

Influence of recurrent mobility patterns on the spread of vector-borne diseases

David Soriano-Paños^{1,2}, Sandro Meloni², Juddy Heliana Arias-Castro³, and Jesús Gómez-Gardeñes^{1,2}

¹Departamento de Física de la Materia Condensada, Universidad de Zaragoza, 50009 Zaragoza, Spain

²Instituto de Biocomputación y Física de Sistemas Complejos (BIFI), Universidad de Zaragoza, 50018 Zaragoza, Spain

²Departamento de Matemáticas, Universidad del Valle, 25360 Cali, Colombia

Contagious diseases cause more than millions of deaths all over the world according to the World Health Organization [1]. There exists a great variety of contagious diseases depending on the mechanism that drives the epidemic spreading. In this talk, we are going to focus on vector-borne diseases, which are indirectly transmitted among humans via the intermediation of some external agents, denoted as vectors, like mosquitoes, sand-flies, ticks, etc.

The impact of these vector-borne diseases, especially in tropical areas, has raised the necessity of making models capable of predicting their incidence as well as their spatio-temporal propagation patterns. In this sense, the most paradigmatic model is the Ross-Macdonald model [2, 3], in which vectors as well humans can adopt two dynamical states: susceptible of contracting the disease or infected by them. The Ross-Macdonald model has been widely studied by following mean field theories and some important analytical results have been obtained such as estimations of the boundaries between the epidemic phase and the disease free one.

However, these results correspond to closed systems in which agents as well as vectors are assumed not to move. In light of the crucial role that human mobility has played on the spread of many diseases, we want to extend the Ross-Macdonald model to account for recurrent human mobility patterns. Based on the equations previously developed for directly transmitted diseases between humans [4], we will propose a new formalism to assess the effects of human mobility on the spread of vector-borne diseases. To check the validity of the proposed model, we will compare its theoretical predictions with results from Monte Carlo simulations. Figure. 1 shows this comparison by using a SF metapopulation as the underlying mobility network.

Once we have checked the validity of our equations, we will be able to deduce an estimation of the epidemic threshold which will shed light on the effects of mobility on the onset of epidemics. In addition to the differences concerning the contagion mechanisms, the consequences of contracting vector-borne diseases are severe and usually prevent the infected agents from moving in a normal way. For this purpose, we will introduce a restriction in the mobility of infected agents. This way, we will study the influence of the interplay between the mobility of both infected and susceptible agents on the epidemic threshold. Interestingly, we will

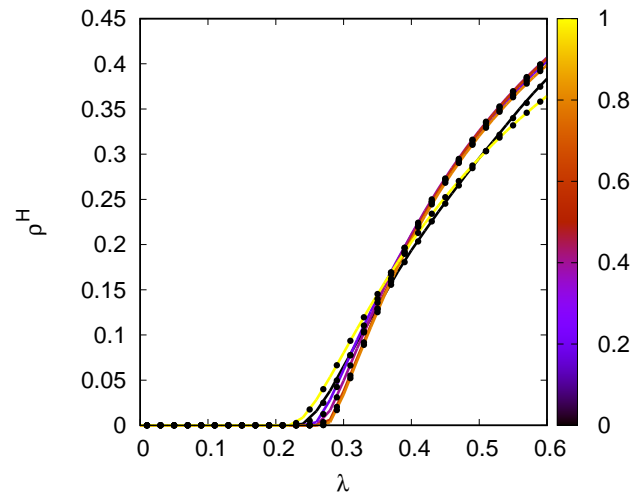


Fig. 1. Total fraction of infected people ρ^h in the stationary state as a function of the infectivity λ between humans and mosquitoes and the mobility, here denoted with the color scale.

reveal that the restriction of mobility of infected agents will be very determinant since it will dramatically change the dependence of the epidemic threshold on the mobility of the susceptible agents.

Finally, we will study the applicability of our model to predict the most affected geographical areas by the outbreak of vector-borne diseases. Thus, we will show that our model is able to capture them for the case of Dengue outbreaks in the city of Cali, Colombia.

[1] WHO Fact sheet N°38 (2014).

[2] R. Ross, *The Prevention of Malaria* (John Murray, London, 1911).

[3] D. L. Smith, K. E. Battle, S. I. Hay, C. M. Barker, T. W. Scott, and F. E. McKenzie, *PLoS Pathog.* **8**, e1002588 (2012).

[4] J. Gómez-Gardeñes, D. Soriano-Paños, and A. Arenas, *Nat. Phys.* **14**, 391 (2018).