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A network model for Ebola spreading

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HIGHLIGHTS

- We define a realistic Ebola model that does not rely on homogeneous mixing.
- We reproduce the dynamics of the 2014–2015 Ebola outbreak in Liberia.
- We model non-ideal and time-varying intervention policies.
- We assess the efficacy intervention policies with respect to their application time.

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ABSTRACT

The availability of accurate models for the spreading of infectious diseases has opened a new era in management and containment of epidemics. Models are extensively used to plan for and execute vaccination campaigns, to evaluate the risk of international spreadings and the feasibility of travel bans, and to inform prophylaxis campaigns. Even when no specific therapeutical protocol is available, as for the Ebola Virus Disease (EVD), models of epidemic spreading can provide useful insight to steer interventions in the field and to forecast the trend of the epidemic. Here, we propose a novel mathematical model to describe EVD spreading based on activity driven networks (ADNs). Our approach overcomes the simplifying assumption of homogeneous mixing, which is central to most of the mathematically tractable models of EVD spreading. In our ADN-based model, each individual is not bound to contact every other, and its network of contacts varies in time as a function of an activity potential. Our model contemplates the possibility of non-ideal and time-varying intervention policies, which are critical to accurately describe EVD spreading in afflicted countries. The model is calibrated from field data of the 2014 April-to-December spreading in Liberia. We use the model as a predictive tool, to emulate the dynamics of EVD in Liberia and offer a one-year projection, until December 2015. Our predictions agree with the current vision expressed by professionals in the field, who consider EVD in Liberia at its final stage. The model is also used to perform a what-if analysis to assess the efficacy of timely intervention policies. In particular, we show that an earlier application of the same intervention policy would have greatly reduced the number of EVD cases, the duration of the outbreak, and the infrastructures needed for the implementation of the intervention.

1. Introduction

Since the discovery of Ebola viruses in 1976, the 2014–2015 outbreak of the Ebola Virus Disease (EVD) has been the largest in terms of number of countries involved, reported cases, and casualties. As of December 13, 2015 the Centers for Disease Control and Prevention (CDC) have reported more than 28,600 cases in six West African countries, of which about 15,200 have been laboratory confirmed, totaling more than 11,300 casualties (Centers for Disease Control and Prevention, 2014a). Outside of these regions, one case has been reported in Spain, one in the United Kingdom, and four in the United States of America, one of which has resulted in a casualty (Centers for Disease Control and Prevention, 2014b). While massive interventions are currently underway in afflicted countries, unaffected countries worldwide are striving to strengthen their preparedness and response plans through clinical

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and non-clinical interventions (Centers for Disease Control and Prevention, 2014c). In this context, mathematical modeling of infectious disease spreading can provide paramount information on the progression of EVD and on short/long-term outcomes of the epidemics. At the same time, policy makers could benefit from quantitative and qualitative information afforded by such mathematical models that directly assess the effectiveness of intervention policies (Keeling and Eames, 2005; Legrand et al., 2007; Brauer and Castillo-Chavez, 2011; Keeling and Rohani, 2011; Althaus, 2014; Fisman et al., 2014; Gomes et al., 2014; Meltzer et al., 2014; Nishiura and Chowell, 2014; Rivers et al., 2014; Towers et al., 2014; Merler et al., 2015; Valdez et al., 2015; Webb et al., 2015).

As in the study of many other infectious diseases (Keeling and Eames, 2005; Brauer and Castillo-Chavez, 2011; Keeling and Rohani, 2011), modeling efforts on EVD have mainly focused on mean-field compartmental models, either deterministic or stochastic, and agent-based models (Chowell et al., 2004; Althaus, 2014; CDC Stacks, 2014; Fasina et al., 2014; Fisman et al., 2014; Gomes et al., 2014; Kiskowski, 2014; Lewnard et al., 2014; Meltzer et al., 2014; Nishiura and Chowell, 2014; Pandey et al., 2014; Poletto et al., 2014; Rivers et al., 2014; Towers et al., 2014; Merler et al., 2015; Valdez et al., 2015; Webb et al., 2015). Although these models are valuable tools for simulation and prediction of EVD scenarios, they suffer from limitations that reduce their capability to accurately-and-quickly assess the effectiveness of specific intervention policies and pathways for their improvement.

Mean-field compartmental models are based on deterministic or stochastic differential equations, in which relevant variables, called compartments, evolve in time to describe the fraction of the population in a given state of the epidemic model (Brauer and Castillo-Chavez, 2011; Keeling and Rohani, 2011). Several mean-field compartmental models have been recently formulated to describe the spreading of EVD and assess the impact of non-pharmaceutical interventions (Chowell et al., 2004; Althaus, 2014; CDC Stacks, 2014; Fasina et al., 2014; Fisman et al., 2014; Kiskowski, 2014; Lewnard et al., 2014; Meltzer et al., 2014; Nishiura and Chowell, 2014; Pandey et al., 2014; Rivers et al., 2014; Towers et al., 2014; Webb et al., 2015). These models are usually calibrated through least-squares optimization on available epidemic data (World Health Organization, 2014a). Then, several instances of the model are studied, varying one or more parameters, to anticipate plausible scenarios for the evolution of the outbreak in terms of the total number of infections and casualties.

Mean-field approximations are effective to enable a first, mathematically rigorous understanding of EVD spreading, but suffer from several limitations. While these models are computationally simple and theoretically tractable, they do not take into account the inherently time-varying nature of human behavior, which is influenced by several factors, such as health status or risk perception (Ferguson, 2007; Funk et al., 2010; Manfredi and D'Onofrio, 2013). In their basic incarnation, they rely on the assumption of homogeneous mixing, whereby each individual contacts every other. This assumption typically yields an overestimation of cases (Lewnard et al., 2014; Merler et al., 2015), since social interactions in populations are heterogeneous in both number and intensity (Barrat et al., 2008; Holme and Saramäki, 2012; Perra and Goncalves, 2015). Although heterogeneities could be included by refining and increasing the spectrum of compartments (Brauer, 2008; Choe and Lee, 2015), such an approach may challenge rigorous analytical treatment and parameter identification.

On the opposite side of the spectrum from mean-field compartmental models in terms of complexity are agent-based models. These models are based on the stochastic simulation of individuals' motion and interaction, following specific rules, spatial constraints, and mobility patterns (Ajelli et al., 2010). A comprehensive agent-based model for worldwide simulation, the Global Epidemic and Mobility Model (GLEAMviz) (van den Broeck et al., 2011), has been used to assess the international spreading risk associated with the 2014 EVD outbreak, taking into account several realistic factors that influence the spreading (Gomes et al., 2014; Poletto et al., 2014). A detailed agent-based model, accounting for the spatial distribution of households and hospitals, geographic, and demographic information, and mobility patterns of individuals, has been presented in Merler et al. (2015) to assess the effectiveness of non-pharmaceutical intervention in Liberia. Agent-based models are very refined, but they provide valuable information only in extensive simulation campaigns with a deep knowledge of human behavior, and they are not amenable to analytical treatment.

The typical time scales of the progress of infectious diseases and the present lifestyle, with fast and frequent national and international travels, suggest that homogeneous mixing should be overcome in favor of approaches that explicitly account for the concurrent evolution of the dynamics of infectious diseases and formation of the network of contacts. Activity driven networks (ADNs) have been recently introduced to describe contact processes that evolve over time-varying networks (Perra et al., 2012), when timing and duration of connections happen over short time scales (Morris and Kretzschmar, 1997; Moody, 2002; Ghoshal and Holme, 2006; Butts, 2009; Holme and Saramäki, 2012), comparable with the dynamics of the process running on the network nodes. This modeling paradigm contrasts that of traditional connectivity-driven networks, where links between nodes have a long life span (Centola et al., 2007; Volz and Meyers, 2008; Schwartz and Shaw, 2010; Shaw and Schwartz, 2010; Jolad et al., 2012), resulting in the separation between the time scales of the dynamics of the network connections and the process evolution.

ADNs have been successfully used to study disease spreading in susceptible–infected–susceptible (SIS) and susceptible–infected–removed (SIR) models (Liu et al., 2014). Through a heterogeneous mean-field approach (Perra et al., 2012; Liu et al., 2014), spreading and immunization thresholds have been computed. These thresholds have been found to be considerably different from those computed on static networks, highlighting the need for more in-depth studies of epidemics on time-varying networks. ADNs can thus afford the possibility of formulating mathematically tractable, yet accurate, models of epidemic spreading, which overcome key limitations of mean-field compartmental and agent-based models. However, research on ADNs is in its infancy, and many efforts are currently under way to advance this field of investigation (Medus and Dorso, 2014; Rizzo et al., 2014; Sousa da Mata and Pastor-Satorras, 2015; Starnini and Pastor-Satorras, 2014; Sun et al., 2014). Toward a more realistic treatment of human factors, in Rizzo et al. (2014), we have studied the effect of individual behavior on the spreading of the epidemic in an SIS process. In particular, we have considered reduced activity of infected individuals, due to quarantine or to their debilitating health status, and self-protective behavior of healthy individuals on the basis of their risk perception. In Sun et al. (2014), the effect of memory phenomena on the epidemic threshold of SIS and SIR processes has been studied. These efforts have focused on hypothetical epidemic processes, and the validation of ADN models against real epidemic data is currently untapped.

In this paper, we formulate an ADN-based mathematical model of the 2014–2015 EVD outbreak in Liberia. The motivation for the selection of ADNs to model EVD is twofold. First, the incubation time of EVD, with a minimum of 2 and a maximum of 21 days (World Health Organization, 2014b), is compatible with the time scale of individual mobility patterns (González et al., 2008; Poletto et al., 2013). This implies that time-scale separation assumptions may yield incorrect predictions on the spread of the epidemic (Merler et al., 2015). Second, ADNs can be adapted to account for realistic phenomena that may be critical to the assessment of the severity and