

Structural Analysis of Dynamical Networks: *BDC-Decomposition and Influence Matrix*

Giulia Giordano * Franco Blanchini **

* *Department of Automatic Control, Lund University,
Box 118, SE-221 00 Lund, Sweden. E-mail: giulia.giordano@uniud.it*
** *Department of Mathematics, Computer Science and Physics, University of
Udine, via delle Scienze 206, 33100 Udine, Italy. E-mail: blanchini@uniud.it*

Abstract: *Dynamical networks*, composed of dynamical subsystems that interact according to a given interconnection topology, can model several complex systems, ranging from natural systems to engineering applications. Dynamical networks admit a graph representation, where nodes represent subsystems and arcs represent interconnections, and have a peculiar feature: the global behaviour is the outcome of an ensemble of local interactions. A structural analysis of dynamical networks aims at providing parameter-independent results, based on the topology of the interconnection graph (*i.e.*, the system structure); a structural approach is particularly well suited to explain the extraordinary robustness of natural systems in spite of intrinsic uncertainties and variability. We present the *BDC-decomposition*, which describes the structure of a wide class of dynamical networks: we show that it provides not only a local, but also a global description of the system, and that it can help structurally assess many relevant properties. In particular, we focus on a *BDC*-based vertex algorithm that allows us to analyse the system steady-state input-output behaviour and to compute the system *influence matrix*, representing the structural steady-state effect on each of the variables of a persistent input applied to each of the system equations.

Keywords: dynamical networks, biochemical systems, structural analysis, influence matrix

1. INTRODUCTION

Complex systems in several contexts, ranging from biological, social and economical to man-made systems, can be regarded as *dynamical networks*: phenomena related both to the evolution of quantities over time (*dynamics*) and to interconnections among several units/components/agents (*networks*) are ubiquitous both in natural and in artificial systems. A dynamical network is composed of subsystems, each having its own dynamics, which interact according to a given interconnection topology. Although the interactions are *local*, they have *global* consequences, affecting the behaviour of the overall system (Giordano 2016).

A wide variety of real-world systems can be modelled in a dynamical-network framework (Barrat et al. 2008; Easley and Kleinberg 2010; Mesbahi and Egerstedt 2010; Ren and Cao 2010; Barabási 2012): chemical, biochemical and biomolecular processes (Feinberg 1987; Alon 2006; Chen et al. 2005; Del Vecchio and Murray 2014); biological and ecological systems (Levins 1968; May 1974; Levins 1975; Puccia and Levins 1985; Dambacher et al. 2003b,a; Edelstein-Keshet 2005; Dambacher et al. 2005; Dambacher and Ramos Jiliberto 2007; Dambacher et al. 2009; Marzloff et al. 2011); social and economical interaction systems and opinion dynamics (Friedkin and Johnsen 1999; Altafini 2012, 2013; Altafini and Lini 2015; Frasca et al. 2015; Friedkin 2015; Ravazzi et al. 2015; Blanchini et al. 2015); telecommunication and data communication networks (Moss and Segall 1982; Ephremides and Verdú 1989; Iftar and Davison 1990, 2002); inventory management and production-distribution systems (Silver and Peterson 1985; Boukas et al. 1995; Blanchini et al. 1997, 2000; Bertsimas and Thiele 2006; Sarimveisa et al. 2008; Bauso et al. 2010); water distribution networks (Larson and Keckler 1969; Bauso et al. 2013); transportation networks

(Ataslar and Iftar 1998; Mudchanatongsuk et al. 2008); traffic and congestion management systems (Iftar 1999); vehicle platooning and formation flight of aircrafts (D'Andrea 1998); and flow networks in general (Atamtürk and Zhang 2007; Ordóñez and Zhao 2007; Bauso et al. 2010; Wei and van der Schaft 2013). Regardless of the specific application, the structure of a dynamical network can be effectively visualised as a *graph*, in which the nodes correspond to subsystems (or to variables, as a particular case) and the edges are associated with interactions.

For any system whose Jacobian is the positive linear combination of rank-one matrices, the *BDC*-decomposition (related to the graph representation) proposed by Blanchini et al. (2012); Blanchini and Giordano (2014); Giordano et al. (2015); Giordano (2016) expresses the system Jacobian as the product of three matrices, one depending on a vector of positive unknown parameters, the other two capturing the system structure. Based on an integral formula (Khalil 2002), we show here that the *BDC*-decomposition is not only a *local*, but also a *global* property. For systems admitting a *BDC*-decomposition, important quantities associated with the Jacobian matrix, *e.g.*, the coefficients of the characteristic polynomial, are multi-affine functions of the positive parameters: methods exploiting multi-affinity have been proposed to structurally detect properties (Giordano 2016), such as the capacity of exhibiting oscillations or perfect adaptation (Blanchini et al. 2012), and stability (Blanchini and Giordano 2014). In particular, here we show how the *BDC*-decomposition can help analyse the steady-state behaviour of a dynamical network, in terms of structural steady-state input-output influences: the structural sign of the variation of the steady-state output value, upon a perturbation due to a constant input, can be easily computed with a vertex algorithm (Giordano et al. 2015).

2. THE BDC-DECOMPOSITION

We begin by introducing the *BDC*-decomposition for a generic nonlinear system

$$\dot{x}(t) = g(x(t)), \quad (1)$$

where $x \in \mathcal{D} \subseteq \mathbb{R}^n$, $g : \mathcal{D} \subseteq \mathbb{R}^n \rightarrow \mathbb{R}^n$ is a continuously differentiable function, and \mathcal{D} is an open, convex domain.

Definition 1. System (1) admits a *BDC*-decomposition iff, for any $x \in \mathcal{D}$, $J(x) = \partial g / \partial x$ can be written as the positive linear combination of rank-one matrices, namely

$$J(x) = \sum_{h=1}^q R_h D_h(x) = \sum_{h=1}^q B_h D_h(x) C_h^\top, \quad (2)$$

where B_h and C_h^\top are column and row vectors, respectively, so that $R_h = [B_h C_h^\top]$ are constant rank-one matrices,¹ while $D_h(x)$, $h = 1, \dots, q$, are positive scalar functions depending on x . \diamond

In a compact form,

$$J(x) = BD(x)C,$$

where $D(x)$ is a diagonal matrix with positive diagonal entries $D_h(x)$, B is the matrix formed by the columns B_h and C is the matrix formed by the rows C_h^\top . The above definition holds for any x in the domain \mathcal{D} , hence, in particular, for any equilibrium point $\bar{x} \in \mathcal{D}$ (such that $g(\bar{x}) = 0$).

Not any system admits a *BDC*-decomposition. However, for a wide class of models, including (bio)chemical reaction networks, a *BDC*-decomposition (having a graph interpretation that will be described later) always exists, and can be easily and systematically computed. Consider the system

$$\dot{x}(t) = Sf(x(t)) + f_0, \quad (3)$$

where $x(t) \in \mathbb{R}_+^n$, $f(x(t)) \in \mathbb{R}^m$ and $f_0 \in \mathbb{R}^m$ is a constant vector ($f_0 \geq 0$ componentwise); $S \in \mathbb{Z}^{n \times m}$ can be regarded as the stoichiometric or flow matrix of the system; \bar{x} denotes the equilibrium point, $Sf(\bar{x}) + f_0 = 0$. This class of models includes any chemical reaction network, or any phenomenological biomolecular model (e.g., gene regulatory models, signalling networks, etc.) that can be written as an equivalent chemical reaction network. Also models typically used in ecology and population dynamics can be rewritten as in (3).

Assumption 2. Each function $f_j(\cdot)$, for $j = 1, \dots, m$, is nonnegative and continuously differentiable, with sign-definite (i.e., always positive, always negative or always zero) partial derivatives in the interior of the positive orthant. \diamond

Assumption 3. Each function $f_j(\cdot)$, for $j = 1, \dots, m$, is zero if and only if at least one of its arguments is zero. Furthermore, if $[S]_{ij} < 0$, then $f_j(\cdot)$ must have $x_i(t)$ as an argument. \diamond

Remark 4. Assumption 3 ensures that (3) is a positive system (in fact, $\dot{x}_i \geq 0$ for $x_i = 0$), since the considered class of systems models biochemical and biological systems. However, system positivity is not necessary in general for the existence of a *BDC*-decomposition: the fundamental requirement is the sign-definiteness of the partial derivatives. For instance, the system

$$\begin{cases} \dot{a} = -k_1 a - k_2 b + a_0, \\ \dot{b} = h_1 a - h_2 b, \end{cases}$$

with $k_1, k_2, h_1, h_2 > 0$, is not necessarily positive (when $a = 0$, \dot{a} may be negative if b is large enough), but its Jacobian admits a *BDC*-decomposition. Depending on the considered domain \mathcal{D} ,

¹ A rank-one matrix R_h can always be written as the product of a column vector B_h and a row vector C_h^\top .

the same system may or may not admit a *BDC*-decomposition; and it may happen that the system admits a *BDC*-decomposition if $\mathcal{D} = \mathbb{R}_+^n$, but not if $\mathcal{D} = \mathbb{R}^n$. For example, the system

$$\begin{cases} \dot{a} = -ab - a + a_0, \\ \dot{b} = -ab - b + b_0, \end{cases}$$

whose Jacobian is

$$J(a, b) = \begin{bmatrix} -(b+1) & -a \\ -b & -(a+1) \end{bmatrix},$$

admits a *BDC*-decomposition if the domain is the positive orthant, but not if it is the whole plane (because, in this latter case, the variables are no longer sign-definite). \diamond

The following result guarantees that systems of the form (3) always admit a *BDC*-decomposition.

Proposition 5. Any system falling in the class (3) admits a *BDC*-decomposition: $J(x) = BD(x)C$. Matrices B and C can be built systematically, based on matrix S and on qualitative information about $f(\cdot)$.

Proof. The statement is proved constructively by Giordano et al. (2015); Giordano (2016): equation (3) is rewritten as

$$\dot{x} = \sum_{j=1}^s S_j f_j(x) + f_0,$$

where S_j is the j th column of matrix S . The corresponding Jacobian is

$$J(x) = \sum_{j=1}^s S_j \begin{bmatrix} \frac{\partial f_j}{\partial x_1} & \frac{\partial f_j}{\partial x_2} & \dots & \frac{\partial f_j}{\partial x_n} \end{bmatrix}.$$

Denoting by $D_1(x), D_2(x), \dots, D_q(x)$ the absolute values of all the non-zero partial derivatives, it can be written

$$J(x) = \sum_{h=1}^q B_h D_h(x) C_h^\top,$$

where

- $D_h(x) = \left| \frac{\partial f_j}{\partial x_i} \right|$ for some i and j ;
- $B_h = S_j$, the column of S associated with f_j ;
- C_h^\top has a single non-zero entry in the i th position, equal to the sign of $\frac{\partial f_j}{\partial x_i}$. \blacksquare

Example 6. Consider the chemical reaction network $\emptyset \xrightarrow{a_0} A$, $\emptyset \xrightarrow{b_0} B$, $A + B \xrightleftharpoons[f_c(c)]{f_{ab}(a,b)} C$, $A + C \xrightarrow{f_{ac}(a,c)} \emptyset$, $B \xrightarrow{f_b(b)} \emptyset$, corresponding to the system

$$\begin{cases} \dot{a} = a_0 - f_{ab}(a, b) - f_{ac}(a, c) + f_c(c), \\ \dot{b} = b_0 - f_{ab}(a, b) - f_b(b) + f_c(c), \\ \dot{c} = f_{ab}(a, b) - f_{ac}(a, c) - f_c(c), \end{cases}$$

which can be rewritten as in model (3) by setting $x = [a \ b \ c]^\top$,

$$S = \begin{bmatrix} -1 & 1 & -1 & 0 \\ -1 & 1 & 0 & -1 \\ 1 & -1 & -1 & 0 \end{bmatrix}, \quad f(x) = \begin{bmatrix} f_{ab}(a, b) \\ f_c(c) \\ f_{ac}(a, c) \\ f_b(b) \end{bmatrix}, \quad f_0 = \begin{bmatrix} a_0 \\ b_0 \\ 0 \end{bmatrix}.$$

Denoting the positive partial derivatives as $\alpha = \frac{\partial f_{ab}(a,b)}{\partial a}$, $\beta = \frac{\partial f_{ab}(a,b)}{\partial b}$, $\gamma = \frac{\partial f_c(c)}{\partial c}$, $\delta = \frac{\partial f_{ac}(a,c)}{\partial a}$, $\varepsilon = \frac{\partial f_{ac}(a,c)}{\partial c}$, $\zeta = \frac{\partial f_b(b)}{\partial b}$, the Jacobian matrix and its *BDC*-decomposition are

$$J = \begin{bmatrix} -(\alpha + \delta) & -\beta & \gamma - \varepsilon \\ -\alpha & -(\beta + \zeta) & \gamma \\ \alpha - \delta & \beta & -(\gamma + \varepsilon) \end{bmatrix}$$

$$= \underbrace{\begin{bmatrix} -1 & -1 & 1 & -1 & -1 & 0 \\ -1 & -1 & 1 & 0 & 0 & -1 \\ 1 & 1 & -1 & -1 & -1 & 0 \end{bmatrix}}_{=B} \underbrace{\text{diag}\{\alpha, \beta, \gamma, \delta, \varepsilon, \zeta\}}_{=D} \underbrace{\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \\ 0 & 1 & 0 \end{bmatrix}}_{=C}.$$

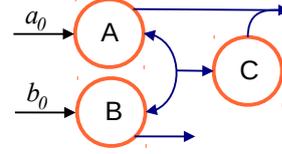


Fig. 1. The graph associated with the system in Example 6.

To compute the BDC -decomposition, an order must be chosen for the positive partial derivatives. Then, since the first derivative is $\alpha = \frac{\partial f_{ab}(a,b)}{\partial a}$, the first column of B corresponds to S_1 , associated with the reaction rate function $f_{ab}(\cdot, \cdot)$, and the first row of C has a 1 entry in the first position, corresponding to variable a ; and so on. Note that columns S_1 and S_3 are repeated twice in B because $f_{ab}(\cdot, \cdot)$ and $f_{ac}(\cdot, \cdot)$ have two arguments. \diamond

Remark 7. The BDC -decomposition is not unique. Even when an order for the diagonal entries of D is assigned, the sign of both B_k and C_k^\top can be changed, resulting in matrices \hat{B} and \hat{C} , and still $J = \hat{B}\hat{D}\hat{C}$. More in general, B_k can be divided and C_k^\top can be multiplied by the same quantity. The only requirement is that matrix D , containing the free positive parameters, is diagonal. \diamond

The proposed approach for computing the BDC -decomposition can be extended to non-positive systems (cf. Remark 4) and also to the case of dependencies between partial derivatives. For instance, the system

$$\begin{cases} \dot{a} = a_0 - f_{ab}(a-b) \\ \dot{b} = f_{ab}(a-b) - f_b(b) \end{cases}$$

with

$$S = \begin{bmatrix} -1 & 0 \\ 1 & -1 \end{bmatrix}, \quad f = \begin{bmatrix} f_{ab}(a-b) \\ f_b(b) \end{bmatrix}, \quad f_0 = \begin{bmatrix} a_0 \\ 0 \end{bmatrix},$$

would have the BDC -decomposition

$$J = \begin{bmatrix} -\alpha & \beta \\ \alpha & -(\beta + \gamma) \end{bmatrix} = \underbrace{\begin{bmatrix} -1 & -1 & 0 \\ 1 & 1 & -1 \end{bmatrix}}_{=B} \underbrace{\text{diag}\{\alpha, \beta, \gamma\}}_{=D} \underbrace{\begin{bmatrix} 1 & 0 \\ 0 & -1 \\ 0 & 1 \end{bmatrix}}_{=C}$$

if considering the three parameters $\alpha = \partial f_{ab}/\partial a > 0$, $\beta = |\partial f_{ab}/\partial b|$ and $\gamma = \partial f_b/\partial b > 0$. However, since $\beta = \alpha$, two parameters only, α and γ , are needed. Hence:

$$J = \begin{bmatrix} -\alpha & \alpha \\ \alpha & -(\alpha + \gamma) \end{bmatrix} = \underbrace{\begin{bmatrix} -1 & 0 \\ 1 & -1 \end{bmatrix}}_{=B} \underbrace{\text{diag}\{\alpha, \gamma\}}_{=D} \underbrace{\begin{bmatrix} 1 & -1 \\ 0 & 1 \end{bmatrix}}_{=C}.$$

Also when the Jacobian of system (3) has independent (hence sign-definite, due to Assumption 2) entries, the system always admits a BDC -decomposition.

The BDC -decomposition can help assess *structural* properties: indeed, for a *family* of systems admitting a BDC -decomposition, the *structure* is given by the matrices B and C ; a *realisation* of the structure is given by a choice of the positive diagonal entries of D , $D_k > 0$, $k = 1, \dots, q$.

The BDC -decomposition is not only related to the system Jacobian, but also to the graph representing the system, whose nodes and arcs denote, respectively, state variables and interactions among them. For instance, the dynamical network in Example 6 corresponds to the graph in Fig. 1. Arcs are associated with

positive parameters that are in the diagonal of D ; if an arc has k tails, it is associated with k parameters and it corresponds to k identical columns of matrix B (having a negative entry in the positions associated with the nodes from which the arc tails start, a positive entry in the positions associated with the nodes reached by the arc arrows, zero entries elsewhere) and to k rows of matrix C , each having a single non-zero entry in one of the positions associated with the nodes from which the arc tails start.

2.1 BDC -Decomposition: a Global Property

Although the BDC -decomposition has an obvious connection with the system Jacobian, it is not just a local property, or a linearisation: based on a simple but powerful integral formula, it can be shown that the BDC -decomposition associated with a system is not only a local, but also a *global* property.

Generalising a result by Khalil (2002) (p. 108, Exercise 3.23), it can be shown that, given a continuously differentiable function $g(x)$, $g: \mathcal{D} \subset \mathbb{R}^n \rightarrow \mathbb{R}^n$, where \mathcal{D} is an open convex domain,

$$g(x) - g(0) = \left(\int_0^1 \frac{\partial g}{\partial x}(\sigma x) d\sigma \right) x, \quad \forall x \in \mathcal{D}. \quad (4)$$

In fact, denoting by $\varphi(\sigma) \doteq g(\sigma x)$ for $0 \leq \sigma \leq 1$,

$$g(x) - g(0) = \varphi(1) - \varphi(0) = \int_0^1 \varphi'(\sigma) d\sigma = \int_0^1 \frac{\partial g}{\partial x}(\sigma x) d\sigma x,$$

since

$$\frac{d\varphi}{d\sigma}(\sigma) = \frac{\partial g}{\partial x}(\sigma x) \frac{d(\sigma x)}{d\sigma} = \frac{\partial g}{\partial x}(\sigma x)x.$$

Consider system (3), with $x \in \mathcal{D}$ open and convex,

$$\dot{x}(t) = Sf(x(t)) + f_0,$$

along with the equilibrium condition

$$0 = Sf(\bar{x}) + f_0.$$

Denoting $z \doteq x - \bar{x}$ and subtracting the two equations, the shifted system

$$\dot{z} = S[f(z + \bar{x}) - f(\bar{x})] \quad (5)$$

is obtained; since the system admits a BDC -decomposition, as previously shown, for any fixed equilibrium \bar{x} its Jacobian can be written as $J(z) = BD(z)C$, hence the system can be equivalently rewritten (not linearised) as

$$\dot{z} = [BD(z)C]z. \quad (6)$$

In fact, an immediate application of the integral formula (4) to the right-hand side of system (5) provides

$$\dot{z} = \left[\int_0^1 J(\sigma z + \bar{x}) d\sigma \right] z.$$

In view of the BDC -decomposition, equivalently

$$\dot{z} = \left[B \left(\int_0^1 \text{diag} \left\{ \frac{\partial f_i(\sigma z + \bar{x})}{\partial x_j} \right\} d\sigma \right) C \right] z.$$

Therefore, denoting by

$$\Gamma_{ij}(z) = \int_0^1 \frac{\partial f_i(\sigma z + \bar{x})}{\partial x_j} d\sigma, \quad (7)$$

it follows that

$$\begin{aligned} D(z) &= \int_0^1 \text{diag} \left\{ \frac{\partial f_i(\sigma z + \bar{x})}{\partial x_j} \right\} d\sigma \\ &= \text{diag} \left\{ \int_0^1 \frac{\partial f_i(\sigma z + \bar{x})}{\partial x_j} d\sigma \right\} = \text{diag} \{ \Gamma_{ij}(z) \}. \end{aligned} \quad (8)$$

Due to monotonicity of the functions $f_i(\cdot)$, whose integral is computed on a non-zero interval, $\Gamma_{ij}(z)$ is strictly positive and admits a maximum and a minimum in any closed and bounded domain:

$$v < v_{ij} \leq \Gamma_{ij}(z) \leq \mu_{ij} < \mu.$$

Hence, a system admits a global *BDC*-representation of the form (6) if and only if it admits a local *BDC*-decomposition $J = BDC$.

Proposition 8. (Giordano 2016) A nonlinear system (3), admitting equilibrium \bar{x} , can be equivalently written in the form

$$\dot{z} = BD(z)Cz,$$

where $z = x - \bar{x}$, if and only if it admits a *BDC*-decomposition, according to Definition 1.

Proof. If $J(x) = BD(x)C$ for any x in the domain, then, denoting $z = x - \bar{x}$, $J(z) = BD(z)C$ holds for any z . Then, integration exploiting the integral formula (4) entails the result, as shown in the derivation above. Conversely, if system (3) is equivalent to $\dot{z} = BD(z)Cz$, then linearisation immediately provides $J(z) = BD(z)C$, hence $J(x) = BD(x)C$. ■

Note that, if \bar{x} is not an equilibrium point, the nonlinear system (3) can be equivalently written as

$$\dot{z} = BD(z)Cz + \hat{f}_0,$$

where $z = x - \bar{x}$ and $\hat{f}_0 = Sf(\bar{x}) + f_0$.

3. SOME *BDC*-BASED RESULTS

Based on the *BDC*-decomposition, interesting structural results can be derived, which hold regardless of the value of the positive diagonal entries of matrix D . A first result concerns the number of equilibrium points of the nonlinear system.

Theorem 9. (Giordano 2016) Consider a nonlinear system (3), defined on an open and convex domain \mathcal{D} , admitting a *BDC*-decomposition with D having a positive diagonal. If in \mathcal{D} there are more than one distinct equilibrium points, then the system Jacobian $J = BDC$ cannot be structurally nonsingular.

Proof. Given the system $\dot{x} = Sf(x) + f_0$, consider two distinct equilibrium points \bar{x} and \tilde{x} . Then, both equilibrium conditions $0 = Sf(\bar{x}) + f_0$ and $0 = Sf(\tilde{x}) + f_0$ must hold. Since the equality $S[f(x) - f(\bar{x})] = BD(z)Cz$, with $z = x - \bar{x}$, can be written for any x , it is possible to choose $x = \tilde{x}$. This choice provides $S[f(\tilde{x}) - f(\bar{x})] = BD(z)Cz = 0$, in view of the equilibrium conditions. Since $z = \tilde{x} - \bar{x} \neq 0$, being $\tilde{x} \neq \bar{x}$ (the equilibria are distinct by assumption), then $BD(z)C$ must be singular. ■

Therefore, if $J = BDC$ is structurally nonsingular, the equilibrium (if any) must be unique.

Another results concerns monotonicity (Hirsch 1988; Smith 2008). Recall that a monotone nonlinear system has a Jacobian matrix that is Metzler, when evaluated at any equilibrium point.

Proposition 10. (Giordano 2016) The system (3), admitting a *BDC*-decomposition

$$J(x) = \sum_{k=1}^q B_k C_k^\top D_k(x),$$

is structurally monotone if and only if $B_k C_k^\top$ are Metzler matrices for all k .

Proof. Sufficiency is immediate, since the positive linear combination of Metzler matrices is of course a Metzler matrix. Necessity can be proved by contradiction: should $B_k C_k^\top$ have a negative off-diagonal entry, for some k , then, for large enough values of $D_k(\bar{x})$, the resulting matrix $J(\bar{x})$ would have a negative off-diagonal entry as well, hence it would not be Metzler for some \bar{x} , and the system would not be structurally monotone. ■

3.1 *BDC*-based Computation of Polyhedral Lyapunov Functions for Structural Stability

The global representation provided by system (6) allows to absorb the original nonlinear system in a *linear differential inclusion* (LDI). Indeed, assuming that the equilibrium is at zero, $\bar{x} = 0$, system (6) becomes

$$\dot{x}(t) = BD(x(t))Cx(t).$$

Then it suffices to replace $D(x(t))$ with $D(t)$ to get the LDI

$$\dot{x}(t) = BD(t)Cx(t),$$

such that all the trajectories of the original systems are also trajectories of the LDI. This can help assessing the stability properties of its equilibrium in a structural fashion. In fact, after absorbing the nonlinear system equations in a *BDC*-based LDI, a polyhedral Lyapunov function can be found, based on the network structure only (namely, on matrices B and C only): the existence of a polyhedral Lyapunov function is shown to be equivalent to the stability of a suitable discrete difference inclusion, and a numerical recursive procedure is proposed to generate the unit ball of the polyhedral norm, if any. Whenever a polyhedral Lyapunov function is found, the proposed procedure structurally certifies the stability of the system for any choice of the positive diagonal entries of matrix D . A similar, but less conservative, procedure can be used to assess boundedness of the nonlinear system, by absorbing it in a *positive* linear differential inclusion. Details are in the work by Blanchini and Giordano 2014, 2015b,a.

3.2 *BDC*-Decomposition: Exploiting Multi-affinity

For a system admitting a *BDC*-decomposition as in (2), some important functions, such as the determinant and the coefficients of the characteristic polynomial of the Jacobian, are multi-affine functions of the diagonal entries D_h of matrix D , because $[B_h C_h^\top]$ are rank-one matrices (Barmish 1994). This property can be exploited for structurally assessing properties of the associated system. Indeed, a fundamental result states that a multi-affine function defined on a hypercube reaches its minimum (and maximum) value on a vertex of the hypercube (Barmish 1994, Lemma 14.5.5). Structural analysis provided by Blanchini et al. (2012); Blanchini and Giordano (2014); Giordano et al. (2015) is grounded on the following result.

Theorem 11. Given the hypercube

$$\mathcal{C}_x = \{x \in \mathbb{R}^n : 0 \leq x_k \leq \Phi, k = 1, \dots, n\},$$

and the multi-affine function $h : \mathcal{C}_x \rightarrow \mathbb{R}$, denote by $x^{(v)}$ the vertices of the hypercube \mathcal{C}_x , $v = 1, \dots, 2^n$, where $x^{(1)} = [\Phi \Phi \dots \Phi]$. Then:

- a) $h(x) > 0$ for all x in the interior of \mathcal{C}_x if and only if $h(x^{(v)}) \geq 0$ for all v and $h(x^{(1)}) > 0$;
- b) $h(x) < 0$ for all x in the interior of \mathcal{C}_x if and only if $h(x^{(v)}) \leq 0$ for all v and $h(x^{(1)}) < 0$;
- c) $h(x) = 0$ for all x in \mathcal{C}_x if and only if $h(x^{(v)}) = 0$ for all v .

Proof. Necessity is immediately based on continuity arguments. Sufficiency can be proved by contradiction, based on the fact that a multi-affine function defined on a hypercube reaches its minimum (and maximum) value on a vertex of the hypercube. Details are in Blanchini and Giordano (2014); Giordano et al. (2015); Giordano (2016). ■

Remark 12. If x has n components, it is necessary to check 2^n vertices; hence, an algorithm exploring the sign of $h(x)$ on all vertices has exponential complexity. However, remarkably, checking the sign on a *finite* number of vertices can provide information on the sign in the whole hypercube. ◊

As explained in the following section, this result can be exploited for the efficient computation of *structural steady-state influences*.

4. STRUCTURAL STEADY-STATE INFLUENCE: BDC-BASED COMPUTATION

The (i, j) entry of the Jacobian matrix expresses the *direct influence* of the j th system variable on the i th; when the Jacobian is sign-definite, we know that each variable of the system always has a positive/negative direct influence on each of the others (and this direct influence is visually represented in the associated graph by a positive/negative edge). However, it is also interesting to determine the sign of the *net steady-state influence*, combining all direct and indirect effects. Based on the BDC-decomposition, Giordano et al. (2015) have proposed an efficient approach to compute the so-called *structural influence matrix*, expressing the overall direct and indirect influences, at steady-state, among the state variables of a dynamical network. The problem of determining structural influences is well known in the field of ecology, and is related to the notion of community matrix Levins (1968), which is the Jacobian matrix of the system of growth equations and thus describes interactions among and within species in a community near equilibrium. The community matrix, expressing direct effects only, was first qualitatively analysed in Levins (1974, 1975) in terms of signed entries, graphs and loops. The net steady-state effect, combining all direct and indirect effects, is expressed by the adjoint matrix of the negative of the community matrix. Levins (1974, 1975); Dambacher et al. (2002, 2003b,a, 2005) When the sign of some entries of the adjoint matrix is indeterminate, the net response predicted by the model is uncertain: to quantify this uncertainty, a weighted-predictions matrix was introduced Dambacher et al. (2002); Dambacher and Ramos Jiliberto (2007) that assigns a probability to the predicted sign of the response.

More in general, Giordano et al. (2015) consider the problem of identifying structural influences of external inputs on steady-state outputs (with a special focus on biological network models). A structural influence is identified whenever, upon a perturbation due to a constant input, the ensuing variation of the steady-state output value has the same sign as the input (positive influence), the opposite sign (negative influence), or is zero (perfect adaptation: a variable embedded in a system is adaptive if, in the presence of a persistent input, after a transient it reverts to its pre-perturbation value, and adaptation is perfect if the

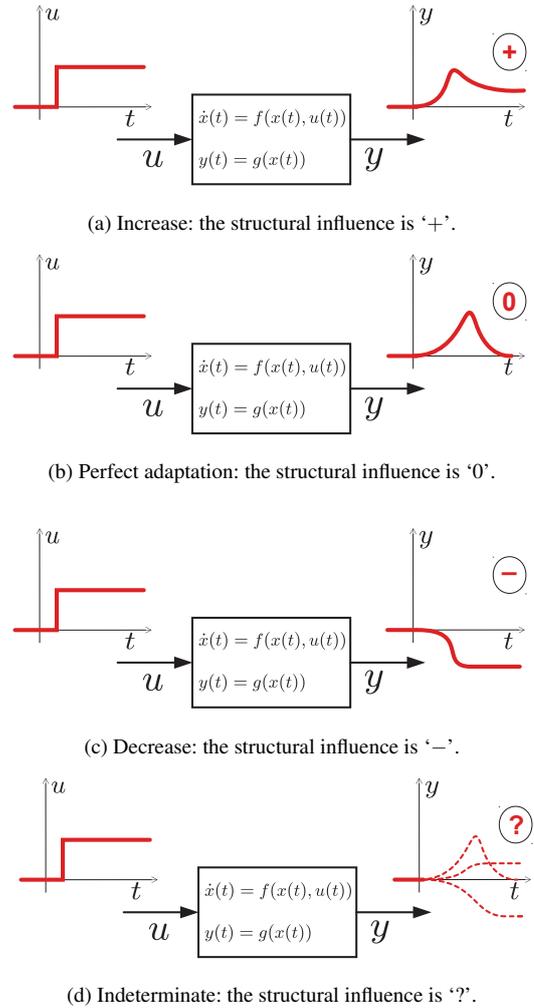


Fig. 2. The structural input-output influence is determinate if a step input yields a positive (a), zero (b), or negative (c) change in the output steady state, for any choice of the parameters. The structural influence is indeterminate when the output variation depends on the system parameters (d). Figure taken from Giordano et al. (2015).

pre-perturbation value is exactly recovered at steady-state, Yi et al. 2000; Sontag 2003; Drengstig et al. 2008), for any feasible choice of the model parameters.

When persistent additive inputs are applied to a single state variable and outputs are taken as single state variables, all the resulting signs and zeros can constitute a *structural influence matrix*, whose (i, j) entry indicates the sign of the *overall* steady-state influence of the j th system variable on the i th variable (namely, the output caused by an external persistent input applied to the j th variable). Each entry is structurally determinate if the sign does not depend on the choice of the parameters, but is indeterminate otherwise: as illustrated in Fig. 2, the structural influence is determinate if, for any feasible choice of the system parameters, the steady-state variation in the output value is zero ('0'), or its sign is concordant ('+') or discordant ('-') with the sign of the external stimulus. In contrast, if the sign of the variation depends on the magnitude of the parameters, the influence is indeterminate ('?'). The structural influence matrix corresponds indeed to the adjoint matrix of the negative of the Jacobian matrix, as is known for ecological models; however, for large-scale systems, an efficient computational

approach is needed. In principle, determining the influence matrix would require exhaustive testing of the system steady-state behaviour in the widest range of parameter values. However, for systems admitting a *BDC*-decomposition (which, as we have seen, include most biological systems), the influence matrix can be evaluated by an algorithm that tests the system steady-state behaviour only at a finite number of points. By means of the same algorithm, the structural effect of any perturbation (such as variations of relevant parameters) can be assessed as well.

Consider a general nonlinear system

$$\dot{x}(t) = f(x(t), u(t)), \quad (9)$$

$$y(t) = g(x(t)), \quad (10)$$

where $f(\cdot, \cdot)$ and $g(\cdot)$ are continuously differentiable, $x \in \mathbb{R}^n$, $u \in \mathbb{R}$ is an input and $y \in \mathbb{R}$ is an output. Assume that there exists an equilibrium point $\bar{x} > 0$ (componentwise), corresponding to \bar{u} , such that $f(\bar{x}, \bar{u}) = 0$, and consider the corresponding output steady-state value $\bar{y} = g(\bar{x})$. So both the steady-state values $\bar{x}(u)$ and $\bar{y}(u)$ are functions of u . Also, assume that the considered equilibrium \bar{x} is asymptotically stable, that the input perturbation u is small enough to ensure that the stability of $\bar{x}(u)$ is preserved, and that the system admits a *BDC*-decomposition.

The influence is determined by the derivative of the steady-state map that relates a given input u to a specific output y . For system (9)-(10), the implicit function theorem provides an analytical expression for the derivative of the steady-state input-output map:

$$\frac{\partial \bar{y}}{\partial \bar{u}} = \frac{\partial g}{\partial x} \bigg|_{\bar{x}} \left(- \frac{\partial f}{\partial x} \bigg|_{(\bar{x}, \bar{u})} \right)^{-1} \frac{\partial f}{\partial u} \bigg|_{(\bar{x}, \bar{u})}. \quad (11)$$

Consider the linear approximation of the nonlinear system in a neighbourhood of the equilibrium \bar{x} . Then, denoting by $z(t) = x(t) - \bar{x}$, $v(t) = u(t) - \bar{u}$, $w(t) = y(t) - \bar{y}$, the linearised system is

$$\begin{cases} \dot{z}(t) = Jz(t) + Ev(t), \\ w(t) = Hz(t), \end{cases}$$

where $[J]_{ij} = \frac{\partial f_i}{\partial x_j} \bigg|_{(\bar{x}, \bar{u})}$, $[E]_i = \frac{\partial f_i}{\partial u} \bigg|_{(\bar{x}, \bar{u})}$ and $[H]_j = \frac{dg}{dx_j} \bigg|_{\bar{x}}$. J is the Jacobian matrix, while E and H are a column and a row vector representing, respectively, how the input acts on the system state and how the output depends on the system state in the linearised system.

As shown by Giordano et al. (2015), for system (9)-(10),

$$\frac{\partial \bar{y}}{\partial \bar{u}} = H(-J)^{-1}E = \frac{1}{\det(-J)} \det \begin{bmatrix} -J & -E \\ H & 0 \end{bmatrix}. \quad (12)$$

Since the equilibrium is assumed to be stable, $\det(-J)$ is always positive; since the system admits a *BDC*-decomposition, to *structurally* evaluate the sign of $\frac{\partial \bar{y}}{\partial \bar{u}}$, we can check whether function

$$r(D) \doteq \det \begin{bmatrix} -J & -E \\ H & 0 \end{bmatrix} = \det \begin{bmatrix} -BDC & -E \\ H & 0 \end{bmatrix} \quad (13)$$

is sign-definite, namely, it has the same sign for all the possible choices of $D \succ 0$. If the sign is not the same for all possible choices, then the influence is not structurally determined. The *structural* sign of $r(D)$ can be determined by checking a *finite* number of points: the vertices of the unit hypercube

$$\mathcal{C}_D = \{D_k : 0 \leq D_k \leq 1, k = 1, \dots, q\}.$$

Theorem 13. (Giordano et al. 2015) Denote by $D^{(v)}$ the matrices corresponding to the vertices of the hypercube \mathcal{C}_D , $v = 1, \dots, 2^q$. Then:

- $r(D) > 0$ structurally if and only if $r(D^{(v)}) \geq 0$ for all v and $r(D) > 0$ for $D = I$;
- $r(D) < 0$ structurally if and only if $r(D^{(v)}) \leq 0$ for all v and $r(D) < 0$ for $D = I$;
- $r(D) = 0$ structurally if and only if $r(D^{(v)}) = 0$ for all v .

Remark 14. The proof of Theorem 13 is based on Theorem 11. Although the vectors E and H are in general functions of the parameters, namely, of the partial derivatives (with respect to x and to u): $[E]_i = \frac{\partial f_i}{\partial u} \bigg|_{(\bar{x}, \bar{u})}$ and $[H]_j = \frac{dg}{dx_j} \bigg|_{\bar{x}}$, this not an issue, because $r(D)$ is still a multi-affine function of the parameters. \diamond

We have then the following numerical procedure.

Algorithm 1. Vertex algorithm.

Input: Matrices B and C of the *BDC*-decomposition and matrices E and H appearing in (13).

Output: The steady-state structural influence sign $\sigma \in \{+, -, 0, ?\}$.

- Let $\omega_{max} = \omega_{min} := 0$.
- For $k = 0, 1, \dots, 2^q - 1$, consider its binary representation $k_{bin} := [D_1, D_2, \dots, D_q] \in \{0, 1\}^q$.
 - Let $D = \text{diag}\{D_1, D_2, \dots, D_q\}$.
 - Let $\omega_{min} := \min\{\omega_{min}, \text{sign}[r(D)]\}$.
 - Let $\omega_{max} := \min\{\omega_{max}, \text{sign}[r(D)]\}$.
- IF $\omega_{min} = 0$ and $\omega_{max} = 1$, then $\sigma := +$;
- IF $\omega_{min} = -1$ and $\omega_{max} = 0$, then $\sigma := -$;
- IF $\omega_{min} = 0$ and $\omega_{max} = 0$, then $\sigma := 0$;
- IF $\omega_{min} = -1$ and $\omega_{max} = 1$, then $\sigma := ?$.

The outcome of the procedure is one of the four cases represented in Fig. 2.

The proposed approach can be used to establish the existence of a structural influence of *any input* on a given output. Since uncertain parameters can be considered as inputs subject to variations, the method can be applied to identify the structural influence of a system parameter on the system outputs.

When a persistent additive input is applied to a single state variable and a single state variable is taken as the system output, the results for all the possible input-output pair combinations can be visualised in the structural influence matrix, whose entries express the sign of the steady-state influence on each variable of an external persistent input applied to each variable. To assess the structural influence on the i th variable of a persistent, additive input applied to the j th variable (Giordano et al. 2015), consider a system (9)-(10) of the form

$$\dot{x}(t) = f(x(t)) + Eu(t), \quad (14)$$

$$y(t) = Hx(t), \quad (15)$$

and take vectors $E = E_j$ and $H = H_i$ with a single non-zero entry equal to one

$$E_j = [0 \dots 0 \underbrace{1}_{\text{position } j} 0 \dots 0]^T, \quad H_i = [0 \dots 0 \underbrace{1}_{\text{position } i} 0 \dots 0].$$

If the system admits a *BDC*-decomposition, then each entry $[M]_{ij}$ of the influence matrix $M \in \mathbb{R}^{n \times n}$ can be generated by means of the numerical vertex Algorithm 1, choosing the corresponding E_j and H_i . $[M]_{ij}$ is:

- '+' if the influence is positive for any realisation of the structure;

- ‘0’ if there is perfect adaptation for any realisation of the structure;
- ‘−’ if the influence is negative for any realisation of the structure;
- ‘?’ if the influence is not structurally sign-definite.

Remark 15. Also when considering their signed influence matrix, monotone systems enjoy particular properties. Indeed, as shown by Giordano et al. (2015), the influence matrix associated with a monotone system (hence, with a Metzler or a positive Jacobian matrix) has exclusively ‘+’ or ‘0’ entries; and exclusively ‘+’ entries if, furthermore, the Jacobian is irreducible. Monotonicity is a sufficient, but not a necessary condition: there are systems that enjoy the same positive-influence-matrix property without being monotone. \diamond

Interestingly, several complex dynamical networks in nature admit signed influence matrices that are highly determined: an example is given by the model of EnvZ-OmpR osmoregulation in *E. coli* proposed by Shinar and Feinberg (2010), whose influence matrix has been computed by Giordano et al. (2015) based on Algorithm 1 and is reported in Fig. 3, along with the corresponding graph.

Remark 16. (Global, not local!) The BDC-based method for computing structural steady-state input-output influences is *not* a local method based on linearisation, which would be valid exclusively for infinitesimal deviations from the equilibrium point. Of course, as stated earlier, the perturbation must be small enough to ensure that stability is preserved; however, the perturbation might drive the system from the stable equilibrium \bar{x}_E to another stable equilibrium \bar{x}_A , and the analysis would still be valid. In fact, as an alternative proof, we can show that the approach simply relies on stability assumptions and on the knowledge of matrices B and C , which are the same for any equilibrium point of the system, since, as proved in Section 2.1, the BDC-decomposition is a global property: therefore, even though the system parameters (accounted for by matrix D) are completely different at the two equilibria, the system structure (matrices B and C) is unchanged. Assume for instance that $\bar{x}_E = 0$ when $u = 0$; the application of a persistent step input $u = \bar{u}$ drives the system to the new equilibrium \bar{x}_A , such that

$$0 = BD(\bar{x}_A)C\bar{x}_A + E\bar{u}.$$

Then, under stability assumptions, matrix $BD(\bar{x}_A)C$ is invertible and the proposed procedure can assess the structural sign of the steady-state variation in each state variable,

$$\bar{x}_A = [BD(\bar{x}_A)C]^{-1}E\bar{u},$$

which is determinate if the components of $[BD(\bar{x}_A)C]^{-1}E\bar{u}$ have the same sign for all matrices D with positive diagonal entries. \diamond

5. CONCLUSION

The proposed results rely on a peculiar aspect of dynamical networks: *local* interactions have consequences on the *global* behaviour of the system. Hence, structural analysis can examine what characteristic behaviour can be produced by local interactions having a given structure, or how local interactions with a given structure can result in a given behaviour. The BDC-decomposition can capture the fact that the global behaviour is due to the combination of several local interactions, representing a meaningful picture of the “local interactions, global behaviour” effect; based on the BDC-decomposition, structural, parameter-free criteria can be devised to assess fundamental properties of the system, such as the capacity of exhibiting oscillations

(Blanchini et al. 2012) and the system stability (Blanchini and Giordano 2014). In particular, here we have focused on the steady-state input-output behaviour: by exploiting the multi-affinity properties of the BDC-decomposition, numerical procedures can be devised to provide guarantees on the sign of suitable functions in a whole hypercube, based on the computation of the function on its vertices only. This allows the efficient computation of the steady-state influence matrix (Giordano et al. 2015), representing the structural steady-state effect on each of the variables of a persistent input applied to each of the system equations, but the same procedure can be applied to assess the effect of variations in significant parameters.

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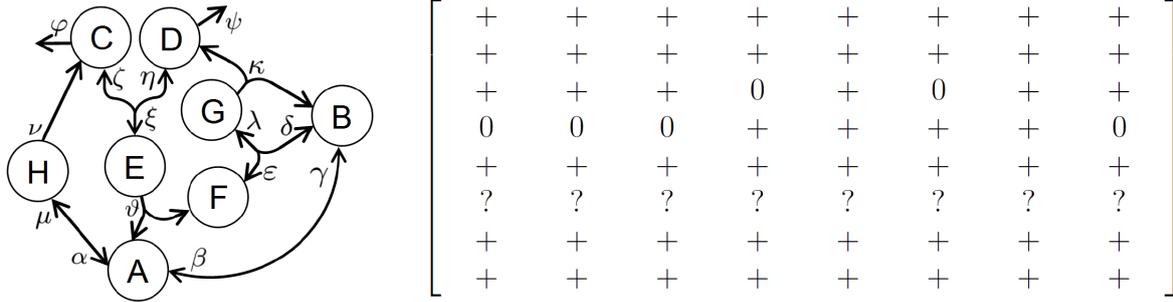


Fig. 3. Graph associated with the *E. coli* EnvZ-OmpR osmoregulation model by Shinar and Feinberg (2010) and corresponding signed influence matrix, computed by Giordano et al. (2015). Figure taken from Giordano et al. (2015).

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