Sufficient Condition for Survival of the Fittest in a Bi-virus Epidemics

Augusto Santos*, José M. F. Moura*, and João M. F. Xavier†

Abstract—**We study the spread of two strains of virus competing for space in a network modeled by the classical logistic ordinary differential equations. In large-scale complex networks, the underlying nonlinear dynamical system is high-dimensional and performing qualitative analysis of the differential equation becomes prohibitive. The study of such systems is often deferred to numerical simulations or local analysis about equilibrium points of the system. In this paper, we extend the work developed in [1], to formally establish a simple sufficient condition for (exponentially fast) survival of the fittest in a bi-layer weighted digraph: the weaker strain dies out regardless of the initial conditions if its maximum in-flow rate of infection across nodes is smaller than the minimum in-flow rate of the stronger strain. We bound any solution of the logistic ODE by one-dimensional solutions over certain *homogeneous* networks, for which the system is well understood. Our global stability approach via bounds readily applies to the discrete-time logistic model counterpart.**

I. INTRODUCTION

What we study. We study bi-virus epidemics on bi-layer networks where each layer renders the net-flow of infection associated with each strain of virus as illustrated in Fig.1. The dynamics is assumed to be the
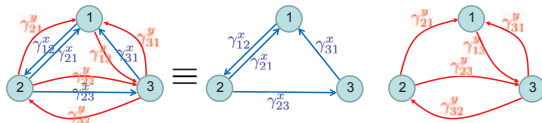

Figure 1: Bi-layer weighted network. The red (blue) arrows represent the flow of infection associated with the red (blue) strain of virus. The parameters γ_{ij}^z are cast as the rate of infection from node i to node j by the strain z, as properly introduced in Section II.

classical logistic ODE model referred to in equations (1)-(2). In particular, we will establish a simple selective advantage over the rate parameters γ that leads to survival

of the fittest between the two competing strains: if the maximum in-flow of strain y, across nodes, is smaller than the minimum in-flow of x, then the y-strain will vanish exponentially fast. Our approach rests upon global qualitative analysis of the ODE model that is quite hard to attain in general as the classical tools of Lyapunov and Ergodic theory are hardly applicable. Rather, we bound general solutions of the ODE (1)-(2) by those on homogeneous networks – networks whose in-flow rates are constant across nodes as it will be properly defined. We explore the fact that the dynamics is much simpler to be studied in homogeneous networks. Hence, our general principle is to approximate, i.e., bound, the *hard* dynamics on general bi-layer networks, by simpler dynamics on homogeneous networks to extract valuable exact global stability information, in particular, a simple sufficient condition for survival of the fittest.

Why we study it. Bi-virus dynamics may model the evolution of the fraction of infected vs vaccinated individuals in an interconnected set of communities. In particular, the population of i) infected individuals, ii) healthy not-vaccinated individuals, and iii) healthy vaccinated individuals evolve in a coupled manner. This coupling is not captured by standard single-virus models and moreover, one cannot understand the bi-virus dynamics of virus-vaccines by studying it separately (i.e., via the single-virus dynamics). The logistic bi-virus ODE that we study in this paper emerges naturally as the fluid limit dynamics from a microscopic peer-to-peer model of infection among individuals in different densely connected communities. A detailed motivation on the underlying epistemology of the bi-virus logistic ODE can be found, e.g., in Chapter 1 of [2].

Complex networked dynamical systems. The long-term behavior of the state of any dynamical system requires global qualitative analysis – characterizing the attractors and corresponding basins of attraction – which is in general hard to attain and often ignored in the literature. Most of the existing literature, e.g., references [3], [4] for single virus, or [5], [6], [7] on bi-virus dynamics, deal only with *local* analysis, i.e., determine properties of the equilibria, or study the dynamical system on *small* neighborhoods of the equilibrium points, or develop heuristics for their transitory behavior. The challenge to perform global analysis has been noted by the complex networked dynamical systems literature in

general, and reference [8] provides a recent overview on classical dynamical models over networks highlighting the challenges that arise when studying such systems. We remark, for instance, that the discrete-time counterpart of the logistic ODE (1)-(2) exhibits *chaotic* behavior and do not, in general, converge to the equilibria (refer to the discussion on the logistic map in [9]). Thus, local analysis often provides rather contrived conclusions and rigorous results and techniques on the global stability of a system are crucial to understand the long-term behavior of its solutions.

Main contribution of this paper. We identify a monotonous structure on the bi-virus logistic ODE to obtain a global stability result under certain parameter configurations, by bounding solutions to general weighted systems by simpler solutions on homogeneous networks. We established a survival of the fittest phenomenon.

II. PROBLEM FORMULATION

In this paper, we devise a sufficient condition for survival of the fittest between two strains of virus competing for space in a network. To address this problem, we study the global qualitative behavior of the logistic dynamical model

$$\dot{x}_i(t) = \left(\sum_{j \to i} \gamma_{ji}^x x_j(t) \right)(1 - x_i(t) - y_i(t)) - x_i(t) \quad (1)$$

$$\dot{y}_i(t) = \left(\sum_{j \to i} \gamma_{ji}^y y_j(t) \right)(1 - x_i(t) - y_i(t)) - y_i(t). \quad (2)$$

For analytical purposes, this is a dynamical system over a bi-layer weighted digraph as sketched in Fig. 1, where x_i and y_i represent the states of node i, and the weight of the edge (i, j) in the layer x (respectively, y) is γ_{ij}^x (respectively, γ_{ij}^y). We denote $G^z = (V, \Gamma^z)$ as the weighted graph associated with the strain z, where $\Gamma^z = (\gamma_{ij}^z)_{ij}$ is the matrix of weights and V is the set of nodes. From now on, we replace the term *weighted digraph* by *e-network*. We represent a bilayer e-network as a pair $\mathbf{G} = (G^x, G^y)$. In this model, one may construe the state variables $x_i(t)$ and $y_i(t)$ as

• the probability of infection of node i in an epidemics at time t, as motivated in [10];

• the fraction of infected individuals in a community i within a densely connected supernetwork of communities in the limit of large communities, as established in [2].

The parameters γ_{ji}^z stand for the rates of infection from community or node j to community or node i due to strain z.

We are to prove a simple sufficient condition on the parameters Γ^x and Γ^y under which

$$\liminf_t x_i(t) > 0$$
$$\lim_t y_i(t) = 0,$$

for all $i = 1, 2, \ldots, N$. Our methodology readily applies to the (chaotic) discrete-time logistic model.

Note that the underlying vector field of the ODE (1)-(2) is Lipschitz and thus, to each initial condition, there is associated a unique solution. Moreover, the compact set

$$\mathcal{D} = \left\{ (\mathbf{x}, \mathbf{y}) \in [0, 1]^N \times [0, 1]^N : x_i + y_i \leq 1 \right\}$$

is invariant for the dynamics and, therefore, solutions are well-defined for all $t \geq 0$.

Define the incidence vector rate $\mathbf{r}(G^z)$ of a weighted graph $G^z = (V, \Gamma^z)$ as

$$\mathbf{r}(G^z) := \left(\sum_{j \to 1} \gamma_{j1}^z, \ldots, \sum_{j \to N} \gamma_{jN}^z \right).$$

We call the weighted directed graph G^z homogeneous whenever

$$\mathbf{r}(G^z) \triangleq r^z \mathbf{1}_N$$

for some $r^z \in \mathbb{R}_{++}$, i.e., the in-flow rates are constant across nodes. The notation $\mathbf{1}_N$ stands for the N-dimensional vector of 1's. In this case, we may also call G^z an r^z-homogeneous e-network. Note that this definition makes no reference to the out-flow rates γ_{ij}^z of a node i. In fact, the out-flow rates may differ and the e-network G^z may still be homogeneous. When both G^x and G^y are homogeneous, we call $\mathbf{G} = (G^x, G^y)$ an homogeneous bilayer e-network.

Before proceeding, we summarize some important notation

• $\mathbf{x}(t, (\mathbf{x}_0, \mathbf{y}_0); \mathbf{G}) = (x_1(t), \ldots, x_N(t))$: vector collecting the state $x_i(t)$ of each node $i = 1, \ldots, N$ associated with the strain x at time t, assuming initial condition $(\mathbf{x}(0), \mathbf{y}(0)) = (\mathbf{x}_0, \mathbf{y}_0)$ and underlying e-network $\mathbf{G} = (G^x, G^y)$;

• $(\mathbf{x}(t, (\mathbf{x}_0, \mathbf{y}_0); \mathbf{G})) = (x_1(t), \ldots, x_N(t))$: associated orbit, i.e., curve over time $t \geq 0$. It will be also referred as flow to (1)-(2).

Similar notation is adopted for the strain y.

III. BI-VIRUS RESULTS

In this Section, we establish a sufficient condition for survival of the fittest as formally stated in Corollary 4. Given two pairs

Let

$$(x_1, y_1), (x_2, y_2) \in \mathbb{R}^N \times \mathbb{R}^N,$$

we define the binary relation $\succeq_\preceq$ as

$$(x_1, y_1) \succeq_\preceq (x_2, y_2) \overset{\triangle}{\Longleftrightarrow} (x_1 \geq x_2) \wedge (y_1 \leq y_2).$$

It is trivial to check that $\succeq_\preceq$ is a partial order on $\mathbb{R}^N \times \mathbb{R}^N$. We refer to $\succeq_\preceq$ as skew-inequality.

The next Lemma states that the dynamical system (1)-(2) is much simpler over homogeneous networks and with even initial conditions.

Lemma 1 (Homogeneous bilayer e-network). *Let* $\mathbf{G} = (G^x, G^y)$ *be a bilayer e-network so that* G^x *and* G^y *are* r^x*-homogeneous and* r^y*-homogeneous, respectively. Then,*

$$\begin{cases} \mathbf{y}(0) = y_0 \mathbf{1}_N \\ \mathbf{x}(0) = x_0 \mathbf{1}_N \end{cases}$$
$$\Downarrow$$
$$\begin{cases} \mathbf{y}(t, \mathbf{x}(0), \mathbf{y}(0); \mathbf{G}) = y(t, x_0, y_0) \mathbf{1}_N \\ \mathbf{x}(t, \mathbf{x}(0), \mathbf{y}(0); \mathbf{G}) = x(t, x_0, y_0) \mathbf{1}_N \end{cases}$$

where $(x(t, x_0, y_0), y(t, x_0, y_0))$ *is the flow to the 2D ODE*

$$\begin{aligned} \dot{y}(t) &= r^y y(t) (1 - x(t) - y(t)) - y(t) \\ \dot{x}(t) &= r^x x(t) (1 - x(t) - y(t)) - x(t) \end{aligned} \quad (3)$$

Proof. We only need to show that

$$(\mathbf{y}, \mathbf{x})(t, x_0 \mathbf{1}_N, y_0 \mathbf{1}_N; \mathbf{G})$$
$$=$$
$$(y(t, x_0, y_0) \mathbf{1}_N, x(t, x_0, y_0) \mathbf{1}_N)$$

is solution to (1)-(2) and therefore, the unique solution as the underlying vector field $\mathbf{F}$ is Lipschitz. Indeed,

$$\dot{\mathbf{y}}(t, x_0 \mathbf{1}_N, y_0 \mathbf{1}_N; G)$$
$$=$$
$$\dot{y}(t, x_0, y_0) \mathbf{1}_N$$
$$=$$
$$((r^y y(t))(1 - y(t) - x(t)) - y(t)) \mathbf{1}_N$$
$$=$$
$$F_1(x(t)\mathbf{1}_N, y(t)\mathbf{1}_N) = F_1(\mathbf{x}(t), \mathbf{y}(t))$$

and the same for x. $\qquad \square$

The next Theorem states that under certain conditions of homogeneity, the dynamical system (1)-(2) preserves the skew-inequality, and we can bound general solutions by solutions on homogeneous e-networks.

Theorem 2 (Bounds). *Let* $\mathbf{G} = (G^x, G^y)$ *be so that*

$$(\mathbf{r}(G^x), \mathbf{r}(G^y)) \succeq_\preceq (r^x \mathbf{1}_N, r^y \mathbf{1}_N),$$

i.e.,

$$\begin{aligned} \mathbf{r}^x &\overset{\triangle}{=} \mathbf{r}(G^x) \geq r^x \mathbf{1}_N \\ \mathbf{r}^y &\overset{\triangle}{=} \mathbf{r}(G^y) \leq r^y \mathbf{1}_N. \end{aligned}$$

Then,

$$(\mathbf{x}(0), \mathbf{y}(0)) \succeq_\preceq (x_0 \mathbf{1}_N, y_0 \mathbf{1}_N)$$
$$\Downarrow$$
$$((\mathbf{x}, \mathbf{y})(t, \mathbf{x}(0), \mathbf{y}(0); \mathbf{G}))$$
$$\succeq_\preceq$$
$$(x(t, x_0, y_0) \mathbf{1}_N, y(t, x_0, y_0) \mathbf{1}_N)$$

for all $t \geq 0$, *where the flow* $(x(t, x_0, y_0), y(t, x_0, y_0))$ *is the solution to the ODE* (3).

Proof. We assume that

$$r^y \geq \sum_{j \to i} \gamma_{ji}^y \quad \text{and} \quad y_i(0) \leq y_0$$
$$r^x \leq \sum_{j \to i} \gamma_{ji}^x \quad \text{and} \quad x_i(0) \geq x_0$$

for all $i = 1, \ldots, N$, with strict inequality for (at least) some node m in the e-network:

$$r^y(m) < r^y \text{ or } y_m(0) < y(0),$$

or

$$r^x(m) > r^x \text{ or } x_m(0) > x(0).$$

Note that, if no strict inequality holds, then from Lemma 1,

$$(\mathbf{x}, \mathbf{y})(t, \mathbf{x}(0), \mathbf{y}(0); \mathbf{G}) = (x(t, x_0, y_0), y(t, x_0, y_0)),$$

and, thus, Theorem 2 holds true. Define the *hitting time*

$$T = \inf \{t \geq 0 : \mathbf{y}(t) \not\preceq y(t)\mathbf{1}_N \vee \mathbf{x}(t) \not\succeq x(t)\mathbf{1}_N\}$$

and assume finiteness $T < \infty$. To ease the notation, we say that the hitting time T is ϵ-extendable with respect to y_i, (respectively, x_i), whenever there exists an $\epsilon > 0$ such that $y_i(t) < y(t)$ (respectively, $x_i(t) > x(t)$) for all $t \in (T, T + \epsilon)$. Note that if T is extendable with respect to y_i and x_i for all $i = 1, \ldots, N$, then T cannot be finite and we reach a contradiction. That is our goal in this proof.

Note first that strict inequality holds at T

$$x_m(T) > x(T) \text{ or } y_m(T) < y(T)$$

for some m, otherwise

$$(\mathbf{x}(T), \mathbf{y}(T)) = (x(T)\mathbf{1}_N, y(T)\mathbf{1}_N)$$

violates uniqueness of the ODE. Assume that $y_m(T) < y(T)$ for some m (the case $x_m(T) > x(T)$ is analogous). Define

$$I^y = \{j : y_j(T) = y(T)\}$$

and

$$I^x = \{j : x_j(T) = x(T)\}.$$

Remark that if $I^x \cup I^y = \emptyset$, then T is obviously ϵ-extendable w.r.t. $\mathbf{x}$ and $\mathbf{y}$, which contradicts the finiteness $T < \infty$. Now, assume $I^y \neq \emptyset$ and let $k \in I^y$.

Assume first that $m \in \mathcal{N}(k)$. Then, comparing termwise the equations

$$\dot{x}_i(t) = \underbrace{\left(\sum_{j \to i} \gamma_{ji}^x x_j(t)\right)}_{A} \underbrace{(1 - x_i(t) - y_i(t))}_{B} - \underbrace{x_i(t)}_{C}$$

$$\dot{y}_i(t) = \underbrace{\left(\sum_{j \to i} \gamma_{ji}^y y_j(t)\right)}_{D} \underbrace{(1 - x_i(t) - y_i(t))}_{E} - \underbrace{y_i(t)}_{F}$$

$$\dot{x}(t) = \underbrace{r^x x(t)}_{A'} \underbrace{(1 - x(t) - y(t))}_{B'} - \underbrace{x(t)}_{C'}$$

$$\dot{y}(t) = \underbrace{r^y y(t)}_{D'} \underbrace{(1 - x(t) - y(t))}_{E'} - \underbrace{y(t)}_{F'}$$

we have $F = F'$, $E \leq E'$ and $D < D'$ due to the assumption $m \in \mathcal{N}(i)$. Therefore, $\dot{y}_i(T) < \dot{y}(T)$ and there exists $\epsilon_i^y > 0$ such that

$$y_i(t) < y(t) \; \forall t \in (T, T + \epsilon_i^y). \tag{4}$$

If $m \in \mathcal{N}^{(n)}(i)$ with $n > 1$ then, similarly to as done in [1], we can show by induction on the neighborhood order that $\overset{(k)}{y}_i(T) \geq \overset{(k)}{y}(T)$ and $\overset{(n)}{y}_i(T) > \overset{(n)}{y}(T)$. In any case, (4) holds.

Now, if $x_j(T) = x(T)$ for any $j \in \mathcal{N}(i)$ and with the initial assumption that $y_m(T) < y(T)$ for some neighbor $m \in \mathcal{N}(i)$ then, $\dot{x}_i(T) = x(T)$, but we can compare the equations for the second derivative $\ddot{x}_i(t)$

$$\ddot{x}_i(t) = \underbrace{\left(\sum_{j \to i} \gamma_{ji}^x \dot{x}_j(t)\right)(1 - x_i(t) - y_i(t))}_{A}$$

$$\underbrace{- \left(\sum_{j \to i} \gamma_{ji}^x x_j(t)\right)(\dot{x}_i(t) + \dot{y}_i(t))}_{B} - \underbrace{\dot{x}_i(t)}_{C}$$

$$\ddot{x}(t) = \underbrace{(r^x \dot{x}(t))(1 - x(t) - y(t))}_{A'}$$

$$\underbrace{- (r^x x(t))(\dot{x}(t) + \dot{y}(t))}_{B'} - \underbrace{\dot{x}(t)}_{C'}$$

to readily see that: i) $C = C'$; ii) $B > B'$ since $\dot{y}_i(T) < \dot{y}(T)$, as we have seen; iii) $A > A'$ since $\dot{x}_m(T) > \dot{x}(T)$ as can be easily checked. Therefore, $\ddot{x}_i(T) > x(T)$ and there is an ϵ_i^x such that $x_i(t) > x(t)$ for all $t \in (T, T + \epsilon_i^x)$. In case, $y_m(T) < y(T)$ (or $x_m(T) > x(T)$) only for some m n-hops away from i, then one can prove by induction that $x_i^{(n+1)}(T) > x^{(n+1)}(T)$ (or $x_i^{(n)}(T) > x^{(n)}(T)$). In any case we have that there exists

$$\epsilon_1^x, \ldots, \epsilon_N^x > 0 \text{ and } \epsilon_1^y, \ldots, \epsilon_N^y > 0$$

with

$$y_i(t) < y(t) \; \forall t \in (T, T + \epsilon_i^y)$$
$$x_i(t) > x(t) \; \forall t \in (T, T + \epsilon_i^x)$$

for all i and thus,

$$\mathbf{y}(t) < y(t)\mathbf{1}_N$$
$$\mathbf{x}(t) > x(t)\mathbf{1}_N$$

for all $t \in (T, T + \epsilon)$, with

$$\epsilon \triangleq \min_{z = x, y; k = 1, \ldots, N} \{\epsilon_k^z\}.$$

We reached a contradiction on the assumption $T < \infty$.
$\square$

The next Theorem states the long term behavior on homogeneous e-networks.

Theorem 3. *Consider the 2D ODE*

$$\dot{x}(t) = (\gamma^x x(t))(1 - x(t) - y(t)) - x(t)$$
$$\dot{y}(t) = (\gamma^y y(t))(1 - x(t) - y(t)) - y(t).$$

If $\gamma^y < \gamma^x$ and $x(0) > 0$, then $y(t) \longrightarrow 0$, exponentially fast, regardless of the initial conditions $x(0)$ and $y(0)$.

Proof. Define $z(t) \triangleq \frac{y(t)}{x(t)}$ and observe that

$$\begin{cases} \frac{d}{dt} z(t) &= \frac{x(t)y(t)(\gamma^y - \gamma^x)(1 - x(t) - y(t))}{(x(t))^2} \\ &= z(t)(\gamma^y - \gamma^x)(1 - x(t) - y(t)) \quad (5) \\ z(t) &> 0 \end{cases}$$

for all $t \geq 0$. Note that, if $x(0) \neq 0$ then, $x(t) \neq 0$ for all t and the derivative in equation (5) is well defined. By Gronwall's inequality,

$$z(t) \leq z(0) e^{(\gamma^y - \gamma^x) \int_0^t 1 - x(s) - y(s) ds} \tag{6}$$

and note that $\gamma^y - \gamma^x < 0$. Also, we observe that the positive quantity $1 - x(t) - y(t)$ is bounded away from 0. Indeed, let $w(t) \triangleq x(t) + y(t)$

$$\frac{d}{dt} w(t) = (\gamma^x x(t) + \gamma^y y(t))(1 - x(t) - y(t))$$
$$- (x(t) + y(t))$$
$$= (\gamma^x (x(t) + y(t)) + (\gamma^y - \gamma^x) y(t)) \times$$
$$\times (1 - x(t) - y(t)) - (x(t) + y(t))$$
$$= (\gamma^x w(t))(1 - w(t)) - w(t)$$
$$+ \underbrace{((\gamma^y - \gamma^x) y(t))(1 - w(t))}_{<0}$$

and since the latter term is negative for all time, we have

$$w(0) \leq v(0) \Rightarrow w(t) \leq v(t) \; \forall t \geq 0,$$

where $(v(t))$ is solution to the 1D single-virus logistic

ODE

$$\frac{d}{dt}v(t) = (\gamma^x v(t))(1 - v(t)) - v(t).$$

Now, it is trivial to check that $v(t)$ converges monotonously to $1 - \frac{1}{\gamma^x} < 1$, and, therefore, for any initial condition

$$x(0) + y(0) \le v(0) < (1 - \epsilon) \wedge \left(1 - \frac{1}{\gamma^x}\right)$$

we have,

$$x(t) + y(t) \le v(t) < (1 - \epsilon) \wedge \left(1 - \frac{1}{\gamma^x}\right)$$

for all $t \ge 0$ and $z(t) \longrightarrow 0$, exponentially fast, – with a rate of at least $(\gamma^x - \gamma^y)\left(\epsilon \vee \frac{1}{\gamma^x}\right)$ – from equation (6). In particular, $y(t) \longrightarrow 0$, exponentially fast, as $x(t)$ is bounded. $\square$

The next Corollary establishes the main result of this paper.

Corollary 4 (Survival of the fittest). *Let* $\mathbf{G} = (G^x, G^y)$ *be so that*

$$r^x \triangleq \min_{i \in V} \left\{ \sum_{j \to_x i} \gamma_{ji}^x \right\} > \max_{i \in V} \left\{ \sum_{j \to_y i} \gamma_{ji}^y \right\} \triangleq R^y.$$

Then,

$$\mathbf{y}(t, \mathbf{x}_0, \mathbf{y}_0) \longrightarrow \mathbf{0}_N,$$

exponentially fast, for any initial condition $(\mathbf{x}_0, \mathbf{y}_0)$ *with* $\mathbf{x}_0 \ne \mathbf{0}$.

Proof. Let $\mathbf{x}_0 > 0$. From Theorem 2, we have that

$$(\mathbf{x}, \mathbf{y}(t, \mathbf{x}_0, \mathbf{y}_0)) \succeq_\preceq (x(t, x_0, y_0)\mathbf{1}_N, y(t, x_0, y_0)\mathbf{1}_N)$$

where $(x(t, x_0, y_0), y(t, x_0, y_0))$ is solution to

$$\dot{x}(t) = (\tilde{r}^x x(t))(1 - x(t) - y(t)) - x(t)$$
$$\dot{y}(t) = \left(\tilde{R}^y y(t)\right)(1 - x(t) - y(t)) - y(t).$$

with,

$$r^x > \tilde{r}^x > \tilde{R}^y > R^y,$$

for some $\tilde{r}^x, \tilde{R}^y$. From Theorem 3,

$$\mathbf{y}(t, \mathbf{x}_0, \mathbf{y}_0) \le y(t, x_0, y_0)\mathbf{1}_N \longrightarrow 0$$

exponentially fast.

If $\mathbf{x}_0 \not> \mathbf{0}$ and $\mathbf{x}_0 \ne \mathbf{0}$, then it is easy to show that $\mathbf{x}(t, \mathbf{x}_0, \mathbf{y}_0) > 0$ for any $t > 0$ and the convergence above still holds. $\square$

IV. CONCLUDING REMARKS

We presented a global qualitative analysis technique that allows to develop relevant results for a complex networked dynamical system – namely survival of the fittest – by analyzing much simpler dynamical systems. The results presented in this paper extend those in reference [1]. Our approach readily extends to the discrete time bi-virus logistic difference equations, namely, all relevant Theorems in the previous Section hold for the discrete-time model with obvious adaptations. Moreover, similar analysis holds for a broader class of dynamical models other than the logistic equations. For instance, it naturally applies to establish survival of the fittest for the more general dynamics

$$\dot{x}_i(t) = \left(\sum_{j \to i} \gamma_{ji}^x \sqrt[n]{x_j(t)}\right)(1 - x_i(t) - y_i(t)) - x_i(t)$$

$$\dot{y}_i(t) = \left(\sum_{j \to i} \gamma_{ji}^y y_j^n(t)\right)(1 - x_i(t) - y_i(t)) - y_i(t).$$

where $\mathbf{y}(t) \to 0$ whenever the parameter conditions in Corollary 4 hold. The global stability property arises without the need for further analysis of the system. An extension of our results for more general vector fields is ongoing.

REFERENCES

[1] A. Santos, J. M. F. Moura, and J. M. F. Xavier, "Bi-virus SIS epidemics over networks: Qualitative analysis," *IEEE Transactions on Network Science and Engineering*, vol. 2, no. 1, pp. 17–29, Jan 2015.

[2] A. Santos, *Bi-virus Epidemics over Large-scale Networks: Emergent Dynamics and Qualitative Analysis*. Ph.D. Thesis, Carnegie Mellon University, Sep 2014.

[3] A. Barrat, M. Barthélemy, and A. Vespignani, *Dynamical Processes on Complex Networks*. London, UK: Cambridge University Press, November 2012.

[4] M. O. Jackson, *Social and Economic Networks*. Princeton University Press, 2008.

[5] X. Wei, N. Valler, B. Prakash, I. Neamtiu, M. Faloutsos, and C. Faloutsos, "Competing memes propagation on networks: A network science perspective," *Selected Areas in Communications, IEEE Journal on*, vol. 31, no. 6, pp. 1049–1060, June 2013.

[6] B. Karrer and M. E. J. Newman, "Competing epidemics on complex networks," *Phys. Rev. E*, vol. 84, p. 036106, Sep 2011. [Online]. Available: http://link.aps.org/doi/10.1103/PhysRevE.84.036106

[7] C. Darabi Sahneh, Faryad; Scoglio, "May the best meme win!: New exploration of competitive epidemic spreading over arbitrary multi-layer networks," *eprint arXiv:1308.4880*, August 2013.

[8] M. A. Porter and J. P. Gleeson, "Dynamical systems on networks: a tutorial," 2015. [Online]. Available: arXiv:1403.7663v2.

[9] M. Mitchell, "Complexity: a guided tour," *Genetic Programming and Evolvable Machines*, vol. 11, no. 1, pp. 127–128, 2010. [Online]. Available: http://dx.doi.org/10.1007/s10710-009-9097-y

[10] P. Van Mieghem, J. Omic, and R. Kooij, "Virus spread in networks," *IEEE/ACM Transactions on Networking*, vol. 17, no. 1, pp. 1 –14, February 2009.