2022 European Control Conference (ECC)
July 12-15, 2022. London, United Kingdom

Analysis and On/Off Lockdown Control for Time-Varying SIS Epidemics with a Shared Resource

Sebin Gracy, Irinel Constantin Morărescu, Vineeth S. Varma, and Philip E. Paré

Abstract— **The paper studies the spread of a virus over a (possibly) time-varying graph, with the spread being (possibly) worsened by the presence of a shared resource. We propose a time-varying susceptible-infected-water-susceptible (SIWS) model, with the water compartment representing the contamination level in the shared resource. We say that the system is in the disease-free equilibrium (DFE) if none of the nodes (representative of sub-populations, such as cities, districts, etc.) are infected, and the shared resource is contaminant-free. We identify multiple sufficient conditions for exponential convergence to the DFE. Based on one of the aforementioned sufficient conditions, an on/off lockdown strategy that eradicates the infection spread is proposed. More specifically, we design a switching rule between lockdown and free (i.e., no lockdown) modes to guarantee exponential convergence to the DFE.**

I. INTRODUCTION

Spreading processes such as epidemics, information in social networks, etc., have drawn the attention of several research communities ranging from physics and computer science to economics and sociology. The earliest work in the direction of studying epidemic spread is the model for the smallpox virus formulated and analysed by Daniel Bernouli [1]. Mathematical epidemiology, as a discipline, advanced rapidly during the 20th century; see [2]–[5], with [4] being one of the seminal works. Given that the destruction that epidemics leave in their wake is often times unprecedented, the fundamental questions of interest in the aforementioned works revolves around understanding how a disease spreads, what causes it to become persistent in the population, how can the spread be mitigated or eradicated, etc. While there are several models proposed in the literature, the present paper focuses on the susceptible-infected-susceptible (SIS) model, that was originally developed in [6].

Networked SIS models with static graphs (where the graphs represent the interaction between the various population nodes) have been well-studied; for continuous-time setting, see [7], [8], whereas for discrete-time setting, see [9], [10]. Given that modern societies involve mobile agents thus imposing a time-varying topology on the interconnection graph, it is natural to consider networked SIS models that also account for time-varying graphs. Such models have been proposed in [11], [12]. The present paper focuses on time-varying networked SIS models.

A major drawback with traditional epidemic models is that these assume that the only way an epidemic could spread is through node-to-node interaction. However, other pathways also exist, for instance spread of viruses through a shared resource such as a water distribution network [13], neighborhood supermarkets, infected hospital surfaces [14], etc. Addressing this gap, a networked continuous-time SIS model that also accounts for the presence of a shared resource was first proposed by [15], referred to as susceptible-infected-water-susceptible (SIWS) model. For the SIWS model, a sufficient condition for asymptotic convergence to the disease-free equilibrium (DFE) (i.e., the state where each agent is healthy, and the shared resource is contamination-free) has been identified in [15], whereas a sufficient condition for the existence, uniqueness and asymptotic convergence to the endemic equilibrium (i.e., the state where each agent has a non-trivial infection level, and the shared resource is contaminated) has been identified in [16]. Building off of the SIWS model, a model that accounts for the presence of *multiple* shared resources, referred to as the *layered networked SIWS model*, has been proposed in [17]. However, both the SIWS model and the layered networked SIWS model only account for static interaction graphs, and neither of these works propose a control scheme that involves manipulating the weights on the edges between the nodes (the so-called lockdown approach). The present paper aims to address these shortcomings.

Our main contributions are as follows:

i) We develop a model that captures the spread of a virus in a population where the interconnection among the agents (possibly) are time-varying, and also accounts for the presence of a shared resource that is accessed by (possibly) the entire population.
ii) Identify a sufficient condition for global exponential stability (GES) of the DFE, both for homogeneous spread, and for heterogeneous spread; see Theorem 1 and Theorem 2, respectively.
iii) Identify a less restrictive sufficient condition, which can be checked easily, for exponential convergence to the DFE; see Theorem 3.
iv) Finally, we design a switching rule between lockdown and free (i.e., no lockdown) modes to control the infection spreading. To be specific, the overall switching system satisfies the conditions in the previous item (i.e.,

---

Sebin Gracy is with the Division of Decision and Control Systems, School of Electrical Engineering and Computer Science, KTH Royal Institute of Technology, and Digital Futures, Stockholm, Sweden. Email: gracy@kth.se. This work was supported in part by the Knut and Alice Wallenberg Foundation, Swedish Research Council under Grant 2016-00861. I.C. Morărescu and V.S. Varma are with Université de Lorraine, CNRS, CRAN, F-54000 Nancy, France. Emails: constantin.morarescu@univ-lorraine.fr; vineeth.satheeskumar-varma@univ-lorraine.fr. This work was supported in part by the ANR through the grant NICETWEET ANR-20-CE48-0009. Philip E. Paré is with the Elmore Family School of Electrical and Computer Engineering at Purdue University. Email: philpare@purdue.edu. This work was supported in part by the National Science Foundation, grants NSF-CNS #2028738 and NSF-ECCS #2032258.

978-3-907144-07-7 ©2022 EUCA

item iii)) and consequently, the dynamics, regardless of the initial condition (i.e., infected or otherwise), converges to the DFE exponentially fast; see Lemma 2.

Paper Outline

The rest of the paper is organized as follows. We conclude the present section by listing the notations that will be used in the sequel. We introduce the model, and formally present the main problems of interest in Section II. The main results are spread out across two sections, namely in Section III we identify sufficient conditions for GES of the DFE. Building on the aforementioned sufficient conditions, a control strategy for efficient management of the epidemic is proposed in Section IV. We illustrate our theoretical findings in Section V. Finally, we summarize the paper, and highlight some problems of possible interest to the wider community in Section VI.

Notation

Let $\mathbb{R}$, $\mathbb{R}_{\geq 0}$, and $\mathbb{N}$ denote the set of real numbers, nonnegative real numbers, and positive integers, respectively. For any positive integer n, we have $[n] = \{1, \ldots, n\}$. Given a matrix A, supposing its spectrum is real, $\lambda_1(A)$ denotes the maximum eigenvalue of A; the largest real-valued part of the eigenvalues of A is denoted by $r_1(A)$. We use $\mathbf{0}$ and $\mathbf{1}$ to denote the vectors whose entries all equal 0 and 1, respectively, and use I to denote the identity matrix, while the sizes of the vectors and matrix are to be understood from the context. For any two real matrices $A, B \in \mathbb{R}^{n \times m}$, we write $A \geq B$ if $A_{ij} \geq B_{ij}$ for all $i \in [n]$, $j \in [m]$, and $A > B$ if $A \geq B$ and $A \neq B$.

II. MODEL

Consider a population of individuals, divided into n subpopulation nodes in a network, with a resource W that is shared among (possibly) all of the population nodes. Suppose that a virus is active in the aforementioned population. The spread of the virus among the n nodes can be represented by a (possibly) directed time-varying graph $\mathcal{G}(t) = \{\mathcal{V}, \mathcal{E}(t)\}$, where $\mathcal{V} = \{1, 2, \ldots, n\}$ are the nodes (which represent subpopulations), with, at time t, existence of a directed edge from node j to node i if, at time t, individuals in node j can infect those in node i. We also assume that not only does a node get (possibly) infected due to contact with W but also that W could be contaminated whenever an infected population node comes in contact with it. Thus, at each t, each node in $\mathcal{G}(t)$ possibly has bidirectional connections with W.

Each population node i, contains N_i individuals, at time t, has birth rate $\mu_i(t)$, death rate $\bar{\mu}_i(t)$, and, at time t, $S_i(t)$ denotes the number of susceptible individuals, while $I_i(t)$ denotes the number of individuals infected by the virus. For each node i, at time $t \geq 0$, infected individuals have a recovery rate $\gamma_i(t)$. We denote the infection rate of node i, at time t, as $\beta_i(t)$. Let $\alpha_{ij}(t)(\geq 0)$ denote, at time t, the strength of interconnection (could also be interpreted as the frequency of interactions) between an individual in node i and an individual in node j. Clearly, if node j is not connected to node i at time t, then $\alpha_{ij}(t) = 0$; otherwise, $\alpha_{ij}(t) > 0$. Let $z(t)$ denote, at time t, the concentration of the virus in the shared resource W. The rate at which the virus decays in the shared resource, at time t, is denoted by $\delta_w(t)$, while the concentration of the virus in the shared resource W grows at a rate proportional to the sum of $I_i(t)$ scaled by $\zeta_i(t)$, where $\zeta_i(t)$ denotes, at time t, the rate at which the resource gets contaminated due to node i. The resource-to-node infection rate for node i at time t is denoted by $\alpha_{iw}(t)$.

Given the interactions between different individuals in a population node (resp. between different individuals in different population nodes), the fraction of infected individuals in a population node changes with time. More precisely, the evolution of the number of susceptible and infected individuals in node i can be represented as follows:

$$\begin{aligned}
\dot{S}_i(t) =& \mu_i(t)N_i - \bar{\mu}_i(t)S_i(t) + \gamma_i(t)I_i(t) \\
&- \big(\alpha_{iw}(t)W(t) - \textstyle\sum_{j=1}^n \beta_i(t)\alpha_{ij}(t)\frac{I_j(t)}{N_i}\big)S_i(t), \\
\dot{I}_i(t) =& -\ (\bar{\mu}_i(t) + \gamma_i(t))I_i(t) \\
&+ \big(\alpha_{iw}(t)W(t) + \textstyle\sum_{j=1}^n \beta_i(t)\alpha_{ij}(t)\frac{I_j(t)}{N_i}\big)S_i(t), \\
\dot{W}(t) =& -\delta_w(t)W(t) + \textstyle\sum_{j=1}^n \zeta_j(t)I_j(t).
\end{aligned} \tag{1}$$

We define new variables to simplify the system. Let:

$$x_i(t) = \frac{I_i(t)}{N_i},\ z(t) = \frac{\delta_w(t)W(t)}{\sum_{j=1}^n \zeta_j(t)N_j},\ \delta_i(t) = \gamma_i(t) + \mu_i(t),$$

$$\beta_{ij}(t) = \beta_i(t)\alpha_{ij}(t)\frac{N_j}{N_i},\ \beta_{iw}(t) = \frac{\alpha_{iw}(t)}{\delta_w(t)}\textstyle\sum_{j=1}^n \zeta_j(t)N_j,$$

$$c_i(t) = \frac{\zeta_i(t)N_i}{\sum_{j=1}^n \zeta_j(t)N_j}. \tag{2}$$

Then, assuming that, at each time $t \geq 0$, the birth rates and the death rates are equal, (1) can be rewritten as:

$$\begin{aligned}
\dot{x}_i(t) =& -\delta_i(t)x_i(t) \\
&+ \big(1 - x_i(t)\big)\big(\beta_{iw}(t)z(t) + \textstyle\sum_{j=1}^n \beta_{ij}(t)x_j(t)\big),
\end{aligned} \tag{3}$$

$$\dot{z}(t) = \delta_w(t)\Big(- z(t) + \textstyle\sum_{i=1}^n c_i(t)x_i(t)\Big). \tag{4}$$

Observe that assuming that the parameters in system (3) and (4) are time-independent, we recover the time-invariant SIWS model proposed in [15]. Likewise, in the absence of the shared resource (i.e., setting $z(t) = 0$), we recover the time-varying SIS networked model studied in [12].

The model from (3)-(4) in vector form becomes:

$$\begin{aligned}
\dot{x}(t) = \big(- D(t) + B(t) - X(t)B(t)\big)x(t) \\
+ \big(I - X(t)\big)b(t)z(t)
\end{aligned} \tag{5}$$

$$\dot{z}(t) = -\delta_w(t)z(t) + c(t)^\top x(t)\ , \tag{6}$$

where $D(t) = \mathrm{diag}(\delta_i(t))$, $B(t) = [\beta_{ij}(t)]_{n \times n}$, $X(t) = \mathrm{diag}(x(t))$ [1], $b(t)$ is a column vector in $\mathbb{R}^n$ with its i^{th}

---

[1] When clear from context, for ease of notation, we will drop the time index, and use X instead of $X(t)$.

element being $\beta_{iw}(t)$, and $c(t)^\top$ is a row vector in $\mathbb{R}^n$ whose i^{th} element is $\delta_w(t)c_i(t)$. Defining $\bar{B}(t) := \operatorname{diag}(\beta_i(t))$ and $A(t) := [\alpha_{ij}(t)\frac{N_j}{N_i}]_{n\times n}$, we have that $B(t) = \bar{B}(t)A(t)$. System (5)-(6) can be written more compactly using

$$y(t) := \begin{bmatrix} x(t) \\ z(t) \end{bmatrix},\ X(y(t)) := \begin{bmatrix} \operatorname{diag}(x(t)) & 0 \\ 0 & 0 \end{bmatrix},$$
$$B_w(t) := \begin{bmatrix} B(t) & b(t) \\ c^\top(t) & 0 \end{bmatrix},\ \text{and } D_w(t) := \begin{bmatrix} D(t) & 0 \\ 0 & \delta_w(t) \end{bmatrix}.$$

With the new notations in place, system (5)-(6) can be rewritten as:

$$\dot{y}(t) = \big(-D_w(t) + (I - X(y(t)))B_w(t)\big)y(t). \tag{7}$$

Observe that if $x = \mathbf{0}$, and $z = 0$, then none of the nodes are infected nor is there any contamination in the shared resource. Furthermore, $(\mathbf{0}, 0)$, is an equilibrium of system (7). Hence, we call this equilibrium the *disease-free equilibrium* (DFE).

With the setup as given in (7), the problems being investigated in this paper are as follows.

i) Assuming the graph $\mathcal{G}(t)$ is, for each t, symmetric, and that $\beta_i(t) = \beta(t)$ for all $i \in [n]$ and for each t, identify a sufficient condition such that $y(t)$ converges to $\mathbf{0}$ exponentially fast.
ii) Accounting also for (possibly) directed graphs $\mathcal{G}(t)$, and also heterogeneous spread, identify a sufficient condition such that $y(t)$ converges to $\mathbf{0}$ exponentially fast.
iii) Ensure that the convergence to the DFE is exponential even in finite time and not just asymptotic to ensure that critical health constraints are not violated. Thus, for a given initial time t_0 and $y(t_0)$, we want to ensure that

$$\|y(t)\| \le \exp(-\lambda_0(t - t_0))\gamma\|y(t_0)\|, \tag{8}$$

for all $t \ge t_1$, for some finite $t_1 \ge t_0$ and $\gamma > 0$.

We require the following assumptions on the model parameters.

Assumption 1: Suppose that, for each $t \in \mathbb{R}_{\ge 0}$, $\delta_i(t) > 0$, and $\delta_w(t) > 0$. Suppose that, for each $t \in \mathbb{R}_{\ge 0}$, $\beta_{ij}(t) \ge 0$ for all $i, j \in [n]$, and $\beta_{iw}(t) > 0$, $c_i(t) > 0$, for all $i \in [n]$.

Given that we are interested in identifying sufficient conditions for exponential convergence to the DFE, we recall the following definition.

Definition 1: Consider a system, described as follows:

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

where $f : \mathbb{R}_{\ge 0} \times \mathbb{R}^n \to \mathbb{R}^n$ is locally Lipschitz. The origin is a GES equilibrium point of (9) if there exist positive constants α and η, with $0 \le \eta < 1$, such that

$$\|x(t)\| \le \alpha\,\|x(t_0)\|\,\eta^{(t-t_0)}, \quad \forall\ t, t_0 \ge 0, \forall\ x(t_0) \in \mathbb{R}^n.$$

Since each x_i represents the fraction of infected individuals in group i, it is immediate that the initial value of x_i is in $[0, 1]$, because otherwise the value of x_i will lack physical meaning for the epidemic model considered here. Similarly, it is also natural to assume that the initial value of z measured, for instance, in milligrams per litre is nonnegative. Consequently, we can say that the DFE of system (7) is GES if the condition in Definition 1 is satisfied for all $x_0 \in [0, 1]^n$ and $z(0) \ge 0$. Hence, we can restrict our analysis to the set:

$$\mathcal{D} := \{y(t) : x(t) \in [0, 1]^n, z(t) \in [0, \infty)\}. \tag{10}$$

The following lemma establishes that the set $\mathcal{D}$ is positively invariant.

Lemma 1: Consider system (7) under Assumption 1. If $x_i(0) \in [0, 1]$ for all $i \in [n]$, and $z(0) \ge 0$, then $x_i(t) \in [0, 1]$ for all $i \in [n]$, and $z(t) \ge 0$, $\forall t \ge 0$.
Proof: See proof of [18, Lemma 1].

III. CONVERGENCE TO THE DFE

In this section, we identify sufficient conditions for GES of the DFE. We first consider the case where the spread is homogeneous (i.e., all agents have the same infection rate, for all time instants) and the underlying graph is symmetric and undirected, then we consider the case where the spread could also be heterogeneous (i.e., not all of the agents have the same infection rate for all time instants) and the underlying graph could also be directed.

A. Homogeneous case

We consider the case where each node has the same infection rate, i.e., $\beta_i(t) = \beta(t)$ for all $i \in [n]$, and for all $t \in \mathbb{R}_{\ge 0}$. Furthermore, we assume that the interconnection graph, represented by the matrix $A(t)$, is undirected, and has symmetric weights, i.e., for each $t \in \mathbb{R}_{\ge 0}$, $a_{ij}(t) = a_{ji}(t)$. We have the following result, which is partly inspired from [12, Theorem 1].

Theorem 1: Consider system (7) under Assumption 1. Suppose that, for each $t \in \mathbb{R}_{\ge 0}$, $\beta_i(t) = \beta(t)$ for all $i \in [n]$, $A(t), b(t), c(t), D(t)$ and $\delta_w(t)$ is piecewise continuous in t, and bounded. Suppose that, for each $t \in \mathbb{R}_{\ge 0}$, $A(t) = A(t)^\top$, and $b(t) = c(t)$. If $\sup_{t\ge 0} \lambda_1(-D_w(t) + B_w(t)) < 0$, then the DFE of (7) is GES.
Proof: See proof of [18, Theorem 1].

B. Heterogeneous case

We now consider the case where the infection rates are not necessarily the same for every node; the interconnection graph could be directed.. We have the following result.

Theorem 2: Consider system (7) under Assumption 1, with $B_w(t)$ and $D_w(t)$ to be continuously differentiable. Suppose that

i) there exists $L > 0$ such that $\|B_w(t) - D_w(t)\| \le L\ \forall t$;
ii) for some $\alpha_1 > 0$ $\sup_{t\ge 0} r_1(B_w(t) - D_w(t)) < -\alpha_1$; and
iii) there exists $\kappa > 0$ such that $\sup_{t\ge 0}\|\frac{d}{dt}\big(B_w(t) - D_w(t)\big)\| < \kappa$.

If κ is sufficiently small, then the DFE of (7) is GES.

Remark 1: The proof technique is closely related to that of [12, Theorem 2] and [19]; in the interest of completeness, we provide the details here.
Proof: See proof of [18, Theorem 2].

Remark 2: Particularized to the setting without a shared resource, the difference between Theorem 2 and [12, Theorem 2] is as follows: Theorem 2 does not assume the existence of a constant that upper bounds the Lyapunov function $V(y,t)$; it turns out that the existence of such a constant is a direct consequence of the first two conditions in Theorem 2 being satisfied. The result [12, Theorem 2], to the contrary, assumes that such a constant exists and is well-defined, and together with conditions in Theorem 2 establishes exponential convergence to the DFE. Therefore, even particularized to the setting without a shared resource, Theorem 2 is more general than [12, Theorem 2].

Remark 3: The third condition in Theorem 2 could be slightly relaxed as follows while (assuming that the first two conditions are fulfilled) still guaranteeing GES [20]:

$$\int_t^{t+T} \|\dot{B}_w(s) - \dot{D}_w(s)\| ds \leq \mu T + \eta, \ \forall t \geq 0, \ \forall T \geq 0, \tag{11}$$

where $\eta > 0$ is some scalar, and μ depends on L and α_1.

Observe that both Theorem 2, and its relaxation in Remark 3, require $B_w(t)$ and $D_w(t)$ to be continuously differentiable. For linear time-varying systems, a sufficient condition for GES that does not insist on the state matrix being continuously differentiable has been identified in [21, Theorem 3]. Extending [21, Theorem 3] to also account for nonlinear time-varying systems of the kind in (7) is beyond the scope of the present paper, and is left for future work.

Observe that Theorems 1 and 2 insist on the matrix $-D_w(t) + B_w(t)$ being Hurwitz for *each* $t \geq 0$. Consequently, it becomes extremely hard to verify this condition. As such, we are interested in seeking less restrictive sufficient condition(s). Towards this end, we need the following assumption.

Assumption 2: Suppose that

i)

$$\lim_{T\to\infty} \frac{1}{T}\int_{t_0}^{t_0+T} \|-D_w(s) + B_w(s)\| ds \leq \alpha < \infty, \forall t_0 \geq 0. \tag{12}$$

ii) for some $v > 0$, there exists an $h > 0$ such that

$$\|-D_w(t+h) + B_w(t+h) + D_w(t) - B_w(t)\| \leq vh^\gamma, \tag{13}$$

for all $t \geq 0$, and for some γ such that $0 < \gamma \leq 1$.

iii)

$$\frac{1}{T}\int_{t_0}^{t_0+T} r_1(-D_w(s) + B_w(s)) ds \leq \bar{\sigma}, \tag{14}$$

for all $t_0 \geq 0$, $T \geq T_0$ and for some $\bar{\sigma} < 0$ and $T_0 > 0$.

Theorem 3: Consider system (7) under Assumptions 1 and 2. The DFE is GES, and

$$\|y(t)\| \leq \exp(-\lambda_0(t - t_0))\gamma\|y(t_0)\|, \tag{15}$$

for all $t \geq t_1$, for some finite $t_1 \geq t_0$ and $\lambda_0, \gamma > 0$.

Proof: See proof of [18, Theorem 3].

IV. CONTROL STRATEGIES FOR AN EFFICIENT LOCKDOWN

We study the case in which the epidemics is controlled by a lockdown procedure. In its natural state, i.e., without a lockdown, we consider that the population behaves in such a way that

$$\sup_{t\geq t_0} r_1(B_w(t) - D_w(t)) < \bar{\sigma}_N, \tag{16}$$

for all $t_0 \geq 0$, with $\bar{\sigma}_N > 0$.

On the other hand, during lockdown, the behavior for the population is such that Assumption 2 is satisfied and

$$\frac{1}{T}\int_{t_0}^{t_0+T} r_1(-D_w(s) + B_w(s)) ds \leq \bar{\sigma}_L, \tag{17}$$

for all $t_0 \geq 0$, with $\bar{\sigma}_L < 0$ as long as $T \geq T_{\min}$, with $T_{\min} > 0$ known.

Assuming that switching between the two strategies preserves the properties (12)-(13), our goal is to find a switching rule which ensures that all the conditions in Assumption 2 are satisfied, and therefore, guarantees the DFE is GES and the system's trajectory satisfies (8).

For any given t_0, let us first denote the sequence of switching times by $\{t_k, k \in \mathbb{N}\}$. We assume that a switching to a lockdown mode is done at any t_{2k}, $k \in \mathbb{N}$, while a switching to free (no lockdown) mode is done at any t_{2k+1}, $k \in \mathbb{N}$. We also assume that the lockdown is initiated at t_0 to control the epidemic.

Lemma 2: Assuming (16) and (17) hold true, if the switching sequence $\{t_k, k \in \mathbb{N}\}$ is chosen such that $t_{2k+1} - t_{2k} \geq T_{min}$, $\forall k \in \mathbb{N}$ and

$$\sum_{k=0}^{K} (\bar{\sigma}_L(t_{2k+1} - t_{2k}) + \bar{\sigma}_N(t_{2k+2} - t_{2k+1})) \leq \bar{\sigma}, \tag{18}$$

for all $K \in \mathbb{N}$, then (14) holds true with $T_0 = T_{\min}$.

Proof: See proof of [18, Lemma 2].

Due to Lemma 2, we can minimize the time spent in lockdown as well as ensure an exponential convergence to the disease free equilibrium for all $t > t_0 + T_{\min}$ by selecting a switching rule that satisfies (18) with the inequality replaced by an equality. The details on how to do so are left for future work.

V. SIMULATION

We now illustrate the analysis and control results via simulations. To capture the time-varying structure of the model, we model the adjacency matrix as the following:

$$a_{ij}(t) = \begin{cases} e^{-\|\chi_i(t)-\chi_j(t)\|^2}, & \text{if } \|\chi_i(t) - \chi_j(t)\| < r \\ 0, & \text{otherwise,} \end{cases} \tag{19}$$

where $\chi_i(t) \in \mathbb{R}^2$ is the position of node i and can change as a function of time. We assume that each node has the same population size, thus implying that $\frac{N_j}{N_i} = 1$, for all $i, j \in [n]$. Hence, $a_{ij}(t) = \alpha_{ij}(t)$ for each t. We also define

$$[c(t)]_i = \begin{cases} e^{-\|\chi_i(t)\|^2}, & \text{if } \|\chi_i(t)\| < r \\ 0, & \text{otherwise,} \end{cases} \tag{20}$$

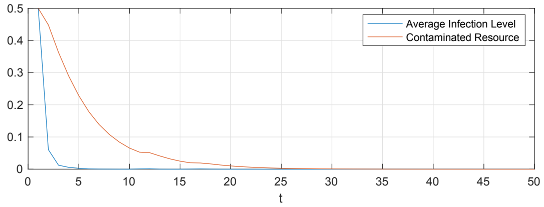

Fig. 1: Average infection level ($\frac{1}{n}\sum_{i=1}^{n} x_i(t)$) and $z(t)$ in illustration of Theorem 1, with $\beta = 1$, $\delta = 3$, $\delta_w = 0.25$, and $z(0) = 0.5$.

which is assuming that the location of the shared resource is fixed and located at $(0, 0)$. We set $b(t) = c(t)$. Also, note that, from (19), $A(t)$ is symmetric. While these symmetry assumptions are only needed for Theorem 1, we factor the infection rates in a similar manner and employ the symmetric graph structure for simplicity in all the simulations.

For movement of the nodes, we assume piece-wise constant drift, confining the nodes to a fixed region. The positional dynamics of each node i are given by

$$\dot{\chi}_i(t) = \phi_i, \tag{21}$$

where $\phi_i \in \mathbb{R}^2$ with

$$\phi_{ik} = \begin{cases} -\phi_{ik}, & \text{if } z_k = z_{c_k} + l/2 \text{ or } z_k = z_{c_k} - l/2 \\ \phi_{ik}, & \text{otherwise,} \end{cases} \tag{22}$$

for each dimension $k = 1, 2$, where z_c is the center of a square that the nodes are bouncing around. In other words, if an agent arrives at a boundary of the box, the velocity of the agent in the corresponding dimension changes sign. Note that the simulation setup follows [12] except with the shared resource added.

For all the simulations we set $r = 10$. We assume there are 10 nodes ($n = 10$) that bounce around a box of dimension 5×5, centered at $z_c = (2.5, 2.5)$. A randomly infected set of nodes is initially infected ($x_i(0) = 1$). We assume time-invariant homogeneous viral spread, that is, the same β and δ for each node.

We first simulate a scenario that meets the assumptions of Theorem 1. We set $\beta = 1$, $\delta = 3$, and $\delta_w = 0.25$, and $z(0) = 0.5$. The average infection level ($\frac{1}{n}\sum_{i=1}^{n} x_i(t)$) and the resource contamination level ($z(t)$) are plotted in Fig. 1. The maximum eigenvalue for the simulation is plotted over time in Fig. 2. Note that the assumptions of Theorem 1 are met, with the largest eigenvalue always remaining below zero. Consistent with Theorem 1, the virus and the resource contamination die out quickly; see the blue line and red line, respectively.

We also simulated a system that violated the assumptions of all the results. We set $\beta = 2$, $\delta = 2$, $\delta_w = 0.5$, and $z(0) = 0.5$. The average infection level and the resource contamination level are plotted in Fig. 3 with the corresponding maximum eigenvalues plotted over time in Fig. 4. Note that the eigenvalues are mostly greater than zero and the virus persists in the system.

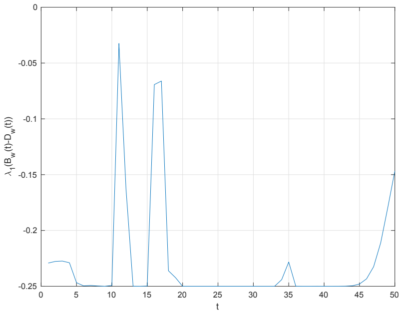

Fig. 2: Maximum eigenvalue of the simulation in Fig. 1. Note that the maximum eigenvalue is always less than zero and the system converges to the DFE rapidly consistent with Theorem 1.

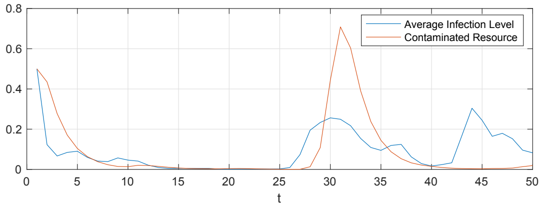

Fig. 3: Average infection level and $z(t)$ in illustration of system with $\beta = 2$, $\delta = 2$, $\delta_w = 0.5$, and $z(0) = 0.5$. The lack of lockdown measures causes the infection level to rise rapidly around $t = 30$.

In order to enact the on/off lockdown control policy proposed in Section IV, we devise the following social distancing protocol that is implemented for ten time steps. While not letting node i leave the square region,

$$\dot{\chi}_i(t) = \frac{\sum_{j, a_{ij}(t) > 0.001} \chi_i - \chi_j}{\| \sum_{j, a_{ij}(t) > 0.001} \chi_i - \chi_j \|}, \tag{23}$$

forcing the nodes to separate from each other. We implement this algorithm every 20 time steps, starting at time $t = 10$, for the endemic system from Fig. 3. The average infection level and the resource contamination level are plotted in Fig. 5 with the corresponding maximum eigenvalues plotted over time in Fig. 6. Note that the eigenvalues are almost always less than zero, the 20-time step average is always below zero, and the virus no longer persists in the system, dying out quite quickly, consistent with the result in Lemma 2.

VI. CONCLUSION

In this paper, we proposed a SIWS model that also accounts for time-varying interactions between the agents. We identified several sufficient conditions for exponential convergence to the DFE; a difficult-to-check condition, and, an easily checkable one. Both the conditions also account for heterogeneous spread, and directed graphs. We have also proposed a control strategy guaranteeing that the DFE is GES. This control strategy is based on switching between a lockdown and a free (no-lockdown mode), and maintaining lockdown measures for sufficiently long time periods of time.

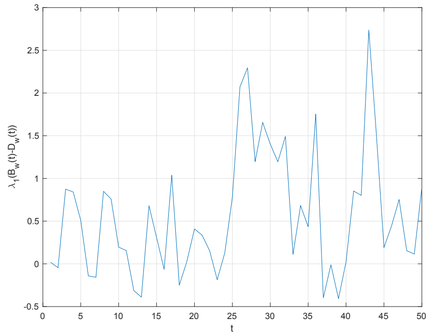

Fig. 4: Maximum eigenvalue of the simulation in Fig. 3. Note that the maximum eigenvalue is greater than zero most of the time and the virus persists in the network (see Fig. 3).

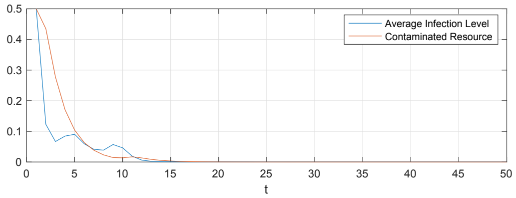

Fig. 5: Average infection level and $z(t)$ in illustration of the endemic system from Fig. 3 with the social distancing policy from (23) every 20 time steps, starting at time $t = 10$. With the on/off lockdown strategy implementation added, the virus in Fig. 3 is eradicated.

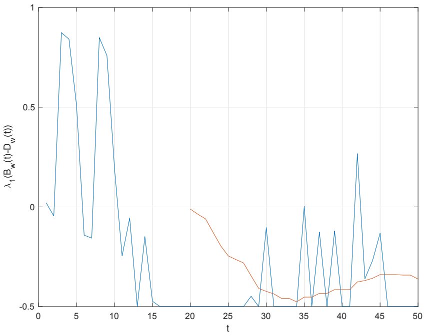

Fig. 6: Maximum eigenvalue of the simulation in Fig. 5 plotted in blue and the 20-time step average plotted in red. Note that the average is always below zero, satisfying the conditions of Lemma 2; the control strategy eradicates the virus (see Fig. 5).

We illustrated our theoretical findings using an extensive set of simulations.

REFERENCES

[1] Daniel Bernoulli. Essai d'une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l'inoculation pour la prévenir. *Histoire de l'Acad., Roy. Sci.(Paris) avec Mem*, pages 1–45, 1760.

[2] Niels Becker. The uses of epidemic models. *Biometrics*, pages 295–305, 1979.

[3] William Heaton Hamer. *Epidemic disease in England: the evidence of variability and of persistency of type*. Bedford Press, 1906.

[4] Norman TJ Bailey et al. *The mathematical theory of infectious diseases and its applications*. Charles Griffin & Company Ltd, 5a Crendon Street, High Wycombe, Bucks HP13 6LE., 1975.

[5] Herbert W Hethcote. The mathematics of infectious diseases. *SIAM review*, 42(4):599–653, 2000.

[6] William Ogilvy Kermack and Anderson G McKendrick. Contributions to the mathematical theory of epidemics. ii.—the problem of endemicity. *Proceedings of the Royal Society of London. Series A, containing papers of a mathematical and physical character*, 138(834):55–83, 1932.

[7] A. Lajmanovich and J. A. Yorke. A deterministic model for gonorrhea in a nonhomogeneous population. *Mathematical Biosciences*, 28(3-4):221–236, 1976.

[8] Ali Khanafer, Tamer Başar, and Bahman Gharesifard. Stability of epidemic models over directed graphs: A positive systems approach. *Automatica*, 74:126–134, 2016.

[9] Hyoung Jun Ahn and Babak Hassibi. Global dynamics of epidemic spread over complex networks. In *Proceedings of the 52nd IEEE Conference on Decision and Control*, pages 4579–4585, 2013.

[10] Yang Wang, Deepayan Chakrabarti, Chenxi Wang, and Christos Faloutsos. Epidemic spreading in real networks: An eigenvalue viewpoint. In *Proceedings of the 22nd International Symposium on Reliable Distributed Systems, 2003*, pages 25–34. IEEE, 2003.

[11] V. S. Bokharaie, O. Mason, and F. Wirth. Spread of epidemics in time-dependent networks. In *Proceedings of the 19th International Symposium on Mathematical Theory of Networks and Systems*, pages 1717–1719, 2010.

[12] Philip E Paré, Carolyn L Beck, and Angelia Nedić. Epidemic processes over time-varying networks. *IEEE Transactions on Control of Network Systems*, 5(3):1322–1334, 2018.

[13] Joseph H Tien and David JD Earn. Multiple transmission pathways and disease dynamics in a waterborne pathogen model. *Bulletin of mathematical biology*, 72(6):1506–1533, 2010.

[14] Robert A Weinstein and Bala Hota. Contamination, disinfection, and cross-colonization: are hospital surfaces reservoirs for nosocomial infection? *Clinical infectious diseases*, 39(8):1182–1189, 2004.

[15] Ji Liu, Philip E Paré, Erhu Du, and Zhiyong Sun. A networked SIS disease dynamics model with a waterborne pathogen. In *Proc. 2019 American Control Conference (ACC)*, pages 2735–2740. IEEE, 2019.

[16] A. Janson, S. Gracy, P. E. Paré, H. Sandberg, and K. H. Johansson. Networked multi-virus spread with a shared resource: Analysis and mitigation strategies. To be submitted to a journal, *https://arxiv.org/abs/2011.07569*, 2022.

[17] Philip E Pare, Axel Janson, Sebin Gracy, Ji Liu, Henrik Sandberg, and Karl H Johansson. Multi-layer SIS model with an infrastructure network. IEEE Transactions on Control of Network Systems, *https://arXiv preprint arXiv:2109.09493*, 2020. Note: Under Review, 2^{nd} Round.

[18] Sebin Gracy, Irinel Constantin Morărescu, Vineeth S Varma, and Philip E Paré. Analysis and on/off lockdown control for time-varying sis epidemics with a shared resource. In *Proc. 2022 European Control Conference*. IEEE, 2021.

[19] HH Rosenbrook. The stability of linear time-dependent control systems. *International Journal of Electronics*, 15(1):73–80, 1963.

[20] Petros A Ioannou and Jing Sun. *Robust Adaptive Control*. Courier Corporation, 1996.

[21] Xiaobin Gao, Daniel Liberzon, Ji Liu, and Tamer Başar. Unified stability criteria for slowly time-varying and switched linear systems. *Automatica*, 96:110–120, 2018.