

Markovian Analysis of Reaction-Diffusion Processes in Complex Metapopulations

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During the last decades we have witnessed the onset of several major global health threats such as the 2003 spread of SARS, the H1N1 influenza pandemic in 2009, the western Africa 2014 Ebola outbreaks and more recently the Zika epidemics in the Americas and Caribbean regions during 2015 and 2016. These outbreaks are increasingly characterized by the small elapsed time between initial infections in a single region to the global epidemic state affecting different cities, regions, countries and, in some cases, continents. Thus, in the recent years a great effort has been devoted to adapt classical epidemic models taking into account the multiscale nature of diseases propagation so to reproduce the fast unfold of emergent diseases and serve as theoretical frameworks to design both local and global contention strategies [1, 2].

It is clear that the spread of an emergent infectious disease is the result of human-human interactions in small geographical patches. However, in order to understand the geographical diffusion of diseases one has to combine these microscopic contagion processes with the long-range disease propagation due to human mobility across different spatial scales. To tackle this problem epidemic modeling has relied on reaction-diffusion dynamics in metapopulations [4] so that a population is distributed in a set of patches, being the size (number of individuals) of each patch in principle different. The individuals within each patch are well-mixed, *i.e.*, pathogens can be transmitted from an infected host to any of the healthy agents placed in the same patch.

The second ingredient of metapopulation frameworks concerns the mobility of agents. Each host is allowed to change its current location and occupy another patch, thus fostering the spread of pathogens at the global system level. The non-trivial mobility patterns of real populations and the recent advances of network epidemiology [5] has motivated a thorough analysis about the impact of mobility networks on the onset of global-scale contagions. In the last decade, most of theoretical works have assumed simple mobility patterns and mean-field approximations for hosts and patches behavior, to be able of predicting the onset of an outbreak. In these models random diffusion of agents between patches is often used as proxy of human mobility [6, 7, 8, 9] while, as in the case of the heterogeneous mean field approach in networks, subpopulations with identical connectivity patterns are assumed to be equally affected by the disease.

As data gathering techniques and epidemic surveillance increase their accuracy, metapopulation models face new challenges [10]. In an effort of relaxing the assumption about random diffusion of hosts and approach the realistic mobility patterns used in agent based simulations [11], recently the recurrent and spatially constrained nature of most human movements, such as daily commutes, has been addressed [12, 13], at the expense of considering either mean-field assumptions or simple mobility networks.

In this presentation we aim at going one step beyond mean field models of metapopulations in attempt to increase the realism of epidemiological models without compromising their theoretical analysis. To this aim we propose a novel theoretical framework in which the dynamical variables of each patch forming the metapopulation are treated independently. In addition this framework can accommodate any mobility network from real commuting datasets and is amenable to any particular distribution of the population across the patches. We investigate the effect of the diffusion (mobility) on the spreading of the epidemics, and obtain analytic expressions that relate mobility and incidence in all the phase diagram of the system. Interestingly, we can determine conditions where mobility detracts the spreading of epidemics. We analyze real mobility networks where epidemics is damped by the mobility patterns reported.

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