Modelling SIRS infection with mobility and network structure

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Abstract

In this report we describe the implementation, simulation and analysis of an epidemics spreading over two networks taking into account mobility; in particular, we consider a disease spreading according to a stochastic SIRS process over two networks whose nodes travel with a certain probability according to a commuting pattern. The analysis of the results mainly focuses on how the probability of mobility and the differences in the structure of the networks affect the extinction and the recurrence of the disease.

1. Introduction

When modeling the spreading of a disease, considering a closed population with no interactions with other communities can be a very strong assumption: as we will show in this report mobility between two communities can play a fundamental role in the recurrence of a disease and its persistence. In a more positive context, we can think of a small community in which some traditions and folklore are kept alive as the "hotbed" of our disease; if we introduce a mobility pattern between this and another community in which those traditions disappeared we could observe the restoration of some lost knowledge.
In the following paragraphs we will firstly describe the theoretical basis of our model: each community is represented by a network, which allows us to also investigate the role of structure in the spreading. Each node represents an individual which can be in one of three different states at a given time step: susceptible, infected or recovered. We then introduce the chosen mobility pattern, in the form of commuting, and the probability of travel, the main variable of our model.
In the final paragraph we will discuss the results of our simulations, assessing the importance of mobility and discussing the lack of dependency of the results on the initial conditions and the underlying network structure.

2. Theory

In this section we describe and analyse from a theoretical point of view the main ingredients of our model.
Firstly, we introduce the stochastic SIRS model over a network; we then proceed in describing the chosen mobility pattern and how this was modeled taking into account the topology of the networks. Lastly, we explain the choice of the SIRS model, highlighting the difference between this model and an SIR with demography, and justify how the epidemics parameters are selected in order to make future analysis.
In the following we will refer to groups/cities as networks, in which each individual is represented by a node.

2.1. Epidemics model: SIRS

The SIRS model in its simplest form is a compartmental model in which an individual at each time step can be in one of three different states: susceptible (S), infected (I) or recovered (R). A susceptible individual can contract the disease if it comes into contact with an infected individual. At each time step an infected individual can transition to recovered: in this state the subject cannot contract the disease and it is not infectious anymore. With a given probability a recovered node transitions to susceptible again. This last transition is what differentiates the SIRS model from the plain SIR, in which a recovered individual has eternal immunity to the disease.
The model outlined is based on some assumptions that are not necessary and can be removed to obtain a more realistic description of the phenomenon that we have in mind:

1. Homogeneous mixing: all nodes are treated as equals, e.g. with the same amount of contacts $\langle k \rangle$, all with the same degree $\langle k \rangle$.

2. Each node interacts with $\langle k \rangle$ out of N nodes selected at random at each time step. In this

way each individual changes its contacts every time, coming effectively in contact with all the other individuals throughout the simulation.

If now we define λ as the probability of disease transmission in a contact between a susceptible and an infectious subject, we can for example approximate the number of new infected individuals as $\beta \frac{SI}{N}$, where $\beta = \langle k \rangle \lambda$.

2.2. Stochastic SIRS on a network

We now explain the two changes that we introduced in the SIRS model:

1. Take into account the actual contact network between individuals.
2. Use a stochastic individual-based dynamics.

Introducing a bit of notation, we define the state of individual i as $\overline{\sigma}_i = (S_i, I_i, R_i)$, that is a vector with 3 entries X_i, $X \in \{S, I, R\}$, that are equal to 1 if the individual i is in state X, 0 otherwise. In this way we can encode in a matrix $\Sigma = (\overline{\sigma}_1, \ldots, \overline{\sigma}_N)$ the complete status of all individuals at a given time. We also denote with $\overline{X} = (X_1, \ldots, X_N)$, $X \in \{S, I, R\}$, the susceptible, infected or recovered vectors.
At each time step a node changes its status with a certain probability given by the rates in Table 1.

Transition	Probability
S $\longrightarrow$ I	λ · number of infected neighbours
I $\longrightarrow$ R	μ
R $\longrightarrow$ S	γ

Table 1: *Transitions in a stochastic SIRS model with topology*

To compute the probability of a susceptible node to become infected we should in theory compute the probability that the given node gets the infection from at least one of its neighbours, that is

$$P_i[at\ least\ 1] = 1 - \prod_{j=1}^{N} (1 - \lambda A_{ij} I_j)$$

where A is the adjacency matrix of the network. Actually we approximate it with just the first order term in λI_j (that is a good approximation when there is a low fraction of infected in the system) obtaining

$$P_i[at\ least\ 1] \approx \lambda \sum_{j=1}^{N} A_{ij} I_j$$

In this way at each time step we estimate the probability that each susceptible node has to contract the infection, then draw a random number u uniformly between 0 and 1 and if $u < P_i[at\ least\ 1]$ then node i becomes infected; this is how we simulate a stochastic contact process.
In a similar but simpler way we consider a stochastic dynamics for the $I \longrightarrow R$ and $R \longrightarrow S$ transitions, where again we draw a random number u uniformly distributed in $[0, 1]$ and make the transitions happen if $u < \mu$ or $u < \gamma$ respectively (of course we use a different random number for each transition of each individual at each step).

2.3. Mobility model: two-steps commuting

In this paragraph we describe how mobility is modeled taking into account the structure of the networks involved. In our treatment mobility follows a commuting pattern, meaning that at each time step in our simulation a traveling node detaches from its network, visits the other network and then goes back to its original position. We refer to this as "two-steps commuting" as the spreading of the epidemics happens in two steps: when the traveling node reaches the new network and when the traveling node returns to its own community.
The probability of travel p_{mob} is the fraction of nodes in a network that travels at each time step, namely $n_{travellers} = N * p_{mob}$ where N is the number of nodes in each network. At the beginning of the simulation $n_{travellers}$ are chosen uniformly at random in each network and they will be the nodes that at each iteration of the simulation leave their network and visit the other. The travelling nodes attach to the other network keeping their original degree (i.e. making as many contacts as they had in the original network) and following the degree distribution of the target network. This choice, in our opinion, reflects a likely real scenario and allows us to take into account characteristics of both the origin of the individual and of the target.

2.4. Choice of the model and the epidemics parameters

In our case of study we need a model that, under specific conditions, admits an endemic equilibrium solution: the basic idea is to choose the parameters of the model to be in a critical region between the endemic equilibrium and the disease-free equilibrium and see how mobility between the communities can reintroduce the disease. In this context the role of demography is fundamental as we need to reintroduce susceptible individuals in the system; for this reason the ideal model would have been an SIR with demography. However, reintroducing nodes in

a network can be computationally very expensive as it means re-computing its adjacency matrix anytime a new node is added. By choosing the SIRS model we avoid this step and reintroduce susceptible individuals without actually adding new nodes.
As we mentioned, our goal is to study if and under which conditions the introduction of mobility between two networks sustains or reintroduces an otherwise disappearing disease.
In order to do so, once the model is outlined, we have to identify some "critical parameters" for it, namely those values of β, μ and γ for which the spreading over two uncoupled networks ends up, on average, with the extinction of the disease.
A real life case of a disease following an SIRS model is influenza. We thus set our parameters to be as similar as possible to those of influenza for which the basic reproductive ratio R_0[1] ranges between 0.9 and 2.1 and the infectious period[2] lasts for about 5 to 7 days, meaning that $\mu \in [\frac{1}{5} \sim \frac{1}{7}] = [0.14 \sim 0.2]$ if we consider a simulation step as a day. β was computed as $\beta = R_0 * \mu$ and topology was taken into account computing $\lambda = \frac{\beta}{\langle k \rangle}$. Lastly we chose a transition time for $R \longrightarrow S$ of an average of 60 days: this value and the final values of the other parameters were chosen running some simulations on the two uncoupled networks and choosing those values for which the disease died out in the majority of the cases but not in all of them. This behaviour, in our opinion, showed that the disease was not "strong" enough to sustain itself but that the parameters were in a critical region that sometimes allowed it to survive. The initial ranges and final values of the parameters are listed in Table 2.

Parameter	Range	Value
R_0	$0.9 \sim 2.1$	2
μ	$0.14 \sim 0.20$	0.15
β	$0.13 \sim 0.42$	0.3
$\lambda(\langle k \rangle = 4)$	$0.03 \sim 0.1$	0.075
γ	—	0.016

Table 2: *Epidemics parameters*

3. Analysis and results

In this section we present the results of our simulations.

We considered two kinds of networks, one that presents a power law degree distribution (denoted as "scale free" - SF) and the other one that is the Erdős-Rènyi (ER) graph (degree follows a binomial distribution), both with $N = 1000$ nodes and average degree $\langle k \rangle = 4$.

[1]https://www.ncbi.nlm.nih.gov/pubmed/19545404
[2]https://www.cdc.gov/flu/professionals/acip/clinical.htm

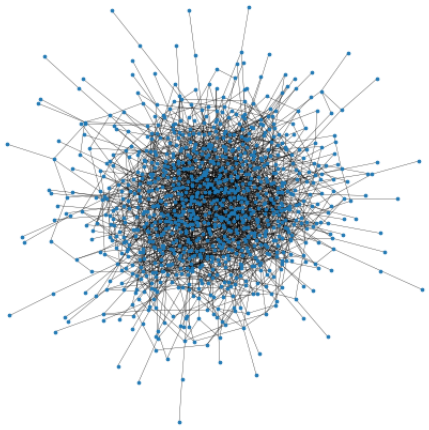

Figure 1: *Example of Erdős-Rènyi with 1000 nodes and average degree 4.*

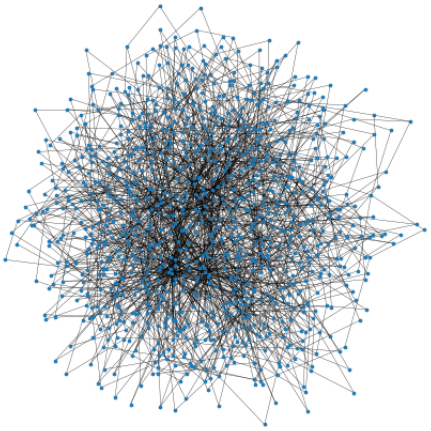

Figure 2: *Example of scale-free with 1000 nodes and average degree 4.*

The main objective of our analysis is to see if and how mobility between two networks affects the persistence of a disease.
We use two different metrics to do that: the probability of extinction p_{ext} and the fraction of cumulative time spent as disease-free dt_{ext} (let's just call it cumulative extinction time for simplicity). Given n runs of the simulation with the same parameters, the first metric is defined as the fraction of simulations in which at least for a time step a system was disease-free after having presented the disease; the second metric is the number of time steps in which a system was disease-free divided by the total number of time steps (a.k.a. iterations).
Furthermore we inquire the following dependencies for the probability of extinction and the cumulative extinction time:

1. Dependence on the topology of the network (SF

vs ER).

2. Dependence on the topology of the coupled network (SF with ER against SF with SF).

3. Dependence on the initial conditions (number of initial infected of each network).

More in concrete, we considered 20 values of the probability of mobility p_{mob} evenly spaced between 0.03 and 0.2 and simulated for each parameter:

1. 100 runs of a system composed by a SF network with 5 initial infected (SF_5) and a ER network with 0 initial infected (ER_0).

2. 50 runs of a system composed by a SF network with 5 initial infected (SF_5) and a SF network with 0 initial infected (SF_0).

3. 50 runs of a system composed by a SF network with 3 initial infected (SF_3) and a SF network with 2 initial infected (SF_2): since the two networks are almost symmetric both in structure and in initialization we aggregate the results of this simulation in order to build faster the same statistics. Basically we are assuming $(SF_3, SF_2) \approx (SF_{sym}, SF_{sym})$ and we will show the aggregated data like if it was obtained from a single net SF_{sym} in 100 runs of (SF_{sym}, SF_{sym}).

These simulations provide us with the raw information to test all the dependencies that we have listed above.
First of all we can see in Fig. 3 and Fig. 4 that both metrics decrease as the fraction of individuals interested by mobility increases.
Furthermore we can see in Fig. 3 that the probability of extinction is higher for SF_5 network w.r.t. the ER_0 network, whereas the fraction of cumulative extinction time is basically the same. Our hypothesis is that this is an artifact due to the chosen initialization for the infected, because there can be cases where the disease dies out in the SF_5 network without ever travelling to the ER_0 one, hence for the probability of extinction metric in the second network the disease never become extincted in that particular run, lowering the average probability of extinction. Unfortunately we had not the time to simulate the inverse case (SF_0, ER_5) and the results from the (SF_5, SF_0) and (SF_3, SF_2) simulations are not precise enough to support or contradict this hypothesis, as can be seen in Fig. 5. From this we can conclude that the fraction of cumulative extinction time is much more reliable as a metric for the effects of mobility on spreading epidemics.
An interesting fact is that the fraction of cumulative extinction time of two coupled networks tends to be the same, as can be seen in Fig. 4 for the pair (SF_5, ER_0) and in Fig. 6 for both pairs.

4. Conclusions

In this work we simulated the stochastic spreading of an SIRS-like disease on two systems connected by commuting patterns, taking also into account the underlying network structure of the two systems.
The main result that we achieved was to show that the probability of a node to travel from one system to the other affects the persistence of the disease, decreasing both the probability of extinction and the fraction of time in which the system is disease-free as the probability of mobility increases.
We then tried to test some dependencies of the disease's persistence (properly measured with two different metrics), namely the dependence on the topology of the networks and on the initial conditions, but, using as metric the fraction of cumulative extinction time, we did not find dependence on the first factor.
Furthermore, simulations on paired scale-free networks seemed to show that there is no dependence on the initial conditions of the two systems, as long as the total number of initial infectious individuals is the same.
Future developments of this work could be to test this model against a stochastic SIRS with mobility without taking into account the structure, to see if the predictions of the two models differ or not and to test it with different sizes and average degrees, in order to study if changing these parameters shifts the model into more interesting regimes, where the differences in the network structure can be appreciated.

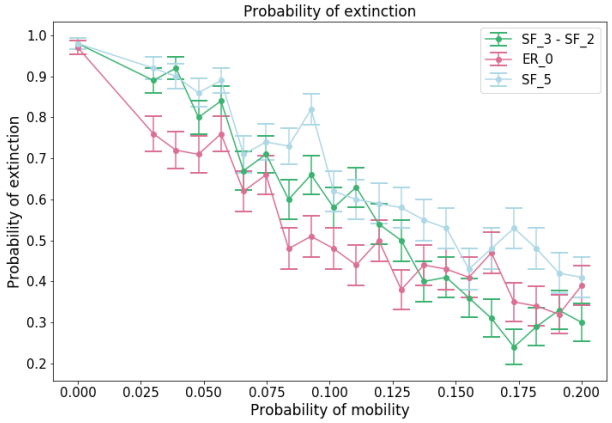

Figure 3: *Probability of extinction for the networks used in the simulations of (SF_5, ER_0) and (SF_3,SF_2). The data from the second simulation has been aggregated like if they were 100 runs from the same network instead of 50 and 50 for symmetry reasons.*

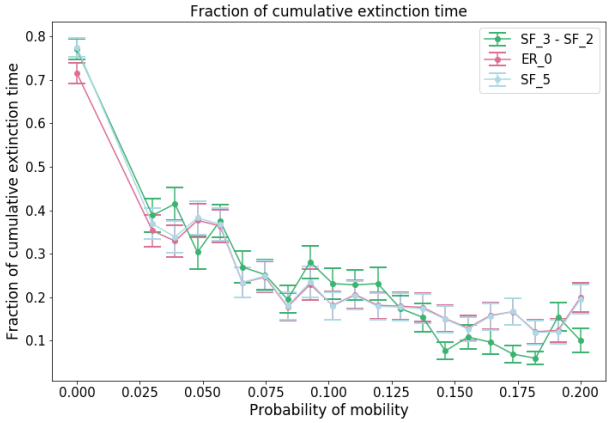

Figure 4: *Fraction of cumulative extinction time for the networks used in the simulations of (SF_5, ER_0) and (SF_3,SF_2). The data from the second simulation has been aggregated like if they were 100 runs from the same network instead of 50 and 50 for symmetry reasons.*

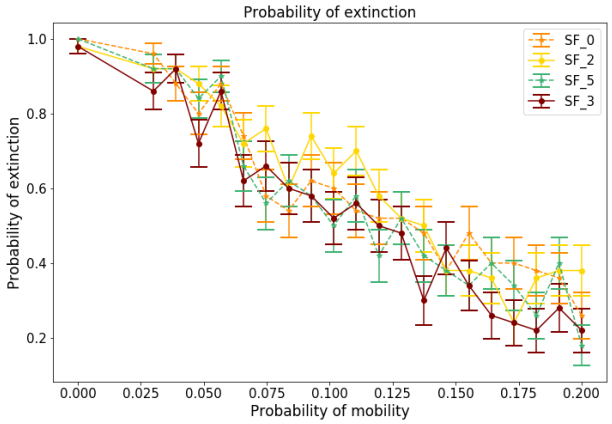

Figure 5: *Probability of extinction for the networks used in the simulations of (SF_5, SF_0) and (SF_3,SF_2). No clear dependence on the initial condition emerges, but the variance of the simulations would cover every signal of that dependence.*

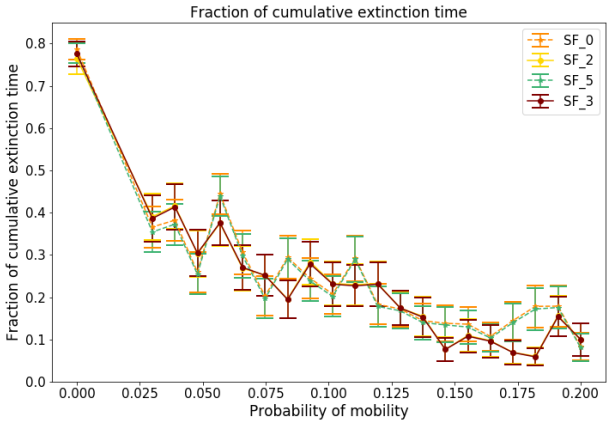

Figure 6: *Fraction of cumulative extinction time for the networks used in the simulations of (SF_5, SF_0) and (SF_3,SF_2). It can be seen how the variables are almost identical for the pairs of coupled networks.*