Deterministic and stochastic mean-field SIRS models on heterogeneous networks

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In this paper we study a model for the spread of an SIRS-type epidemics on a network, both in a deterministic setting and under the presence of a random environment, that enters in the definition of the infection rates of the nodes. Accordingly, we model the infection rates in the form of independent stochastic processes. To analyze the problem, we apply a mean field approximation that is known in the literature as NIMFA model, which allows to get a differential equation for the probability of infection in each node. We discover a sufficient condition which guarantees the extinction of the epidemics both in the deterministic and in the stochastic setting.

I. INTRODUCTION

Differential models for population dynamics are necessary tools to make predictions and analysis in many fields of science, starting from the early contributions in epidemic models due to Kermack and McKendrick [11] which were concerned with the spread of infectious diseases.
The name *epidemic model*, that in the origin was actually referred to the spread of infections in human populations, is currently used to cover the spreading of many other threats in a population, cultural beliefs [5, 25], drug and alcohol addictions [19], as well as digital populations: diffusion of computer viruses and worms, spreading of informations (news, rumors, messages) in on-line social networks [23].

The epidemic models generally assume that individuals are divided into classes that represent the status of the individual itself. The main classes are: susceptibles (S), that are healthy and can contract the infection, infected and infectious (I) and recovered and immune (R). In general, the model assumes that susceptible individuals can get infected, usually, through interaction with other infected individuals. An infected individual remains in such state for a certain period of time, and then recovers: in classical SIS models, the recovered individual returns to the class of susceptibles, while in SIR models it becomes immune for the remaining time (perfect vaccination). In this paper, we consider a SIRS model, that is an intermediate case between SIS and SIR dynamics. The recovered individual receives a temporary immunity, i.e. the immunity wanes after some time (called latency period) before the individual returns to the susceptible class [2]. In order to introduce heterogeneity of the population it is necessary to introduce a network-based approach, where inhomogeneous contact rates and individual responses to the infection are introduced [4, 14, 18].

Under some standard mathematical simplification, we can describe the epidemic spreading using the theory of Markov chains in discrete and continuous time [1]. This approach is often use to describe epidemic models based on their deterministic formulations. In most cases, the deterministic model is a good representation of the process, however, is important to include in the analysis also a stochastic effect in order to cover more realistic situations.
There are different possible way to include stochasticity in the model, both from a mathematical and a biological perspective, one of the approaches is to consider stochastic differential equations [1]. Another way to introduce a stochastic perturbation consists of replacing one or more parameters of the deterministic model by the corresponding stochastic counterparts, indeed, the parameters may have a great variability [6, 16].

Our epidemic spreading process is described by an individual-based mean-field approximation [20]. The idea is to write down the equations of the evolution in time of the probability of every node to be in each class assuming independence between the state of every couples of nodes.
After a mean-field approximation, the non linear system considered has two different solutions, the first is the trivial one that represent the absorbing state, the second is the nonzero steady-state solution called metastable state [13, 20]. This behaviour depends on the effective infection rate $\tau = \beta/\delta$, the ratio between infection rate and curing rate. If this quantity is above a critical threshold τ_c i.e., $\tau > \tau_c$, the infection spreads and there exist a nonzero fraction of infected nodes, while, if $\tau \leq \tau_c$, the epidemic dies out quickly.
Computing the critical threshold for the SIRS mean-field model in the discrete homogeneous case, we observe that it coincides with the critical threshold for the SIS model and the metastable state of the SIRS case is proportional to that of the SIS model.
Throughout the paper we shall discuss the long time behaviour of the solution both in deterministic and stochastic case finding conditions which guarantee the extinction of the epidemics. For the asymptotic stability of the stochastic case we use a result in [17] and we found a sufficient condition for the exponential stability of the solution. Since the condition is only sufficient, in some cases the solution wanes even if the condition is not satisfied; we analyse this behaviour by means of some simulations in a given graph.

The paper is organized as follows. In the Section II we describe the SIRS model in the deterministic case and we introduce the related individual-based mean-field ap-

proximation that we use to obtain a system of differential equation for each node. Then, in Section III we study the behaviour of the solution over time, finding the stability properties of the system obtained. At first, we consider the homogeneous case and we study the epidemic spreading to changing the effective infection rate which is the ratio between the infection rate β and the recovery rate δ. Then we extend the results to the heterogeneous setting. In Section V we include stochasticity in the parameters of the model, we prove that the unique global solution remains in $(0,1)^{3N}$ whenever it starts from this region and we study the stability properties. Finally, in Section IV we provide some numerical results for the heterogeneous case in order to better investigate the behaviour of the solution.

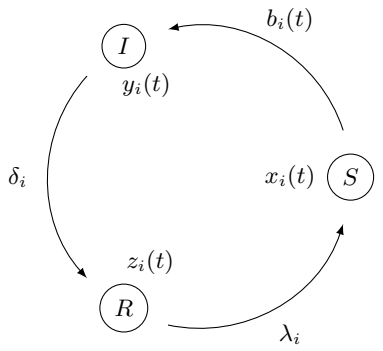


FIG. 1. State transition diagram for node v_i

II. THE DETERMINISTIC MODEL

The spatial structure of the population is encoded by a *network*, i.e., an undirected graph $G(E,V)$ with set of vertices (nodes) $V = \{\mathsf{v}_1, \dots, \mathsf{v}_N\}$ (N being the total amount of the population) and set of links E. The geometry of the network is described by the symmetric adjacency matrix A, in which the element $a_{ij} = a_{ji}$ is either 1 if the nodes v_i and v_j are connected, or 0 otherwise. We shall further denote d_i the degree of the node v_i.

In a classical SIS model, the state of an individual at time t is represented by a Bernoulli random variable $X_i(t)$, where $X_i = 0$ represents the healthy, susceptible state and $X_i = 1$ the infected state. Therefore, the state of the system can be represented by the quantity $p_i(t) = \mathbb{P}(X_i(t) = 1)$, which represents the probability that the i-individual is infectious at time t.
On the other hand, in a SIRS model the random variable $X_i(t)$ needs to take three different values (which represent the states S, I and R, respectively) and the state is described by three quantities, $x_i(t) = \mathbb{P}(X_i(t) = S)$, $y_i(t) = \mathbb{P}(X_i(t) = I)$ and $z_i(t) = \mathbb{P}(X_i(t) = R)$. The total probability theorem implies that

$$x_i(t) + y_i(t) + z_i(t) = 1 \tag{1}$$

for every time $t \geq 0$.
The infection of an individual i is a Poisson process with rate $b_i(t)$ which depends on the state of the other individuals. More precisely, the probability that a node i in a susceptible state receives infections from its neighbors is given by

$$b_i(t) = 1 - \prod_{j:j \text{ neighbors of } i} (1 - \beta_j y_j(t)),$$

where β_j is the rate at which individual j tries to infect its neighbors. By means of the adjacency matrix A, previous expression becomes

$$b_i(t) = 1 - \prod_{j=1}^{N} (1 - a_{ij}\beta_j y_j(t)). \tag{2}$$

We assume that the curing process per the node v_i is a Poisson process with rate δ_i, and that the period of latency is exponentially distributed with rate λ_i, All involved Poisson processes are independent.

We are thus lead to the following *mean field* model for the SIRS epidemics

$$\begin{cases} x_i'(t) = -b_i(t)x_i(t) + \lambda_i z_i(t) \\ y_i'(t) = b_i(t)x_i(t) - \delta_i y_i(t) \\ z_i'(t) = \delta_i y_i(t) - \lambda_i z_i(t) \end{cases} \tag{3}$$

Obviously, it is sufficient to solve just two of them, thanks to (1).

A justification of Eq.(3) can be given in terms of a mean-field approximation for the exact Markov process on the space $\{S,I,R\}^N$, following the ideas in [20]. For instance, the exact Markovian equation governing the state of individual i implies that the transition probability for the node v_i to move from the susceptible to the infected state is given by

$$B_i(t) = 1 - \prod_{j=1}^{N} \left(1 - \beta_j a_{ij} \mathbf{1}_{X_j(t)=I}\right)$$

where the indicator function is 1 if the node v_j is in the state I at time t and it is 0 otherwise. Therefore, this coupling is a random variable, and the process is, in some sense, "doubly stochastic" and actually not Markovian. Van Mieghem [20, 21] proposed to replace the actual, random infection rate $B_i(t)$ with its average $b_i(t)$, which can be interpreted as a mean-field approximation of the exact model.
A different, but related, justification of Eq.(3) can be given by taking expectation in the governing equation of transition rate for the Markov process on the space $\{S,I,R\}^N$. The equation for the probability of node i

being in state I is given by

$$\frac{d}{dt}\mathbb{E}[\mathbf{1}_I(X_i(t))] = \mathbb{E}\left[-\delta_i \mathbf{1}_I(X_i(t)) + \mathbf{1}_S(X_i(t))1 - \prod_{j=1}^{N}\left(1-\beta_j a_{ij}\mathbf{1}_{X_j(t)=I}\right)\right]$$

As one can see, the equation contains the joint probabilities for the random variables $X_i(t)$. Therefore, the system does not contain enough equations for getting a solution. However, instead of adding more and more equations, which should allow to solve also for the joint probabilities, we propose to close the system by assuming independence between the infection state of every couple of nodes. This approximation is also called a mean-field approximation [24].
It shall be noticed that this second approach leads to a model which is formally defined by Eq.(3), but in this case the coefficients $b_i(t)$ have a different expression, i.e.,

$$\tilde{b}_i(t) = \sum_{j=1}^{N} a_{ij}\beta_j y_j(t).$$

We shall often use, in the sequel, the following observation.

Remark 1. *The function $\tilde{b}_i(t)$ is a first-order approximation of $b_i(t)$ for small values of the parameters β.*

III. THE CRITICAL THRESHOLD

Since the early models, it is known that the time behavior of an epidemics' spreading depends on the ratio $\tau = \beta/\delta$ between infection rate over the curing rate[**?**]: if this quantity is below a critical threshold τ_c then the epidemics dies out exponentially fast, otherwise the epidemics becomes endemic in the population, meaning that there exists a positive lower bound on the probability of being infected [15].
It is our interest to extend the above result to a spatially structured population. In the analysis of a SIS epidemics in an homogeneous population, the analysis in [20] provides the determination of the epidemic threshold $\tau_c = 1/\lambda_1$ of the mean-field N-intertwined model as the inverse of the largest eigenvalue λ_1 of the adjacency matrix A. It is our aim the extension of this result to the SIRS epidemic model.

In the first part of this section, we provide a sufficient condition for the epidemics to die out exponentially fast. In order to simplify the analysis, we explicitly solve the steady state problem associated to (3) in case of constant parameters β, δ and λ. Actually, it becomes necessary to solve the system

$$\begin{cases} y_i'(t) = (1 - y_i(t) - z_i(t))\, b_i(t) - \delta y_i(t) \\ z_i'(t) = \delta y_i(t) - \lambda z_i(t) \end{cases} \tag{4}$$

Since both functions $y_i(t)$ and $z_i(t)$ take values in $[0,1]$, we can bound the first equation as

$$\begin{cases} y_i'(t) \leq 1 - \prod_{j=1}^{N}(1 - a_{ij}\beta y_j(t)) - \delta y_i(t) \\ z_i'(t) = \delta y_i(t) - \lambda z_i(t) \end{cases}$$

Taking into account the first order expansion of the product in previous formula, i.e.,

$$\prod_{j=1}^{N}(1 - a_{ij}\beta y_j(t)) \geq 1 - \sum_{j=1}^{N} a_{ij}\beta y_j(t)$$

we obtain the following

$$\begin{cases} y_i'(t) \leq \beta \sum_{j=1}^{N} a_{ij} y_j(t) - \delta y_i(t) \\ z_i'(t) = \delta y_i(t) - \lambda z_i(t) \end{cases} \tag{5}$$

Define the vector $\eta = (y_1, \ldots, y_n, z_1, \ldots, z_n)^\star \in \mathbb{R}^{2n}$ and consider the block matrix

$$C = \left(\begin{array}{c|c} \beta A - \delta I_n & 0 \\ \hline \delta I_n & -\lambda I_n \end{array}\right)$$

We consider the differential systems

$$\begin{aligned} \eta'(t) &\leq C\eta(t) \\ \eta(0) &= \eta_0 \end{aligned} \tag{6}$$

and

$$\begin{aligned} \tilde{\eta}'(t) &= C\tilde{\eta}(t) \\ \tilde{\eta}(0) &= \eta_0 \end{aligned} \tag{7}$$

Let us recall that a comparison principle for linear equations implies that for $0 \leq \eta_{0;i} \leq 1$ then $0 \leq \eta_i(t) \leq \tilde{\eta}_i(t)$ for every $t > 0$. Moreover, the null solution of the linear differential system (7) is asymptotically stable if and only if the real parts of every eigenvalue of C is negative.

Theorem 1. *Assume that the ratio $\tau = \beta/\delta$ satisfies*

$$\tau < 1/\lambda_1(A). \tag{8}$$

Then the SIRS epidemic model (3) *vanishes exponentially fast for every possible initial condition.*

The proof follows from the analysis of the eigenvalues of the matrix C. The real parts of every eigenvalue of C have to be negative.
Using the properties of block matrices we have that the eigenvalues of C are: $-\lambda$, coming from the second block on the diagonal, that is negative, and

$$\lambda_i(\beta A - \delta I_n) = \beta\lambda_i(A) - \delta$$

and, in order to get the asymptotically stability we have to impose the following condition

$$\lambda_1(\beta A - \delta I_n) = \beta\lambda_1(A) - \delta < 0$$

which reads

$$\frac{\beta}{\delta} < \frac{1}{\lambda_1(A)}.$$

We see that the presence of a latency period does not affect the critical threshold. We then proceed to analyse how the latency rate λ influence the model above threshold.
Our aim is the computation of the steady-state vector $\eta_\infty(y_1,\dots,y_n,z_1,\dots,z_n)^\star \in \mathbb{R}^{2n}$ that satisfies

$$\begin{cases} 0 = (1-y_i-z_i)\, b_i - \delta y_i \\ 0 = \delta y_i - \lambda z_i \end{cases} \tag{9}$$

where

$$b_i = 1 - \prod_{j=1}^{N} (1 - a_{ij}\beta y_j).$$

We can assume that near the critical threshold the steady-state has the form

$$\eta = \varepsilon\tilde{\eta},$$

where $\tilde{\eta}$ is a vector with all positive elements (compare e.g. [22]). Then we proceed to analyse Eq.(9). Using the second equation in system (9) we obtain that the system is determined by the value of the projection of η on the first n components: $Y = (y_1,\dots,y_n)^\star$

$$\delta y_i = (1 - (1 + \frac{\delta}{\lambda}) y_i)\, b_i$$

We expect $y_i = \varepsilon\tilde{y}_i$, hence we perform an asymptotic expansion in the small parameter ε;

$$\delta\varepsilon\tilde{y}_i = (1 - \varepsilon(1+\frac{\delta}{\lambda})\tilde{y}_i) \left(\sum_{j=1}^{N} \beta a_{ij} \varepsilon \tilde{y}_j + O(\varepsilon^2) \right).$$

If we simplify previous expression and take the limit for $\varepsilon \to 0$, we see that under condition (8) there exists only the null solution to previous equation, while a non trivial stable state $\eta = \varepsilon\tilde{\eta}$ exists if τ is larger than the critical threshold. We summarise what we've found in the following

Theorem 2. *Under condition* (8)*, there exists only one stable solution for the SIRS model* (3) *that is the trivial one, and the system converges to the trivial solution exponentially fast.*
If the ratio $\tau = \beta/\delta$ satisfies $\tau > 1/\lambda_1(A)$, then the trivial steady state is unstable and there exists a non-trivial steady state η_∞ that is asymptotically stable.

A. Computing the meta-stable state

In this section we are interested in the computation of the meta-stable state for the SIRS model (3) in the over-critical case $\tau > 1/\lambda_1(A)$. We shall provide a description of the situation in either the case described by the mean field model with infection rate $b_i(t)$ and in the first order approximation $\tilde{b}_i(t)$.
At first, we give an explicit formula for the solution in the case of the approximating infection rate $\tilde{b}_i(t)$. In order to compute the value of $\eta_\infty = (Y,Z)^\star$, we consider the system

$$\begin{cases} 0 = (1-y_i-z_i)\, \tilde{b}_i - \delta y_i \\ 0 = \delta y_i - \lambda z_i \end{cases} \tag{10}$$

Then, by the second equation we get that

$$z_i = \frac{\delta}{\lambda} y_i$$

and we arrive at the equation

$$\delta y_i = \left(1 - \left(1 + \tfrac{\delta}{\lambda}\right) y_i\right) \beta (AY)_i$$

Let us introduce $\lambda^* = 1 + \frac{\delta}{\lambda}$; then a little algebra leads to

$$\lambda^* y_i = 1 - \frac{1}{1 + \tau(A\lambda^* y)_i}$$

The above system for the unknowns $Y = (y_1,\dots,y_n)$ can be solved by means of a recursive argument

$$\lambda^* y_i^{(k+1)} = 1 - \frac{1}{1 + \tau(A\lambda^* y^{(k)})_i}$$

which, even after a few iterations, gives a good approximation of the exact value. Moreover, we recognize the above formula from the analog computation in the SIS case [21].
A similar computation can be made for the SIRS model described in model (3) with infection rate $b_i(t)$.
We aim to emphasize that the first order approximation shows a good agreement with the mean field model. Let us consider for instance the spread of an SIRS epidemics on the network plotted in Fig. 3(a), which corresponds to a graph with $|V| = 18$ nodes and $|E| = 25$ vertices. In Fig.2 we provide a numerical computation for the overall percentage of infected individuals in the meta-stable state for the mean field approximation model (with coefficients $b_i(t)$) and its first order approximation (with coefficients $\tilde{b}_i(t)$). It is apparent that these models share the same qualitative features.

Theorem 3. *The average incidence of the epidemics for the SIRS model, in the over-threshold case $\tau > 1/\lambda_1(A)$ (that coincides with the critical region for the SIS model), is equal to that of the SIS model rescaled by a factor $\frac{\lambda}{\lambda+\delta} < 1$ which depends on the latency rate λ.*

In the meta-stable state, the average number of susceptible, infected and recovered individuals is given by,

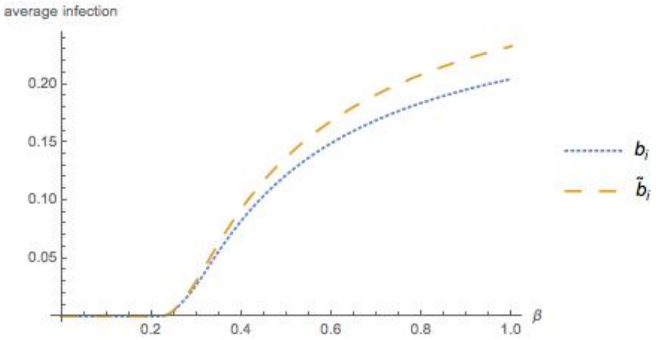


FIG. 2. In this graph, we plot the overall infected individuals in the meta-stable state as the (uniform) infection rate in the nodes β varies between 0 and 1, in either the case of mean field approximation model (with coefficients $b_i(t)$) and its first order approximation (with coefficients $\tilde{b}_i(t)$). The underlying network is depicted in Fig. 3(a). The other parameters are $\delta = 1$ (arbitrary units), $\lambda = 0.5$ (latency period is the double of the curing period). Critical threshold $\tau_c = 1/\lambda_1(A) = 0.24263$

respectively,

$$S = \sum_{i=1}^{n} x_i(t) = N\left(1 - \frac{\lambda+\delta}{\lambda}\frac{I}{N}\right),$$
$$I = \sum_{i=1}^{n} y_i(t), \qquad R = \sum_{i=1}^{n} z_i(t) = \frac{\delta}{\lambda} I.$$

For a latency period going to 0 (which corresponds to $\lambda \to \infty$) we get that the SIRS model converges to the SIS model; conversely, if $\lambda \to 0$ (there is no return to the susceptible state), then the quantity of infected individuals converges to 0, as in the SIR model.

B. The heterogeneous case

In this section we extend the above result to the heterogeneous setting, where we include the possibility for both the infection rates and the curing rates to be different for each node. As we have seen before, in this case, the governing equation is given by system (3). Actually, it is necessary to solve

$$\begin{cases} y_i'(t) = (1 - y_i(t) - z_i(t))\, b_i(t) - \delta_i y_i(t) \\ z_i'(t) = \delta_i y_i(t) - \lambda_i z_i(t) \end{cases} \tag{11}$$

Taking into account that $y_i(t)$ and $z_i(t)$ take values in $[0, 1]$ and considering the first order expansion of the product in $b_i(t)$ i.e.

$$\prod_{j=1}^{N}(1 - a_{ij}\beta y_j(t)) \geq 1 - \sum_{j=1}^{N} a_{ij}\beta y_j(t)$$

we obtain a generalization of the system (5)

$$\begin{cases} y_i'(t) \leq \sum_{j=1}^{N} a_{ij}\beta_j y_j(t) - \delta_i y_i(t) \\ z_i'(t) = \delta_i y_i(t) - \lambda_i z_i(t) \end{cases}$$

As in the homogeneous case we consider the block matrix

$$C = \left(\begin{array}{c|c} A\,\mathrm{diag}(\beta_i) - \mathrm{diag}(\delta_i) & 0 \\ \hline \mathrm{diag}(\delta_i) & -\mathrm{diag}(\lambda_i) \end{array}\right)$$

and the differential systems

$$\begin{aligned} \eta'(t) &\leq C\eta(t) \\ \eta(0) &= \eta_0 \end{aligned} \tag{12}$$

and

$$\begin{aligned} \tilde{\eta}'(t) &= C\tilde{\eta}(t) \\ \tilde{\eta}(0) &= \eta_0 \end{aligned} \tag{13}$$

In order to understand when the null solution of the linear differential system (13) is asymptotically stable we analyse the eigenvalue of the matrix C. We have to study when the real part of every eigenvalue of C is negative. For the property of the block matrix it is sufficient to understand when the matrix $A\mathrm{diag}(\beta_i) - \mathrm{diag}(\delta_i)$ is semidefinite negative.
Since the sign of the matrix $A\mathrm{diag}(\beta_i) - \mathrm{diag}(\delta_i)$ is equivalent to that of the matrix $A - \mathrm{diag}(\delta_i/\beta_i)$, a sufficient condition for this matrix to be (semi-)negative defined is

$$\lambda_1(A) \leq \min\left\{\frac{\delta_i}{\beta_i}\right\} \tag{14}$$

We can improve previous estimate. Recall that the discrete Laplacian operator $\mathcal{L} = \mathrm{diag}(\mathsf{d}(\mathsf{v}_i)) - A$ is semidefinite positive, where $\mathsf{d}(\mathsf{v})$ is the degree of vertex v [22]; hence, writing

$$\begin{aligned} &A - \mathrm{diag}(\delta_i/\beta_i) \\ &\quad = [A - \mathrm{diag}(\mathsf{d}(\mathsf{v}_i))] + [\mathrm{diag}(\mathsf{d}(\mathsf{v}_i)) - \mathrm{diag}(\delta_i/\beta_i)] \end{aligned}$$

we obtain the following sufficient condition for the matrix $A\mathrm{diag}(\beta_i) - \mathrm{diag}(\delta_i)$ to be (semi-)negative defined:

$$\max\left\{\mathsf{d}(\mathsf{v}_i) - \frac{\delta_i}{\beta_i}\right\} \leq 0 \tag{15}$$

For a regular graph, say of degree $\mathsf{d}(\mathsf{v}) = r$, it holds that $\lambda_1(A) = r$, which means that conditions (14) and (15) coincide.

Remark 2. *In order to justify our preference for condition* (15)*, we propose the following problem. We are given a population, whose spatial structure is described by a graph G with adjacency matrix A. Assume that the infection rates are constant throughout the population at a level β. Assume that a cure is available, and can be distributed to the population, with a cost for each individual*

that is proportional to the efficiency (measured in terms of the rate δ_i). Then, according to the policy in (14)*, it is necessary to distribute (pay) a quantity proportional to $N\lambda_1(A)$ units in order to guarantee the vanishing of the epidemics.*
However, according to the policy in (15)*, the total cost of the cure is proportional to $\sum_{i=1}^{N} \mathsf{d}(\mathsf{v}_i)$. Since $N\lambda_1(A) \geq \sum_{i=1}^{N} \mathsf{d}(\mathsf{v}_i)$ (compare [22, Eq.(3.31)]), it follows that condition* (15) *is globally better than* (14)*.*

Now, we compute the metastable state for the SIRS model in the heterogeneous case. We consider the system

$$\begin{cases} 0 = (1 - y_i - z_i)\,\tilde{b}_i - \delta y_i \\ 0 = \delta_i y_i - \lambda_i z_i \end{cases} \tag{16}$$

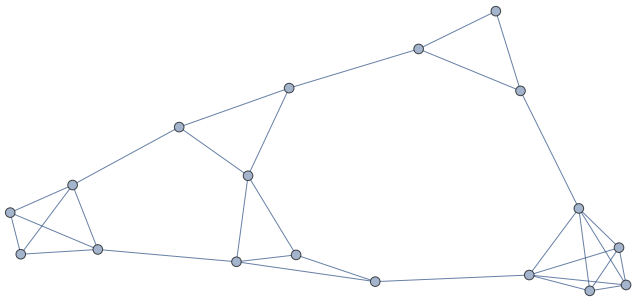
from which we get

$$\delta_i y_i = \left(1 - \left(1 + \tfrac{\delta_i}{\lambda_i}\right) y_i\right) \sum_{j=1}^{N} a_{ij}\beta_j y_j$$

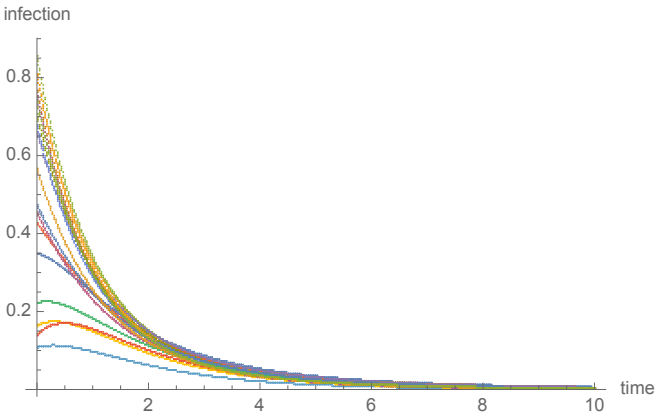
that yields the nodal steady state equation

$$\sum_{j=1}^{N} a_{ij}\beta_j y_j = \frac{\delta_i y_i}{1 - \left(1 + \tfrac{\delta_i}{\lambda_i}\right) y_i}$$

We recognize the above formula from the heterogeneous SIS case [21, Eq.(6)]. In particular, we see that for a latency period going to 0 (which corresponds to $\lambda \to \infty$) we get that the SIRS model converges to the SIS model.



(a)The model network for this simulation. It contains $|V| = 18$ nodes and $|E| = 25$ edges



(b)Total rate of infection for the above network in the under-threshold regime

FIG. 3. In (b), the rate of infection in the network provided in (a) as a function of time, for different values of the initial infection rate. In the simulation we fix $\delta = 1$, $\lambda = .5$ and we choose arbitrary values β_i such that $\max\{\beta_i\} \leq \frac{1}{\lambda_1(A)} = 0.242431$

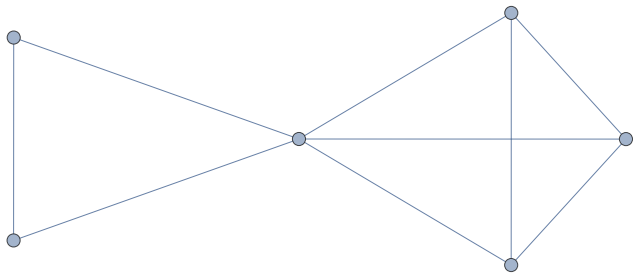
IV. SIMULATIONS FOR THE DETERMINISTIC HETEROGENEOUS CASE

In the first example, described in Figure 3, we consider the sufficient condition (14). We associate to every node a different value of the infection rate β_i chosen arbitrarily in the interval $(0.1, 0.23)$. The sufficient condition for stability, stated in (14), is $\max\{\beta_i\} \leq \frac{1}{\lambda_1(A)} = 0.242431$; therefore, our system is in the under-threshold regime. The simulation shows that the epidemic level decreases to zero uniformly in the whole network.

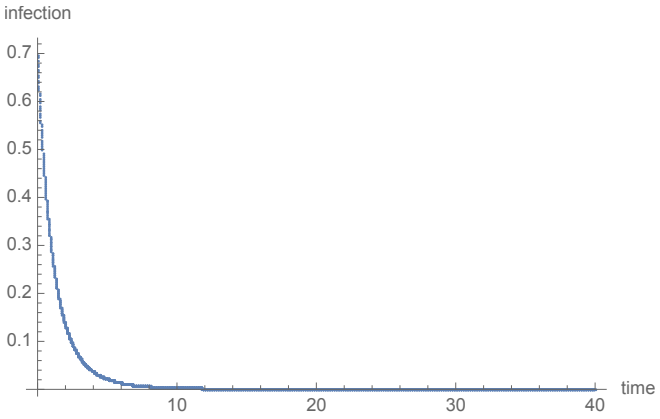
The next example shows that the sufficient conditions (15) and (14) are not necessary. Consider the simple graph in Figure 4. We observe the following behaviours, according to the different values of the parameters β_j: when the sufficient condition (15) is verified, then the graph converges exponentially fast to the zero solution (absence of infection). Otherwise, the topological structure of the graph shall play a rôle. In both the examples depicted in Fig. 5, the system does not satisfy the sufficient conditions above. As far as condition (14) is concerned, we have $\frac{1}{\lambda_1(A)} = 0.306579$ but $\max\{\beta_i\} = 0.8$, hence the inequality is not satisfied. Moreover, condition (15) requires $\max\{\beta_i \mathsf{d}(\mathsf{v}_i)\} \leq 1$. Since in (a): $\beta_4 \mathsf{d}(\mathsf{v}_4) = 4$ while in (b) $\beta_6 \mathsf{d}(\mathsf{v}_6) = 1.6$, condition (15) fails to hold too.
However, in the case in Figure 5(a), when the central node has a large infectivity rate, the system converges to a metastable state where the average infection rate of the nodes is positive ($\bar{y} = 0.0235458$), while in case (b), when the large infectivity rate is associated with a peripheral node, the system converges to zero.

V. STOCHASTIC SIRS MODEL

In order to make things formal, we shall introduce a standard n-dimensional Brownian motion $W(t) = (w_1(t), ..., w_n(t))$ defined on a stochastic basis $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}, \mathbb{P})$ that satisfies the standard assumptions.
In the epidemiology literature, despite the potential importance of the environmental noise, stochastic models have received relatively little attention. In the aggregated models, there are mainly two ways to introduce a

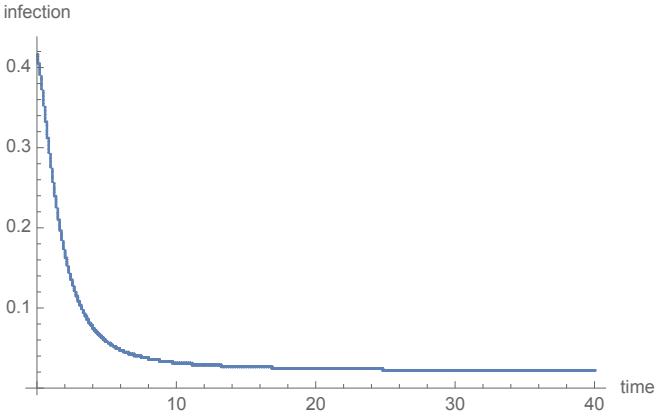


(a)The model network for this simulation. It contains $|V| = 6$ nodes and $|E| = 9$ edges

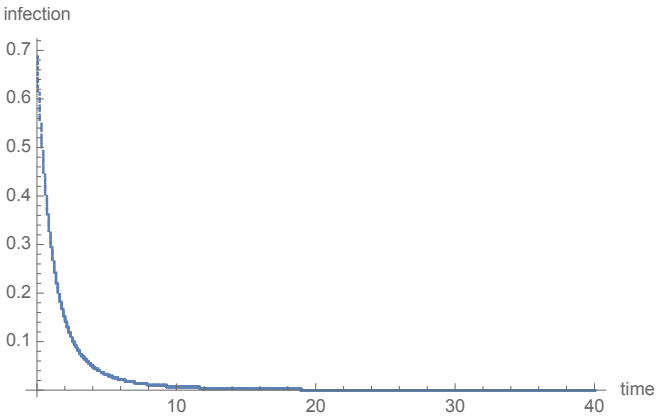


(b)Total rate of infection for the above network in the under-threshold regime

FIG. 4. In the simulation we fix $\delta = 1$, $\lambda = .5$ and the we choose arbitrary values β_i such that $\max\{\beta_i\} \leq \frac{1}{\lambda_1(A)} = 0.306579$



(a)Total rate of infection in the network in Fig. 4(a) when the central node is highly infective



(b)Total rate of infection in the network in Fig. 4(a) when only a peripheral node is highly infective

FIG. 5. In the simulation we fix $\delta = 1$, $\lambda = .5$. In (a) we consider all $\beta_i = 0.2$ except $\beta_4 = 0.8$ (v_4 is the central node). The system converges to a meta-stable state. In (b) we consider all $\beta_i = 0.2$ except $\beta_6 = 0.8$ (v_6 is the rightmost node). The system converges to the null state. Sufficient conditions for stability: (14) means $\max\{\beta_i\} \leq \frac{1}{\lambda_1(A)} = 0.306579$, which fails to hold, while condition (15) requires $\max\{\beta_i \mathsf{d}_i\} \leq 1$. Since $\mathsf{d}_6 = 2$, condition (15) fails to hold too.

stochastic perturbation. In the first, one replaces one or more of the parameters of the deterministic model by the corresponding stochastic counterparts (see for instance [16]). In a second way, one can add randomly fluctuation affecting directly the deterministic model (see for instance [9, 10]).

Here, we consider the mean field model for the SIRS epidemics (3), and we assume that the infection rate $b_i(t)$ is perturbed by a stochastic term having the form $\sigma_i \frac{y_i(t)}{1+\alpha y_i(t)} \dot{w}_i(t)$ (compare system (2) in [12] or [6]), thus leading to the stochastic differential system

$$\begin{cases} \mathrm{d}x_i(t) = [-b_i(t)x_i(t) + \lambda_i z_i(t)]\,\mathrm{d}t - \sigma_i \dfrac{x_i(t)y_i(t)}{1+\alpha y_i(t)}\,\mathrm{d}w_i(t) \\ \mathrm{d}y_i(t) = [b_i(t)x_i(t) - \delta_i y_i(t)]\,\mathrm{d}t + \sigma_i \dfrac{x_i(t)y_i(t)}{1+\alpha y_i(t)}\,\mathrm{d}w_i(t) \\ \mathrm{d}z_i(t) = [\delta_i y_i(t) - \lambda_i z_i(t)]\,\mathrm{d}t \end{cases} \tag{17}$$

We shall denote $P(t) = \big(\underline{x}(t), \underline{y}(t), \underline{z}(t)\big)$ the solution of (17) with the standard notation $\underline{x} = (x_1, \ldots, x_n)$.

Remark 3. *In* (17) *we have chosen the stochastic perturbation term in such a way that the disturbance is small provided that the state of the node is far from infection. This also implies the viability of the system in the set* $[0,1]^{3N}$*, since a diffusion coefficient independent of the infection level would have implied a stochastic variability also near the zero level, thus allowing the solution to go below zero, which does not have any physical meaning.*

Theorem 4. *For any initial condition* $(\underline{x}, \underline{y}, \underline{z}) \in D := (0,1)^{3N}$ *the solution of system* (17) *has an infinite lifespan and, moreover, it remains inside the domain* D *for all times, almost surely.*

Since the coefficients of the equation are locally Lipschitz continuous, for any given initial value $P(0) = (\underline{x}, \underline{y}, \underline{z})$ there is a unique local solution on $t \in [0, \tau_e)$,

where τ_e is the explosion time (see for instance [3]).
To show this solution is global, we need to show that $\tau_e = \infty$ a.s. This is achieved if we prove a somehow stronger property of the solution, namely that it never leaves the domain D. The following computations are somehow standard (compare for instance [6]). Let $N_0 > 0$ be sufficiently large for $p_i(0) \geq \frac{1}{N_0}$, $p \in \{x, y, z\}$, for all $i = 1, \dots n$. For each integer $N \geq N_0$, define the stopping time

$$\tau_N = \inf \left\{ t \in [0, \tau_e) : \inf_{p \in \{x,y,z\}, i \in \{1,\dots,n\}} p_i(t) < 1/N \right\},$$

where, as customary, $\inf \emptyset = +\infty$ (with $\emptyset$ denoting the empty set).
Clearly τ_N is increasing as $N \to \infty$ and letting $\tau_\infty = \lim_{n\to\infty} \tau_N$, we have $\tau_\infty \leq \tau_e$ a.s. Hence we basically need to show that $\tau_\infty = \infty$ a.s; if this were not so, there would exists a pair of constants $T > 0$ and $\epsilon \in (0, 1)$ such that

$$\mathbb{P}\{\tau_\infty \leq T\} > \epsilon.$$

Accordingly, there is an integer $N_1 \geq N_0$ such that

$$\mathbb{P}\{\tau_N \leq T\} \geq \epsilon/2 \qquad \forall N \geq N_1. \tag{18}$$

Now we define a function $V : D \to \mathbb{R}^+$ as

$$V(P(t)) = -\sum_{i=1}^{n} \log\left[x_i(t) y_i(t) z_i(t)\right].$$

By Itô's formula we have

$$\begin{aligned} \mathrm{d}V(P(t)) = &\sum_{i=1}^{n} \left(b_i(t) + \delta_i + \lambda_i + \frac{1}{2}\sigma_i^2 \frac{x_i(t)^2 + y_i(t)^2}{(1 + \alpha y_i(t))^2} \right. \\ &\left. -\lambda_i \frac{z_i(t)}{x_i(t)} - b_i(t)\frac{x_i(t)}{y_i(t)} - \delta_i \frac{y_i(t)}{z_i(t)} \right) \mathrm{d}t \\ &+ \sum_{i=1}^{n} \sigma_i \frac{y_i(t) - x_i(t)}{1 + \alpha y_i(t)} \, \mathrm{d}w_i(t) \end{aligned}$$

Therefore, in $[0, \tau_N)$ we have, by using the positivity of the components of $P(t)$, and the simple bounds $b_i(t) \leq 1$ and $x_i^2 + y_i^2 \leq 2$:

$$\begin{aligned} V(P(t)) - V(P(0)) \leq &\sum_{i=1}^{n} \left(1 + \delta_i + \lambda_i + \sigma_i^2\right) t \\ &+ M(t) \end{aligned} \tag{19}$$

where $M(t)$ is the (local) martingale defined by

$$M(t) = \sum_{i=1}^{n} \sigma_i \int_0^t \frac{y_i(s) - x_i(s)}{1 + \alpha y_i(s)} \, \mathrm{d}w_i(s).$$

Taking the expectation in (19) we arrive to

$$\begin{aligned} \mathbb{E}[V\left(P(\tau_n \wedge T)\right)] &\leq \mathbb{E}[V(P(0))] + K\,\mathbb{E}(\tau_n \wedge T) \\ &\leq \mathbb{E}[V(P(0))] + KT. \end{aligned} \tag{20}$$

Set $\Omega_N = \{\tau_N \leq T\}$ for $N \geq N_1$. By (18) we have $P(\Omega_N) \geq \epsilon/2$. Since for every $\omega \in \Omega_N$, there is at least one of the $p_i(\tau_N, \omega)$, $p \in \{x, y, z\}$, equal to $1/N$, then it holds

$$V\left(P(\tau_N, \omega)\right) \geq -\log \frac{1}{N}. \tag{21}$$

Then from (20) and (21) it follows that

$$V(P(0)) + KT \geq \mathbb{E}\left[\chi_{\Omega_N} V\left(P(\tau_N, \omega)\right)\right] \geq \epsilon/2 \log(N)$$

where χ_{Ω_N} is the indicator function of Ω_N. Letting $N \to \infty$ we have the following contradiction

$$\infty > V(P(0)) + KT \geq \lim_{N\to\infty} \epsilon/2 \log(N) = \infty,$$

that is a contraddiction. Hence we must have $\tau_\infty = \infty$ a.s. and the proof is complete.

The concept of asymptotic stability for dynamical system was introduced in 1892 by Lyapunov: roughly speaking, it means that the system converges to the equilibrium solution for large time, independently by the initial condition. Later, in the 1960's, the concept was extended to stochastic systems by Bucy, Arnold, Has'minskii and many others. Let us briefly recall the main definitions we shall need in this section.

Definition 5. *The trivial solution of the equation*

$$\begin{aligned} \mathrm{d}x(t) &= f(t, x(t))\,\mathrm{d}t + g(t, x(t))\,\mathrm{d}W(t) \\ x(0) &= x_0 \end{aligned} \tag{22}$$

is said to be stochastically asymptotically stable if

(i) it is stochastically stable:

$$\mathbb{P}\{|x(t; x_0) < r \text{ for all } t > 0\} \geq 1 - \varepsilon$$

(ii) moreover, for every $\varepsilon \in (0, 1)$, there exists a $\delta_0 = \delta_0(\varepsilon) > 0$ such that

$$\mathbb{P}\{\lim_{t\to\infty} |x(t; x_0) = 0\} \geq 1 - \varepsilon$$

whenever $|x_0| < \delta_0$.

In the sequel, we adapt the presentation of Arnold [3] to our case. In particular, we shall exploit the invariance of the domain D and consider all the following construction restricting the functions, and inequalities, to D.

A continuous function $V(x)$ defined on $D \cap B_h(0)$ is said to be positive-definite (in the sense of Lyapunov) if $V(0) = 0$ and $V(x) > 0$ on $|x| > 0$.
A function V is said to be negative-definite if $-V$ is positive-definite.
The diffusion operator associated to (22) is

$$Lv(x) = \left(\sum f_i(t, x) \frac{\partial}{\partial x_i} + \frac{1}{2} \sum \left[g(t, x) g^\star(t, x)\right]_{ij} \frac{\partial^2}{\partial_i x_j} \right) v(x).$$

In order to prove asymptotic stability of the solution, we shall appeal to the following result (compare [17, Ch.4, Thm.2.2]).

Proposition 6. *If there exists a positive-definite function $V(x)$ such that $LV(x)$ is negative-definite, then the trivial solution of equation* (22) *is stochastically asymptotically stable.*

It shall be noted that in the above result the functions V and LV are given in the whole space. However, since we only allow initial conditions in the invariant domain D, a sufficient condition for the relevant inequality $\mathbb{E}LV(X_t^x) \leq 0$ is $LV(x)$ negative defined in D.

In this section we consider the unknown $P(t) = (\underline{y}(t), \underline{z}(t))$ and the corresponding equation

$$\begin{cases} \mathrm{d}y_i(t) = [b_i(t)(1 - y_i(t) - z_i(t)) - \delta_i y_i(t)]\,\mathrm{d}t + \sigma_i \dfrac{(1 - y_i(t) - z_i(t))y_i(t)}{1 + \alpha y_i(t)}\,\mathrm{d}w_i(t) \\ \mathrm{d}z_i(t) = [\delta_i y_i(t) - \lambda_i z_i(t)]\,\mathrm{d}t \end{cases} \tag{23}$$

In order to study asymptotic stability, we consider the function $V(P) = \sum \log(1 + y_i) + \varepsilon \sum z_i$ on the domain $D \cap B_h(0)$ for some $h > 0$. This function is positive-definite (in the sense of Lyapunov), hence we shall prove that $LV(P)$ is negative-definite, where

$$LV(P) = \sum_{i=1}^{n} [b_i(t)(1 - y_i(t) - z_i(t)) - \delta_i y_i(t)] \frac{1}{1 + y_i(t)}$$

Proof. We compute

$$\begin{aligned} b_i(t) =& 1 - \prod_{j=1}^{N} (1 - a_{ij}\beta_j y_j(t)) = 1 - (1 - a_{i1}\beta_1 y_1)(1 - a_{i2}\beta_2 y_2) \dots (1 - a_{iN}\beta_N y_N) \\ =& 1 - (1 - \sum_{j=1}^{N} a_{ij}\beta_j y_j + \sum_{j,k=1}^{N} a_{ij}a_{ik}\beta_j\beta_k y_j y_k - \dots) \\ =& \sum_{j=1}^{N} a_{ij}\beta_j y_j - (\sum_{j,k=1}^{N} a_{ij}a_{ik}\beta_j\beta_k y_j y_k - \sum_{j,k,l=1}^{N} a_{ij}a_{ik}a_{il}\beta_j\beta_k\beta_l y_j y_k y_l + \dots) \end{aligned}$$

where, taking into account that $0 \leq y_i \leq h$, for h small enough, we get

$$\sum_{j,k=1}^{N} a_{ij}a_{ik}\beta_j\beta_k y_j y_k \geq \sum_{j,k,l=1}^{N} a_{ij}a_{ik}a_{il}\beta_j\beta_k\beta_l y_j y_k y_l \geq \dots$$

and all the differences between successive pair of sums inside the brackets are positive. This implies that

$$b_i(t) \leq \sum_{j=1}^{N} a_{ij}\beta_j y_j = \tilde{b}_i(t)$$

as claimed. □

We thus estimate

$$LV(P) \leq -\sum_{i=1}^{n} \left(-\beta \mathrm{deg}(\mathsf{v}_i) + \delta_i \left(\frac{1}{1+h} - \varepsilon \right) \right) y_i$$

$$- \sum_{i=1}^{n} \left(\sigma_i \frac{(1 - y_i(t) - z_i(t))y_i(t)}{1 + \alpha y_i(t)} \right)^2 \frac{1}{(1 + y_i(t))^2}$$
$$+ \varepsilon \sum_{i=1}^{n} [\delta_i y_i(t) - \lambda_i z_i(t)]$$

Claim 1 It holds that $b_i(t) \leq \tilde{b}_i(t)$ for $P \in D \cap B_h(0)$.

$$- \varepsilon \sum_{i=1}^{n} \lambda_i z_i$$

(the diffusion term is negative and goes to zero as y^2 hence it is negligible) and, due to the arbitrariness of h and ε, we arrive at the following result.

Theorem 7. *The sufficient condition* (15) *for the exponential stability of the solution of the deterministic problem* (3) *is also a sufficient condition for the exponential stability of the solution of the stochastic problem* (17)*.*

VI. CONCLUSION

In this paper we study the behaviour of an epidemics spreading in a population with homogeneous and inhomogeneous contact rates, where the rates at which each

individual can be infected from its neighbours are considered as independent stochastic processes.
We start from the deterministic case obtained after a mean field approximation, where the infection rate β between each two given individuals is either zero, if they are not in contact, or a given constant, if they are connected.
However, since epidemic processes are usually affected by random disturbances, we introduce in this model a stochastic heterogeneity of the population by taking into account a variability in time of the parameters. Precisely, we assume that the rate of receiving the infection, for each individual, varies around a common average value under the action of a family of independent, identically distributed Brownian motions.
We observe that the steady state solution of the SIRS model can be exactly mapped to that of the SIS model, via the identification of the density of infected individuals. Therefore, all the critical properties of the SIRS model are very similar to the SIS model.
In the last part, we consider the stochastic system and we prove that $(0,1)^{3N}$ is invariant. We study the asymptotic behaviour of the solution finding a sufficient condition for the stochastic asymptotic stability of the solution.

ACKNOWLEDGMENTS

The authors wish to thank dr. Stefania Ottaviano and prof. Delio Mugnolo for many interesting discussions, and the anonymous referee for the invaluable help to improve the presentation of the paper.

November 19, 2019

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