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Multiple peaks in network SIR epidemic models

Martina Alutto, Leonardo Cianfanelli, Giacomo Como, *Member, IEEE,* and Fabio Fagnani

Abstract— We study network SIR (Susceptible—Infected—Recovered) epidemic models in the case of two interacting populations. We analyze the dynamics behavior of the fractions of infected individuals in the two populations. In contrast to the classical scalar SIR epidemic model, where the fraction of infected individuals is known to have an unimodal behavior (either decreasing throughout time or initially increasing, until reaching a peak and decreasing everafter), we show the possible occurrence of a novel multimodal behaviors in the network SIR model. Specifically, we show that the curve of the fraction of infected individuals in a population may incur in a change of monotonicity even when it starts with a decreasing trend. Our analysis focuses on a homogeneous mixing model, whereby all contacts have unitary frequency. We study the initial conditions and network characteristics sufficient for the aforementioned multimodal behavior to emerge and those that instead guarantee the classical unimodal behavior.

Index Terms— Epidemic models, Susceptible-Infected-Recovered model, reproduction number.

I. INTRODUCTION

The study of compartmental models to forecast the evolution of epidemics has received large attention in the past decades. Within this class of models, a population of individuals is split into compartments based on their state. The evolution of the fraction of individuals in each state is then described by autonomous ordinary differential equations, without keeping track of the state of the single individuals. One of the most popular compartmental epidemic models is the SIR epidemic model [1]. The SIR epidemic model considers three compartments (susceptible, infected and recovered) and assumes that the rate of new infections in the population is proportional to the product of the fraction of susceptible individuals times the fraction of infected individuals due to pairwise interactions, while the rate of new recoveries is proportional to the number of infected individuals, due to spontaneous healing. The underlying assumption is that the population is homogeneously mixed.

The SIR epidemic model is well studied in the literature. A classical result already proved by Kermack and McKendrick [1] is that the growth rate of fraction of infected individuals in the population is captured by a time-dependent scalar quantity, known as the *reproduction number* and denoted by $R(t)$, which describes how many new infections on average an infected individual will produce in the population. If $R(t) < 1$, then the fraction of infected individuals is

The authors are with the Department of Mathematical Sciences "G.L. Lagrange," Politecnico di Torino, Corso Duca degli Abruzzi 24, 10129 Torino, Italy (e-mail: {martina.alutto; leonardo.cianfanelli}@polito.it, {giacomo.como; fabio.fagnani}@polito.it). G. Como is also with the Department of Automatic Control, Lund University, BOX 118, SE-22100 Lund, Sweden.

decreasing at time t. On the other hand, if $R(t) > 1$, then the fraction of infected individuals increases, so there is an epidemic outbreak at time t. It can then be proved that the reproduction number $R(t)$ is monotonically decreasing in t and eventually becomes less than 1. From that point on, the fraction of infected individuals decreases monotonically to 0. As a consequence, in the SIR epidemic model the diffusion of the disease is *unimodal*, meaning that the curve of infected individuals in the population has just one local maximum in $t \geq 0$, to be referred as its *peak*. Such unimodal behavior is also at the basis of several control strategies, including some recently proposed in the context of the COVID-19 pandemic, see, e.g., [2] and [3].

The underlying assumption of homogeneous mixing of the population in the classical SIR epidemic model can prove too restrictive in many applications of interest. To include some kind of heterogeneity, the SIR epidemic model has been generalized into the *network SIR model* [4]. In this model, nodes of a finite graph represent meta-populations of indistinguishable individuals and the interactions between individuals of different nodes may be heterogeneous. The network SIR model (or generalizations including more than three compartments) finds application to study the heterogeneous spread of a disease in different geographical areas [5]–[7], or to study the spread of the disease in sub-populations defined with respect to demographic aspects (e.g., the age), that determine different responses to the disease and different interaction levels (e.g., students tend to interact more with students than with older individuals) [8].

From now on, to distinguish the network SIR model from the standard SIR model, we shall refer to the latter one by *scalar SIR model*. The network SIR model has been analysed from a theoretical perspective in [9], where the authors identified a network reproduction number that plays a role similar to the one played by the reproduction number of the scalar SIR model. If this new reproduction number is below 1, then a certain weighted average of the infected individuals decreases; otherwise the weighted average of the infected average increases, until the reproduction number eventually becomes smaller than 1. In [10], it is instead analysed how the heterogeneity affects the final size of the outbreak. Both analyses in [9] and [10] are at the aggregate level and no information on the single node dynamics is provided. However, in many applications this local information is important. Nodes may represent populations of individuals belonging to the same age group or to the same geographical area and understanding the epidemic evolution at node level (e.g., the modal behavior of the curve) can be crucial to plan specific and more effective control policies [8].

In this paper, we analyze this issue for the simple case of a network SIR model with just two nodes, derived from a scalar model where a population satisfying the homogeneous mixing hypotheses has been split into two arbitrary groups. While the parameters are uniform across the two nodes, initial conditions may differ. We show that, surprisingly, this distinction is sufficient for the dynamics to exhibit multi-modal behaviors, which cannot be observed in the scalar SIR model. Our contribution is two-fold. First, we provide sufficient conditions for, respectively, unimodal and multi-modal behaviors to arise in a single node. Second, we show that in every node the infected curve cannot exhibit more than two local maxima.

The rest of the paper is organized as follows. In Section II we describe the network SIR model and its properties. In Section III, we define our case-study and provide our theoretical results. In Section IV some simulations on different network are shown. Finally, in Section V we summarize our work and discuss future research lines.

II. NETWORK SIR EPIDEMIC MODEL

In this section, we introduce the network SIR epidemic model. Let us consider a weighted graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, A)$ with finite set of nodes $\mathcal{V} = \{1, 2, \ldots, n\}$, set of directed links $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$, and a matrix A in $\mathbb{R}_+^{n \times n}$, whose entries embody the strength of both the infection and the contact frequency between individuals of subpopulation i and individuals of subpopulation j. For a given recovery rate $\gamma > 0$, the SIR model on a graph $\mathcal{G} = (\mathcal{V}, \mathcal{E}, A)$ is the dynamical system

$$\begin{cases} \dot{x}_i = -x_i \sum_j a_{ij} y_j \\ \dot{y}_i = x_i \sum_j a_{ij} y_j - \gamma y_i \\ \dot{z}_i = \gamma y_i \end{cases} \quad (1)$$

for $i = 1, \ldots, n$, where x_i, y_i, and z_i represent respectively the fractions of susceptible, infected, and recovered individuals in population i. Notice that (1) can be more compactly rewritten in its vectorial form

$$\begin{cases} \dot{x} = -diag(x)Ay \\ \dot{y} = diag(x)Ay - \gamma y \end{cases} \quad (2)$$

This model has been studied in [9] and [11]. If there is a positive initial fraction of infected individuals, the strict positivity of solutions has been shown. This result will be useful in the following theorems. The dominant eigenvalue of the nonnegative matrix $diag(x)A$, has been shown to be crucial in the dynamics of this model. Indeed, it has been proven under the assumption of strong connectivity of the graph $\mathcal{G}$, that the quantity

$$R(t) = \lambda_{\max}(\operatorname{diag}(x(t))A)/\gamma,$$

is decreasing along solutions and represents a kind of reproduction number, as the one in the scalar SIR case. Depending on its value, two different epidemics behaviors may occur. In particular, the analysis conducted in [9] is focused on the behavior of a weighted average of infected individuals, whose weight is $v(t)$, i.e., the corresponding left-eigenvector

of $\lambda_{\max}$ of the matrix $\operatorname{diag}(x(t))A$. Specifically, if $R(\tau)$ is less than 1 for some time instant $\tau \geq 0$, then the weighted average of the infected $v(\tau)'y(t)$ will be monotonically decreasing to 0 for $t \geq \tau$. Otherwise, if $R(0)$ is greater than 1, then the weighted average $v(0)'y(t)$ increases and then, there exists some time instant at which the new defined reproduction number becomes less than or equal to 1 and the weighted average will become monotonically decreasing to 0 for subsequent time instants.

This result makes possible a comparison with the scalar SIR model theory. However, the average view does not provide a direct knowledge of how the dynamics is developing at individual nodes. Numerical simulations show how the dynamical behavior at individual nodes can exhibit atypical phenomena compared to the unimodal or monotonically decreasing behavior of the scalar case. We shall investigate these phenomena in the next section, trying to determine sufficient conditions for multimodal and unimodal behaviors to occur at a single node level. For this analysis from now on, we will focus on the case of a network consisting of two nodes.

III. TWO-NODES HOMOGENEOUS NETWORK

In this section, we will deal with the case of a network composed of two nodes and we will investigate different behaviors of the infected fraction at node level, on the basis of particular initial conditions and characteristics of the network.

We assume a network with uniform mixing, so the infection/contact matrix is

$$A = \begin{pmatrix} \beta & \beta \\ \beta & \beta \end{pmatrix},$$

where $\beta > 0$. Therefore, the model analysed is

$$\begin{cases} \dot{x}_i = -\beta x_i(y_1 + y_2) \\ \dot{y}_i = \beta x_i(y_1 + y_2) - \gamma y_i \qquad i = 1, 2 \,. \\ \dot{z}_i = \gamma y_i \end{cases} \quad (3)$$

Note that this scenario corresponds to arbitrarily dividing a completely homogeneous population into two portions. In this way, it is possible to study the separate dynamics occurring in the two portions of the population having different initial conditions. This type of model has been analysed to study the effects of targeted lockdown strategies when individuals are classified based on their age, under the assumption that intra-group and inter-groups contact rates are uniform [8].

Our work will show new behaviors with respect to the classical scalar SIR theory, which could pave the way for further control applications. Our goal is to show that the disease may have multiple peaks at a single node level. In this analysis, we assume for simplicity of notation $z(0) = (0, 0)$, but the results can be extended to the general case without loss of generality. In order to study the behavior of the fraction of infected individuals at single node level, we will focus on a particular scenario in which only one node

has an initial small fraction of infected individuals, while the other one is initially totally susceptible.

For simplicity of notation, we will consider the special case in which $\beta = \gamma = 1$, but the following result remains valid for general infection, recovery rates and initial condition for the second node.

Proposition 1: Consider the network SIR model (3). Let the initial condition be

$$x_1(0) = 1 - \varepsilon, \quad y_1(0) = \varepsilon, \quad x_2(0) = 1, \quad y_2(0) = 0,$$

for some $0 < \varepsilon < \bar{\varepsilon}$, where

$$\bar{\varepsilon} = \min\left\{\varepsilon \in [0,1] : \varepsilon = \frac{1-\varepsilon}{2-\varepsilon}(1 - \ln(2 - \varepsilon))\right\}.$$

Then, the fraction of infected individuals in the first population y_1 changes monotonicity at least twice along the solution.

Remark 1: Notice that $\bar{\varepsilon}$ always exists. Indeed, by letting

$$g(\varepsilon) = \frac{1-\varepsilon}{2-\varepsilon}(1 - \ln(2 - \varepsilon)) - \varepsilon,$$

it is easy to show that $g(\varepsilon)$ admits a zero in $[0,1]$. This follows immediately from $g(0) = 1/2(1 - \ln 2) > 0$ and $g(1) = -1 < 0$.

Proof: The dynamics is given by

$$\dot{x}_i = -2x_i\bar{y}, \qquad \dot{y}_i = 2x_i\bar{y} - y_i, \qquad i = 1, 2,$$

where $\bar{x} = (x_1 + x_2)/2$, $\bar{y} = (y_1 + y_2)/2$ are the mean aggregate variables. Notice that

$$\dot{\bar{x}} = -2\bar{x}\,\bar{y}, \qquad \dot{\bar{y}} = (2\bar{x} - 1)\bar{y},$$

so that by scalar theory the quantity $\bar{x} + \bar{y} - \frac{1}{2}\ln\bar{x}$ remains constant along solutions, i.e. for every $t \geq 0$

$$\bar{x}(t) + \bar{y}(t) - \frac{1}{2}\ln\bar{x}(t) = \bar{x}(0) + \bar{y}(0) - \frac{1}{2}\ln\bar{x}(0). \quad (4)$$

On the other hand, whenever $x_2 > 0$, we have

$$\left(\frac{x_1}{x_2}\right)^{\cdot} = \frac{\dot{x}_1 x_2 - x_1 \dot{x}_2}{x_2^2} = 0$$

so that the ratio x_1/x_2 remains constant along solutions, i.e.,

$$x_i(t)\bar{x}(0) = x_i(0)\bar{x}(t), \quad \forall t \geq 0, \ i = 1, 2. \quad (5)$$

Observe that

$$\dot{y}_1(0) = 2x_1(0)\bar{y}(0) - y_1(0) = -\varepsilon^2 < 0,$$

whereas,

$$\dot{\bar{y}}(0) = (2\bar{x}(0) - 1)\bar{y}(0) = (1 - \varepsilon)\varepsilon/2 > 0.$$

Let $t^* > 0$ be the aggregate peak time, i.e., the time such that $\dot{\bar{y}}(t^*) = 0$, which implies $\bar{x}(t^*) = 1/2$. It follows from (4) that aggregate peak is

$$\bar{y}(t^*) = \bar{x}(0) + \bar{y}(0) - \frac{1}{2}\ln\bar{x}(0) - \bar{x}(t^*) + \frac{1}{2}\ln\bar{x}(t^*)$$

$$= \frac{1}{2}\left(1 - \ln(2 - \varepsilon)\right),$$

while evaluating (5) in t^*, we get that

$$x_1(t^*) = \frac{x_1(0)\bar{x}(t^*)}{\bar{x}(0)} = \frac{1 - \varepsilon}{2 - \varepsilon}. \quad (6)$$

Now, assume by contradiction that

$$\dot{y}_1(t) \leq 0, \qquad \forall t \geq 0. \quad (7)$$

In particular, this would imply that at t^*

$$0 \geq \dot{y}_1(t^*)$$
$$= 2x_1(t^*)\bar{y}(t^*) - y_1(t^*)$$
$$= \frac{1-\varepsilon}{2-\varepsilon}\left(1 - \ln(2 - \varepsilon)\right) - y_1(t^*)$$
$$\geq \frac{1-\varepsilon}{2-\varepsilon}\left(1 - \ln(2 - \varepsilon)\right) - y_1(0).$$

So we would obtain that

$$y_1(0) = \varepsilon \geq \frac{1-\varepsilon}{2-\varepsilon}\left(1 - \ln(2 - \varepsilon)\right).$$

Therefore necessarily $\varepsilon \geq \bar{\varepsilon}$, thus violating the assumption. It then follows that there exists at least a time $\bar{t}$ such that $\dot{y}_1(\bar{t}) > 0$. The claim then follows, since $\dot{y}_1(0) < 0$ and $\lim_{t \to +\infty} y_1(t) = 0$. We have shown that the infected curve in the first node y_1 changes monotonicity at least twice along the solution. ∎

Remark 2: Proposition 1 shows the existence of an atypical behavior, which is not observed in the scalar SIR, in a situation of total homogeneity of the network. We remark that this behavior is only due to the difference between the initial conditions of the two nodes.

Remark 3: Note that at the aggregate level, the dynamics of the model (3) is unimodal. Indeed,

$$\dot{y}_1 + \dot{y}_2 = (\beta(x_1 + x_2) - \gamma)(y_1 + y_2), \quad (8)$$

and since the aggregate curve of susceptible individuals is always decreasing and the aggregate variable of infected individuals is bounded, the latter can assume only two behaviors: either monotonically decreasing or an unimodal behavior.

The scenario studied in the previous proposition concerns the occurrence of an increasing phase of the infected curve in the first node after an initial decreasing trend. This means that under some conditions the infected curve can have at least two peaks, i.e. two local maxima where the first one is not a critical point but it coincides with its initial condition. On the subsequent behavior of the infected curve nothing can be said yet, so there may be multiple peaks. The next proposition, whose proof can be found in the Appendix, allows us to better define the phenomenon, whenever it occurs. In particular, we will ensure that the infected curve can change its monotonicity at most twice if it starts decreasing, otherwise it will show an unimodal behavior.

Proposition 2: Consider the network SIR model (3). Then, the fraction of infected individuals can have at most one internal maximum point in each node.

Proposition 2 characterizes the atypical phenomenon and states that if the infected curve starts increasing, then it will show an unimodal behavior, otherwise if it starts decreasing, then it can change monotonicity and reach a maximum point, after which it becomes decreasing to 0. To complete the analysis, in the next proposition we provide a sufficient condition in order to guarantee a classic behavior, so that the phenomenon analyzed in the previous results does not occur.

Proposition 3: Consider the network SIR model (3). Let the initial conditions such that

$$\beta(x_1(0) + x_2(0)) < \gamma. \tag{9}$$

Then the set $\Omega = \{(x_1, y_1, x_2, y_2) \in [0,1]^4 : \dot{y}_1 \leq 0\}$ is positively invariant.

Proof: Suppose that the initial condition $(x_1(0), y_1(0), x_2(0), y_2(0)) \in \Omega$. We want to prove that the corresponding solution will remain in Ω for all $t \geq 0$. Suppose that it exists an instant t^* such that the solution belongs to $\delta\Omega = \{(x_1, y_1, x_2, y_2) \in [0,1]^4 : \dot{y}_1 = 0\}$ and $(x_1(t), y_1(t), x_2(t), y_2(t)) \in \Omega \quad \forall t < t^*$. Let us consider the first derivative of $\dot{y}_1$ with respect to time t,

$$\ddot{y}_1 = \beta\dot{x}_1(y_1 + y_2) + \beta x_1(\dot{y}_1 + \dot{y}_2) - \gamma\dot{y}_1. \tag{10}$$

From (9) and the monotonically decreasing behavior of $x_1 + x_2$, we have that

$$\beta x_2(t^*) < \gamma - \beta x_1(t^*),$$

thus, evaluating (10) in t^* we get

$$\begin{aligned}
\ddot{y}_1(t^*) &= -\beta^2 x_1(y_1 + y_2)^2 + \beta^2 x_1 x_2(y_1 + y_2) - \gamma\beta x_1 y_2 \\
&< \beta x_1[\beta x_2(y_1 + y_2) - \gamma y_2] \\
&< \beta_1 x_1[\gamma(y_1 + y_2) - \beta x_1(y_1 + y_2) - \gamma y_2] \\
&= \beta_1 x_1[\gamma(y_1 + y_2) - \gamma y_1 - \gamma y_2] = 0,
\end{aligned}$$

where the first inequality follows from the positivity of solution while the last equality from $\dot{y}_1(t^*) = 0$. This leads to a contradiction because $\ddot{y}_1(t^*) < 0$ and, by continuity, we can state that $\ddot{y}_1 < 0$ in a neighborhood $(t^* - \delta, t^*]$. Since $\dot{y}_1$ is decreasing and, by construction, $\dot{y}_1 < 0$ for $t < t^*$, it is not possible that $\dot{y}_1(t^*) = 0$. ∎

Remark 4: From (8), we can note that condition (9) corresponds to a scenario in which the aggregate infection curve is monotonically decreasing to 0, so a level of immunity has been reached in the aggregate model that ensures the decline of the epidemics.

IV. NUMERICAL SIMULATIONS

In this section we will provide some simulations of the model considered in the previous analysis, that is the case of a homogeneous network consisting of two nodes. We will then observe a non-homogeneous network scenario where further phenomena may occur, especially by increasing the number of nodes.

In Figure 1, in the first plot we can observe the occurrence of the atypical behavior in the scenario of a homogeneous
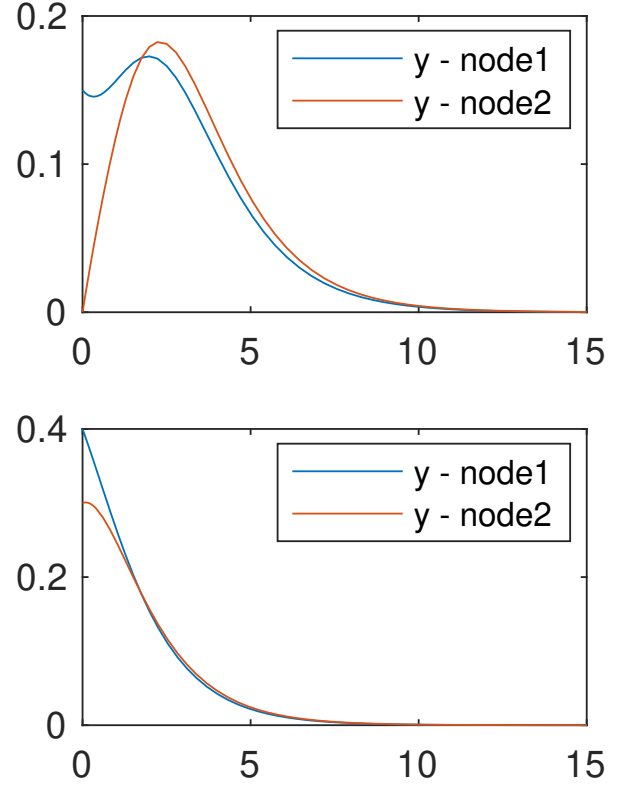

Fig. 1: Simulations of the network SIR model in a homogeneous network in two different cases. On the top, the initial conditions are $(x_1(0) = 0.85 = 1 - y_1(0)$ and $x_2(0) = 1$ $y_2(0) = 0$, the transmission rare is $\beta = 1$, the recovery rate is $\gamma = 0.95$. On the bottom, the initial conditions are $(x_1(0) = 0.6 = 1 - y_1(0)$ and $x_2(0) = 0.7 = 1 - y_2(0)$, the transmission rate is $\beta = 0.65$ and the recovery rate is $\gamma = 1$.

network of two nodes: the curve of the infected in the first node is initially decreasing, then it becomes increasing to a peak of infection, and then decreasing to 0. We have considered a population characterized by a small initial fraction of infected individuals, such as to cause an exponential decrease to 0 if it were isolated, using the scalar SIR epidemic model theory. But if this first population meets a totally healthy one, it begins to infect it and then suffers a return wave of infection with a second peak (the first one is in its initial condition). However, the second plot shows a scenario in which initial conditions satisfies the condition in (9) and the infected curve in both nodes has a classic behavior.

Still considering the case of a graph consisting of only two nodes, it may be interesting to expand the analysis to an arbitrary, non-homogeneous network. In Figure 2, we can observe simulations on these networks and the remarkable thing is that: in addition to the previously observed behaviors, the second simulation also shows a bimodal behavior for the infected curve in the first node, with two local maxima points. In Figure 3, we can observe that by increasing the number of nodes, multimodal behaviors at the single node level can occur.
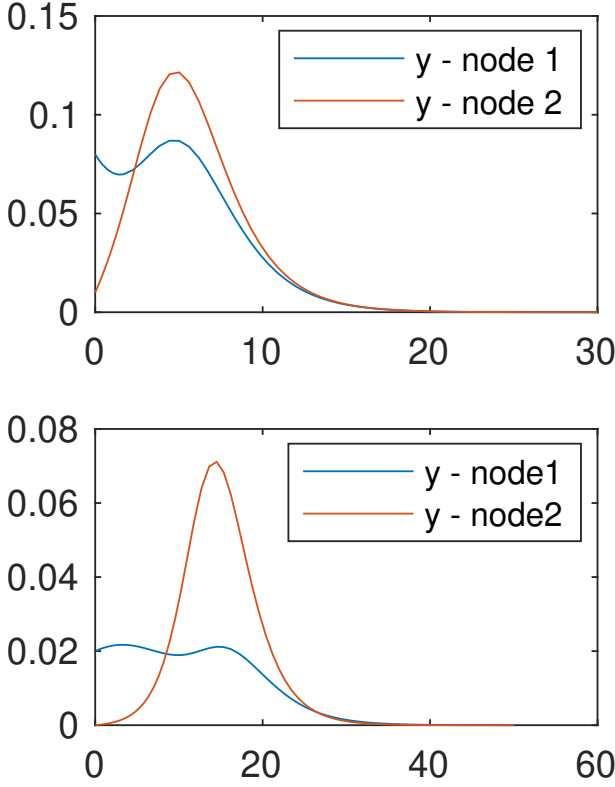
Fig. 2: Numerical simulations of the network SIR model in a non-homogeneous network in two different cases with transmission rate $\beta = 1$. On the top, $x_1(0) = 0.92 = 1 - y_1(0)$, $x_2(0) = 0.99 = 1 - y_2(0)$, $\gamma = 0.9$, and $A = \begin{pmatrix} 0.8 & 0.5 \\ 0.1 & 1.5 \end{pmatrix}$. On the bottom, $x_1(0) = 0.98 = 1 - y_1(0)$, $x_2(0) = 1$, $y_2(0) = 0$, $\gamma = 0.86$, and $A = \begin{pmatrix} [0.93 & 0.08 \\ 0.01 & 1.32 \end{pmatrix}$.

V. Conclusion

In this paper, we have studied the network SIR epidemic model and we have restricted our analysis to a fairly simple scenario: a homogeneous mixing model, in which all contacts have unit weight on a network consisting of only two nodes. We have shown the existence of non-classical behavior in the infected curve at the level of the single node. We have provided a sufficient condition for the occurrence of this atypical behavior and we have guaranteed that the infected curve at single node level can have at most one internal maximum point. In addition, we have shown a sufficient condition for having the unimodal behavior.

Future research will expand the discussion to non-homogeneous arbitrary models trying to define the phenomenon of multiple peaks in the more general cases.
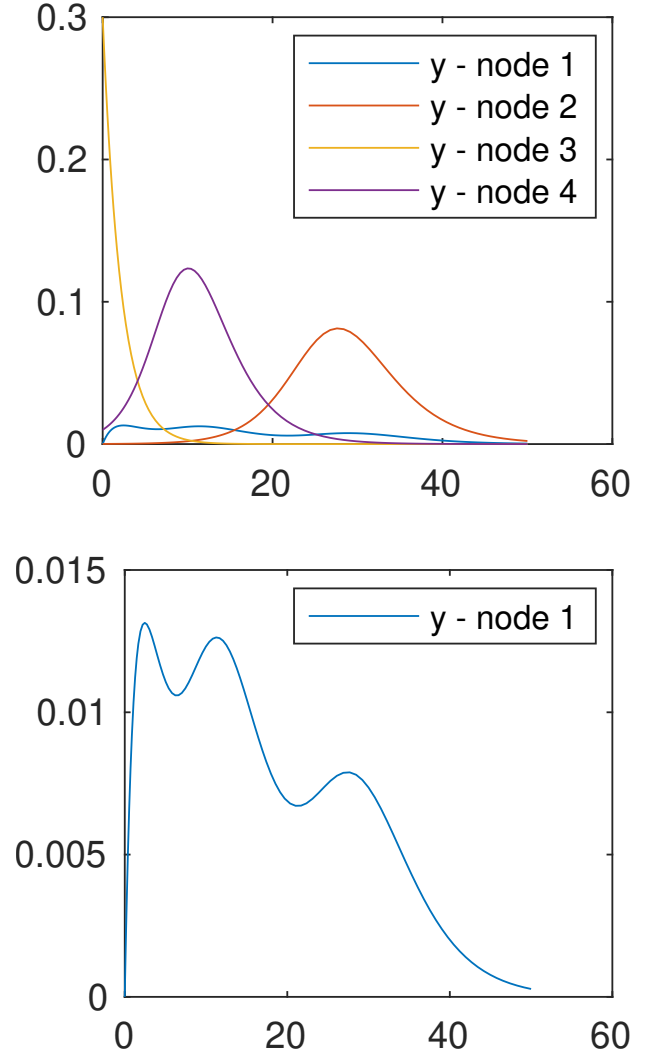
VI. Acknowledgements

Fig. 3: Simulations of the network SIR model in a non-homogeneous network with 4 nodes. Initial conditions are $x_1(0) = x_2(0) = 1$, $y_1(0) = y_2(0) = 0$, $x_3(0) = 0.3 = 1 - y_3(0)$, $x_4(0) = 0.99 = 1 - y_4(0)$, while $\beta = 1$, $\gamma = 0.5$, and $A = \begin{pmatrix} 0.05 & 0.05 & 0.05 & 0.05 \\ 0.0001 & 0.8 & 0.0001 & 0.0001 \\ 0.0001 & 0.0001 & 0.05 & 0.0001 \\ 0.0009 & 0.0009 & 0.0009 & 0.0009 \end{pmatrix}$.

References

[1] W. O. Kermack and A. G. McKendrick, "A contribution to the mathematical theory of epidemics," *Proceedings of the Royal Society of London. Series A*, vol. 115, no. 772, pp. 700–721, 1927.

[2] L. Cianfanelli, F. Parise, D. Acemoglu, G. Como, and A. Ozdaglar, "Lockdown interventions in the SIR model: Is the reproduction number the right control variable?" in *Proceedings of the 60th IEEE Conference on Decision and Control (CDC 2021)*. IEEE, 2021, pp. 4254–4259.

[3] L. Miclo, D. Spiro, and J. Weibull, "Optimal epidemic suppression under an ICU constraint," *Journal of Mathematical Economics*, vol. 101, p. 102669, 2022.

[4] H. W. Hethcote, "An immunization model for a heterogeneous population," *Theoretical Population Biology*, vol. 14, no. 3, pp. 338–349, 1978.

[5] F. Parino, L. Zino, M. Porfiri, and A. Rizzo, "Modelling and predicting the effect of social distancing and travel restrictions on covid-19

spreading," *Journal of the Royal Society Interface*, vol. 18, no. 175, p. 20200875, 2021.

[6] M. Alutto, G. Como, and F. Fagnani, "On sir epidemic models with feedback-controlled interactions and network effects," *2021 60th IEEE Conference on Decision and Control (CDC 2021)*, pp. 5562–5567, 2021.

[7] J. R. Birge, O. Candogan, and Y. Feng, "Controlling epidemic spread: reducing economic losses with targeted closures," *Management Science*, vol. 68, no. 5, pp. 3175–3973, 2022.

[8] D. Acemoglu, V. Chernozhukov, I. Werning, and M. D. Whinston, "Optimal targeted lockdowns in a multigroup sir model," *American Economic Review: Insights*, vol. 3, no. 4, pp. 487–502, 2021.

[9] W. Mei, S. Mohagheghi, S. Zampieri, and F. Bullo, "On the dynamics of deterministic epidemic propagation over networks," *Annual Reviews in Control*, vol. 44, pp. 116–128, 2017.

[10] G. Ellison, "Implications of heterogeneous sir models for analyses of covid-19," National Bureau of Economic Research, Working Paper 27373, June 2020.

[11] C. Nowzari, V. M. Preciado, and G. J. Pappas, "Analysis and control of epidemics: A survey of spreading processes on complex networks," *IEEE Control Systems Magazine*, vol. 36, no. 1, pp. 26–46, 2016.

APPENDIX I
PROOF OF PROPOSITION 2

We start by proving a technical result.

Lemma 1: Consider the network SIR model (3). If

$$\beta(x_1 + x_2) > \gamma,$$

then the set

$$\Omega_1 = \{(x_i, y_i)_i \in [0,1]^4 : -y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2 \leq 0\}$$

is an invariant set for the dynamics.

Proof: Let us consider an initial condition belonging to Ω_1 and let $(x_i(t), y_i(t))_i$ be the corresponding solution. We want to prove that this will belong to Ω_1 for every $t > 0$. Consider an instant $t^* > 0$ such that

$$(x_i(t^*), y_i(t^*))_i \in \delta\Omega_1,$$

where $\delta\Omega_1 = \{(x_i(t), y_i(t))_i \in [0,1]^4 : -y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2 = 0\}$, and $(x_i(t), y_i(t))_i \in \Omega_1$ for every $t < t^*$. Let us define

$$Q(t) = -y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2,$$

and consider its first derivative with respect to time t.

$$\dot{Q}(t) = -\dot{y}_1(y_1 + y_2) - y_1(\dot{y}_1 + \dot{y}_2) + \dot{x}_2 y_1 + $$
$$+ x_2 \dot{y}_1 - \dot{x}_1 y_2 - x_1 \dot{y}_2$$

Notice that at $t = t^*$,

$$\dot{Q}(t^*) = -\beta x_1(y_1 + y_2)^2 + \gamma y_1(y_1 + y_2) - y_1(\dot{y}_1 + \dot{y}_2) + $$
$$- \beta x_2 y_1(y_1 + y_2) + x_2 \dot{y}_1 - \beta x_1 y_2(y_1 + y_2) - x_1 \dot{y}_2$$
$$< \gamma y_1(y_1 + y_2) + \beta x_1 x_2(y_1 + y_2) - \gamma x_2 y_1 + $$
$$- \beta x_1 x_2(y_1 + y_2) + \gamma x_1 y_2 = 0$$

where the first inequality follows from the the positivity of the solution and $\dot{y}_1 + \dot{y}_2 > 0$ by the assumption, while the last equality follows from $Q(t^*) = 0$. Therefore, we have shown that $\dot{Q}(t^*) < 0$. By continuity, we can state that $Q(t)$ is decreasing in a neighborhood of t^*; however by construction, $Q(t) < 0$ for $t < t^*$, therefore it is not possible that $Q(t^*) = 0$ and we have shown the invariance of set Ω_1. Note that a symmetric analysis can be done for the second node. ∎

We can now proceed to the proof of Proposition 2. The analysis is conducted from the perspective of the first node, but Lemma 1 and this proof can be modified from the second node's perspective and symmetric results would be obtained.

We divide the analysis in two possible scenarios, depending on the initial conditions in the first node.

If $\dot{y}_1(0) < 0$, then we can consider two further cases. If $\beta(x_1(0) + x_2(0)) < \gamma$, then by Proposition 3 the set in which the first derivative of $\dot{y}_1$ is negative, is an invariant for the dynamics. Therefore in this case, y_1 will be monotonically decreasing to 0.

If $\beta(x_1(0) + x_2(0)) \geq \gamma$, we have shown the existence of a set of parameters and initial conditions that ensure that y_1 have at least two local maxima. We now show that they cannot be more than two, where one coincides with the initial condition, which means that the infected curve at the single node level can have at most one internal maximum point. Let us consider the second time derivative of y_1,

$$\ddot{y}_1 = \beta \dot{x}_1(y_1 + y_2) + \beta x_1(\dot{y}_1 + \dot{y}_2) - \gamma \dot{y}_1 \tag{11}$$

Let t_1 be the time instant at which $\dot{y}_1 = 0$ for the first time. Observe that the first time derivative of y_1 at t_1 will be the following

$$\ddot{y}_1(t_1) = -\beta^2 x_1(y_1 + y_2)^2 + \beta^2 x_1 x_2(y_1 + y_2) - \gamma \beta x_1 y_2$$
$$= -\gamma \beta y_1(y_1 + y_2) + \gamma \beta x_2 y_1 - \gamma \beta x_1 y_2$$

where the equalities follow from the expression of $\dot{y}_2$ and from $\dot{y}_1(t^*) = 0$, i.e. $\beta x_1(y_1 + y_2) = \gamma y_1$. Since the first time derivative starts negative, we can state that

$$\ddot{y}_1(t_1) = \gamma \beta[-y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2] \geq 0$$

Let now t_2 be the time instant at which $\dot{y}_1 = 0$ for the second time and we get that

$$\ddot{y}_1(t_2) = \gamma \beta[-y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2] \leq 0$$

If there were a third time instant t_3 at which the first derivative of y_1 cancels out, it should occur that

$$\ddot{y}_1(t_3) = \gamma \beta[-y_1(y_1 + y_2) + x_2 y_1 - x_1 y_2] \geq 0$$

but this is an absurd for Lemma 1. Note that it is not possible that $\ddot{y}_1(t_2) = 0$ and $\ddot{y}_1(t_3) = 0$ because if $\ddot{y}_1(t_2)$ had been 0, then its first time derivative will be negative, as shown in Lemma 1. Therefore, we have shown that y_1 changes monotonicity at most twice along the solution, i.e. it can have at most one local maxima at which the first time derivative cancels out.

If $\dot{y}_1(0) \geq 0$, there must be an instant t^* in which $\dot{y}_1$ becomes negative since $\lim_{t \to +\infty} y_i(t) = 0$. At that point,

$$\ddot{y}_1(t^*) = \beta \dot{x}_1(y_1 + y_2) + \beta x_1(\dot{y}_1 + \dot{y}_2) - \gamma \dot{y}_1$$
$$= -\gamma \beta y_1(y_1 + y_2) + \gamma \beta x_2 y_1 - \gamma \beta x_1 y_2 \leq 0$$

For similar considerations as previous case, we can state that there can not exist a second instant at which $\dot{y}_1 = 0$. ∎