Impact of network connectivity on the synchronization and global dynamics of coupled systems of differential equations

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HIGHLIGHTS

- We investigated a general class of coupled dynamical systems on networks.
- We established the global dynamics when the network is not strongly connected.
- We investigated the impact of network connectivity on the global dynamics.
- When vertex systems are gradient, network connectivity completely determines the synchronization.
- We applied the theory to two significant applications in epidemiology and ecology.

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ABSTRACT

The global dynamics of coupled systems of differential equations defined on an interaction network are investigated. Local dynamics at each vertex, when interactions are absent, are assumed to be simple: solutions to each vertex system are assumed to converge to an equilibrium, either on the boundary or in the interior of the feasible region. The interest is to investigate the collective behaviours of the coupled system when interactions among vertex systems are present. It was shown in Li and Shuai (2010) that, if the interaction network is strongly connected, then solutions to the coupled system synchronize at a single equilibrium. We focus on the case when the underlying network is not strongly connected and the coupled system may have mixed equilibria whose coordinates are in the interior at some vertices while on the boundary at others. We show that solutions on a strongly connected component of the network will synchronize. Considering a condensed digraph by collapsing each strongly connected component, we are able to introduce a partial order on the set $\mathcal{P}$ of all equilibria, and show that all solutions of the coupled system converge to a unique equilibrium P^* that is the maximizer in $\mathcal{P}$. We further establish that behaviours of the coupled system at minimal elements of the condensed digraph determine whether the global limit P^* is a mixed equilibrium. The theory are applied to mathematical models from epidemiology and spatial ecology.

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1. Introduction

Coupled systems on networks is a mathematical framework that encompasses many different classes of large-scale artificial and natural systems [1]. A network is given by a weighted digraph $(\mathcal{G}, A)$, where $\mathcal{G}$ is a digraph with vertex set $V(\mathcal{G}) = \{1, 2, \ldots, n\}$, and $A = (a_{ij})_{n \times n} \geq 0$ is the weight matrix. At each vertex i, a differential system $u_i' = f_i(u_i)$ is defined. Inter-connections or coupling among vertex systems are described by the edges of $\mathcal{G}$, and the strength of the coupling described by the weights of edges.

In particular, an edge (i, j) from vertex j to i exists if and only if $a_{ij} > 0$. A coupled system defined on a network $(\mathcal{G}, A)$ can be written in the form

$$u_i' = f_i(u_i) + \sum_{j=1}^{n} a_{ij} g_{ij}(u_i, u_j), \quad i = 1, 2, \ldots, n, \qquad (1)$$

and $g_{ij}(u_i, u_j)$ is a normalized interference function from vertex j to i [1]. System (1) can describe a network of coupled oscillators in which each vertex system is an oscillator and g_{ij} describe the coupling terms. System (1) can also model the flocking of birds, swarms of aerial robots and formation of small satellites, for which $(\mathcal{G}, A)$ describes the communication topology. For ecological systems with spatial dispersal, vertex systems in (1) may model the

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dynamics of species on a single patch, g_{ij} describes the dispersal term and $(\mathcal{G}, A)$ is the dispersal network.

Many mathematical questions can be investigated in the framework of coupled systems on networks. Each vertex system is typically of low dimension and whose dynamics are simple. Assuming that each vertex system has a global attractor that is an equilibrium or a limit cycle, one can ask if the coupled system has a unique equilibrium or limit cycle and if it is globally attracting. The framework is also a natural setting for investigating the emergence of complex patterns and system behaviours from organization of simple dynamics. Of key interest is the impact of network structure, whether geometrical, topological or graph theoretical, on the system behaviours. In this study, we are interested in the impact of network connectivity on the simplest type of invariant sets: the set of equilibria. A motivation for this study comes from modelling of the transmission dynamics of infectious diseases within a heterogeneous host population in mathematical epidemiology. Multi-group models have been used to model heterogeneous transmission of sexually transmitted diseases [2]. A main mathematical question regarding the global dynamics is the threshold theorem: if the basic reproduction number $R_0 \leq 1$ then the unique disease-free equilibrium P_0 is globally stable and the disease dies out; if $R_0 > 1$ then P_0 is unstable and the disease persists. In particular, a unique endemic equilibrium P^* exists and is globally stable with respect to all positive initial conditions. Multigroup models is an example of couple systems on networks in which the network $(\mathcal{G}, A)$ describes cross-transmission among groups. The uniqueness and global stability of the endemic equilibrium for an n-group SIR model with bilinear incidence was first established in [3] using a global Lyapunov function, under the assumption that the cross-transmission network is strongly connected, or in biological terms, if the disease can be transmitted from one group to another group either directly or indirectly through other groups. Using the same technique, the threshold theorem is established for many other heterogeneous epidemic models structured with groups [4,5], infection stages [6] and spatial dispersal [7]. The overarching assumption for these threshold results is that the underlying network is strongly connected. On the other hand, threshold results for heterogeneous epidemic models are not expected to hold when the network is not strongly connected. It is shown in [8] that mixed equilibria, at which some group/patch is disease-free while others are endemic, can exist if the network is not strongly connected. Further studies are needed to investigate the global dynamics of heterogeneous epidemic models without the assumption of strong connectedness, and address the following questions: what are the structures of the set of equilibria? Can a mixed-equilibrium attract all positive solutions, and if so, how to characterize and identify the global attracting equilibrium?

In the present paper, in the general mathematical framework of coupled systems on networks (1), we investigate the structure of the set of equilibrium without the strong connectedness assumption on $\mathcal{G}$. We show that on each strongly connected component H of $\mathcal{G}$ the behaviour of system (1) tends to be synchronized, the equilibrium is either positive or zero at all vertex in H. This allows us to consider a condensed graph $\mathcal{H} = \mathcal{G}/\sim$ by collapsing each strongly connected component to a single vertex. A canonical partial order $\prec$ can be defined on the condensed graph $\mathcal{H}$, which encodes the structure of the set of equilibria. We define an evaluation function E on the ordered condensed graph $(\mathcal{H}, \prec)$, and show that E has a unique maximizer P^*, and that P^* corresponds to a unique equilibrium of (1), either positive or mixed, that attracts all positive solutions.

We present our main theoretic results in Section 2. In Sections 3 and 4, we apply our general approach to well-known examples of coupled systems. In Section 5, we present numerical examples to demonstrate our main results. Numerical simulations of a network of three coupled oscillators are also given in Section 5, to demonstrate the importance of network connectivity on synchronous oscillatory behaviours.

2. Coupled systems on networks

Let $\mathcal{G}$ be a digraph of n vertices. Consider a coupled system on graph $\mathcal{G}$ of form:

$$u_i' = f_i(u_i) + \sum_{j=1}^{n} g_{ij}(u_i, Pu_j), \quad i = 1, 2, \ldots, n, \tag{2}$$

where $u_i \in \mathbb{R}^d, f_i = (f_i^1, f_i^2, \ldots, f_i^d) : \mathbb{R}^d \to \mathbb{R}^d$, and $g_{ij} = (g_{ij}^1, g_{ij}^2, \ldots, g_{ij}^d) : \mathbb{R}^d \times \mathbb{R}^d \to \mathbb{R}^d$. Functions g_{ij} represent the influence of vertex j on vertex i, and an arc from vertex j to i exists if and only if $g_{ij}(u_i, Pu_j) \not\equiv 0$. Matrix P is a $d \times d$ projection matrix, namely $P^2 = P$, and we assume that rank $P = r > 0$. For each $1 \leq i \leq n$, Pu_i are referred to as coupling variables.

Without loss of generality, we assume that the coupling graph $\mathcal{G}$ is connected, since otherwise each connected component of $\mathcal{G}$ gives rise to an independent system and can be treated separately. We make the following general assumptions.

(A$_1$) For $\forall 1 \leq i \leq n, 1 \leq m \leq d, f_i^m(u_i)\big|_{u_i^m=0} \geq 0$; and

$f_i^m(u_i)\big|_{u_i^m=0} = 0$ only if $Pu_i = 0$.

(A$_2$) For $1 \leq i, j \leq n, u_i, u_j \geq 0, Pg_{ij}(u_i, Pu_j) \geq 0$; if $Pg_{ij} \not\equiv 0$, then $Pg_{ij}(u_i, Pu_j) \neq 0 \Leftrightarrow Pu_j \neq 0$.

Assumption (A$_1$) requires that the vector field f_i is either tangent to or crosses each boundary subspace $u_i^m = 0$ of $\mathbb{R}_+^d$ to the interior. This ensures that the nonnegative orthant $\mathbb{R}_+^d$ is positively invariant for each vertex system $u_i = f_i(u_i)$, which is motivated by applications in population biology. Assumption (A$_2$) is regarding the non-negativity of the coupling term g_{ij}. We do not require that all entries in the vector g_{ij} to be nonnegative, and only that the coupling entries Pg_{ij} are nonnegative.

An equilibrium $u^* = (u_1^*, \ldots, u_n^*)$ is said to be *nonnegative* if it belongs to the nonnegative orthant $\mathbb{R}_+^d \times \cdots \times \mathbb{R}_+^d$ of the phase space. From assumption (A$_1$), we can deduce that at a nonnegative equilibrium u^*, for each vertex i, we have either $Pu_i^* > 0$ or $Pu_i^* = 0$, namely, there is no i such that vector Pu_i^* has both positive and zero coordinates. Equilibrium u^* is said to be *positive* if $Pu_i^* > 0$ for all i, and u^* is said to be *mixed* if there exist i, j such that $Pu_i^* = 0$ and $Pu_j^* > 0$. When matrix P has full rank, then $Pu_i^* > 0$ if and only if $u_i^* > 0$. In this case, a positive equilibrium belongs to the interior of the nonnegative orthant. Generally, if $Pu_i^* = 0$ for some i, then the equilibrium u^* belongs to the boundary of the nonnegative orthant, and is also called a boundary equilibrium. A mixed equilibrium is necessarily a boundary equilibrium, while a boundary equilibrium may not be mixed since we can have $Pu_i^* = 0$ for all i.

Define a partial order $\preceq$ among vertices of the digraph $\mathcal{G}$ as follows: for vertices $i, j, i \preceq j$ if there exists an oriented path from i to j. We say $i \sim j$ if $i \preceq j$ and $j \preceq i$. It can be verified straightforwardly that relation "$\sim$" is an equivalence relation.

Proposition 2.1. *Relation $\sim$ is an equivalence relation.*

Let $V(\mathcal{G})$ be the vertex set of digraph $\mathcal{G}$. Define $\mathcal{H}$ as the condensed graph of $\mathcal{G}$, which is formed by collapsing each strongly connected component to a single vertex. Then $V(\mathcal{H}) = V(\mathcal{G})/\sim$, and each vertex $H \in V(\mathcal{H})$ represents a strongly connected component of $\mathcal{G}$. If $\mathcal{G}$ is strongly connected, then $V(\mathcal{H}) = \{\mathcal{G}\}$ is a singleton. For $H, H' \in \mathcal{H}$, a directed edge from H to H' exists if there exist $i \in V(H)$ and $j \in V(H)$ such that a directed edge from i to j exists in $\mathcal{G}$. A canonical partial order $\prec$ can be defined in $\mathcal{H}$ as follows: for $H, H' \in V(\mathcal{H}), H \prec H'$ if there exist $i \in H, j \in H'$, such that $i \preceq j$. If $H, H' \in V(\mathcal{H})$ satisfy both $H \prec H'$ and $H' \prec H$, then H and H' are the same strongly connected component. This implies that $\prec$ is a strict partial order. Thus there exist minimal and maximal elements in $V(\mathcal{H})$ with respect to the strict partial order $\prec$ (see Fig. 1).