Modeling epidemics dynamics on heterogenous networks

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Abstract

The dynamics of the SIS process on heterogenous networks, where different local communities are connected by airlines, is studied. We suggest a new modeling technique for traveler's movement, in order to avoid an interference of the movement with the demographic parameters characterizing the metapopulation. A solution to the deterministic reaction-diffusion equations that emerge from this model on a general network is presented. A typical example of heterogenous network, the star structure, is studied in detail both analytically and using agent-based simulations. The interplay between demographic stochasticity, spatial heterogeneity and the infection dynamics is shown to produce some counterintuitive effects. In particular it was found that, while movement always increases the chance of an outbreak, it may decrease the steady-state fraction of sick individuals. The importance of the modeling technique in estimating the outcomes of a vaccination campaign is demonstrated.

1. Introduction

One of the major threats for any living species is the outbreak of an infectious disease. Even after the development of modern medicine and the appearance of antibiotics, the human population is still at risk for the appearance of resistent strains of bacteria or lethal, infectious virus species. A series of epidemic and pandemic events in the last hundred years - from the Spanish flu through the spread of AIDS to the recent avian and swine flu - remind us that the danger still exists. The study of infection dynamics - its spread, the chance of an outbreak, the effects of pathogen infectivity, virulence and so on - is thus of extreme importance and constitutes of a substantial part of current ecology literature (Anderson & May, 1992; Bailey, 1975; Murray, 1993).

The recent outbreaks of various human epidemics were characterized by very fast, and nonlocal, geographic spreads. The old scenario, known from the middle ages - like, say, the spread of the bubonic plague - when the disease propagated locally from town to the neighboring villages and then to the next town - is replaced nowadays by almost instantaneous prevalence around the globe due to the intensive use of air-traffic. This poses an urgent need for a new type of infection dynamics models, and a new series of works by Colizza, Vespignani and coworkers (Colizza & Vespignani, 2008, 2007; Colizza *et al.*, 2007, 2006) have addressed this issue.

The classical mathematical models in epidemiology - SIR (susceptible-infected-recovered) and SIS (susceptible-infected-susceptible) have been presented originally for a well mixed, uniformed population (Kermack & McKendrick, 1927; Bailey, 1975; Weiss & Dishon, 1971). In the original form these models admit no age nor spatial/social structure and the analysis was bases on deterministic differential equations. In the last decades much work has been done in extending these models in order to include structured populations. Moreover, for small groups of individuals and for the first steps of the epidemics the number of infected agents is small, hence the stochastic nature of the infection-recovery process must be

taken into account. See review at (Vespignani, 2008).

A stochastic model with a spatial structure - a metapopulation divided among habitat patches on a regular lattice with an inter-patch infectivity that differs from the intra-patch one - has been presented recently. This system was subject to extensive numerical studies (Getz *et al.*, 2005) with a few analytic results presented (Kessler & Shnerb, 2008). To model actual human dynamics in modern world, Colizza et. al. have extended this type of models even further, taking into account the heterogenous structure of urban populations and airline connectivity. Their model describes a segregated population for which the connections between subcommunities obey a scale-free statistics, in agreement with recent observations regarding air-traffic networks (Guimerà *et al.*, 2005).

Here we show that the heterogeneity of the network poses a new complication in the modeling procedure: on an irregular network the movement of individual agents interferes with the demography of the subpopulations. Allowing migration between nodes on an irregular network yields a nontrivial steady state size distribution for the nodes that differs, almost surely, from the initial conditions imposed in a simulation. As a result the dynamics is affected heavily by the demographic changes as the population approaches the steady state. Here we suggest a "travelers model", within which individuals stay on their original node while infecting others on neighboring sites. In this model the size of a site is kept fixed so the modeler may introduce any realistic initial conditions.

The main aim of this work is to explain and discuss this travelers dynamic within which no such interference between demography and motion occurs. En passant, a few interesting observations are made:

1. On heterogenous networks an increase in the movement of agents may *decrease* the size of the epidemic at the steady state, although it increases the chance of an outbreak.
2. These contradicting effects of movement make the estimation of R_0 using the steady state densities quite problematic.
3. Simple heterogenous networks, like a star structure, yield results that are very similar to a full scale-free network model (Baxter *et al.*, 2008)
4. The effect of immunization of a fraction of the hub population is pronounced, as opposed to the prediction based on former models.

Why there is an interference between demography and movement on heterogenous network? On regular networks all "nodes" (locations, cities, habitat patches) have the same number of "links", i.e., of routes agents may use to migrate to other nodes. Starting, say, from a uniform state where all local populations are equal, the influx of immigrant into a node is balanced by the outbound flow of emigrants, and in steady state all nodes admit the same population (up to small fluctuations that may appear due to some type of noise). On heterogenous networks, on the other hand, the number of links is varying among nodes. There are a few "hubs" with thousands of links (like big cities or airfields where headquarters of airline carriers are located), and many dead ends (end nodes) connected only a few, or even a single, link. In such a case density independent migration must introduces a drift, either towards the hubs (if the chance per agent to move is fixed) or from the hub (if the chance of migration per link is fixed).

Indeed, Colizza and coworkers (Colizza *et al.*, 2007) have assumed the following movement model: any individual agent emigrates with a certain probability pet unit time; upon emigration, the agent chooses its destination at random from all sites connected to its original location with equal chance. As explained, such a procedure induces a drift into the hubs. This effect may be easily recognized by looking at the star structure presented in Fig. 1. Any individual that leaves the end sites must choose the hub as its destination, while the one emigrating from the hub chooses one of eight end-sites. Accordingly, starting from equal subpopulation on any node, the movement dynamics leads to a steady state in which the hub community is much larger. As the size of the subcommunity is a major factor determining the chance of local outbreaks, the resulting epidemic dynamics will be correlated almost solely with the events on the hub, where the rest of the network remains more or less passive.

The accumulation of agents on the hubs in the

steady state of (Colizza *et al.*, 2007) (the "migration model") is not unrealistic, as indeed airtraffic hubs as described above are typically found at the proximity of big cities and megalopolises. However, it is clear that the logic beyond this phenomenon should be reversed: people have not accumulated in Chicago or in Houston because of their large airports. The large population of a city is the reason for the existence of an airport in its vicinity, not its result.

Here we suggest a simple movement model for which, even on heterogenous networks, agent migration does not interfere with the demographic properties of the subpopulations. The basic idea is simple: since the vast majority of the airline travelers porches round-trip tickets travelers will reach their destination, stay there for a relatively short time, and then fly back. In that sense the passengers act like mosquitos in the process of vector transition, and induce "long range infection" between subcommunities. In the next sections this basic insight will be integrated into a formal model, then the model is analyzed from various aspects including its ability to predict the effect of imperfect immunization.

2. The travelers model

Following (Getz *et al.*, 2005; Lloyd-Smith *et al.*, 2005; Kessler & Shnerb, 2008) we suggest a *travelers model* for the movement of human population. The population is divided into L local communities, each admits an integer number of individuals N_i, $i = 1..L$. The set of N_is determines the demographic structure of the metapopulation and is kept fixed in time; this reflects the assumption that the timescale for demographic shifts is much larger than the timescale associated with the disease outbreak. The topology of the network is determined by links connecting subpopulations, where these links correspond to airlines. The degree of a node (number of bidirectional connection to other nodes) is k. In Fig. 2 a concrete example is illustrated: for this star configuration $L = 9$, for the hub $k = 8$ and all the end nodes have $k = 1$.

Along this paper we keep using the star structure as a toy model for a full scale free network. This setup is fairly simple to simulate. It is interesting to note that the results from this star arrangement are very similar to those obtained from the a full scale-free topology (Colizza *et al.*, 2007) - it may be the case that this toy model captures, at least for some range of parameters, the involved hierarchy of a real network.

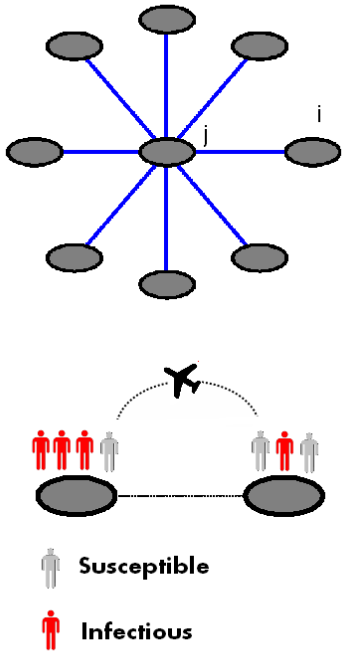

Figure 1: A schematic figure illustrated as a heterogenous metapopulation network represented with a star structure. Individuals are divided in two groups: susceptible and infected.

Now let us specify the dynamics of the disease. We consider here an SIS infection model with frequency dependent transition [type II in the terminology of Anderson and May (Anderson & May, 1992; McCallum *et al.*, 2001)]. The dynamics of the infectious pathogen is determined by three parameters: β measures the infectivity, μ is the recovery rate and χ is the chance that an individual travels and infects peo-

ple somewhere else rather than in its own community. If S_i is the number of susceptible on the ith site and I_j is the number of infected individuals on the j site, the reaction kinetics is described schematically by,

$$\begin{aligned} S_i + I_i &\xrightarrow{\beta(1-\chi)/N_i} 2I_i \\ S_i + I_j &\xrightarrow{\beta\chi/N_i} I_i + I_j \\ I &\xrightarrow{\mu} S. \end{aligned} \quad (1)$$

For a well mixed population of size N the basic reproduction number for type II infection is $R_0 = \beta/\mu$, in contrast with $R_0 = \beta N/\mu$ for the type I model (frequency independent transition). While R_0 is independent of N, the chance of an outbreak is still N dependent as will be shown below. The reason for that is the effect of demographic stochasticity: for small N an outbreak may be avoided or a spontaneous fadeout may occur even if $R_0 > 1$, as fluctuations drive the pathogen to extinction.

We have studied this model using Monte-Carlo individual based simulation and analytic mean-field approach. For the simulation, each node was occupied by N inhabitants (here we considered only the case where N is the same for all subpopulations), each of which may be either susceptible or infected. The update form t to $t + \Delta t$ has been carried out as follows: the nodes are visited sequentially. If the number of infected persons on certain node (say, the i-th patch) is an integer I_i, p of them recover (become susceptible) where p is another integer taken from the binomial distribution $B(\mu\Delta t, I_i)$. We now calculate the parameter

$$\tilde{I}_i = (1-\chi)I_i + \sum_j \chi I_j/k_j,$$

where the sum over j runs on all sites connected to the i-th one. $\tilde{I}_i$ is a measure for the number of sick persons that may infect a susceptible on this site, and the division of I_j by k_j reflects the fact that a traveler from the j site chooses its destination with equal chance among all k_j patches connected to j. Given $\tilde{I}_i$, q of the susceptible change their status to infected, where q is another integer taken from the binomial distribution

$$B(1 - [1 - \frac{\beta\Delta t}{N_i}]^{\tilde{I}_i}, S_i).$$

Note that $1 - \beta\Delta t/N_i$ is the chance of a susceptible to escape infection from a single sick person.

3. Results

We have simulated the travelers IBM described above on the star network of Fig. 2 (with 10 end nodes), and compare our results with those obtained from the model of Colizza *et al.* (2007). The only difference between the two approaches is the spatial dynamics of agents: in our model the demography is kept fixed, while the former model allows for migration of individuals from site to site. As explained above, since any emigrant chooses its destination at random from all possible sites connected to its original location, a drift towards the hub appears and the demography changes in the migration model, and the demography is kept fixed in the travelers model. All simulations starts with the same number of individuals on each site.

This difference between models manifests itself in Fig. 3. A single infected individual has been placed on one end node, an outbreak occurs, and the number of susceptible and sick persons is plotted until the system reaches its steady state. [Indeed this is a metastable state as any finite epidemic should disappear at the end due to large fluctuation (fadeout). However the timescale related to this rare events is exponentially large in the total number of sick people and is way beyond the times considered here. (Kessler & Shnerb, 2007)]. A typical time evolution is plotted separately for the hub and for the average over all end nodes. The results of the interference between agents dynamics and local demography are clearly seen in the lower panel; evidently the drift towards the hub causes a demographic steady state that involves a strong depletion of the population on the end nodes along time. As a result almost all the activity takes place on the hub, and the overall time evolution summed over all sites (inset) is very similar to that of the hub alone. This should be compared with the fixed demography travelers model suggested here (upper panel), where a substantial part of the activity takes place on the end nodes.

Another moral that one can gather from Fig. 3 is that, even when the demography is kept fixed (travel-

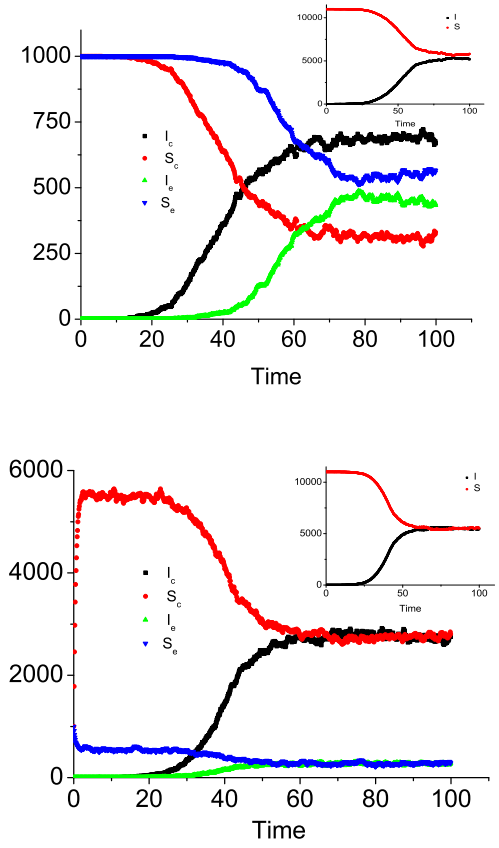

Figure 2: Upper Panel: Typical time development of the disease, using the fixed population dynamics suggested here, on a star network. The results of a fully stochastic simulation is presented, with 1000 individuals on each site, $\chi = 0.1$ and $R_0 = 2$. The number of susceptible and infected on the center (I_c and S_c) and the average number of the end sites (I_e and S_e) are indicated separately. The graphs follow the development of the outbreak from the introduction of a single sick subject to the steady state. In the inset the global dynamics of the disease (total numbers of infected and susceptible vs. time) is presented. Lower panel: the same outcomes are graphed for the movement model considered by (Colizza *et al.*, 2007). Clearly, the drift towards the center increases the population, the majority of dynamics happen there.

ers model, upper panel), the size of the epidemic on the end nodes is substantially smaller than its size on the hub. This happens because any susceptible on the hub may be infected by all sick persons in the system, while the end sites could be infected only by the hub. In terms of the ecology of the pathogen, the end sites act almost like "sinks" as it is relatively hard for a sick person there to infect a susceptible on the hub. Indeed, the mean-field deterministic approximation discussed below predicts that the total number of infected individuals in the system is inversely proportional to the level of motion (travel) described by the parameter χ. This surprising effect is demonstrated in Figure 3.

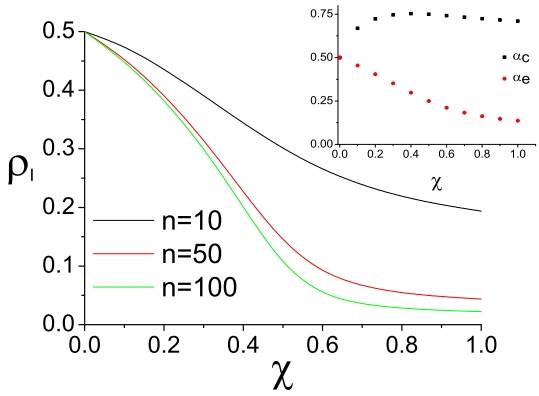

Figure 3: The total density of infected individuals ρ_I vs. the travel parameter χ for the star network with parameters $R_0 = 2$, $n = 10$, 50 and 100. Results obtained from the analytic-deterministic approximation, Eq. (14). While the number of infected individuals grows on the center as χ increases, the disease at the end sites is less and less frequent. See inset where the corresponding system with $R_0 = 2, n = 10$, where α_c and α_e, the fraction of infected individuals on the hub and on the end sites respectively, are plotted vs. χ.

Figure 3 summarizes the results for the chance of an outbreak and the steady state epidemic size for both models. It shows again that while an outbreak is more likely for strong dispersal, the corresponding steady state size of the epidemic ρ_I is (in the travelers model) lowered.

This is somewhat surprising result. It is known

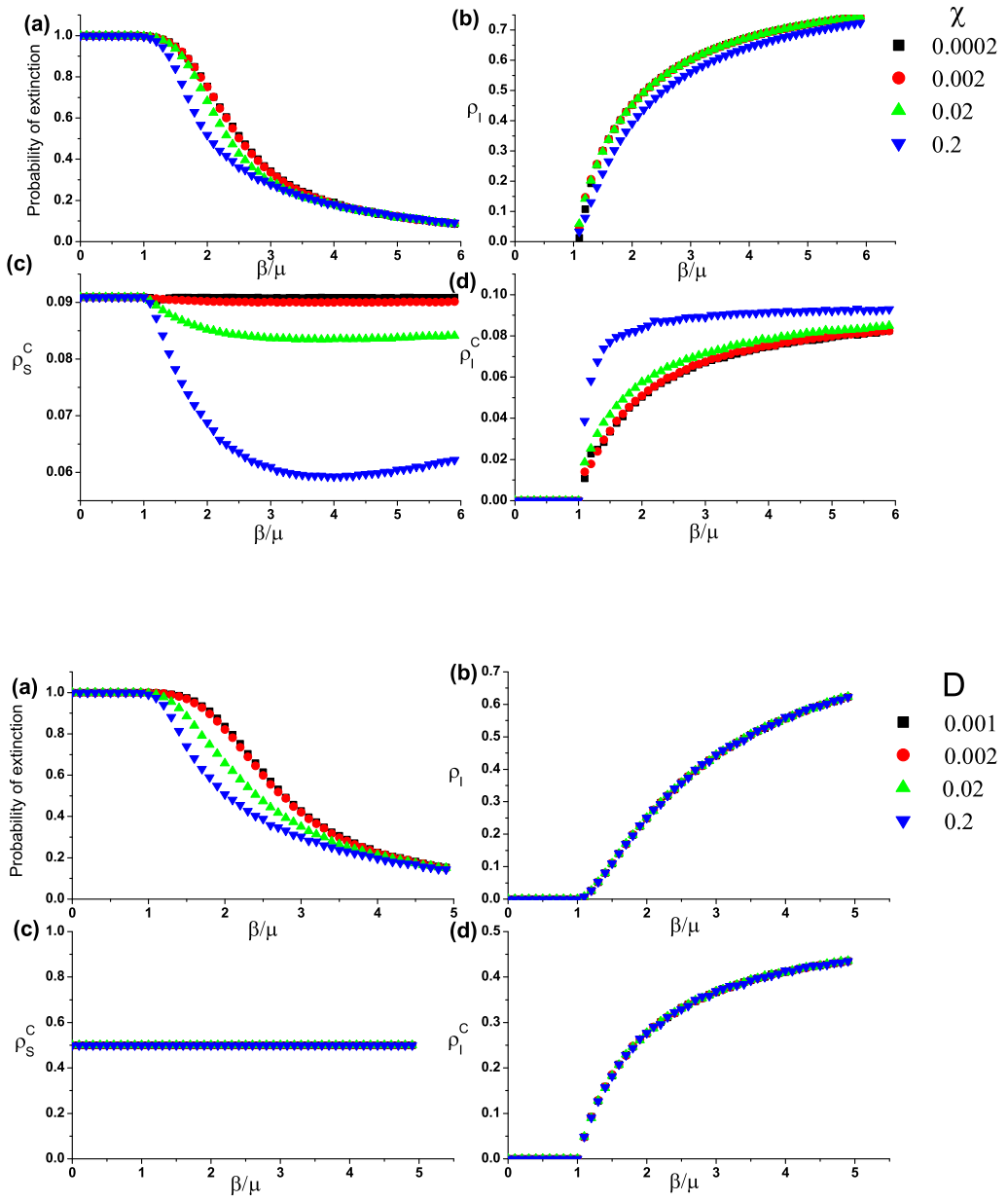

Figure 4: Some characteristics of the stochastic simulations, all obtained for the Travelers model (upper panel) and the migration (lower panel) model on the star geometry. Each panel shows 4 subfigures. (a) Is the chance that there is no outbreak when a single sick individual is introduced. This chance is 100% below the critical R_0 and is finite above criticality as a result of demographic stochasticity. Note that as χ grows the chance of an outbreak increases, as expected. The steady state value of ρ_I is plotted in (b) as a function of R_0, emphasizing that in the round-trip travelers model the density of infectious *decreases* when there are more travelers, as opposed to (a). In the migration model the differences are negligible. (c) and (d) illustrate the dynamics on the center node, correspond to the fraction of the suspectable ρ_S^c (out of the total number of susceptible) and the fraction of the sick persons ρ_I^c on the center node as a function of R_0. Compering the upper and lower panels indicates again that the outbreak in the migration model happens due to the growth in the total population on the center.

that the movement of individuals *facilitates* the spread of an epidemic, and in particular that the critical infection rate R_c for a spatially segregated population decreases as χ grows (see, e.g., (Getz *et al.*, 2005; Lloyd-Smith *et al.*, 2005; Kessler & Shnerb, 2008)). One may expects, thus, that the number of healthy people will by smaller if the migration rate is larger. What we observe here is that, on heterogenous networks, increased mobility facilitates the outbreak but *reduces* the size of the epidemic at the steady state.

This effect may, or may not, appear in the model used by Colizza at. al., where migration act to increase the total population on the hub. Concentration of the total population acts in favor of the disease and this (at least for some topologies) may invert the sign of the response function $d\rho_I/d\chi$. As seen in Figure 3, for the set of parameters used for our simulation the steady state size of the infection is independent of χ in the migration model.

The contradicting roles played by migration in nonuniform spatial models - lowering R_c while decreasing ρ_I, may pose a serious problem if one is trying to use the steady-state size of the epidemic ρ_I in order to retrieve R_0. The standard method (Anderson & May, 1992), based on the assumption of a well-mixed large population, obtains R_0 from the relation $R_0 = 1/(S/N)$, where S/N is the steady state fraction if the susceptibles. This method has already been criticized (Keeling & Rohani, 1995), but now we see that it may fail on heterogenous network just because of the topology: a glance in fig. 3 convinces one that totally a different estimation may be obtained for R_0 although the threshold for an outbreak is the same, $R_0 = 1$, for all cases. Steady state estimations not only fail to give the right value, they even fail to give the right *order*: a pathogen with smaller ρ_I may be more dangerous, in terms of the chance for an outbreak, than one that has larger ρ_I.

3.1. Vaccination strategy

Many recent studies were focused on the case of limited immunization (Pastor-Satorras & Vespignani, 2002; Cohen *et al.*, 2000b,a, 2003; Chen *et al.*, 2008), trying to explain how to immunize a population with a minimal number of immunization supplies. This question has became very important since the last pandemic spread very fast while the immunization is under preparation, limited and/or very expensive.

These studies showed that the random uniform immunization is a highly inefficient strategy on scale-free networks. These networks provides an ideal environment for the spreading of infective agents through the hubs, and random immunization can not avoid percolation through the network. On the other hand, immunization based on the nodes connectivity hierarchy (the vaccination of hubs takes place before the vaccination of the end sites) should be used in order to avoid outbreak. (Pastor-Satorras & Vespignani, 2002).

We examine now a vaccination strategy with a fixed, limited number of immunization supplies on the star network. It is already known that one should deposit all the immunizations on the hub, trying to disconnect different parts of the network. How does the immunization affect the outbreak if only a fraction of the hub population is immunized? Let us check the results and compare between the travelers scenario and the migration model.

Figure 3.1 presented the results from our IBM Monte-Carlo. First, we initialize the network with N suspectable individuals per site. One sick individual was introduced into the system and the process continue according to the algorithm described above. Once the system reached 10% of infectious people we immune $f \times N$ suspectable on the central node where f stands for the fraction of immunity (between 0 and 1). Only healthy subjects were immunized, so the effect of immunization is to decrease, effectively, the population on the hub.

The results are depicted in Fig. 3.1. In the travelers model the effect of immunization is evident and an increase of f leads to an appreciable reduction of the chance of an outbreak. In the immigration model the effect is much less pronounced, since there is a flow of agents to the hub.

4. General mean-field solution

In this section we present an analytic solution to the deterministic equations describing the dynamic of a spatial infection process. We consider the travelers model when the effect of stochasticity may be

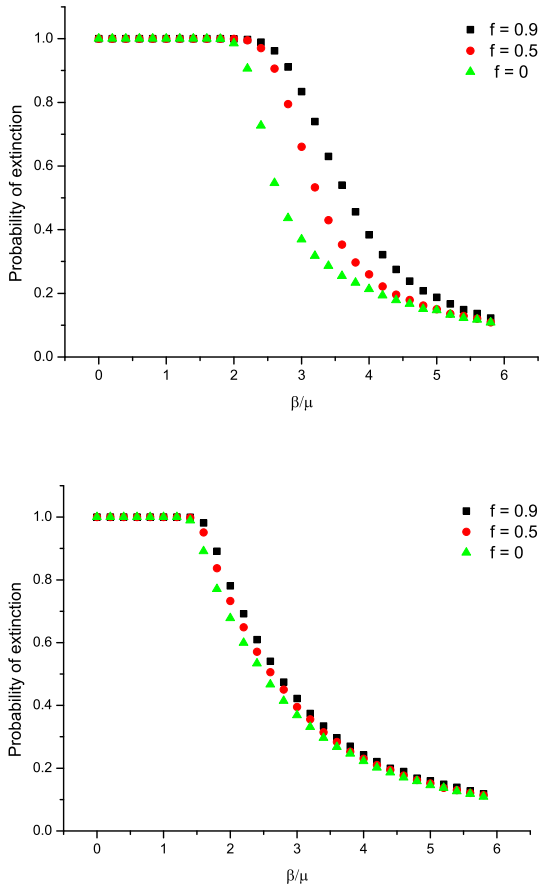

Figure 5: The effect of immunization for the travelers model (upper panel) and the migration (lower panel) model both examined using the stochastic simulation on the star geometry ($N = 100$). Here the chance of pathogen extinction (one minus the chance for an outbreak) is plotted against R_0. In the travelers model immunizing of agents on the central node affect strongly persistence of the pathogen, while the migration model yields much smaller effect.

neglected. As in the simulations we assume here the same number of individuals N on each site; I_k and S_k stand for the average infectious population and the suspectable population respectively with the same k . Following the standard procedure for networks we assume that all nodes of degree k admit the same dynamics.

Using the method presented by (Colizza & Vespignani, 2008) the rate equation for the infected population is defined through,

$$\frac{\Delta I_k}{\Delta t} = I_k^{in} - I_k^{out}, \tag{2}$$

that represent the total difference of the infectious population during a small time interval Δt. I_k^{in} and I_k^{out} are the number of susceptibles who become sick or recover, correspondingly, within Δt. Clearly,

$$I_k^{out} = \mu I_k, \tag{3}$$

μ stands for the recovery rate, which is the only means of exiting I_k class. the influx is,

$$I_k^{in} = (1-\chi)\frac{\beta}{N} S_k I_k + \frac{\beta}{N} S_k k \sum_{k'} P(k'|k)\frac{\chi}{k'} I_{k'}, \tag{4}$$

where the first term stands for the contagion of an infectious to a susceptible individual on the same node, and the second term describes the ability of being infected by travelers from connected nodes. The summation is over k', the degree of the linked sites, and $P(k'|k)$ stand for the probability of a site with k links will be connected to a site with k' links.

Assuming uncorrelated network, $P(k'|k) = k'P(k')/\langle k\rangle$ (Pastor-Satorras *et al.*, 2001; Dorogovtsev & Mendes, 2003), thus,

$$\frac{\partial I_k}{\partial t} = (1-\chi)\frac{\beta}{N} S_k I_k + \chi \frac{\beta}{N\langle k\rangle} S_k k \sum_{k'} P(k') I_{k'} - \mu I_k. \tag{5}$$

In the same manner, the equation for S_k takes the form,

$$\frac{\partial S_k}{\partial t} = \mu I_k - (1-\chi)\frac{\beta}{N} S_k I_k - \chi \frac{\beta}{N\langle k\rangle} S_k k \sum_{k'} P(k') I_{k'}. \tag{6}$$

One can easily verify that these equations conserve the local population, $d(S_k + I_k)/dt = 0$. This is a result of the assumption standing in the base of the analysis that N is time independent.

4.1. The outbreak

The basic reproductive number R_0 plays a major role in the early stages of the pandemic. R_0 is essentially the average number of successful offsprings that a parasite is intrinsically capable of producing (Anderson & May, 1992). Introducing a single infected individual is equivalent, under the deterministic approximation, to initial conditions for which I is slightly larger than zero, such that $I/S \to 0$ so $S \simeq N$, $S/N \simeq 1$. Using that the relation $\sum_{k'} P(k')I_{k'} = \langle I \rangle$ eq. (5) takes the form

$$\frac{\partial I_k}{\partial t} = (1-\chi)\beta I_k + \frac{\beta}{\langle k \rangle}\chi k \langle I \rangle - \mu I_k. \tag{7}$$

Let $\tilde{I}$ denote $\langle I \rangle$. When multiplying the above expression by $\sum_k P(k)$, one obtains a simple equation for $\tilde{I}$

$$\frac{\partial}{\partial t}\sum_k P(k)I_k = \frac{\partial \tilde{I}}{\partial t} = (\beta - \mu)\tilde{I}, \tag{8}$$

using

$$\tilde{I}_0 \equiv \langle I_k|_{t=0} \rangle \equiv \sum_k p(k)I_k|_{t=0}, \tag{9}$$

the solution for this equation is

$$\tilde{I} = \tilde{I}_0 e^{(\beta-\mu)t}. \tag{10}$$

So we have obtained the classical result that an outbreak may occur when $R_0 = \frac{\beta}{\mu} > 1$.

The deterministic models predict a critical value $R_0 = 1$. However, it is known (Getz *et al.*, 2005; Lloyd-Smith *et al.*, 2005; Kessler & Shnerb, 2008) that stochastic fluctuations may cause a spontaneous fadeout even above this critical value. For example if $\beta = 2$ and $\mu = 1$ then $R_0 = 2$, it means that on average two persons are infected by a sick individual before it recovers. Yet there is a finite chance for the recovery of the single infected introduced (the founder) before the first infection. As shown by the figures above below the critical R_0 outbreaks never appear, but above this value the chance for an outbreak is not 1. This effect of stochasticity can not be seen within this mean-field framework. This point is discussed in detail below.

4.2. Steady state of a pandemic

In the steady state,

$$\frac{\partial I_k}{\partial t} = I_k^{in} - I_k^{out} = 0, \tag{11}$$

using eq. (5) and that $S_k = N - I_k$, we get

$$(1-\chi)\frac{\beta}{N}(N-I_k)I_k + \chi\frac{\beta}{N\langle k \rangle}(N-I_k)k\langle I_k \rangle - \mu I_k = 0. \tag{12}$$

We define α as the fraction of the infectious in the group of sites with connectivity k, i.e., $I_k = \alpha_k N$. Substituting this into the above equation, one may easily get a general description of the steady state:

$$(1-\chi)R_0(1-\alpha_k)\alpha_k + \chi\frac{R_0}{\langle k \rangle}(1-\alpha_k)k\langle \alpha_k \rangle - \alpha_k = 0. \tag{13}$$

For simplicity, we will focus from now on on the star structure with L sites (see Figure 1). In this case we can divide the nodes into two classes: the central node that holds $L-1$ links and "end nodes" holding only one connection. We define I_c, S_c, I_e, S_e as the susceptible and infectious densities on the center and on the end nodes respectively. The steady state equations for the infectious on the central node and on the end nodes reads as follows,

$$\begin{aligned}(1-\chi)R_0\alpha_c(1-\alpha_c) + R_0(1-\alpha_c)(L-1)\chi\alpha_e - \alpha_c = 0,\\ (1-\chi)R_0\alpha_e(1-\alpha_e) + R_0(1-\alpha_e)\frac{\chi}{(L-1)}\alpha_c - \alpha_e = 0.\end{aligned} \tag{14}$$

This set of equation may be solved numerically, and the results are depicted in Fig. 3. While the migration rules in our model keeping the overall size of any subpopulation fixed and for the case considered each site admits the same population, the steady state shows different density of infected individuals. As χ grows, the infected fraction on the hub grows, but on the end site the epidemic size decreases. The overall density per site of infected population, $\rho_I \equiv (\alpha_c + (n-1)\alpha_e)/n$, *decreases* with χ. It is

easy to verify that this effect is weak if the movement is rare (the first order correction to ρ_I, evaluated perturbatively for small χ, vanishes) but is pronounced when the travel parameter χ is large. In particular for $\chi = 1$ (infection only to neighboring sites) $\alpha_c = 1 - 1/R_0^2$ (growth with respect to the value $1 - 1/R_0$ for zero migration) but α_e scales like $1/n$, so all the $n-1$ nodes yield non-extensive contribution to ρ_I.

4.3. Stochastic vs. deterministic models

We stress again that movement does facilitate the outbreak of an epidemic, but this effect is invisible in the deterministic model solved above. As seen in Fig. 3b the chance of an outbreak is larger when movement is larger. This, however, comes from the effect of demographic fluctuations. Dispersal decreases the effect of "kin competition" between pathogens: as the number of individuals on each site is fixed, larger migration avoids an effective decrease in the infection rate resulted from the depletion of susceptible population (Keeling & Rohani, 1995). One of the approximations that lead to the deterministic theory is the replacement of numbers by densities, which implicitly assumes infinite number of individuals on each site such that the effect of kin competition vanishes. Kin competition manifests itself only in stochastic models of discrete individuals, like the Hamilton-May model for dispersal (Hamilton & May, 1977; Comins *et al.*, 1980).

Hamilton and May have considered two species which are identical in all aspects except of migration rate. On a regular lattice or any other type of homogenous environment the fast must win (we neglect for the moment the migration cost introduced by Hamilton and May, and assume that each emigrant reaches its destination). The reason is that agents do not have to compete with their offspring on the local resources, as the offspring leave the habitat patch occupied by the parent. On heterogenous substrate, on the other hand, there is an advantage to the slow species that may "stick" to the oases and will suffer less demographic losses due to migration into bad spatial domains. While the second effect is deterministic, the first one is stochastic and disappears in the continuum limit, since in that limit the number of individuals allowed on a patch is infinite. For that reason the model of Hastings and coworkers (Hastings, 1983) - which is a spatial version of Hamilton-May with no migration cost - failed to retrieve Hamilton-May results and suggested that the best strategy is to decrease migration rate to zero. A recent discussion of the relation between stochastic and deterministic models in the context of the evolution of dispersal rates may be found in (Kessler & Sander, 2009).

Similarly, here we have dealt with rate equations based on the continuum approximation, thus we realize only the suppressive effect of migration: the increase of χ induces a drift of infected individuals towards the hubs, that acts like a "trap". Actually, in disordered system like here there is a natural "dispersal cost" as some of the propagules end up in unfavored sites; this effect leads to maximal epidemic size at $\chi = 0$, as obtained by Hastings (Hastings, 1983), and has been proven recently by Dockery et. al. (Dockery *et al.*, 2007). As shown above, although in a fully stochastic model a larger dispersal facilitates the outbreak of the disease, the effect considered here does not disappear and in the steady state, for the range of N considered below, ρ_I is smaller when χ is larger.

5. Conclusions

The basic motivation of this work comes from the pioneering studies of Colizza and coworkers, who first suggested a realistic extension of the traditional epidemiological models to real human populations. These authors correctly assumed that the large hubs of the air traffic network correspond to sites with large population. Still their movement model mixes the local demography with the migration dynamics such that the modeler can not determine the steady state demography. Here we have presented an improved model in which round-trip travelers are modeled as a vector for transition; using our scheme one may plug the actual demographic numbers without an interference of the steady state with the law of motion of the agents.

We did not try to model a realistic airline network in all its glory as did (Colizza *et al.*, 2007). Instead

we have discussed in detail the simple case of star geometry using our technique. The results show a very interesting difference between the outbreak dynamics and the steady state behavior of the epidemic. The main take-home message is that birth-death processes on heterogenous networks may differ strongly from their counterparts in a well mixed population or on a regular networks, and in particular that the steady state size of the epidemic may not reflect the right R_0. Further extensions of this work to socially structured population are also possible.

Finally, we have addressed another issue: the impact of a vaccination campaign. It turns out that the immigration model underestimates the impact of vaccination on the hub as it allows for immigration of susceptible individuals into the hub during the outbreak. Say it another way, the spatial structure is not so important in the migration model since virtually all the activity happens on the hub. Conversely, in the travelers model vaccination campaign is much more effective as it allows for isolation of different parts of the network, thus the infection can not "percolate" in space.

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Anderson, R. & May, R. (1992). *Infectious Diseases in Humans.* Oxford: Oxford University Press.

Bailey, N. T. J. (1975). *The Mathematical Theory of Infectious Diseases.* London: Griffin.

Baxter, G. J., Blythe, R. A. & McKane, A. J. (2008). Fixation and consensus times on a network: a unified approach. *Phys. Rev. Lett.* **101**, 258701.

Chen, Y., Paul, G., Havlin, S., Liljeros, F. & Stanley, H. E. (2008). Finding a better immunization strategy. *Phys. Rev. Lett.* **101**, 058701.

Cohen, R., Erez, K., ben Avraham, D. & Havlin, S. (2000a). Breakdown of the internet under intentional attack. *Phys. Rev. Lett.* **86**, 3683.

Cohen, R., Erez, K., ben Avraham, D. & Havlin, S. (2000b). Resilience of the internet to random breakdowns. *Phys. Rev. Lett.* **85**, 4626.

Cohen, R., Havlin, S. & ben Avraham, D. (2003). Efficient immunization strategies for computer networks and populations. *Phys. Rev. Lett.* **91**, 247901.

Colizza, V., Barrat, A., Barthe'lemy, M. & Vespignani, A. (2006). The role of the airline transportation network in the prediction and predictability of global epidemics. *Proc. Natl Acad. Sci. USA* **103**(7), 2015–2020.

Colizza, V., Pastor-Satorras, R. & Vespignani, A. (2007). Reaction-diffusion processes and metapopulation models in heterogeneous networks. *Nature Physics* **3**, 276–282.

Colizza, V. & Vespignani, A. (2007). Invasion threshold in heterogeneous metapopulation networks. *Phys. Rev. Lett.* **99**, 148701.

Colizza, V. & Vespignani, A. (2008). Epidemic modeling in metapopulation systems with heterogeneous coupling pattern: Theory and simulations. *J. Theor. Biol.* **251**(3), 450 – 467.

Comins, H., Hamilton, W. & May, R. (1980). Evolutionary stable dispersal strategies. *J. Theor. Biol.* **82**, 82.

Dockery, J., Hutson, V., Mischaikow, K. & Pernarowski, M. (2007). The evolution of slow dispersal rates: a reaction diffusion model. *Jour. Stat. Phys.* **127**, 861–886.

Dorogovtsev, S. & Mendes, J. (2003). *Evolution of networks: From biological nets to the Internet WWW.* Oxford: Oxford University Press.

Getz, W. M., Lloyd-Smith, J. O., Cross, P. C., Bar-David, S., Johnson, P. L., Porco, T. C. & Sanchez, M. S. (2005). Modeling the invasion and spread of contagious disease in heterogeneous populations. In: *Disease Evolution: Models, Concepts and Data Analyses* (Feng, Z., Dieckmann, U. & Levin, S. A., eds.), vol. 71. AMS-DIMACS, pp. 113–144.

Guimerà, R., Mossa, S., Turtschi, A. & Amaral, L. A. N. (2005). The worldwide air transportation network: Anomalous centrality, community structure, and cities' global roles. *Proc. Natl. Acad. Sci. USA* **102**(22), 7794–7799.

Hamilton, W. & May, R. (1977). Dispersal in stable habitats. *Nature* **269**, 578.

Hastings, A. (1983). Can spatial variation alone lead to selection for dispersal? *Theor. Popul. Biol.* **24**, 244–251.

Keeling, M. J. & Rohani, P. (1995). Estimating spatial coupling in epidemiological systems: A mechanistic approach. *Ecol. Lett.* **5**, 2029.

Kermack, W. O. & McKendrick, A. G. (1927). A contribution to the mathematical theory of epidemics. *Proc. R. Soc. A* **115**, 700–721.

Kessler, D. & Sander, L. (2009). Fluctuations and dispersal rates in population dynamics. *Phys. Rev. E.* **80**, 041907.

Kessler, D. & Shnerb, N. (2007). Extinction rates for fluctuation-induced metastabilities: A real-space wkb approach. *Journal of Statistical Physics* **127**, 861–886.

Kessler, D. & Shnerb, N. (2008). Novel exponents control the quasi-deterministic limit of the extinction transition. *J. Phys. A Math. Theor.* **41**, 292003.

Lloyd-Smith, J. O., Cross, P. C., Briggs, C. J., Daugherty, M., Getz, W. M., Latto, J., Sanchez, M. S., Smith, A. B. & Swei, A. (2005). Should we expect population thresholds for wildlife disease? *Trends Ecol. Evol.* **20**(9), 511 – 519.

McCallum, H., Barlow, N. & Hone, J. (2001). How should pathogen transmission be modelled? *Trends Ecol. Evol.* **16**(6), 295 – 300.

Murray, J. D. (1993). *Mathematical Biology.* New York: Springer.

Pastor-Satorras, R. & Vespignani, A. (2002). Immunization of complex networks. *Phys. Rev. E* **65**, 036104.

Pastor-Satorras, R., Vzquez, A. & Vespignani, A. (2001). Dynamical and correlation properties of the internet. *Phys. Rev. Lett.* **87**, 258701.

Vespignani, A. (2008). Reaction-diffusion processes and epidemic metapopulation models in complex networks. *Eur. Phys. J. B* **64**, 349–353.

Weiss, G. H. & Dishon, M. (1971). On the asymptotic behavior of the stochastic and deterministic models of an epidemic. *Math. Biosci.* **11**, 261265.