifolds in which synchrony of groups of systems is conserved or reinforced. Since the number of these invariant manifolds depends only on the coupling architecture of the network, it can be proposed as a purely topological indicator of synchronization propensity. The proposal is empirically validated through the detailed study of an ecological application.

1.1 Introduction

All properties of networks of N interacting dynamical systems depend, in general, upon network topology, coupling strength and local dynamics, and the most challenging problem is to identify the dependence upon topology (Strogatz, 2001; Boccaletti *et al.*, 2006). This is what we do here by suggesting a purely topological indicator for estimating the propensity of the network to synchronize, namely to have all systems or groups of them behaving in unison at least intermittently if not permanently (Pikovsky *et al.*, 2003). This indicator is particularly useful for detecting the impact of changes in the coupling architecture: for example, it could be used to

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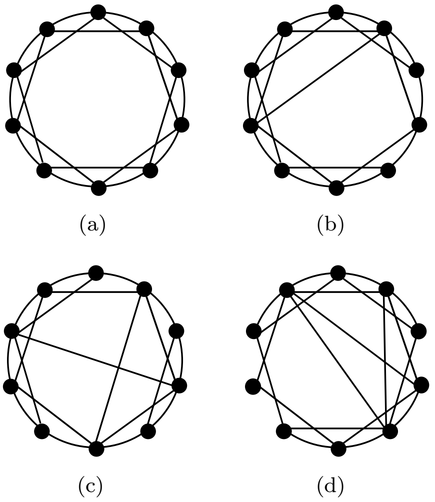
establish if the randomization of a regular network (see Fig.1.1) enhances or reduces the chances of synchronization, independently upon local dynamics and coupling strength. Our analysis differs from previous ones (Wu and Chua, 1996; Pecora and Carroll, 1998; Belykh *et al.*, 2005) which refer only to the special case in which all systems behave in unison (complete synchronization). The proposed topological indicator is based on the number S of partitions (here called synchronous) of the nodes of the network satisfying a special topological relationship.

The reason for suggesting this indicator is purely theoretical and based on the fact that all synchronous partitions are in one-to-one correspondence with invariant manifolds in state space in which groups of systems behave in unison (this is often called cluster or concurrent synchrony). Properties of these invariant manifolds have been discussed in Belykh *et al.* (2000); Pham and Slotine (2007); Belykh *et al.* (2008) yet without stressing the relationship with network topology. If the state of the network is in one of these manifolds, synchronization can not be lost (and can actually be strengthened), while if the state of the network approaches the manifold and remains close to it for a while then synchronization shows up only temporarily. Thus, the greater is S, the higher are the chances to be in (or be attracted by) a permanent or intermittent synchronous regime.

This study suggests, in a sense, what might be intuitively expected,


(a) (b)

(c) (d)

Fig. 1.1 Networks with 10 identical systems and different coupling architectures. Networks (b),(c),(d) are obtained from (a) by randomly rewiring $m = 1, 2, 3$ connections.

namely that regular networks (for which S turns out to be high) can more easily support synchrony than other networks. However, the problem is not as simple as one could imagine, because perceiving if S is high or low by a simple inspection of the coupling architecture is very difficult, if not impossible.

1.2 Synchronous partitions

Consider a network of N identical dynamical systems described by

$$\dot{x}_h(t) = f(x_h(t)) + D \sum_{k \in \mathcal{N}} c_{hk}(x_k(t) - x_h(t)), \quad h \in \mathcal{N} \tag{1.1}$$

where $\mathcal{N} = \{1, 2, \ldots, N\}$, is the set of systems, x_h is the n-dimensional state vector of system h, $f(\cdot)$ is the function describing the local dynamics $\dot{x} = f(x)$ of each system when isolated, $c_{hk} = c_{kh}$ is equal to 1 when systems h and k are connected and 0 otherwise, and D is a non-zero $n \times n$ matrix. When D is diagonal, model (1.1) allows one to deal with the majority of applications involving diffusion of energy, populations, and matters (Strogatz, 2001; Boccaletti *et al.*, 2006; Pikovsky *et al.*, 2003). In such a case the diagonal elements of D are standard diffusion rates.

System (1.1) is usually associated with an undirected graph in which the set of nodes is $\mathcal{N}$ and the arcs are systems connections.

We now consider partitions $\Pi = \{\pi_1, \pi_2, \ldots, \pi_p\}$ of the set $\mathcal{N}$ where π_i is a subset of the nodes of the graph, i.e. a group of systems in the network. Among all possible partitions, S of them, here called *synchronous partitions*, satisfy the following topological condition:

$$n_{h_1 \pi_j} = n_{h_2 \pi_j} \quad \forall h_1, h_2 \in \pi_i \quad \forall (i,j) : i \neq j \tag{1.2}$$

where $n_{h_l \pi_j}$ indicates the number of arcs connecting a node h_l of a set π_i with a disjoint set of nodes π_j. In words, a partition $\Pi = \{\pi_1, \pi_2, \ldots, \pi_p\}$ is synchronous if for all pairs of groups of nodes, all nodes of the first group are connected with the same number of arcs to the second group. For example, condition (1.2) is satisfied in the partition of Fig.1.2a but not in that of Fig.1.2b.

We can now prove the following

Theorem 1.1. *If* $\Pi = \{\pi_1, \pi_2, \ldots, \pi_p\}$ *is a synchronous partition, the manifold*

$$x_{h_1} = x_{h_2} \quad \forall h_1, h_2 \in \pi_i \quad \forall i \in \{1, 2, \ldots, p\} \tag{1.3}$$

is an invariant manifold of system (1.1).

Proof. Consider a generic point ($x_h = x^{(i)} \quad \forall h \in \pi_i \quad \forall i$) of manifold (1.3) as initial state at time t_0 of system (1.1). Thus, for $h \in \pi_i$ we have

$$\begin{aligned}\dot{x}_h(t_0) &= f(x^{(i)}) + D \sum_{k \in \mathcal{N} - \pi_i} c_{hk}(x_k(t_0) - x^{(i)}) \\ &= f(x^{(i)}) + \sum_{j \neq i} n_{h\pi_j} D(x^{(j)} - x^{(i)}).\end{aligned}$$

But condition (1.2) says that $n_{h\pi_j}$ for $h \in \pi_i$ does not depend on h, so that $\dot{x}_h(t_0)$ is the same for all $h \in \pi_i$. This means that the solution of (1.1) remains in manifold (1.3) which is therefore invariant.

□

In words, Theorem 1.1 says that if the state of the network belongs at a given time to manifold (1.3), characterized by the synchrony of groups of systems, then this synchrony is conserved forever and possibly enhanced because the states of two different groups of systems might asymptotically converge one to each other. This is why partitions satisfying condition (1.2) have been called synchronous.

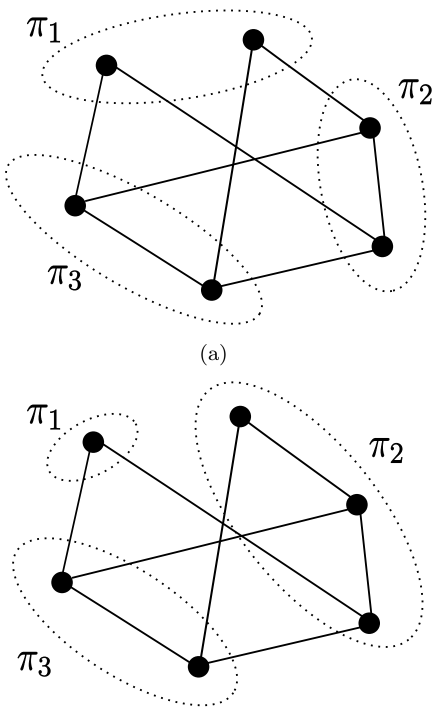
In principle, there could exist manifolds preserving synchrony different from those pointed out by Theorem 1.1. Fortunately, this possibility is ruled out by the following

Theorem 1.2. *If a manifold with groups of synchronous systems of the form (1.3), where* $\Pi = \{\pi_1, \pi_2, \ldots, \pi_p\}$ *is a partition of* $\mathcal{N}$*, is invariant, then* Π *is a synchronous partition.*

Proof. When the system starts at time t_0 in the invariant manifold (1.3), the state vectors of all the systems of the same group π_i are identical, so that two different systems h_1 and h_2 belonging to the same group π_i are described by

$$\begin{aligned}\dot{x}_{h_1}(t_0) &= f(x^{(i)}) + D \sum_{j \neq i} n_{h_1\pi_j}(x^{(j)} - x^{(i)}) \\ \dot{x}_{h_2}(t_0) &= f(x^{(i)}) + D \sum_{j \neq i} n_{h_2\pi_j}(x^{(j)} - x^{(i)})\end{aligned}$$

But $\dot{x}_{h_1}(t_0)$ must be equal to $\dot{x}_{h_2}(t_0)$ because manifold (1.3) is invariant, so that



(a)

(b)

Fig. 1.2 The partition in (a) is synchronous while the partition in (b) is not synchronous

$$\sum_{j\neq i}(n_{h_1\pi_j}-n_{h_2\pi_j})(Dx^{(j)}-Dx^{(i)})=0 \quad .$$

Since this condition must hold for any arbitrary vector $(Dx^{(j)}-Dx^{(i)})$ in the range of D, which is at least one-dimensional because $D\neq 0$, we must have $n_{h_1\pi_j}-n_{h_2\pi_j}=0 \quad \forall j\neq i$ which is, indeed, condition (1.2).

□

Thus, S represents the number of manifolds in which synchrony is preserved (if not enhanced). S can be computed by an algorithm that checks if the topological condition (1.2) is satisfied for each partition. A Matlab version of this algorithm that takes advantage of an incremental construction of the possible partitions using a tree structure and a prune strategy which prematurely discards families of partitions that early violate condition (1.2) is available on request.

1.3 Topological indicators of synchronization propensity

All forms of synchrony of system 1.1 depend on network topology (matrix $[c_{hk}]$), local dynamics (function f) and dispersal (matrix D). Functions that depend only on topology and capture the probability that a particular form of synchrony is present, when local dynamics and dispersal belong to a suitably defined admissible class, are called *topological indicator of synchronization propensity.* In this section we first review the three known topological indicators of synchronization propensity and then present a new one based on the notion of synchronous partitions discussed in the previous section.

The first topological indicator denoted by (a) in the following, has been proposed by Wu and Chua (see Wu and Chua (1996)) and refers to complete synchrony, namely to the case where all systems in the network behave in unison and return to this peculiar collective behavior after any small perturbation. The topological indicator (a) is theoretically justified when the admissible local dynamics are characterized by Master Stability Functions (Pecora and Carroll, 1998), which are negative above a threshold value $\underline{\varepsilon}$. In fact, under these conditions, the completely synchronous regime is stable for small perturbations provided

$$\lambda_2 > \frac{\underline{\varepsilon}}{d} \tag{1.4}$$

where $d = \sqrt{d_1^2 + \ldots + d_n^2}$ and λ_2 is the minimum non-zero eigenvalue of the connectivity matrix (Pecora and Carroll, 1998) (We recall that the connectivity matrix is a zero row sum matrix in which g_{ij}, $i \neq j$, is equal to -1 if systems i and j are coupled and equal to 0 otherwise, whereas g_{ii} is the degree of system i, namely the number of systems directly coupled with i). Since λ_2 depends on topology, while $\underline{\varepsilon}$ and d depend on local dynamics and dispersal and are therefore randomly selected within their admissible sets, we can summarize condition (1.4) by saying that topologies with higher values of λ_2 have higher probabilities of giving rise to complete synchronization in (1.1).

The second topological indicator, denoted by (b), also refers to local stability of the completely synchronous state, but the set of admissible local dynamics is not constrained to the functions f with Master Stability Functions negative above a threshold $\underline{\varepsilon}$. Indeed, the property required for the Master Stability Functions is weaker, namely to be negative in an interval $(\underline{\varepsilon}, \overline{\varepsilon})$. Under these assumptions, it can be proved (Pecora and Carroll, 1998) that the stability condition of the completely synchronous state is

$$\frac{\lambda_2}{\lambda_N} > \frac{\underline{\varepsilon}}{\overline{\varepsilon}} \tag{1.5}$$

where λ_N is the maximum eigenvalue of the connectivity matrix. Thus, $\underline{\varepsilon}/\overline{\varepsilon}$ being a random variable selected within the admissible sets, we can conclude that topologies with higher values of λ_2/λ_N have higher chances to give rise to complete synchrony.

The third topological indicator of synchronization propensity, denoted by (c), still refers to the completely synchronous state, but pretends that the network returns to it after any perturbation and not only after small perturbations. This property (global stability) can be studied using suitable Liapunov functions, as done in Belykh *et al.* (2005), and the final result is that the completely synchronous state has higher chances to be globally stable if the inverse of the highest sum of the lengths of all shortest paths in the network passing through the same arc is higher.

The fourth topological indicator of synchronization propensity, denoted by (d) in the following, is the one we propose in this paper. It is radically different from the three other indicators (a), (b) and (c) because it does not refer only to complete synchrony but also to weak forms of synchrony, like partial (cluster) synchrony and intermittent synchrony. Since the probability of being in a state of weak synchrony certainly increases with the number of manifolds where partial synchrony is preserved (if not enhanced), on the basis of the two theorems reported in the previous section we can propose the number S of synchronous partitions as topological indicator of synchronization propensity.

In order to compare the four indicators we have just described, we can consider the regular network of Fig.1.1a and the families of networks obtained from it by randomly rewiring $m = 1, 2, 3$ connections, with the aim of determining if this randomization increases or decreases the chances of synchronization. In the following section we will go into more details on this problem by making reference to a specific ecological application.

For the network in Fig.1.1a, corresponding to $m = 0$, the four indicators can be easily computed (the value of the indicator (d) computed with our algorithm is $S = 64$). But the four indicators can also be computed for the less regular networks shown in Fig.1.1 (for example, our algorithm gives $S = 7, 5, 3$, respectively, for the networks with $m = 1, 2, 3$ in Fig.1.1). Computing the four indicators for many randomly generated networks with the same m one obtains the four curves reported in Fig.1.3. The curves (a), (b), (c) show that randomization has only a small impact on synchronization, while curve (d) predicts just the opposite, namely a dramatic drop of synchrony with randomization. However, these conflicting results can be easily justified if one recalls that the topological indicator (d) refers to all forms of synchrony while the indicators (a), (b), and (c) refer only to the strongest form of synchrony.

1.4 An ecological application

Spatially extended ecological systems are often composed of N very similar, if not identical, patches in each one of which n species dynamically interact. Some of the patches are connected by channels through which individuals of different species can migrate at various rates. Thus, eq. (1.1) can be used to model such ecosystems.

If some patches are synchronous, even intermittently, then all populations of the same species of those patches reach their minimum density at the same time. This is a highly risky situation because if an environmental shock of large spatial scale occurs exactly at that time, there are high chances that all individuals of the species in those patches die. For this reason high probabilities of synchronization are usually perceived by ecologists as high probabilities of extinction. This justifies studies in which relationships are established between probabilities of synchronization and topological characteristics of the network.

We consider from now on a spatially extended ecosystem composed of n species living in 10 patches located on a circle. Migration of all species is possible from each patch to its four neighbors (two on the left and two on the right), as shown in Fig.1.1a. Networks of this kind mimic aquatic or terrestrial ecosystems distributed around islands or lakes. Moreover, we assume to be interested in knowing if randomization of the migration channels in the form shown in Fig.1.1 is beneficial or not in terms of risk of extinction. The problem can be immediately solved by using the topological indicator (d) described in the previous section because in this application we are interested in all forms of synchrony. The answer is therefore given by the curve (d) of Fig.1.3 which allows one to conclude that randomization reduces very effectively the risk of extinction.

In order to verify if this is indeed the case, we assume that there are only two species, namely a prey x_1 and a predator x_2, described by the

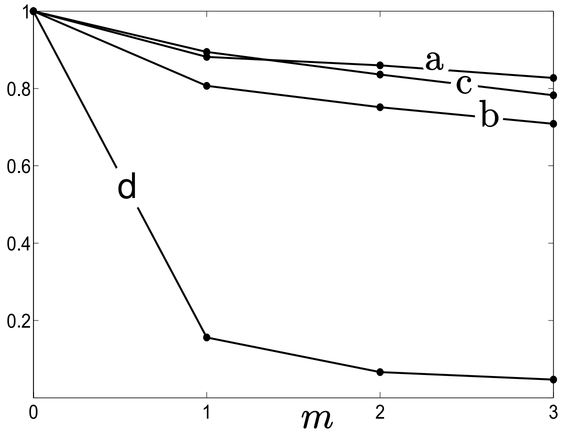


Fig. 1.3 Topological indicators of synchronization propensity for the networks of Fig.1. Each curve (normalized to 1 for $m = 0$) represents the mean values of 100 randomly generated networks for every m.

most standard model used in ecology (Rosenzweig and MacArthur, 1963):

$$\begin{aligned} \dot{x}_1 &= f_1(x_1, x_2) = rx_1\left(1 - \frac{x_1}{K}\right) - \frac{ax_1}{b + x_1}x_2 \\ \dot{x}_2 &= f_2(x_1, x_2) = e\frac{ax_1}{b + x_1}x_2 - zx_2 \end{aligned} \tag{1.6}$$

where

r and K are net growth rate and carrying capacity of the prey, $ax_1/(b+x_1)$ is the Holling type II functional response of the predator and e and z are predator efficiency and mortality. Thus, model (1.1) is completely specified because $f(\cdot)$ is given by (1.6), the matrix D is a 2×2 diagonal matrix with migration rates d_1 and d_2 on its diagonal and the elements c_{hk} are specified by the graphs of Fig.1.1.

In order to estimate the synchronization propensity in the network we can use a pragmatic approach somehow similar to those used by field ecologists (Koenig, 1999; Liebhold *et al.*, 2004). Here we closely follow Holland and Hastings (2008) who have studied, through extensive simulations, the dependence of synchrony on various factors in the networks of Fig.1.1 with model (1.6). More precisely, we integrate Eq.(1.1) for a given initial condition and determine, through correlation analysis, how many are the groups of patches (p) that can be roughly considered to be synchronous after the system has settled on one of its numerous attractors (limit cycles, tori and strange attractors). Then, we repeat this procedure for 100 randomly generated initial conditions, as well as for many different graphs with the same value of m, thus estimating the distribution of the number p of synchronous groups of patches for each m. Since $p = 1$ and $p = 10$ indicate completely synchronous and asynchronous regimes respectively, we extract from each distribution the probability P that $p \leq 5$, i.e. that the groups of synchronous patches are at most 5 and consider this as the probability of synchronization. Finally, in order to check the robustness of our results we have repeated all computations for more than 10 parameter settings of model (1.6) and for various values of the migration rates. All the computed probabilities decline with m, as shown in the four examples reported in Fig.1.4, and therefore confirm the prediction of our topological indicator (see curve (d)) in Fig.1.3). The curves in Fig.1.4 compare favorably with the analysis performed by Holland and Hastings (see Figs. 11a, 10b, 3, 9a in Holland and Hastings (2008)).

It is worth noticing, however, that in this specific application millions of long simulations of 20 ODE's are needed to obtain the same conclusions that can be obtained in a few minutes with our indicator. Moreover, thanks to our theorems we can state that the results are valid not only for other prey-predator communities but also for any other model.

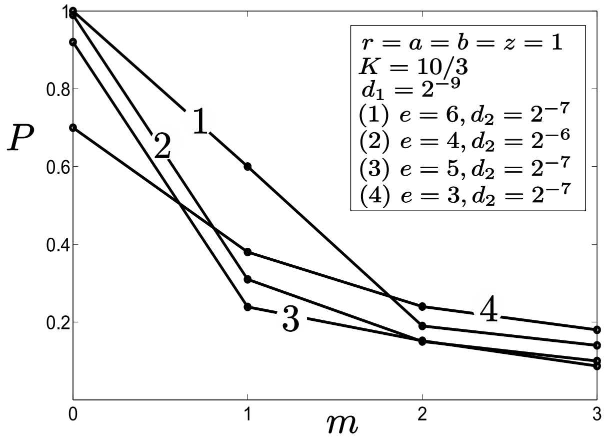


Fig. 1.4 Probability P that at most 5 groups of patches are synchronous in the networks of Fig.1.1.

1.5 Concluding remarks

The results presented in this paper are certainly worth to be extended to more complex networks, in particular those described by directed graphs, and to different types of coupling rules like periodic or aperiodic couplings (e.g. Belykh *et al.* (2004); Wu (2007); Rinaldi (2009)), which are important when migration or diffusion can occur only in specific seasons or during rare and random events. Moreover, since high values of our topological indicator are not necessarily correlated with high chances of complete synchronization, it would make sense to try to identify more complex indicators that might also include the propensity to complete synchronization. Finally, our indicator could be used to identify the coupling architectures that are most promising for controlling epidemics in social networks, since this problem has been shown to be critically influenced by synchrony (Earn *et al.*, 2000).

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