

Epidemics in networked and multiplex metapopulations

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During recent years, we have witnessed the outbreak of some important diseases such as the H1N1 pandemic in 2009, Ebola in 2014 and Zika in 2015. A common feature of these illnesses is they were originated in a little region and then, after some elapsed time, they propagate at large scale to turn into worldwide epidemics. This fact have encouraged the researchers to do models capable of taking into account the contagious processes at a local scale and also the large scale mobility processes which lead to the global propagation. By this way, metapopulation models have emerged.

A metapopulation is a complex network where nodes are associated to places in which the agents live. These agents can move over the network, being their displacements determined by the links. Therefore mobility patterns are encoded by links. Even though first metapopulation models relied on diffusion processes to represent the movements of the agents, we have considered commuting processes where each agent have a node identified with his residence and his movements consist of going to one of the neighbours, staying there for a while and then return to his residence. The main reason for this consideration is the high frequency of this kind of movements in our routine. In this sense, several articles have been written proposing models in order to face the large scale spread of a disease considering commuting processes [1, 2, 3]. Even though some interesting results have been obtained, all these models make some assumptions, mainly heterogeneous mean field, which limit their predictability.

In order to avoid this fact, we have left this assumption and make all the agents statistically independent. Under this premise and considering commuting processes, we have proposed a model (MIR Model) using a MMCA (Markovian Microscopic Chain Approach) which exhibits a perfect agreement with numerical results obtained by simulations based on Monte-Carlo algorithms (see Fig 1). In our model, as we have said before, each agent has a node associated to him. For each time step, agents decide whether staying in their node or going to another node with a probability p . If they decide to move, they choose their target in function of the weights of the mobility matrix \mathbf{W} . Once all the agents have moved, contagious processes take place. In order to characterise them, we have considered a SIS model and also a well mixed population inside each node, so that each agent interacts with the rest who are inside his node. After all agents have updated their dynamical state according to the SIS model, we force the agents to return to their residence. Finally, we do iteratively all these processes until the epidemic reaches the stationary state.

Even though metapopulations are structures with a considerably high degree of complexity, they have some limitations such as they do not allow to introduce different mobility patterns of the people who reside in the same node. For

example, metapopulation models suppose that a rich person visit the same places than a poor one who reside in his same node. To solve this problem, and thanks to the high predictability of the MIR model, we have extended it easily to the case of a multiplex network in which each layer encode different mobility patterns. To conclude, we have checked how this more realistic model about the propagation of diseases keeps predicting with a surprising accuracy their impact after their onset.

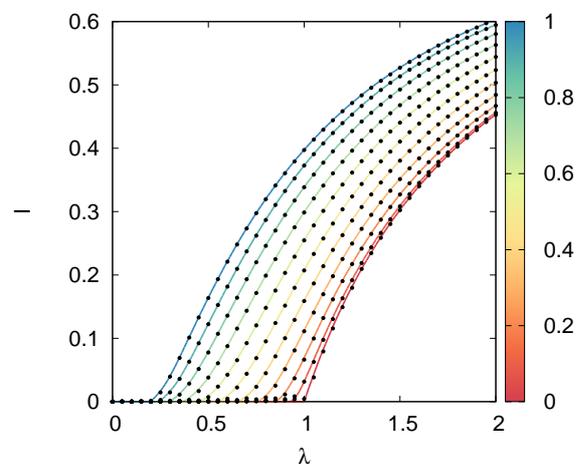


Figure 1: Total fraction of infected people in function of λ after the onset of a SIS disease over a SF network. The network we have used have 1000 nodes homogeneously populated by 5000 agents. Solid lines, whose colours represent different values of the mobility of the agents (p), correspond to the predictions of our MIR model, whereas black dots are the numerical results from MC simulation.

- [1] D. Balcan, and A. Vespignani. Phase transitions in contagion processes mediated by recurrent mobility patterns. *Nature Phys.* **7**, 581–586 (2011).
- [2] V. Belik, T. Geisel and D. Brockmann. Natural Human Mobility Patterns and Spatial Spread of Infectious Diseases. *Phys. Rev. X* **1**, 011001 (2011).
- [3] V. Belik, T. Geisel and D. Brockmann. Recurrent host mobility in spatial epidemics: beyond reaction-diffusion. *Eur. Phys. J. B* **84**, 579–587 (2011).