Invasion Threshold in Heterogeneous Metapopulation Networks

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We study the dynamics of epidemic and reaction-diffusion processes in metapopulation models with heterogeneous connectivity patterns. In susceptible-infected-removed-like processes, along with the standard local epidemic threshold, the system exhibits a global invasion threshold. We provide an explicit expression of the threshold that sets a critical value of the diffusion/mobility rate below which the epidemic is not able to spread to a macroscopic fraction of subpopulations. The invasion threshold is found to be affected by the topological fluctuations of the metapopulation network. The results presented provide a general framework for the understanding of the effect of travel restrictions in epidemic containment.

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The role of heterogeneity has been acknowledged as a central question in the study of population biology of infectious diseases [1–3] and revamped recently with the evidence that a large number of real world networks exhibit complex topological properties [4–6]. These features, often mathematically encoded in a heavy-tailed probability distribution \(P(k)\) that any given node has degree \(k\), were shown to affect the system evolution, altering the threshold behavior and the associated dynamical phase transition [7–9]. These studies have mainly focused on networked systems where each node corresponds to a single individual, and only recently the study of the impact of heterogeneous topologies on bosonic systems, where nodes can be occupied by any number of particles, has been initiated [10]. Examples are provided by reaction-diffusion systems used to model a wide range of phenomena in chemistry and physics [11], and metapopulation epidemic models [2,3,12–16] where particles represent people moving across different subpopulations (nodes) such as city or urban areas, and the reaction processes account for the local infection dynamics.

Here we analyze epidemic metapopulation models characterized by an infection dynamics within each node (or subpopulation) that follows a Susceptible-Infected-Removed (SIR) model. The mobility rate \(p\) of individuals defines the coupling process among the subpopulations. In the real world, the networks representing the mobility pattern of individuals among different subpopulations are in many cases highly heterogeneous [17–21]. For this reason, the connectivity pattern of the metapopulation network is described as a random graph with arbitrary degree distribution \(P(k)\). By using a mechanistic approach it is possible to show that along with the usual epidemic threshold condition \(R_0 > 1\) on the basic reproductive number, the system exhibits a global invasion threshold setting the condition for the infection of a macroscopic fraction of the metapopulation system [22,23]. The threshold condition on \(R_0\) ensures the local outbreak at the subpopulation level [1,10], whereas the explicit expression obtained for global invasion threshold \(R_g > 1\) provides a critical value for the diffusion rate \(p\), below which the epidemic cannot propagate to a relevant fraction of subpopulations. We find that the global invasion threshold is affected by the topological fluctuations of the underlying network. The larger the network heterogeneity, the smaller the value of the critical diffusion rate above which the epidemic may globally invade the metapopulation system. The present results can be generalized to more realistic diffusion and mobility schemes and provide a framework for the analysis of realistic metapopulation epidemic models [24–28].

A simplified mechanistic (i.e., microscopic in the epidemic terminology) approach to the metapopulation spread of infectious diseases uses a markovian assumption in which at each time step the movement of individuals is given in terms of a matrix \(d_{ij}\) that expresses the probability that an individual in the subpopulation \(i\) is traveling to the subpopulation \(j\). Several modeling approaches to the large-scale spread of infectious diseases [24–27,29] use this mobility process based on transportation networks combined with the local evolution of the disease. The markovian character lies in the assumption that at each time step the same traveling probability applies to all individuals in the subpopulation without having memory of their origin. This mobility scheme coupled with an infection dynamics at the local level can be generally viewed as equivalent to classic reaction-diffusion processes with no constraint on the occupation numbers \(N_i\) of each subpopulation. The total population of the metapopulation system is \(N = \sum_i N_i\), and each individual diffuses along the edges with a diffusion coefficient \(d_{ij}\) that depends on the node degree, subpopulation size, and/or the mobility matrix. The metapopulation system is therefore composed of a network substrate connecting nodes—each corresponding to a subpopulation—over which individuals diffuse. We consider that each node \(i\) is connected to other \(k_i\) nodes according to...
its degree, resulting in a network with degree distribution $P(k)$ and distribution moments $(k^n) = \sum k^n P(k)$.

In the following, as a simplified diffusion process we assume that the mobility is equivalent to a diffusion rate along any given link of a node with degree $k$ simply equal to $d_{kk} = p/k$. This is obviously not the case in a wide range of real systems where the extreme heterogeneity of traffic is well documented, and more realistic processes will be considered elsewhere. This simple process, however, automatically generates a stationary distribution of occupation numbers that is better described by grouping subpopulations according to their degree $k$:

$$N_k = \frac{k}{\langle k \rangle} \bar{N},$$

(1)

where $\bar{N}$ is the average subpopulation size.

In each subpopulation $j$ the disease follows an SIR model, and the total number of individuals is partitioned in the compartments $S_j(t)$, $I_j(t)$, and $R_j(t)$, denoting the number of susceptible, infected, and removed individuals at time $t$, respectively. The infection dynamics proceeds as follows. Each susceptible individual has a transition rate to the infected state expressed as $\beta I_j/N_j$, where $\beta$ is the disease transmissibility rate and $I_j/N_j$ is the force of infection in the homogeneous mixing assumption. Analogously, each infected individual enters the removed compartment according to the recovery rate $\mu$. The basic SIR rules thus define a reaction scheme of the type $S + I \rightarrow 2I$ and $I \rightarrow R$, which conserves the number of individuals. The SIR epidemic model is characterized by the reproductive number $R_0 = \beta/\mu$, which defines the average number of infectious individuals generated by one infected individual in a fully susceptible population. The epidemic is able to generate a number of infected individuals larger than those who recover only if $R_0 > 1$, yielding the classic result for the epidemic threshold [1]. If the spreading rate is not large enough to allow a reproductive number larger than 1 (i.e., $\beta > \mu$), the epidemic outbreak will quickly die out. This result is valid at the level of each subpopulation and holds also at the metapopulation level where $R_0 > 1$ is a necessary condition to have the growth of the epidemic [10].

The intuitive result on the subpopulation epidemic threshold, however, does not take into account the effects due to the finite size of subpopulations, the discrete nature of individuals, and the stochastic nature of the reaction and diffusion processes. These effects have been shown to have a crucial role in the problem of resurgent epidemics, extinction, and eradication [22,23,30,31]. Also, in the present framework indeed each subpopulation may or may not transmit the infection to a neighboring subpopulation upon the condition that at least one infected individual is moving onto the noninfected subpopulations during the epidemic outbreak. Given an SIR model with $R_0 > 1$, the total number of infected individuals generated within a subpopulation and the mobility rate must be large enough to ensure the seeding of other subpopulations before the end of the local outbreak [22,23].

As a simple example of this effect let us consider a metapopulation system in which the initial condition is provided by a single infection in a subpopulation with degree $k$ and $N_k$ individuals, given $R_0 > 1$. In the case of a macroscopic outbreak in a closed population, the total number of infected individuals during the outbreak evolution will be equal to $\alpha N_k$, where $\alpha$ depends on the specific disease model and parameter values used. Each infected individual stays in the infectious state for an average time $1/\mu$ equal to the inverse of the recovery rate, during which it can travel to the neighboring subpopulation of degree $k'$ with rate $d_{kk'}$. We can therefore consider that on average the number of new seeds that may appear in a connected subpopulation of degree $k'$ during the duration of the local outbreak is given by

$$\lambda_{kk'} = d_{kk'} \frac{\alpha N_k}{\mu}.$$  

(2)

In this perspective we can provide a characterization of the invasion dynamics at the level of the subpopulations, translating epidemiological and demographic parameters into Levins-type metapopulation parameters of extinction and invasion rate. Let us define $D_k^n$ as the number of diseased subpopulation of degree $k$ at generation $n$, i.e., those which are experiencing an outbreak at the beginning of the process. Each infected subpopulation will seed—during the course of the outbreak—the infection in neighboring subpopulations defining the set $D_k$ of infected subpopulations at generation 1, and so on. This corresponds to a basic branching process [22,32,33] where the $n$th generation of infected subpopulations of degree $k$ is denoted $D_k^n$.

In order to describe the early stage of the subpopulations’ invasion dynamics we assume that the number of subpopulations affected by an outbreak (with $R_0 > 1$) is small, and we can therefore study the evolution of the number of diseased subpopulations by using a branching process approximation relating $D_k^n$ with $D_k^{n-1}$. Let us consider a metapopulation network with degree distribution $P(k)$ and $V$ subpopulations and write the number of subpopulations of degree $k$ invaded at the generation $n$ as

$$D_k^n = \sum_k D_k^{n-1}(k'-1) \left[ 1 - \frac{1}{R_0} \right] P(k)\frac{k'}{V} \left( 1 - \frac{D_k^{n-1}}{V_k} \right).$$

(3)

This equation assumes that each infected subpopulation of degree $k'$ of the $(n-1)$th generation, $D_k^{n-1}$, will seed the infection in a number $(k'-1)$ of subpopulations corresponding to the number of neighboring subpopulations $k'$ minus the one that originally transmitted the infection, the probability $P(k|k')$ that each of the $k'-1$ not yet infected neighboring subpopulations has degree $k$, and the probability to observe an outbreak in the seeded subpopulation, i.e., $(1 - R_0^{-\lambda_{kk'}})$ [34]. The last factor stems from the proba-
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assuming a diffusion probability for each individual along each link of the subpopulation of the form \( d_{kl} = p/k \).

A complete analysis of the system phase diagram is obtained by analyzing the behavior of the global attack rate \( R(\infty)/N \), defined as the total fraction of cases in the metapopulation system at the end of the epidemic, as a function of both \( R_0 \) and \( p \). Figure 1 reports the global attack rate surface in the \( p-R_0 \) space and clearly shows the effect of different couplings as expressed by the value of \( p \) in reducing the final size of the epidemic at a given fixed value of \( R_0 \). The smaller the value of \( R_0 \), the higher the coupling needs to be in order for the virus to successfully invade a finite fraction of the subpopulations, in agreement with the analytic result of Eq. (7). This provides a clear illustration of the varying global invasion threshold as a function of the reproductive rate \( R_0 \). Furthermore, it is possible to study the effect of the heterogeneity of the metapopulation structure on the global epidemic threshold. Figure 2 shows the results obtained by comparing two random metapopulation networks, one with Poissonian degree distribution (homogeneous network) and one with heavy-tailed \( [P(k) \sim k^{-2.1}] \) degree distribution (heterogeneous network). Despite the two models having the same average degree and disease parameters, the fluctuations of the power-law network increase the value of \( R_\ast \), thus lowering the critical value of the mobility.

The present analysis provides insights in setting a framework for the analysis of large-scale spread of epidemics in realistic mobility networks. Furthermore, these results open the path to future work aimed at analyzing refined metapopulation infection models.

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