

Epidemic spreading in localized environments with recurrent mobility patterns

Clara Granell^{1,2,3} and Peter J. Mucha³

¹Departament de Física de la Matèria Condensada, Universitat de Barcelona, Martí i Franquès 1, E-08028 Barcelona, Spain

²Universitat de Barcelona Institute of Complex Systems (UBICS), Universitat de Barcelona, E-08007 Barcelona, Spain

³Carolina Center for Interdisciplinary Applied Mathematics, Department of Mathematics, University of North Carolina, Chapel Hill, NC 27599-3250, USA

The spreading of epidemics is very much determined by the structure of the contact network, which may be impacted by the mobility dynamics of the individuals themselves. In confined scenarios where a small, closed population spends most of its time in localized environments and has easily identifiable mobility patterns—such as workplaces, university campuses or schools—it is of critical importance to identify the factors controlling the rate of disease spread. These kinds of scenarios are usually represented using metapopulation models [3]. In such settings, the nodes of the network represent a population, which is occupied by individuals, and the links of the network represent the migration of individuals from one population to another. This scenario is particularly useful in the study of the spreading of epidemics, given that many real-life patterns of interactions happen in structured, localized populations connected by some degree of migration.

The problem of modeling such scenarios relies on finding the appropriate level of abstraction to grasp the main macroscopic features of the epidemic spreading process for individuals across the particular environment. Traditionally, models for epidemic spreading in metapopulations assume that individuals diffuse randomly and that subpopulations with the same number of connections are treated as statistically equivalent. Although useful, this approach does not capture some important real-world features, like the fact that human dynamics are often dominated by recurrent patterns where individuals have memory of the location they come from and are likely to return to their original location after a short exploration of the network.

In this work we present a discrete-time Markov-chain model for epidemic spreading in structured populations with a recurrent pattern of migrations between the locations in a bipartite network. The aim of this model is to quantify the extent of an SIS-like epidemic in the scenario where each individual spends his time between two locations: their *residence* and *common* locations (where mixing with individuals coming from other residence subpopulations happen). In short, the dynamics are as follows: for each day, agents leave their residence sites with probability p and choose a common location according to the network topology W . Then, both the agents remaining in their residences and the ones that have traveled can get infected by contacting the other agents populating their destination node. After this is done, the individuals return to their residence, and another infection step is performed. Additionally, we introduce a typical mechanism of isolation—such as reducing the mobility of infected individuals—to see if it is able to contain the spreading of the disease.

Our analytical formulation is based on discrete-time Markov-chains [1, 2] and it is able to calculate the fraction of infection at each patch of the metapopulation network. It also allows us to derive analytically the exact expression of the epidemic threshold. We have crosschecked the results

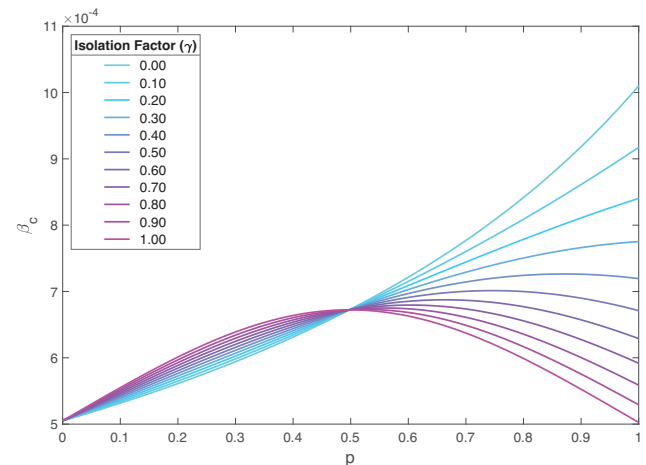


Fig. 1. Epidemic threshold as a function of the mobility parameter p , for different values of the isolation factor γ , where $\gamma = 0$ means that infected individuals cannot travel and $\gamma = 1$ means infected individuals do travel with the same probability than the susceptible ones. For this particular topological configuration, the value of p^* is 0.5, as seen for the curve corresponding to $\gamma = 1$. As the isolation factor γ decreases (more restriction in the mobility of the infected) the optimum mobility p^* is shifted right (the disease is more contained as the mobility increases).

of our model with extensive Monte Carlo simulations, with remarkable correspondence.

Among our findings, we have observed that the curve of the epidemic threshold as a function of the mobility probability p does not have a monotonic behavior. Instead, there is an optimum value of the mobility (p^*), which makes the epidemic threshold maximum. That value is the value of the mobility probability that causes all subpopulations in the network to be of the same (or most similar) effective size during the daytime infection step. We also explored the effect of isolation, i.e., the reduction of mobility of the infected individuals. We find that as the mobility of the infected individuals is more restricted, the epidemic threshold increases with increasing mobility (see Fig. 1), meaning that if infected individuals are contained in their residences, the lower spreading of the disease will happen when the susceptible individuals travel the most out of their residence.

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