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Human mobility and time spent at destination: Impact on spatial epidemic spreading

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HIGHLIGHTS

- We model contagion spreading on a metapopulation model with non-Markovian mobility.
- We assume a heterogeneously distributed length of stay of travelers at destination.
- We find that the length of stay distribution affects the system's epidemic behavior.
- We study the effects of behavioral changes on the global invasion threshold.
- We compare our epidemic results to a Markovian model and find strong differences.

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ABSTRACT

Host mobility plays a fundamental role in the spatial spread of infectious diseases. Previous theoretical works based on the integration of network theory into the metapopulation framework have shown that the heterogeneities that characterize real mobility networks favor the propagation of epidemics. Nevertheless, the studies conducted so far assumed the mobility process to be either Markovian (in which the memory of the origin of each traveler is lost) or non-Markovian with a fixed traveling time scale (in which individuals travel to a destination and come back at a constant rate). Available statistics however show that the time spent by travelers at destination is characterized by wide fluctuations, ranging from a single day up to several months. Such varying length of stay crucially affects the chance and duration of mixing events among hosts and may therefore have a strong impact on the spread of an emerging disease. Here, we present an analytical and a computational study of epidemic processes on a complex subpopulation network where travelers have memory of their origin and spend a heterogeneously distributed time interval at their destination. Through analytical calculations and numerical simulations we show that the heterogeneity of the length of stay alters the expression of the threshold between local outbreak and global invasion, and, moreover, it changes the epidemic behavior of the system in case of a global outbreak. Additionally, our theoretical framework allows us to study the effect of changes in the traveling behavior in response to the infection, by considering a scenario in which sick individuals do not leave their home location. Finally, we compare the results of our non-Markovian framework with those obtained with a classic Markovian approach and find relevant differences between the two, in the estimate of the epidemic invasion potential, as well as of the timing and the pattern of its spatial spread. These results highlight the importance of properly accounting for host trip duration in epidemic models and open the path to the inclusion of such an additional layer of complexity to the existing modeling approaches.

1. Introduction

The spatial distribution of hosts and their mobility behavior represent two key ingredients in the spatial dissemination of an infectious disease affecting the host population. Modeling approaches that take into account these ingredients can address crucial epidemiological issues on the expected outcome, such as the persistence of

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an infection in the population or the conditions for the invasion of an emerging epidemic (Riley, 2007).

An ideal theoretical framework to capture the effects of the spatial structure of a population and to explore its epidemiological implications is given by the metapopulation approach (Hanski and Gilpin, 1997; Grenfell and Harwood, 1997; Tilman and Kareiva, 1997; Bascompte and Solé, 1998; Hanski and Gaggiotti, 2004). This framework has been widely used in population ecology and epidemiology and describes the dynamics of a population in a fragmented environment where a discrete number of localized subpopulations or patches are connected by mobility fluxes. In metapopulation epidemic models, individuals belong to well-defined social or geographical units (e.g. households, towns, or large urban areas) and the coupling among these units is generated by the mobility connections and determines the disease circulation on the spatial system (Hethecote, 1978; May and Anderson, 1984; Bolker and Grenfell, 1995; Sattenspiel and Dietz, 1995; Keeling and Rohani, 2002; Grenfell and Harwood, 1997; Ferguson et al., 2003).

Recently, metapopulation models have been integrated with empirical data on human demography and mobility to create data-driven computational tools for the analysis of large-scale geographic spread of infectious diseases (Grais et al., 2004; Hufnagel et al., 2004; Colizza et al., 2006, 2007a; Cooper et al., 2006; Epstein et al., 2007; Balcan et al., 2009a). The use of real data on human mobility has uncovered the important role of the various heterogeneities that characterize human movement patterns on the resulting epidemic. The network structure of human patterns is usually defined as *complex*, indicating that it displays a large variability, spanning several orders of magnitude, in the number of connections between locations and in the number of travelers between each origin and destination center. Such complex features have been found in the worldwide air travel patterns (Barrat et al., 2004; Guimerá et al., 2005) and in commuting patterns between urban areas (Chowell et al., 2003; Brockmann et al., 2006; González et al., 2008; Balcan et al., 2009a). These fluctuations are particularly relevant when human mobility networks are used as a substrate for metapopulation epidemic models. Under very general assumptions, it has been shown that a metapopulation system may be characterized by two epidemic thresholds: a local epidemic threshold that regulates the spread of the infection within a single subpopulation (Anderson and May, 1992), and a global epidemic threshold that determines if the epidemic invasion can reach a significant fraction of subpopulations (Ball et al., 1997; Cross et al., 2005; Colizza and Vespignani, 2007, 2008; Colizza et al., 2007c). The latter distinguishes cases of spatial invasion from outcomes in which, despite an ongoing outbreak in the seed subpopulation, the epidemic is not able to spread spatially because of a small enough mobility rate, which does not ensure the travel of infected individuals to other subpopulations before the end of the local outbreak, or which produces small enough seeding events not enabling the start of an outbreak in the reached subpopulation due to local extinction events. Assuming that individuals are homogeneously mixed within each subpopulation, the local threshold depends on the disease parameters only, but the global threshold depends also on the statistical fluctuations of the network connectivity and on the mobility fluxes. In case of a broad distribution of connections per subpopulation, while the condition for the occurrence of the local outbreak remains unchanged, the topological fluctuations lower the threshold condition for the global invasion, thus strongly favoring the spatial spread of the epidemic (Colizza and Vespignani, 2007, 2008; Colizza et al., 2007c).

Within the metapopulation framework, such results were obtained under the assumption that the mobility of individuals and the concurrent epidemic process can be modeled as particle reaction–diffusion processes (Colizza et al., 2007c). The first studies also assumed a Markovian dynamics, representing individuals who are indistinguishable regarding their travel pattern, so that at each time step the same traveling probability applies to all individuals without having memory of their origin (Colizza and Vespignani, 2007, 2008; Colizza et al., 2007c). This assumption has also been adopted in several modeling approaches for the data-driven large-scale spreading of infectious diseases (Rvachev and Longini, 1985; Longini, 1988; Flahault and Valleron, 1991; Grais et al., 2003, 2004; Hufnagel et al., 2004; Cooper et al., 2006; Epstein et al., 2007; Colizza et al., 2007a,b; Balcan et al., 2009a), mainly for simplification purposes and the absence of exhaustive detailed origin-destination data. Human mobility has however a clear territorial nature characterized, on average, by individuals spending short periods away of their permanent location. In addition, recent results on the analysis of detailed mobility data at the individual level have pointed out the high level of predictability and recurrence of individual daily travel patterns (Wang and González, 2009; Song et al., 2010a,b). Such recurrent patterns have therefore been included in spatially structured approaches with a specific focus on commuting modes of mobility, that is the type of recurrent daily mobility from the location of residence to the location of work (Sattenspiel and Dietz, 1995; Danon et al., 2009; Keeling et al., 2010; Balcan and Vespignani, 2011, 2012; Belik et al., 2011). This corresponds to recording the subpopulation of residence for each individual, assuming that they spend a fixed time at destination, before returning to their residence at each time step.

Additional modes of mobility, besides the commuting behavior, are characterized by variable lengths of stay at destination, mainly dependent on the purpose of the trip but also on its logistical details and the accessibility of the destinations. Data collected from the office of statistics of several countries worldwide indicate that the time spent by travelers at their destination is broadly distributed and ranges from a single day to months. In Fig. 1 we present some examples that support such empirical evidence for a number of countries. The number of nights spent by foreign travelers in the UK and other European countries span several orders of magnitude, ranging from less than a week to 6 months or more, considering all countries of origin and all travel purposes. Importantly, the average time spent by tourists in different British cities shows strong geographical variations: some locations are characterized by a short length of stay (less than 4 days on average) while in other cities travelers spend on average more than 20 days. The length of stay also depends strongly on the purpose of the trip. As shown by Australian data, business trips tend to be shorter, usually lasting less than 15 days, while educational and employment trips are usually very long and can easily exceed the 3 months duration, on average. Holiday trips show large fluctuations in their duration and can last from few days up to 50 days, on average. Furthermore, similar large fluctuations in the duration of visits were also observed on different time and spatial scales. For instance, the time spent by residents in different locations within a US city during their daily routine varies from few minutes to several hours (Eubank et al., 2004, 2006). Similarly, the analysis of a large dataset of mobile phone records revealed that the time spent by mobile phones users at a given location identified by a phone tower cell, Δt, follows a power law distribution $P(\Delta t) \sim |\Delta t|^{-(1+\beta)}$ with $0 < \beta \leq 1$ (González et al., 2008; Song et al., 2010a).

Prompted by these empirical findings, we study spreading processes on a metapopulation system where individuals have memory of their subpopulation of origin and spend at destination an average length of stay τ that is broadly distributed. This corresponds to focus on an additional level of heterogeneity that is observed in human mobility and that is associated to the timescales of travel movements.

In order to integrate the large fluctuations of τ observed in reality into our modeling framework, we assume that the length of stay of travelers depends on their destination only and it varies from place to place, as a power-law function of the connectivity of a subpopulation,