Consensus over activity-driven networks

Zino, Lorenzo; Rizzo, Alessandro; Porfiri, Maurizio

Consensus Over Activity-Driven Networks

Lorenzo Zino , Alessandro Rizzo , *Senior Member, IEEE*, and Maurizio Porfiri , *Fellow, IEEE*

Abstract—**The problem of self-coordination of a network of dynamical systems toward a common state is often referred to as the consensus problem. In view of its wide range of applications, the consensus problem has been extensively studied in the past few decades. However, most of the available results focus on static networks, challenging our mathematical understanding of coordination in temporal networks. In this article, we study discrete-time stochastic consensus over temporal networks, modeled as activity-driven networks. In this paradigm, each node has a specific tendency to create links in the network, measured through an activity potential. Differences in the activity potential of nodes favor the evolution of heterogeneous networks, in which some nodes are more involved in the process of information sharing than others. Through stochastic stability theory, we characterize the expected consensus state, which is found to be dominated by low-activity nodes. By further leveraging eigenvalue perturbation techniques, we derive a closed-form expression for the convergence rate in a mean-square sense, which points at a detrimental effect of moderate levels of heterogeneity for large networks. Simulations are conducted to support and illustrate our analytical findings.**

Index Terms—**Consensus, convergence rate, heterogeneity, mean-square, stability of linear systems, time-varying networks.**

I. INTRODUCTION

CONSENSUS protocols are a class of distributed algorithms, whose goal is to coordinate the units of a network

L. Zino was with the Department of Mathematical Sciences "G. L. Lagrange, " Politecnico di Torino, 10129 Turin, Italy, and also with the Department of Mechanical and Aerospace Engineering, New York University Tandon School of Engineering, Brooklyn, NY 11201 USA. He is now with the Faculty of Science and Engineering, University of Groningen, 9747 AG Groningen, The Netherlands (e-mail: lorenzo.zino@rug.nl).

A. Rizzo is with the Department of Electronics and Telecommunications, Politecnico di Torino, 10129 Turin, Italy, and also with the Office of Innovation, New York University Tandon School of Engineering, Brooklyn, NY 11201 USA (e-mail: alessandro.rizzo@polito.it).

M. Porfiri is with the Department of Mechanical and Aerospace Engineering and the Department of Biomedical Engineering, New York University Tandon School of Engineering, Brooklyn, NY 11201 USA (e-mail: mporfiri@nyu.edu).

Digital Object Identifier 10.1109/TCNS.2019.2949387

of dynamical systems toward a common state. These protocols find applications in an impressively wide range of research domains, including opinion formation, distributed estimation, and multivehicle coordination [1]–[3].

Because of this wide range of applications, consensus has received extensive attention in the past 15 years. However, most of the research has focused on time-invariant networks [4], and limited efforts have been devoted to time-varying stochastic networks. Criteria for almost sure convergence of consensus protocols over Erdős–Rényi graphs have been originally presented in [5] and later extended to arbitrary weighted graphs [6]–[9].

Building on these early studies, the literature has brought forward a powerful toolbox of analytical tools that can help elucidate stochastic consensus. For example, criteria for exponential convergence and a detailed quantification of the asymptotic consensus state are presented in [10], approximate consensus is examined in [11], convergence bounds are established in [12], and systems resilience is studied in [13]. Several authors have investigated criteria for the computation of convergence rates to consensus [14]–[20].

For specific network models, closed-form results have been established. We mention the gossip communication, where the units asynchronously establish pairwise interactions to exchange information and average their state, and the broadcast gossip communication, where units asynchronously activate and transmit information to the whole network. For the case of bidirectional gossip communication, Boyd *et al.* [21] examine exponential convergence of the consensus problem and of the specific case of average consensus. Unidirectional gossip communication is addressed in [22], where the authors prove asymptotic convergence of the average consensus algorithm using an eigenvalue perturbation argument, and in [23], where exponential convergence is established through a direct computation of the second moment matrix. Exponential and almost sure convergence for the broadcast gossip average consensus are studied in [23] and [24], respectively. Other network models that have been extensively studied, and for which necessary and sufficient conditions for mean-square convergence are available, include numerosity-constrained networks [25] and networks of conspecific agents [26], [27]. Here, we seek to extend the rigorous analysis of networks of conspecific agents in [26] to heterogeneous networks of interactions.

We focus on the paradigm of activity-driven networks (ADNs), which has emerged as a potent tool to faithfully describe the evolution of several networks of interactions [28]. In ADNs, each node is assigned a fixed parameter, called *activity potential*, which encapsulates its propensity to communicate with its peers. Selecting a range of activity potentials

for the nodes in the network allows for elegantly modeling heterogeneity. In the simplest incarnation of ADNs, the activity potential is the probability that a node is *activated* in a time unit. The key advantages of ADNs are that: 1) they allow for reproducing networks with a desired level of heterogeneity, in contrast with existing models of time-varying stochastic networks [28], [29]; and 2) they yield an analytically tractable formulation, which has afforded unprecedented analytical insight into complex problems.

Through the lens of ADNs, researchers have recently established mathematical models for epidemic spreading [30], [31], voting dynamics [32], opinion formation [33], random walks [34], and percolation problems [35]. The ADN paradigm allows for including many features of real-world networks, such as the presence of communities and higher order structures [36], heterogeneous nodes' propensity to attract connections [37], and state-dependent behavioral changes [38], thereby yielding realistic models of social, technical, and sociotechnical systems.

Preliminary results on consensus in ADNs, mostly based on computational methods and time-scale separation between the network evolution and the nodes' dynamics, can be found in [39] and [40]. Here, we build on these endeavors toward a rigorous mathematical treatment of consensus problems over ADNs. Through stochastic stability theory and eigenvalue perturbation methods, we establish closed-form results for the rate of convergence of the mean-square error dynamics and for the expected consensus state of the network. From the analysis of these expressions, we bring forward surprising evidence on the role of heterogeneity on consensus. Our first result, based on a perturbation argument, suggests that the speed of convergence could be hindered by the heterogeneity of the nodes' activity, at least for moderate levels of heterogeneity. Our second result is an exact finding, which holds for any level of heterogeneity, and establishes that low-activity nodes are the most influential in shaping the final state of the network.

The main technical contributions of this article are as follows.

1) We extend the analysis of [25] to analytically study the error dynamics in a mean-square sense for consensus problems over ADNs, where the activities of all the units are generally heterogeneous.

2) We demonstrate the application of perturbation techniques to compute a closed-form expression for the convergence rate to consensus, which helps understanding how even modest heterogeneities in the system could impact the effectiveness of the consensus protocol.

3) We analyze the expected consensus state for arbitrary ADNs and perform once more a perturbation analysis to highlight the sensitivity of consensus to heterogeneities in the nodes' activity.

4) With an eye toward applications of ADNs in real-world problems, we derive a toolbox of asymptotic results for consensus over large networks.

The rest of this article is organized as follows. In Section II, we introduce the problem statement. In Section III, we recall basic notions of stochastic stability theory for consensus protocols. In Section IV, we analyze the consensus protocol on ADNs and present our main results. In Section V, we perform an asymptotic analysis of the system for large-scale networks. Section VI concludes this article and outlines potential avenues of future research.

II. PROBLEM STATEMENT

A. Notation

We gather here the notational convention used throughout this article. $\mathbb{R}$, $\mathbb{R}^+$, and $\mathbb{Z}^+$ are the sets of real, nonnegative real, and nonnegative integer numbers, respectively. $\mathbb{1}$ is the vector of all ones, e_i is a vector with all zeroes but a one in the ith position. Given a vector x, x^T denotes its transpose, $||x||$ its Euclidean norm, and $\mathrm{diag}(x)$ the diagonal matrix with the elements of x on its diagonal. Given a matrix M, we denote its spectral radius as $\rho(M)$. I is the identity matrix. Matrices and vectors' dimensions are omitted when not necessary. The operations $\otimes$ and $\oplus$ denote Kronecker product and sum, respectively. The use of Kronecker algebra will often lead us to work with $n^2 \times n^2$ matrices, where n is the number of nodes. We write these matrices in n^2 blocks of $n \times n$ matrices. More specifically, given an $n^2 \times n^2$ matrix M, we use four labels to denote the blocks (superscript) and the position of the entry in the block (subscript), as follows:

$$M = \begin{bmatrix} M^{11} & \cdots & M^{1n} \\ M^{21} & \cdots & M^{2n} \\ \vdots & \ddots & \vdots \\ M^{n1} & \cdots & M^{nn} \end{bmatrix}, \quad M^{jh} = \begin{bmatrix} M_{11}^{jh} & \cdots & M_{1n}^{jh} \\ M_{21}^{jh} & \cdots & M_{2n}^{jh} \\ \vdots & \ddots & \vdots \\ M_{n1}^{jh} & \cdots & M_{nn}^{jh} \end{bmatrix}.$$

Thus, M_{ik}^{jh} is the entry in the ith row and kth column of the block in the jth row and hth column of M. Similarly, we write n^2-dimensional vectors as $v = [v_1^1, v_2^1, \ldots, v_n^1, \ldots, v_n^n]$. Expected values of random variables are denoted as $\mathbb{E}[\cdot]$.

B. ADNs' Time Evolution

Let $\mathcal{V} = \{1, \ldots, n\}$ be a set of $n \geq 3$ nodes connected through a time-varying directed graph $\mathcal{G}_k = (\mathcal{V}, \mathcal{E}_k)$, where $\mathcal{E}_k$ is the time-varying *link set*, and $k \in \mathbb{Z}^+$ is the discrete time index. The graph $\mathcal{G}_k$ is generated according to a (direct) discrete time ADN [28] with unit time step and nodes' activity potential given by the vector $a \in (0, 1]^n$. Specifically, at each time step, every node $i \in \mathcal{V}$ is activated with probability equal to a_i, independent of others and the past history of the process. A node that is activated generates $m \leq n - 1$ directed links, connecting it with an m-tuple of nodes, selected uniformly among the remaining $n - 1$ nodes. Links are oriented from the activated node toward the selected nodes, and they last for a unit time step. Then, connections are deleted, the time index updated, and the whole process resumes. Should we remove the link directionality, the process would lead to undirected ADNs, typically used in epidemiology [28].

Fig. 1 depicts the formation of an ADN. The figure is helpful in illustrating the richness of the ADN paradigm and its main differences with respect to the other models of temporal networks. Differently from gossip models [21], more than one node can connect with others in one time step, and more than one link can be established in one time step (m for each node
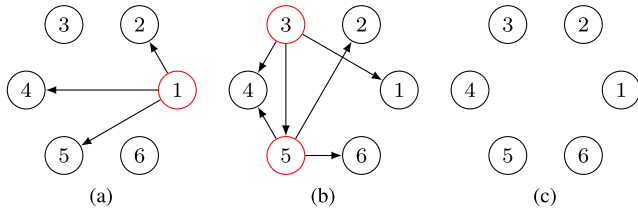
Fig. 1. Exemplary evolution of an ADN. At time $k = 0$, node 1 is activated and generates $m = 3$ directed links. At time $k = 1$, nodes 3 and 5 are activated, generating three links each. At time $k = 2$, none of the nodes is activated. (a) $k = 0$, (b) $k = 1$, (c) $k = 2$.

that is activated), yielding a rich dynamics for the evolving network. In contrast with the broadcast gossip algorithm [24], nodes are allowed to simultaneously update their state and share information with m other nodes. Compared to numerosity-constrained networks [25], only a random fraction of nodes is stochastically activated at each time step. The presence of heterogeneity marks the key difference with respect to networks of conspecific agents [26].

We define the average activity potential and the standard deviation of the activity potential as

$$\bar{a} := \frac{1}{n} \sum_{i=1}^{n} a_i, \quad \sigma := \sqrt{\frac{1}{n} \sum_{i=1}^{n} (a_i - \bar{a})^2}. \tag{1}$$

The standard deviation σ measures the heterogeneity in the nodes' activity potentials. When $\sigma = 0$, the ADN reduces to the model of conspecific agents proposed in [26]. An alternative way of describing such a heterogeneity consists of separating the average activity, as follows:

$$a_i = \bar{a} + \sigma h_i \tag{2}$$

where $h \in \mathbb{R}^n$ measures the deviation of each node from the average. Note that, by definition, $\mathbb{1}^T h = 0$ and $||h|| = \sqrt{n}$.

For any discrete time $k \in \mathbb{Z}^+$, we define the adjacency matrix of the time-varying network as $A_k \in \{0,1\}^{n \times n}$, where $(A_k)_{ij} = 1 \iff (i,j) \in \mathcal{E}_k$, and the Laplacian matrix $L_k := \text{diag}(A_k \mathbb{1}) - A_k$, such that

$$(L_k)_{ij} = \begin{cases} -(A_k)_{ij}, & \text{if } i \neq j \\ \sum_{h \neq i} (A_k)_{ih}, & \text{if } i = j. \end{cases} \tag{3}$$

By construction, matrices L_ks are a sequence of independent and identically distributed (i.i.d.) random variables. To improve the readability of this article, we denote by L a random variable distributed as L_k, for any $k \in \mathbb{Z}^+$, so that we can compute the moments of each of the random variables L_ks by referring to the common random variable L.

C. Consensus Over ADNs

The nodes' dynamics are defined as follows. Each node $i \in \mathcal{V}$ has a continuous state $x_i(k) \in \mathbb{R}$, which evolves according to a discrete-time consensus protocol (see [3, Sec. 3]), starting from an initial condition $x_0 \in \mathbb{R}^n$. At each time step, every node updates its state by averaging with the nodes, with which it is temporarily connected. Specifically, a generic node $i \in \mathcal{V}$

updates its state to

$$x_i(k+1) = (1 - \varepsilon m)x_i(k) + \varepsilon \sum_{j \in \mathcal{V}} (A_k)_{ij} x_j(k) \tag{4}$$

if $(L_k)_{ii} = m$, while it remains $x_i(k+1) = x_i(k)$, if $(L_k)_{ii} = 0$. The parameter $\varepsilon > 0$ is used to capture the nodes' tendency to compromise. Specifically, ε is the weight that each node assigns to the state of its neighbors during the update process: the larger is ε, the more a node will favor the average state of the neighbors against its own during the updating process. Hence, consensus dynamics is described by the following time-varying linear system:

$$x(k+1) = (I - \varepsilon L_k)x(k) := P_k x(k) \tag{5}$$

with initial condition $x(0) = x_0$, where the *consensus matrices* P_ks are a sequence of i.i.d. random variables. In general, P_ks are nonsymmetric, and their entries are not required to be nonnegative. In fact, if $\varepsilon m > 1$, then the diagonal of P_k may include negative entries. We say that the consensus protocol converges to a *consensus state* $\bar{x}$ if $\lim_{k \to \infty} x(k) = \bar{x}\mathbb{1}$, that is, all nodes asymptotically attain the same state. Given that (5) is a stochastic system, convergence must be defined in a stochastic sense [41].

From the literature, almost sure convergence (that is, convergence with probability 1) can be established for slowly updating nodes, that is, $\varepsilon < 1/m$. In this case, matrices P_ks are non-negative and, thus, stochastic (see, for example, [3, Sec. 3]). Here, we focus on mean-square convergence, which places no constraint on the selection of ε and guarantees almost sure convergence in our setting (see, for example, [12], [41], and [42]). Through the lens of mean-square convergence, one can aim at an analytical study of the convergence rate of the protocol, which is known to be unfeasible in an almost sure sense, beyond a few low-dimensional toy problems, where one can compute the largest sample-path Lyapunov exponent (see, for example, [43] and [44]).

III. PRELIMINARY RESULTS

Here, we review some basic notions of stochastic stability and key properties of stochastic consensus protocols. First, we introduce the *agreement subspace* $\mathcal{A} = \{v \in \mathbb{R}^n : v = \mu\mathbb{1}, \ \mu \in \mathbb{R}\}$ and its orthogonal complement $\mathcal{A}^\perp = \{v \in \mathbb{R}^n : v^T u = 0, \ \forall u \in \mathcal{A}\}$, called the *disagreement subspace*. To study the convergence of the consensus protocol to a consensus state, the dynamics $x(k)$ is projected onto the disagreement subspace, by means of a matrix $Q \in \mathbb{R}^{n \times (n-1)}$, such that $Q^T \mathbb{1} = 0$ and $Q^T Q = I$ (see, for example, [25]). The dynamics of the *disagreement vector* $\xi(k) = Q^T x(k)$ is

$$\xi(k+1) = Q^T P_k Q \xi(k) = \tilde{P}_k \xi(k) \tag{6}$$

with initial condition $\xi(0) = \xi_0 = Q^T x_0$. The mean-square stability analysis of the disagreement vector permits to formalize a necessary and sufficient condition for mean-square consentability for a consensus protocol, which is defined as follows.

Definition 1 (see [45, Def. 2]): Consensus protocol (5) is said to be mean-square consentable if for any $i \neq j$, $|x_i(k) - x_j(k)| \to 0$ in a mean-square sense, $\forall \xi_0 \in \mathbb{R}^{n-1}$.

The necessary and sufficient condition for mean-square consentability based on the disagreement vector is the following.

Proposition 1 (see [25, Sec. III.B]): Consensus protocol (5) is mean-square consentable if and only if the disagreement dynamics (6) is mean-square asymptotically stable, that is, $\lim_{k \to \infty} \mathbb{E}[||\xi(k)||^2] = 0$, $\forall \xi_0 \in \mathbb{R}^{n-1}$.

For a linear system like (5), whose matrices P_ks are i.i.d., mean-square convergence implies almost sure convergence; details can be found in [42, Proposition 4.3] and [41, Sec. 2], for the more general case of state matrices from an ergodic Markov chain. Hence, in our setting, mean-square consentability implies almost sure convergence to consensus. In order to quantify the speed of convergence of the protocol toward consensus, we use the asymptotic convergence factor of the disagreement dynamics [12], that is,

$$r := \sup_{||\xi_0|| \neq 0} \lim_{k \to \infty} \left(\frac{\mathbb{E}[||\xi(k)||^2]}{||\xi_0||^2} \right)^{1/k}. \tag{7}$$

The smaller the convergence factor, the faster the convergence of the dynamics is. In [46] and [54], it is proved that $r < 1$ is a necessary and sufficient condition for mean-square consentability. The following result establishes an easy-to-use expression for the convergence factor.

Proposition 2 (see [25, Proposition 1 and Th. 1]): Protocol (5) is mean-square consentable if and only if its convergence factor $r < 1$. The convergence factor is equal to the spectral radius $\rho(G)$ of the second moment consensus matrix

$$G = (R \otimes R) \left(I - \varepsilon \mathbb{E}[L] \oplus \mathbb{E}[L] + \varepsilon^2 \mathbb{E}[L \otimes L] \right) \tag{8}$$

where $R = QQ^T = I - \frac{1}{n} \mathbb{1}\mathbb{1}^T$.

For a mean-square consentable protocol, where convergence to a consensus state $\bar{x}$ is guaranteed almost surely, the expected consensus state $\mathbb{E}[\bar{x}]$ can be computed using the following result, which is indeed valid for the less restrictive case of almost sure convergence.

Proposition 3: Let protocol (5) be mean-square consentable. Then, the expected consensus state is $\mathbb{E}[\bar{x}] = \pi^T x_0$, where π is the left eigenvector associated with the null eigenvalue of $\mathbb{E}[L]$.

Proof: By using (5) recursively and computing the expected value, we obtain

$$\mathbb{E}[x(k)] = \mathbb{E}\left[\prod_{h=0}^{k-1} P_k \right] x(0) = \mathbb{E}[P]^k x_0 \tag{9}$$

where P is a random variable distributed as a generic element of the sequence of i.i.d. random variables P_ks, that is, $P = I - \varepsilon L$. Hence, $\mathbb{E}[x(k)]$ evolves as a time-invariant deterministic protocol with consensus matrix $\mathbb{E}[P]$. According to [3, Th. 2.2], since $\mathbb{E}[x(k)] \to \bar{x}\mathbb{1}$, then $\mathbb{E}[P]^k \to \mathbb{1}\mu^T$. By expressing $\mathbb{E}[P]$ in terms of its Jordan canonical form, we conclude that μ is the left eigenvector associated with the unit eigenvalue of $\mathbb{E}[P]$, which, in turn, coincides with the left eigenvector associated with the null eigenvalue of $\mathbb{E}[L]$. ∎

We note that the same result is proven in [10] and [21], under the assumption that all the P_ks are non-negative. However, the findings in [10] and [21] cannot be directly applied to our setting, unless restricting our analysis to the slowly updating scenario $\varepsilon < 1/m$, in which almost sure convergence is always guaranteed.

IV. ANALYSIS OF THE CONSENSUS PROTOCOL

The analysis of the consensus protocol on ADNs is carried out with two objectives. First, we compute the convergence factor of the consensus protocol by using an eigenvalue perturbation argument. This closed-form result enables us to derive a sufficient condition for almost sure convergence, and it unveils a potentially adversary effect of heterogeneity on the convergence speed of the protocol. Then, we study the effect of the nodes' activity on the formation of the consensus state, under the premise of mean-square consentability. Specifically, we demonstrate that the nodes with low activity influence the expected consensus state the most.

A. Convergence Speed to Consensus

We examine consentability of (5) by computing the convergence factor r, which is equal to the spectral radius of matrix G in (8), according to Proposition 2. The exact computation of $\rho(G)$ for an arbitrary set of activities a_is does not seem feasible when the activity potentials are heterogeneous, due to the nontrivial structure of the two matrices $\mathbb{E}[L] \oplus \mathbb{E}[L]$ and $\mathbb{E}[L \otimes L]$ in Proposition 2.

To address this issue, we study the effect of heterogeneity through a perturbation argument. Specifically, the expression for the activity potentials in (2) enables us to separate the effect of the average activity potential (which is studied through the paradigm of conspecific agents [25]) from the heterogeneity in the activity potential (which acts as a perturbation factor). Hence, we write matrix $G = G_0 + \sigma G_1 + O(\sigma^2)$, where G_0 is the second moment matrix for an ADN with homogeneous activity potentials equal to $\bar{a}$, which is computed using [26, Proposition 3], as

$$G_0 = \left(1 - \frac{n}{n-1} \varepsilon m \bar{a} \right)^2 (R \otimes R) + (I \otimes R)F \tag{10}$$

with

$$F = \frac{\varepsilon^2 \, m^2 \bar{a}^2}{(n-1)^2} F_1 + \frac{\varepsilon^2 \, m^2 \bar{a}}{n-2} F_2 + \frac{\varepsilon^2 \, m \bar{a}}{(n-1)(n-2)} F_3 \tag{11}$$

where matrices F_1, F_2, and F_3 are defined blockwise as

$$F_1^{ii} = -I - n(n-2)e_i(Re_i)^T$$

$$F_2^{ii} = \frac{1}{n}I + \frac{n^2 - 3n + 1}{n-1}e_i(Re_i)^T$$

$$F_3^{ii} = -\frac{1}{n}I + e_i(Re_i)^T \tag{12}$$

for the diagonal blocks and, for $j \neq i$,

$$F_1^{ij} = -I + ne_i(Re_i)^T + ne_j(Re_j)^T$$

$$F_2^{ij} = \frac{1}{n}I + \frac{1}{n-1}e_i(e_i - e_j)^T$$
$$- \frac{n}{n-1}e_i(Re_i)^T - e_j(Re_j)^T$$

$$F_3^{ij} = -\frac{1}{n}I + e_i(e_i - e_j)^T + (ne_i + e_j)(Re_j)^T. \quad (13)$$

Such a perturbation analysis allows for computing the convergence rate of consensus on ADNs in closed form, up to an error of the order of σ^2, shedding light on how a modest heterogeneity in the activity of the nodes influences the consensus dynamics.

To prove our main result, the following intermediate steps are carried out. In Lemma 1, we report the spectral radius of the unperturbed component of matrix G, that is, $\rho(G_0)$, which is computed by specializing the result for networks of conspecific agents in [26]. Then, the first-order perturbation G_1 is evaluated in Lemma 2. In Lemma 3, we reckon that the first-order perturbation of the spectral radius is null. This evidence calls for the evaluation of the first-order perturbation of the associated eigenvector, in Lemma 4, which allows for the computation of the second-order perturbation of the spectral radius. Theorem 1 consolidates these findings into our main result.

Lemma 1 (see [26, Th. 1]): Under the assumptions $m \geq 1$, $\bar{a} \in (0, 1]$, and $\varepsilon > 0$, the spectral radius $\rho_0 := \rho(G_0)$ is associated with a simple eigenvalue, equal to

$$\rho_0 = 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a}m \left[\frac{nm\bar{a}}{(n-1)^2} + m + 1 \right] \quad (14)$$

and its corresponding eigenvector is

$$u_0 = \frac{1}{\sqrt{n-1}} \text{vec}(R). \quad (15)$$

Matrix G_0 has at most three other real eigenvalues

$$\lambda^{(1)} = 0$$

$$\lambda^{(2)} = 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a}m \left[2\frac{nm\bar{a}}{(n-1)^2} + m - \frac{1}{n-1} \right]$$

$$\lambda^{(3)} = \left(1 - \frac{\varepsilon m\bar{a}n}{n-1}\right)^2 \quad (16)$$

whose corresponding eigenspaces are, respectively,

$$\Gamma^{(1)} = \left\{ v \in \mathbb{R}^{n^2} : v = w \otimes \mathbb{1}, \text{ or } v = \mathbb{1} \otimes w, \ w \in \mathbb{R}^n \right\}$$

$$\Gamma^{(2)} = \left\{ v \in \mathbb{R}^{n^2} : v_i = b_i Re_i - \frac{1}{n}\sum_{j \in \mathcal{V}} b_j Re_j \right.$$
$$\left. \mathbb{1}^T b = 0, \ b \in \mathbb{R}^n \right\}$$

$$\Gamma^{(3)} = \left\{ v \in \mathbb{R}^{n^2} : \sum_{i \in \mathcal{V}} v_i = 0, \ v_i^T \mathbb{1} = 0, \ e_i^T v_i = 0 \right\} \quad (17)$$

where the notation $v^T = [v_1^T, \dots, v_n^T]$ is used. The dimensions of $\Gamma^{(1)}$, $\Gamma^{(2)}$, and $\Gamma^{(3)}$ are $2n + 1$, $n - 1$, and $n^2 - 3n - 1$,

respectively, and these spaces are mutually orthogonal and to the span of u_0.

Lemma 2: The first-order perturbation associated with the activity's heterogeneity is $G_1 = (R \otimes R)M$, where

$$M^{jj} = -\varepsilon \left[\frac{n}{n-1} m \, \text{diag}\,(h)R + mh_j I \right]$$
$$+ \varepsilon^2 \frac{nm^2}{n-1} h_j \left[\bar{a}(R - e_j(Re_j)^T) + e_j(Re_j)^T \right]$$
$$+ \varepsilon^2 \frac{nm^2}{n-1} \bar{a} \left[\text{diag}\,(h)(R - e_j(Re_j)^T) \right]$$

$$M^{jh} = \varepsilon \frac{m}{n-1} h_j I + \varepsilon^2 \frac{m}{n-1} h_j e_j [e_h^T - me_j^T]$$
$$- \varepsilon^2 \frac{nm^2}{(n-1)^2} \bar{a} \left[\text{diag}\,(h)(R - e_j(Re_j)^T) \right]$$
$$+ \varepsilon^2 \frac{m(m-1)}{(n-1)(n-2)} h_j e_j \left[\mathbb{1}^T - e_h^T - e_j^T \right]$$
$$- \varepsilon^2 \frac{nm^2}{(n-1)^2} \bar{a} h_j (R - e_j(Re_j)^T), \text{ for } h \neq j. \quad (18)$$

Proof: With respect to its ith row, the random variable L is defined as follows.

1) With probability a_i, $L_{ii} = m$, and m off-diagonal entries, chosen uniformly at random, are equal to -1, while the others are equal to 0.
2) With probability $1 - a_i$, all the entries are equal to 0.

Therefore, we find $\mathbb{E}[L] = \frac{n}{n-1} m \, \text{diag}(a)R$. Through a cumbersome counting argument, we can compute the two matrices $\mathbb{E}[L] \oplus \mathbb{E}[L]$ and $\mathbb{E}[L \otimes L]$. Their expressions, blockwise, are

$$(\mathbb{E}[L] \oplus \mathbb{E}[L])^{jj} = \frac{n}{n-1} m \, \text{diag}(a)R + ma_j I$$

$$(\mathbb{E}[L] \oplus \mathbb{E}[L])^{jh} = -\frac{1}{n-1} ma_j I \quad (19)$$

$$(\mathbb{E}[L \otimes L])^{jj} = \frac{nm^2}{n-1} a_j \left[\text{diag}(a)(R - e_j(Re_j)^T) \right.$$
$$\left. + e_j(Re_j)^T \right]$$

$$(\mathbb{E}[L \otimes L])^{jh} = -\frac{nm^2}{(n-1)^2} a_j \left[\text{diag}(a)(R - e_j(Re_j)^T) \right]$$
$$+ \frac{m(m-1)}{(n-1)(n-2)} a_j e_j \left[\mathbb{1}^T - e_h^T - e_j^T \right]$$
$$+ \frac{m}{n-1} a_j e_j [e_h^T - me_j^T]. \quad (20)$$

The expression for M is obtained by combining the matrices above according to (8), expressing the activity potentials through (2), and collecting all the terms in σ. ∎

Remark 1: While the unperturbed matrix G_0 is symmetric, the first-order perturbation matrix G_1 is in general not symmetric.

Next, we recall the following result from second-order perturbation theory of simple eigenvalues, which is often used in quantum mechanics [47], applied to the spectral radius of G.

Proposition 4 (see [47, Ch. 6.1]): The spectral radius $\rho(G)$ can be written as $\rho(G) = \rho_0 + \sigma\rho_1 + \sigma^2\rho_2 + O(\sigma^3)$. The first-order perturbation is given in terms of u_0 and G_1 as

$$\rho_1 = u_0^T G_1 u_0. \tag{21}$$

The second-order correction requires knowledge of the first-order perturbation to the eigenvector associated with the spectral radius. Specifically, we have

$$\rho_2 = u_0^T G_1 u_1, \quad \text{with} \quad u_1 = \sum_{i=2}^{n^2} \frac{v_i^T G_1 u_0}{\rho_0 - \lambda_i} v_i \tag{22}$$

where $\lambda_2, \ldots, \lambda_{n^2}$ are the $n^2 - 1$ eigenvalues of G_0 in (16), counted with their multiplicity, and $v_2, \ldots, v_{n^2}$ are their corresponding eigenvectors in the eigenspaces in (17).

Vector u_1 represents the first-order perturbation to the eigenvector associated with the spectral radius of G, that is, $u = u_0 + \sigma u_1 + O(\sigma^2)$, with u_0 defined in (15). While in many practical applications, it is sufficient to retain a first-order perturbation to gain insight into the role of a critical parameter [48], consensus over ADNs requires the study of second-order corrections. In fact, the next claim shows that $\rho_1 = 0$.

Lemma 3: Under the assumptions $m \geq 1, \bar{a} > 0$, and $\varepsilon > 0$, the first-order perturbation correction to the spectral radius $\rho(G)$ is $\rho_1 = 0$.

Proof: Based on Proposition 4, we compute $\rho_1 = u_0^T G_1 u_0$. First, recalling (15), we define the vector $\tilde{y} := M u_0$, that is,

$$\tilde{y}_i^j = \sum_{h,k \in \mathcal{V}} M_{ik}^{jh} (u_0)_{kh} = \frac{1}{\sqrt{n-1}} \sum_{h,k \in \mathcal{V}} M_{ik}^{jh} R_{kh}$$

$$= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \sum_{h \in \mathcal{V}} M_{ih}^{jh} - \frac{1}{n} \sum_{h \in \mathcal{V}, k \neq h} M_{ik}^{jh} \right] \tag{23}$$

which can be computed using the explicit expression of M in Lemma 2. Details can be found in the Appendix. Then, we evaluate $y = (R \otimes R)\tilde{y}$ entrywise as

$$y_i^i = \frac{(n-1)^2}{n^2} \tilde{y}_i^i - \frac{n-1}{n^2} \left(\sum_{h \neq i} \tilde{y}_i^h + \sum_{k \neq i} \tilde{y}_k^i \right) + \frac{1}{n^2} \sum_{h,k \neq i} \tilde{y}_k^h \tag{24}$$

and, similarly, for the off-diagonal elements. Explicit computations of vectors $\tilde{y}$ and y are cumbersome, but they follow directly from the expression of M. Details are summarized in the Appendix. Here, we present the final result, that is

$$y_i^j = \begin{cases} \dfrac{n-2}{n} \dfrac{1}{\sqrt{n-1}} \varepsilon m \gamma h_i, & \text{if } i = j \\[2mm] -\dfrac{1}{n\sqrt{(n-1)}} \varepsilon m \gamma (h_i + h_j), & \text{if } i \neq j \end{cases} \tag{25}$$

with

$$\gamma := \frac{2n}{(n-1)^2} \varepsilon m \bar{a} - \frac{2n}{n-1} + \varepsilon m + \varepsilon. \tag{26}$$

In a more compact form, we write

$$y = \sqrt{\frac{n-2}{n-1}} \varepsilon m \gamma q \tag{27}$$

where the unit-norm vector $q^T = [q_1^T, \ldots, q_n^T]$ is

$$q_i := \sqrt{\frac{n}{n-2}} h_i Re_i - \frac{1}{\sqrt{n(n-2)}} \sum_{j \in \mathcal{V}} h_j Re_j. \tag{28}$$

From (17), we note that $y \in \Gamma^{(2)}$. Since eigenspaces are mutually orthogonal, y is orthogonal to u_0. Hence, (21) implies $\rho_1 = u_0^T G_1 u_0 = u_0^T y = 0$. ∎

Thus, a first-order perturbation is not sufficient to elucidate the role of heterogeneity in the nodes' activity on the rate of convergence of the protocol. We use the spectral characterization of G_0 in Lemma 1 to prove the following statement.

Lemma 4: Under the assumptions $m \geq 1, \bar{a} > 0$, and $\varepsilon > 0$, the first-order perturbation correction to the eigenvector of G associated with its spectral radius is

$$u_1 = \frac{\sqrt{(n-2)(n-1)}}{\varepsilon \bar{a} n \left(1 - \dfrac{m\bar{a}}{n-1} \right)} \gamma q \tag{29}$$

where vector q is defined in (28) and parameter γ in (26).

Proof: We split the summation of u_1 in (22) into three terms, one for each eigenspace of G_0, such that

$$u_1 = \left[\frac{1}{\rho_0} \Pi_1 + \frac{1}{\rho_0 - \lambda^{(2)}} \Pi_2 + \frac{1}{\rho_0 - \lambda^{(3)}} \Pi_3 \right] y \tag{30}$$

where Π_i is the matrix associated with the orthogonal projection onto the eigenspace Γ_i, and the vector $y = G_1 u_0$ is computed in (27). Since $q \in \Gamma_2$, the projections $\Pi_1 y = \Pi_3 y = 0$, while $\Pi_2 y = y$. Using Lemma 1, we obtain

$$u_1 = \frac{1}{\rho_0 - \lambda^{(2)}} \sqrt{\frac{n-2}{n-1}} \gamma q = \frac{\sqrt{(n-2)(n-1)}}{\varepsilon \bar{a} n \left(1 - \dfrac{m\bar{a}}{(n-1)} \right)} \gamma q \tag{31}$$

which concludes the proof. ∎

We consolidate our claims in the following theorem, which is the main result of this article.

Theorem 1: Given a consensus protocol over an ADN with activity potentials given by (2), $m \geq 1, \bar{a} > 0$, and $\varepsilon > 0$, the convergence factor is

$$r = 1 - \varepsilon \frac{2\bar{a}mn}{n-1} + \varepsilon^2 \bar{a}m \left[\frac{nm\bar{a}}{(n-1)^2} + m + 1 \right]$$
$$+ \sigma^2 \frac{(n-2)m}{\bar{a}n \left(1 - \dfrac{m\bar{a}}{n-1} \right)} \gamma\beta + O(\sigma^3) \tag{32}$$

where γ is defined in (26), and

$$\beta := \frac{2n}{(n-1)^2} \varepsilon m \bar{a} - \frac{2n}{n-1} + \frac{n-1}{n-2} \varepsilon m - \frac{\varepsilon}{n-2}. \tag{33}$$

Proof: We compute the vector $z^T := u_0^T G_1$ as follows. First, we observe that $u_0^T (R \otimes R) = u_0^T$, since u_0 is an eigenvector associated with the eigenvalue 1 of matrix $R \otimes R$. Then, $z^T = u_0^T M$ is computed by applying the technique used in the proof of Lemma 3. Details can be found in the Appendix. We report the final expression recalling the definition of q in (28),
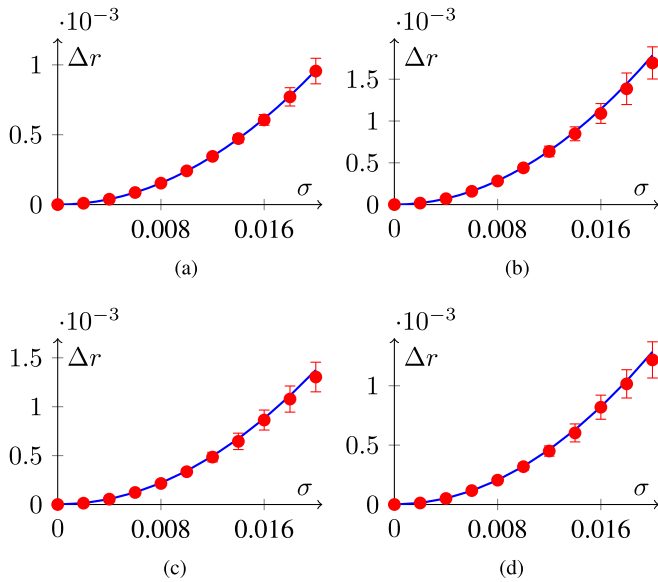
Fig. 2. Variation of the convergence factor Δr with respect to the case of nodes with the same activity, for increasing values of σ, for four choices of the model parameters with increasing network sizes. Vector h is generated uniformly at random under the constraints $\mathbb{1}^T h = 0$ and $\|h\| = \sqrt{n}$. Consequently, the activity potential of node i is $a_i = \bar{a} + \sigma h_i$, for any $i \in \mathcal{V}$. Red circles are Monte Carlo estimations (over 100 realizations of h) with the corresponding 95% confidence intervals, marked by whiskers, and the blue curve is our analytical prediction, up to the second-order power in σ. (a) $n = 30$, $m = 4$, and $\varepsilon = 0.15$. (b) $n = 50$, $m = 10$, and $\varepsilon = 0.05$. (c) $n = 100$, $m = 12$, and $\varepsilon = 0.04$. (d) $n = 200$, $m = 15$, and $\varepsilon = 0.03$.

that is,

$$z = \sqrt{\frac{n-2}{n-1}} \varepsilon m \beta q \tag{34}$$

where β is defined in (33). Using Lemma 4 to evaluate u_1 and applying Proposition 4, we conclude that

$$\rho_2 = \frac{\sqrt{(n-2)(n-1)}}{\varepsilon \bar{a} n \left(1 - \frac{m\bar{a}}{(n-1)}\right)} \gamma \sqrt{\frac{n-2}{n-1}} \varepsilon m \beta q^T q$$

$$= \frac{(n-2)m}{\bar{a} n \left(1 - \frac{m\bar{a}}{n-1}\right)} \gamma \beta \tag{35}$$

which yields the claim. ■

The numerical estimations in Fig. 2 support our analytical predictions and suggest that the accuracy of a parabolic representation for the convergence rate extends beyond the limit of small values of σ, upon which the perturbation analysis rests, to networks with a moderate level of heterogeneity, including small-world networks [49] and many nonscale-free networks, identified from real-world datasets [50].

Remark 2: The estimation in Theorem 1 can inform a qualitative analysis on the effect of the heterogeneity of the nodes' activity on the convergence factor of the consensus protocol. For $\sigma = 0$, the convergence rate is exactly given by the first three summands on the right-hand side of (32), analogously to the consensus protocol over conspecific agents in [26]. By introducing heterogeneity through the ADN paradigm, the convergence fac-
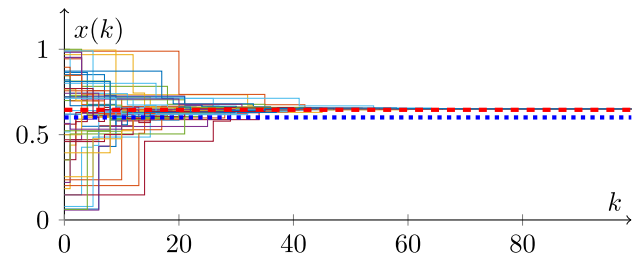
Fig. 3. Sample path of the process and comparison of the evolution of the state variables with the predicted consensus state (red-dashed line). The arithmetic average of the initial conditions, which is the expected steady-state value for homogeneous systems, is shown as a blue-dotted line. Parameters are $n = 50$, $\varepsilon = 0.05$, and $m = 10$. Following [28], activity potentials are distributed according to a rescaled power law with exponent $\gamma = -2.2$ and a lower cutoff $a_{\min} = 0.01$.

tor will vary, so that small values of σ will cause a change of the order of σ^2 in the convergence factor. Whether this change will increase or decrease the value of r depends on the parameters of the ADN (that is, n, m, and $\bar{a}$) and the parameter ε of the consensus protocol. The scenario of large networks, with $n \to \infty$, will be extensively analyzed in Section V, and explicit closed-form results will be derived therein.

B. Expected Consensus State

Assuming that $r < 1$, $x(k)$ converges almost surely to a consensus state $\bar{x}$. Such a state can be characterized through Proposition 3, leading to the following result.

Theorem 2: Given a mean-square consentable protocol (5) over an ADN with activity potentials a_i, $i \in \mathcal{V}$, then $\lim_{k \to \infty} x(k) = \bar{x}\mathbb{1}$ almost surely, with

$$\mathbb{E}[\bar{x}] = \pi^T x_0, \quad \pi_i = \frac{a_i^{-1}}{\sum_{j \in \mathcal{V}} a_j^{-1}}. \tag{36}$$

Proof: By applying Proposition 3, we compute the left eigenvector of $\mathbb{E}[L]$ associated with the null eigenvalue. From the computations in Lemma 2, we recall that $\mathbb{E}[L] = \frac{n}{n-1} \mathrm{diag}(a) R$. Observing that $\mathbb{1}^T R = 0$, we conclude

$$\pi^T \mathbb{E}[L] = 0 \iff \pi^T \mathrm{diag}(a) \propto \mathbb{1}^T \iff \pi_i \propto a_i^{-1}. \tag{37}$$

The normalization of the eigenvector concludes the proof. ■

Remark 3: The consensus protocol over an ADN leads to a consensus state that is not the arithmetic average of the initial states. The initial condition of each node is weighted by the inverse of its activity potential, which can be associated with its resistance to compromise. Nodes with low activity are less inclined to create connections, thus, they will be less prone to compromise their state.

Figs. 3 and 4 illustrate the outcome of numerical simulations that support our findings in Theorem 2. Fig. 3 presents a sample path of the consensus protocol, illustrating that heterogeneity in the nodes' activity causes a shift of the consensus value away from the arithmetic average of initial conditions, which would be expected for a homogeneous systems. Fig. 4 shows results from Monte Carlo simulations that indicate very good agreement between the empirical distribution and analytical predictions of the consensus value.
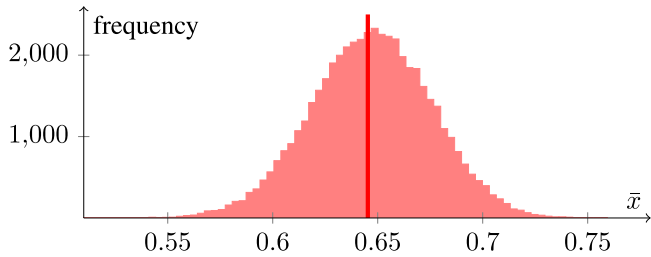
Fig. 4. Empirical distribution of the consensus values for set of Monte Carlo simulations over 50 000 independent runs starting from the same initial condition. The 95% confidence interval of the consensus state from Monte Carlo simulations is [0.6448, 0.6454]. The predicted consensus value from (36), $\mathbb{E}[\bar{x}] = 0.6453$, is plotted as a red line. Parameters are $n = 50$, $\varepsilon = 0.05$, and $m = 10$, and activity potentials are distributed according to a rescaled power law with exponent $\gamma = -2.2$ and a lower cutoff $a_{\min} = 0.01$.

Remark 4: Conducting a Taylor expansion on (36) with respect to σ, we discover that the consensus state is influenced by σ at the very first order, so that

$$\mathbb{E}[\bar{x}] = \frac{1}{n} \sum_{i \in \mathcal{V}} x_{0i} - \sigma \frac{1}{n\bar{a}} \sum_{i \in \mathcal{V}} h_i x_{0i}$$
$$+ \sigma^2 \frac{1}{n\bar{a}^2} \sum_{i \in \mathcal{V}} (h_i^2 - 1) x_{0i} + O(\sigma^3) \qquad (38)$$

where x_{0i} denotes the ith entry of the initial condition vector $x_0 \in \mathbb{R}^n$. For the problem analyzed in Fig. 3, the first-order approximation in (38) would predict a consensus value of 0.6505, while retaining a parabolic expansion would yield 0.6435, with an error less than 0.3%.

Remark 5: Consensus protocols may be implemented over undirected ADNs to model scenarios where information flows along both link directions, similar to epidemics [28]. The adjacency matrix of an undirected ADN at time step k is given by $A_k + A_k^T$, yielding a symmetric Laplacian matrix. Hence, the consensus state coincides with the arithmetic average of the initial conditions [3]. The speed of convergence could be examined by following a perturbation argument similar to the one presented in this article, by leveraging the symmetry of the expected Laplacian to ease the algebraic calculations.

V. APPLICATION TO LARGE NETWORKS

We conclude this article by performing an asymptotic analysis for large networks, in the limit $n \to \infty$. In this practically relevant case, the numerical computation of the spectral radius of G in Proposition 2 would be unfeasible, strengthening the merit of our closed-form solution in Theorem 1 based on perturbation theory. In the homogeneous case, that is, $\sigma = 0$, mean-square consentablility is attained for $\varepsilon(m + 1) < 2$, and given m and $\bar{a}$, selecting $\varepsilon = \varepsilon^* = 1/(m + 1)$ yields the fastest convergence rate [26]. In the presence of heterogeneity in the activity of the nodes, we obtain the following asymptotic expressions.[1]

---

[1]Although $n \to \infty$, r is bounded since m is finite. In fact, a trivial bound on the spectral radius of matrix G can be obtained from (8), based on the fact that $\rho(L) \le \|L\| \le 2\,m$. Hence, $r \le (1 + 2\varepsilon m)^2$, for any value of n.

Corollary 1: In the limit $n \to \infty$, the convergence factor of the consensus protocol (5) has the asymptotic expression

$$r = 1 - 2\varepsilon\bar{a}m + \varepsilon^2\bar{a}m(m + 1)$$
$$+ \sigma^2 \frac{m(2 - \varepsilon(m + 1))(2 - \varepsilon m)}{\bar{a}} + O(\sigma^3). \qquad (39)$$

Proof: For large n, the prediction of Theorem 1 reduces to

$$r = 1 - 2\varepsilon\bar{a}m + \varepsilon^2\bar{a}m(m + 1) + \sigma^2 \frac{m}{\bar{a}}\gamma\beta + O(\sigma^3) \qquad (40)$$

and the expressions for γ and β in (26) and (33), respectively, yields $\gamma = \varepsilon m + \varepsilon - 2$ and $\beta = \varepsilon m - 2$. The proof is completed by substituting these asymptotic expressions in (40). ∎

Remark 6: Small heterogeneities have always a detrimental effect on the convergence factor. For $n \to \infty$, the coefficient of σ^2 in (39) is strictly positive for any choice of the parameters such that $\varepsilon(m + 1) < 2$. Thus, heterogeneity in the nodes' activities decreases the convergence speed, potentially hindering consensus. Given $\varepsilon(m + 1) < 2$, so that $r < 1$ when $\sigma = 0$, the largest level of heterogeneities that can be tolerated by the protocol before losing convergence can be estimated as $\sigma = \bar{a}\sqrt{\frac{\varepsilon}{2 - \varepsilon m}}$. As one might anticipate, the critical value of σ scales with the average activity in the network, such that for ADNs with large values of $\bar{a}$, one may tolerate more severe heterogeneities. Interestingly, the larger is the value of ε, the more the protocol is sensitive to heterogeneities, since the nodes will tend to compromise more with their neighbors, thereby enhancing the overall effect of heterogeneities in the network. Finally, increasing m mitigates the effect of heterogenities.

Remark 7: From (39), we may seek to determine the fastest convergence rate that can be attained by the protocol on a given ADN and determine the value of ε that is conducive to optimal consensus. Toward this aim, we determine

$$\varepsilon^* = \frac{1}{m + 1} + \sigma^2 \frac{1}{\bar{a}^2} + O(\sigma^3) \qquad (41)$$

which yields the optimal asymptotic convergence factor

$$r^* = \frac{1}{n + 1} + \sigma^2 \frac{m(m + 2)}{\bar{a}(m + 1)} + O(\sigma^3). \qquad (42)$$

Predictably, the fastest attainable rate of convergence decreases with σ^2.

Remark 8: In the limit $n \to \infty$, one may offer a probabilistic interpretation of (36). Specifically, let us assume that the initial conditions are drawn from a given scalar distribution X_0 and the activity potentials are also drawn from another, independent, distribution A. This asymptotic result indicates that, when initial conditions and activity potentials are independent, the expected consensus state tends to the average of the initial conditions.

VI. CONCLUSION

In this article, we have analytically studied a discrete-time consensus protocol over ADNs. The ADN paradigm constitutes a powerful viewpoint to examine dynamical systems, in which the time scales of network formation and the node dynamics are comparable. Using stochastic stability theory and eigenvalue

perturbation analysis, we have established closed-form expressions for the rate of convergence to consensus and the expected consensus state, in terms of the distribution of the activity potentials in the network.

Our analytical results suggest that: 1) even a modest amount of heterogeneity in the nodes' activity could affect the consensus protocol by slowing down convergence to the consensus state, and 2) nodes that are less active in generating connections dominate the consensus state of the network. Finally, we have focused on large networks, for which, in the absence of analytical results, the consensus dynamics is difficult to examine because of its computational complexity. In this scenario, we derived the asymptotic expressions for the expected consensus state and for the convergence rate to consensus, demonstrating that heterogeneity is always detrimental to the coordination of large-scale systems.

The main limitation of this study is the lack of an analytical bound for the accuracy of the estimations of the convergence rate and the expected consensus state. Such a limitation is inherent to the perturbation theory, which does not offer a direct way to estimate the residuals in the expansions. Our numerical simulations support that the perturbation analysis is valid for a relatively wide range of parameter values, spanning from low to moderate levels of heterogeneity, whereby a parabolic dependence on the perturbation parameter is in excellent agreement with numerical simulations based on the complete ADN model. In this vein, this work constitutes the first step toward the mathematical treatment of heterogeneity in consensus protocols over temporal networks with rich dynamics. Future efforts should be placed to better elucidate the implication of high levels of heterogeneity. Unlikely, this could be addressed through higher order perturbation arguments, which would yield extremely cumbersome algebraic computations. Matrix inequalities and eigenvalue localization techniques [51] might offer a more viable approach, although it is tenable that only conservative estimates could be obtained.

In contrast with [39], our claims are not based on a time-scale separation between the network evolution and the nodes' dynamics. At each time step, we execute both the averaging process and the network formation, which coevolve within a complex stochastic dynamics. The generality of the framework should be amenable for extension to nonlinear dynamics, critical to shedding light on synchronization phenomena [52]. A master stability function can be likely formulated by extending the line of arguments of [53] to tackle the role of heterogeneity on the linear stability of the synchronization manifold. Another avenue of future research is the study of real-world network features, such as a heterogeneous nodes attractiveness [32], burstiness [55], and leadership [56], toward the analysis of time-resolved datasets of sociotechnical systems.

APPENDIX

We present here the explicit computations of vectors y and z used in Lemma 3 and Theorem 1, respectively. To keep the notation simple, all the summations are to be intended over the set of nodes $\mathcal{V}$, and $\sum_{k \neq i}$ means $\sum_{k \in \mathcal{V} \setminus \{i\}}$. When possible, we omit indices for summations. We start by noticing that

$$\sum_{k \neq i} h_i = h_i \sum_{k \neq i} 1 = (n-1)h_i$$

while

$$\sum_{k \neq i} h_k = \sum h_k - h_i = 0 - h_i = -h_i.$$

For the diagonal elements, we compute

$$\tilde{y}_i^i = \sum_{h,k \in \mathcal{V}} M_{ik}^{ih}(u_0)_{kh} = \frac{1}{\sqrt{n-1}} \sum_{h,k \in \mathcal{V}} M_{ik}^{ih} R_{kh}$$

$$= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \sum_{h \in \mathcal{V}} M_{ih}^{ih} - \frac{1}{n} \sum_{h \in \mathcal{V}, k \neq h} M_{ik}^{ih} \right]$$

$$= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(M_{ii}^{ii} + \sum_{h \neq i} M_{ih}^{ih} \right) \right.$$

$$\left. - \frac{1}{n} \left(\sum_{k \neq i} M_{ik}^{ii} + \sum_{h \neq i} M_{ii}^{ih} + \sum_{h \neq i} \sum_{k \neq i,h} M_{ik}^{ih} \right) \right]$$

$$= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(\varepsilon m h_i(\varepsilon m - 2) + \varepsilon^2 \frac{m}{n-1} \sum_{h \neq i} h_i \right) \right.$$

$$- \frac{1}{n} \left(-\varepsilon \frac{m}{n-1}(\varepsilon m - 1) \sum_{k \neq i} h_i - \varepsilon \frac{m}{n-1}(\varepsilon m - 1) \right.$$

$$\left. \times \sum_{h \neq i} h_i + \varepsilon^2 \frac{m(m-1)}{(n-1)(n-2)} \sum_{h \neq i} \sum_{k \neq i,h} h_i \right) \right]$$

$$= \frac{\varepsilon m h_i}{n\sqrt{n-1}} \left[(n-1)(\varepsilon m - 1) + 2(\varepsilon m - 1) - \varepsilon(m-1) \right]$$

$$= \frac{1}{\sqrt{n-1}} \varepsilon m h_i(\varepsilon m - 2 + \varepsilon)$$

while, following a similar argument, off-diagonal elements are

$$\tilde{y}_i^j = \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(M_{ii}^{ji} + M_{ii}^{jj} + \sum_{h \neq i,j} M_{ih}^{jh} \right) \right.$$

$$- \frac{1}{n} \left(M_{ii}^{jj} + \sum_{h \neq j} M_{ii}^{jh} + \sum_{k \neq i} M_{ik}^{jj} + \sum_{h \neq j} \sum_{k \neq i,j} M_{ik}^{jh} \right) \right]$$

$$= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(-\varepsilon \frac{m}{n-1} [\varepsilon m \bar{a}(h_i + h_j) - h_j] \right) \right.$$

$$- \varepsilon \frac{m}{n-1} [\varepsilon m \bar{a}(h_i + h_j) - h_i] + \varepsilon^2 \frac{m^2}{(n-1)^2}$$

$$\left. \times \sum_{h \neq i,j} (h_i + h_j) \right) - \frac{1}{n} \left(\varepsilon m(h_i + h_j)(\varepsilon m \bar{a} - 1) \right.$$

$$- \varepsilon \frac{m}{n-1} \sum_{h \neq j} [\varepsilon m \bar{a}(h_i + h_j) - h_j]$$

$$- \varepsilon \frac{m}{n-1} \sum_{k \neq i} [\varepsilon m \bar{a}(h_i + h_j) - h_i]$$

$$+ \varepsilon^2 \frac{m^2}{(n-1)^2} \bar{a} \sum_{h \neq j} \sum_{k \neq i,j} (h_i + h_j) \bigg) \bigg]$$

$$= \frac{1}{\sqrt{n-1}} \varepsilon m (h_i + h_j) \frac{1}{n-1} \left(-\frac{n}{n-1} \varepsilon m \bar{a} + 1 \right).$$

Now, we introduce

$$\alpha := (\varepsilon m - 2 + \varepsilon), \quad \delta := \frac{1}{n-1} \left(-\frac{n}{n-1} \varepsilon m \bar{a} + 1 \right)$$

so that

$$\bar{y}_i^i = \frac{1}{\sqrt{n-1}} \varepsilon m \alpha h_i, \quad \bar{y}_i^j = \frac{1}{\sqrt{n-1}} \varepsilon m \delta (h_i + h_j).$$

With this notation, we compute

$$y_i^i = \frac{(n-1)^2}{n^2} \tilde{y}_i^i - \frac{n-1}{n^2} \left(\sum_{h \neq i} \tilde{y}_i^h + \sum_{k \neq i} \tilde{y}_k^i \right) + \frac{1}{n^2} \sum_{h,k \neq i} \tilde{y}_k^h$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \bigg[\frac{(n-1)^2}{n^2} \alpha h_i - \frac{n-1}{n^2} \delta \sum_{h \neq i} (h_i + h_h)$$

$$- \frac{n-1}{n^2} \delta \sum_{k \neq i} (h_k + h_i) + \frac{1}{n^2} \delta \sum_{h \neq i} \sum_{k \neq i,h} (h_h + h_k)$$

$$+ \frac{1}{n^2} \alpha \sum h_h \bigg]$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \bigg[\frac{(n-1)^2}{n^2} \alpha h_i - 2 \frac{(n-1)^2}{n^2} \delta h_i$$

$$+ 2 \frac{n-1}{n^2} \delta h_i + \frac{1}{n^2} \delta \big(-(n-2) h_i + \sum_{h \neq i} (-h_i - h_h) \big)$$

$$- \frac{1}{n^2} \alpha h_i \bigg]$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \bigg[\frac{n-2}{n} \alpha h_i - 2 \frac{(n-1)(n-2)}{n^2} \delta h_i$$

$$+ \frac{2(n-2)}{n^2} \delta h_i \bigg]$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \left(\frac{n-2}{n} \alpha - 2 \frac{n-2}{n} \delta \right) h_i$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \frac{n-2}{n} (\alpha - 2\delta) h_i$$

where we have used the relation

$$\sum_{k \neq i,h} h_k = -h_i - h_h$$

and

$$y_i^j = \varepsilon m \frac{1}{\sqrt{n-1}} \bigg[\frac{(n-1)^2}{n^2} \delta (h_i + h_j) - \frac{n-1}{n^2} \alpha h_i$$

$$- \frac{n-1}{n^2} \delta \sum_{h \neq i,h} (h_i + h_h) - \frac{n-1}{n^2} \alpha h_j$$

$$- \frac{n-1}{n^2} \delta \sum_{k \neq i,h} (h_k + h_j) + \frac{1}{n^2} \alpha \sum_{h \neq i,j} h_h$$

$$+ \frac{1}{n^2} \delta \sum_{n \neq j} \sum_{k \neq i,h} h_k + \frac{1}{n^2} \delta \sum_{h \neq k} \sum_{k \neq i,h} h_h \bigg]$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \bigg[\frac{(n-1)^2}{n^2} \delta (h_i + h_j)$$

$$- \frac{n-1}{n^2} \alpha (h_i + h_j) + \frac{n-1}{n^2} \delta (h_i + h_j)$$

$$+ \frac{n-1}{n^2} \delta (h_i + h_j) - \frac{1}{n^2} \alpha (h_i + h_j)$$

$$- \delta \frac{n-2}{n^2} h_j - \delta \frac{n-1}{n^2} h_i + \frac{1}{n^2} \delta h_j \bigg]$$

$$= \varepsilon m \frac{1}{\sqrt{n-1}} \left(-\frac{1}{n} \alpha + \frac{2}{n} \delta \right) (h_i + h_j)$$

$$= - \varepsilon m \frac{1}{n\sqrt{n-1}} (\alpha - 2\delta)(h_i + h_j).$$

Finally, introducing $\gamma := \alpha - 2\delta$, we obtain the expression for y in (27).

Similarly, vector z is computed as follows:

$$z_i^i = \sum_{h,k \in \mathcal{V}} M_{ki}^{hi} (u_0)_{kh} = \frac{1}{\sqrt{n-1}} \sum_{h,k \in \mathcal{V}} M_{ki}^{hi} R_{kh}$$

$$= \frac{1}{\sqrt{n-1}} \bigg[\frac{n-1}{n} \sum_{h \in \mathcal{V}} M_{hi}^{hi} - \frac{1}{n} \sum_{h \in \mathcal{V}, k \neq h} M_{ki}^{hi} \bigg]$$

$$= \frac{1}{\sqrt{n-1}} \bigg[\frac{n-1}{n} \left(M_{ii}^{ii} + \sum_{h \neq i} M_{hi}^{hi} \right)$$

$$- \frac{1}{n} \left(\sum_{k \neq i} M_{ki}^{ii} + \sum_{h \neq i} M_{ii}^{hi} + \sum_{h \neq i} \sum_{k \neq i,h} M_{ki}^{hi} \right) \bigg]$$

$$= \frac{1}{\sqrt{n-1}} \bigg[\frac{n-1}{n} \left(\varepsilon m h_i (\varepsilon m - 2) + \varepsilon^2 \frac{m}{n-1} \sum_{h \neq i} h_h \right)$$

$$- \frac{1}{n} \left(\varepsilon \frac{m}{n-1} (2 - 2\varepsilon m \bar{a}) \sum_{k \neq i} h_k - 2\varepsilon^2 \frac{m^2}{n-1} \bar{a} \sum_{h \neq i} h_i \right.$$

$$
\left. + \, \varepsilon^2 \frac{m^2}{(n-1)^2} \sum_{h\neq i} \sum_{k\neq i,h} (h_k + h_h) \right) \right]
$$

$$
= \varepsilon m \frac{1}{n\sqrt{n-1}} h_i \left[\varepsilon m \bar{a} \frac{2n(n-2)}{(n-1)^2} - \varepsilon + (n-1)\varepsilon m \right.
$$

$$
\left. - \frac{2n(n-2)}{n-1} \right]
$$

$$
= \varepsilon m \frac{1}{\sqrt{n-1}} \frac{n-2}{n} \beta h_i
$$

and

$$
\tilde{z}_i^j = \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(M_{ii}^{ij} + M_{ji}^{jj} + \sum_{h\neq i,j} M_{hi}^{hj} \right) \right.
$$

$$
\left. - \frac{1}{n} \left(M_{ii}^{jj} + \sum_{k\neq i,j} M_{ki}^{jj} + \sum_{h\neq i,j} M_{ii}^{hj} + \sum_{h\neq j}\sum_{k\neq i,h} M_{ki}^{hj} \right) \right]
$$

$$
= \frac{1}{\sqrt{n-1}} \left[\frac{n-1}{n} \left(-\varepsilon \frac{m}{n-1}(\varepsilon m - 1)(h_i + h_j) \right. \right.
$$

$$
\left. + \varepsilon^2 \frac{m(m-1)}{(n-1)(n-2)} \sum_{n\neq i,j} h_h \right)
$$

$$
- \frac{1}{n} \left(\varepsilon m(\varepsilon m \bar{a} - 1)(h_i + h_j) - 2\varepsilon^2 \frac{m^2}{n-1} \bar{a} \sum_{k\neq i,j}(h_k + h_j) \right.
$$

$$
\left. \left. + 2\varepsilon \frac{m}{n-1} \sum_{k\neq i,j} h_k + \varepsilon^2 \frac{m^2}{(n-1)^2} \bar{a} \sum_{h\neq j}\sum_{k\neq i,h}(h_h + h_k) \right) \right]
$$

$$
= \varepsilon m \frac{1}{n\sqrt{n-1}} (h_i + h_j) \left[-\varepsilon m \bar{a} \frac{2n}{(n-1)^2} + \frac{\varepsilon}{n-2} \right.
$$

$$
\left. + \frac{n-1}{n-2}\varepsilon m - \frac{2n}{n-1} \right]
$$

$$
= -\varepsilon m \frac{1}{n\sqrt{n-1}} \beta(h_i + h_j).
$$

REFERENCES

[1] W. Ren and R. Beard, *Distributed Consensus in Multi-Vehicle Cooperative Control*, 1st ed. London, U.K.: Springer-Verlag, 2008.

[2] R. Olfati-Saber, J. A. Fax, and R. Murray, "Consensus and cooperation in networked multi-agent systems," *Proc. IEEE*, vol. 95, no. 1, pp. 215–233, Jan. 2007.

[3] F. Fagnani and P. Frasca, *Introduction to Averaging Dynamics over Networks*, 1st ed. Cham, Switzerland: Springer, 2017.

[4] Y. Cao, W. Yu, W. Ren, and G. Chen, "An overview of recent progress in the study of distributed multi-agent coordination," *IEEE Trans Ind. Inform.*, vol. 9, no. 1, pp. 427–438, Feb. 2013.

[5] Y. Hatano and M. Mesbahi, "Agreement over random networks," *IEEE Trans. Autom. Control*, vol. 50, no. 11, pp. 1867–1872, Nov. 2005.

[6] C. Wu, "Synchronization and convergence of linear dynamics in random directed networks," *IEEE Trans. Autom. Control*, vol. 51, no. 7, pp. 1207–1210, Jul. 2006.

[7] A. Tahbaz-Salehi and A. Jadbabaie, "A necessary and sufficient condition for consensus over random networks," *IEEE Trans. Autom. Control*, vol. 53, no. 3, pp. 791–795, Apr. 2008.

[8] M. Huang and J. Manton, "Stochastic consensus seeking with noisy and directed inter-agent communication: Fixed and randomly varying topologies," *IEEE Trans. Autom. Control*, vol. 55, no. 1, pp. 235–241, Jan. 2010.

[9] M. Smytnakis, N. M. Freris, and H. Tembine, "Consensus over evolutionary graphs," in *Proc. Eur. Control Conf.*, 2018, pp. 2218–2223.

[10] F. Fagnani and S. Zampieri, "Randomized consensus algorithms over large scale networks," *IEEE J. Sel. Areas Commun.*, vol. 26, no. 4, pp. 634–649, May 2008.

[11] N. Amelina, A. Fradkov, Y. Jiang, and D. J. Vergados, "Approximate consensus in stochastic networks with application to load balancing," *IEEE Trans. Inf. Theory*, vol. 61, no. 4, pp. 1739–1752, Apr. 2015.

[12] J. Zhou and Q. Wang, "Convergence speed in distributed consensus over dynamically switching random networks," *Automatica*, vol. 45, no. 6, pp. 1455–1461, 2009.

[13] H. J. LeBlanc, H. Zhang, X. Koutsoukos, and S. Sundaram, "Resilient asymptotic consensus in robust networks," *IEEE J. Sel. Areas Commun.*, vol. 31, no. 4, pp. 766–781, Apr. 2013.

[14] S. Kar and J. M. F. Moura, "Sensor networks with random links: Topology design for distributed consensus," *IEEE Trans. Signal Process.*, vol. 56, no. 7, pp. 3315–3326, Jul. 2008.

[15] S. S. Pereira and A. Pages-Zamora, "Mean square convergence of consensus algorithms in random WSNs," *IEEE Trans. Signal Process.*, vol. 58, no. 5, pp. 2866–2874, May 2010.

[16] S. Patterson, B. Bamieh, and A. E. Abbadi, "Convergence rates of distributed average consensus with stochastic link failures," *IEEE Trans. Autom. Control*, vol. 55, no. 4, pp. 880–892, Apr. 2010.

[17] M. T. Hale and M. Egerstedt, "Convergence rate estimates for consensus over random graphs," in *Proc. Amer. Control Conf.*, 2017, pp. 1024–1029.

[18] A. Nedic and J. Liu, "On convergence rate of weighted-averaging dynamics for consensus problems," *IEEE Trans. Autom. Control*, vol. 62, no. 2, pp. 766–781, Feb. 2017.

[19] H. K. Mousavi, C. Somarakis, M. Bahavarnia, and N. Motee, "Performance bounds and optimal design of randomly switching linear consensus networks," in *Proc. Amer. Control Conf.*, 2017, pp. 4347–4352.

[20] M. Li and H. Dankowicz, "Impact of temporal network structures on the speed of consensus formation in opinion dynamics," *Phys. A: Stat. Mech. Appl.*, vol. 523, pp. 1355–1370, 2019.

[21] S. Boyd, A. Ghosh, B. Prabhakar, and D. Shah, "Randomized gossip algorithms," *IEEE Trans. Inf. Theory*, vol. 52, no. 6, pp. 2508–2530, Jun. 2006.

[22] K. Cai and H. Ishii, "Average consensus on general strongly connected digraphs," *Automatica*, vol. 48, no. 11, pp. 2750–2761, 2012.

[23] D. Silvestre, J. P. Hespanha, and C. Silvestre, "Broadcast and gossip stochastic average consensus algorithms in directed topologies," *IEEE Trans. Control Netw. Syst.*, vol. 6, no. 2, pp. 474–486, Jun. 2019.

[24] T. C. Aysal, M. E. Yildiz, A. D. Sarwate, and A. Scaglione, "Broadcast gossip algorithms for consensus," *IEEE Trans. Signal Process.*, vol. 57, no. 7, pp. 2748–2761, Jul. 2009.

[25] N. Abaid and M. Porfiri, "Consensus over numerosity-constrained random networks," *IEEE Trans. Autom. Control*, vol. 56, no. 3, pp. 649–654, Mar. 2011.

[26] N. Abaid, I. Igel, and M. Porfiri, "On the consensus protocol of conspecific agents," *Linear Algebra Appl.*, vol. 437, no. 1, pp. 221–235, 2012.

[27] S. Roy and N. Abaid, "On the effect of collaborative and antagonistic interactions on synchronization and consensus in networks of conspecific agents," *IEEE Trans. Autom. Control*, vol. 61, no. 12, pp. 4063–4068, Dec. 2016.

[28] N. Perra, B. Gonçalves, R. Pastor-Satorras, and A. Vespignani, "Activity driven modeling of time varying networks," *Sci. Rep.*, vol. 2, 2012, Art. no. 469.

[29] M. Starnini and R. Pastor-Satorras, "Topological properties of a time-integrated activity-driven network," *Phys. Rev. E*, vol. 87, 2013, Art. no. 062807.

[30] L. Zino, A. Rizzo, and M. Porfiri, "Continuous-time discrete-distribution theory for activity-driven networks," *Phys. Rev. Lett.*, vol. 117, 2016, Art. no. 228302.

[31] M. Ogura, V. Preciado, and N. Masuda, "Optimal containment of epidemics over temporal activity-driven networks," *SIAM J. Appl. Math.*, vol. 79, no. 3, pp. 986–1006, 2019.

[32] A. Moinet, A. Barrat, and R. Pastor-Satorras, "Generalized voterlike model on activity-driven networks with attractiveness," *Phys. Rev. E*, vol. 98, 2018, Art. no. 022303.

[33] D. Li *et al.*, "Opinion dynamics in activity-driven networks," *Europhys. Lett.*, vol. 120, no. 2, 2017, Art. no. 28002.

[34] N. Perra, A. Baronchelli, D. Mocanu, B. Gonçalves, R. Pastor-Satorras, and A. Vespignani, "Random walks and search in time-varying networks," *Phys. Rev. Lett.*, vol. 109, 2012, Art. no. 238701.

[35] M. Starnini and R. Pastor-Satorras, "Temporal percolation in activity-driven networks," *Phys. Rev. E*, vol. 89, 2014, Art. no. 032807.

[36] G. Petri and A. Barrat, "Simplicial activity driven model," *Phys. Rev. Lett.*, vol. 121, 2018, Art. no. 228301.

[37] I. Pozzana, K. Sun, and N. Perra, "Epidemic spreading on activity-driven networks with attractiveness," *Phys. Rev. E*, vol. 96, 2017, Art. no. 042310.

[38] A. Rizzo, M. Frasca, and M. Porfiri, "Effect of individual behavior on epidemic spreading in activity driven networks," *Phys. Rev. E*, vol. 90, 2014, Art no. 042801.

[39] A. Buscarino, L. Fortuna, M. Frasca, L. Gambuzza, and G. Nunnari, "Synchronization of chaotic systems with activity-driven time-varying interactions," *J. Complex Netw.*, vol. 6, no. 2, pp. 173–186, 2018.

[40] M. Ogura, J. Tagawa, and N. Masuda, "Distributed agreement on activity driven networks," in *Proc. Amer. Control Conf.*, 2018, pp. 4147–4152.

[41] Y. Fang, "Stability analysis of linear control systems with uncertain parameters," Ph.D. dissertation, Dept. Syst., Control Ind. Eng., Case Western Reserve Univ., Cleveland, OH, USA, 1994.

[42] Y. Fang, K. A. Loparo, and X. Feng, "Stability of discrete time jump linear systems," *J. Math. Syst., Estimation, Control*, vol. 5, no. 3, pp. 275–321, 1995.

[43] Y. Fang and K. A. Loparo, "On the relationship between the sample path and moment Lyapunov exponents for jump linear systems," *IEEE Trans. Autom. Control*, vol. 47, no. 9, pp. 1556–1560, Sep. 2002.

[44] R. Sturman and J.-L. Thiffeault, "Lyapunov exponents for the random product of two shears," *J. Nonlinear Sci.*, vol. 29, no. 2, pp. 593–620, 2019.

[45] Y. Zhang and Y.-P. Tian, "Consentability and protocol design of multi-agent systems with stochastic switching topology," *Automatica*, vol. 45, no. 5, pp. 1195–1201, 2009.

[46] J. L. Hibey, "Stochastic stability theory for systems containing interval matrices," *IEEE Trans. Aerosp. Electron. Syst.*, vol. 32, no. 4, pp. 1385–1391, Oct. 1996.

[47] D. J. Griffiths, *Introduction to Quantum Mechanics*, 2nd ed. Upper Saddle River, NJ, USA: Pearson, 2005.

[48] G. H. Golub and C. F. Van Loan, *Matrix Computations*, 4th ed. Baltimore, MD, USA: Johns Hopkins Univ. Press, 2013.

[49] D. J. Watts and S. H. Strogatz, "Collective dynamics of 'small-world' networks," *Nature*, vol. 393, no. 6684, pp. 440–442, 1998.

[50] A. D. Broido and A. Clauset, "Scale-free networks are rare," *Nature Commun.*, vol. 10, no. 1, 2019, Art. no. 1017.

[51] D. S. Bernstein, *Matrix Mathematics: Theory, Facts, and Formulas*, 2nd ed. Princeton, NJ, USA: Princeton Univ. Press, 2011.

[52] A. Pikovsky, M. Rosenblum, and J. Kurths, *Synchronization: A Universal Concept in Nonlinear Sciences*. Cambridge, U.K.: Cambridge Univ. Press, 2003.

[53] M. Porfiri, "A master stability function for stochastically coupled chaotic maps," *Europhys. Lett.*, vol. 96, no. 4, 2011, Art. no. 40014.

[54] O. L. V. Costa and M. D. Fragoso, "Comments on 'stochastic stability of jump linear systems'," *IEEE Trans. Automat. Control*, vol. 49, no. 8, pp. 1414–1416, Aug. 2004.

[55] M. Karsai, H.-H. Jo, and K. Kaski, *Bursty Human Dynamics*, 1st ed., New York, NY, USA: Springer, 2018.

[56] Z. Li, Z. Duan, and L. Huang, "Leader-follower consensus of multi-agent systems," in *Proc. Am. Control Conf.*, St. Louis, MO, USA, 2009, pp. 3256–3261.

Lorenzo Zino received the Laurea (B.Sc.) degree in applied mathematics and the Laurea Magistrale (M.S.) degree in mathematical modeling (*summa cum laude*) from the Politecnico di Torino, Torino, Italy, in 2012 and 2014, respectively, and the Ph.D. (Hons.) degree in pure and applied mathematics from the Politecnico di Torino and Università di Torino, Torino (under a joint doctorate program) in 2018.

He has been a Postdoctoral Researcher with the Faculty of Science and Engineering, University of Groningen, Groningen, The Netherlands, since 2019. He was a Research Fellow with the Politecnico di Torino from 2018 to 2019 and a Visiting Research Assistant with the New York University Tandon School of Engineering, Brooklyn, NY, USA, from 2017 to 2018 and in 2019. His current research interests include modeling, analysis, and control of dynamical processes over networks, applied probability, network analysis, and game theory.

Alessandro Rizzo (SM'08) received the Laurea degree (*summa cum laude*) in computer engineering and the Ph.D. degree in automation and electronics engineering from the University of Catania, Catania, Italy, in 1996 and 2000, respectively.

He is currently an Associate Professor with the Politecnico di Torino, Torino, Italy, where he conducts and supervises research on complex networks and systems, nonlinear modeling and control, and robotics. Since 2012, he has also been a Visiting Professor with the New York University Tandon School of Engineering, Brooklyn, NY, USA. He authored two books, two international patents, and more than 150 papers in international journals and conference proceedings.

Prof. Rizzo was the recipient of the award for the Best Application Paper at the IFAC World Triennial Conference in 2002 and the award for the Most Read Papers in *Mathematics and Computers in Simulation* (Elsevier) in 2009. He is also a Distinguished Lecturer of the IEEE Nuclear and Plasma Science Society.

Maurizio Porfiri (SM'12–F'19) received the M.Sc. and Ph.D. degrees in engineering mechanics from Virginia Tech, Blacksburg, VA, USA, in 2000 and 2006, respectively; the Laurea (Hons.) degree in electrical engineering from Sapienza University of Rome, Italy, in 2001; and the Ph.D. degree in theoretical and applied mechanics from Sapienza University of Rome and the University of Toulon, Toulon, France (under a dual-degree program), in 2005.

He is currently a Professor with the Department of Mechanical and Aerospace Engineering and the Department of Biomedical Engineering, New York University Tandon School of Engineering, Brooklyn, NY, USA. He has authored more than 300 journal publications. He is involved in conducting and supervising research on dynamical systems theory, multiphysics modeling, and underwater robotics.

Dr. Porfiri is the recipient of the National Science Foundation CAREER Award. He has been included in the Brilliant 10 list of Popular Science and his research has been featured in all the major media outlets, including CNN, NPR, Scientific American, and Discovery Channel. His other significant recognitions include invitations to the Frontiers of Engineering Symposium and the Japan–America Frontiers of Engineering Symposium organized by the National Academy of Engineering, the Outstanding Young Alumnus Award by the College of Engineering of Virginia Tech, the American Society of Mechanical Engineers (ASME) Gary Anderson Early Achievement Award, the ASME DSCD Young Investigator Award, and the ASME C. D. Mote, Jr., Early Career Award. He has been a Fellow of the ASME since 2019.