

An agent-based modeling approach applied to the spread of cholera



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ARTICLE INFO

Article history:

Received 20 May 2014
Received in revised form
26 August 2014
Accepted 26 August 2014
Available online

Keywords:

Agent-based modeling
Geographical information systems
Disease modeling
Refugee camps
Cholera

ABSTRACT

Cholera is an intestinal disease and is characterized by diarrhea and severe dehydration. While cholera has mainly been eliminated in regions that can provide clean water, adequate hygiene and proper sanitation; it remains a constant threat in many parts of Africa and Asia. Within this paper, we develop an agent-based model that explores the spread of cholera in the Dadaab refugee camp in Kenya. Poor sanitation and housing conditions contribute to frequent incidents of cholera outbreaks within this camp. We model the spread of cholera by explicitly representing the interaction between humans and their environment, and the spread of the epidemic using a Susceptible–Exposed–Infected–Recovered model. Results from the model show that the spread of cholera grows radially from contaminated water sources and seasonal rains can cause the emergence of cholera outbreaks. This modeling effort highlights the potential of agent-based modeling to explore the spread of cholera in a humanitarian context.

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Software availability

Software Requirements: Java, MASON, GeoMason
Programming Language: Java
Program availability and cost: Free, GPL. <http://css.gmu.edu/Cholera/>
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1. Introduction

Cholera is an intestinal disease caused by the bacterium *Vibrio cholerae*, which colonizes the human intestine (Bertuzzo et al., 2010; Sack et al., 2004). The disease is characterized by diarrhea and severe dehydration. The main transmission mechanism for cholera is by drinking water or eating food contaminated by *V. cholerae*, which enters the environment via feces (stools) from infected people. Pandemics of cholera have been seen throughout the world from the Indian sub-continent, Africa, Europe and the Americas (Codeço, 2001; Ali et al., 2012). Even though cholera itself is both preventable and treatable via the treatment of raw sewage or by providing clean drinking water, using oral cholera vaccines or once infected using rehydration therapy, it remains a health hazard

in many developing countries where such care or prevention is not possible. It is extremely difficult to obtain the actual numbers of cases and subsequent deaths per year due to under or no reporting (Ali et al., 2012), but it is estimated that there are between 3 and 5 million cholera cases and 100,000–150,000 deaths per year, mainly in developing countries (Clemens, 2011; Longini et al., 2007; Sack et al., 2004; Waldor et al., 2010). Once cholera arrives into a new region, either carried by an infected person or by contaminated water or food, three different scenarios might arise. The first is that there is no outbreak; the second is an outbreak which is then followed by few waves of outbreaks. This leads to epidemic cholera as the population has little immunity (Clemens, 2011). In the third scenario, an outbreak occurs which is then followed by subsequent out-breaks that have a persistent seasonal pattern (Codeço, 2001). The later is known as endemic cholera as seen in the Ganges Delta (e.g. Clemens, 2011).

While cholera has mainly been eliminated in regions that can provide clean water, adequate hygiene and proper sanitation (Waldor et al., 2010), cholera is an acute problem in Africa. In particular when related to refugee camps as they often suffer from poor sanitation and low per capita availability of water (see Siddique, 1994; Swerdlow et al., 1997; Heyman et al., 1997; Toole and Waldman, 1997; Cronin et al., 2008). For example, 10,000 Rwandan refugees died from cholera in 1994 (Waldor et al., 2010). Within this paper, we focus on one such camp complex: the Dadaab refugee camp, located near the Kenya–Somalia border in the North Eastern Province of Kenya as shown in Fig. 1. This camp complex

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hosts nearly 0.5 million of refugees (UNHCR, 2012) with a high influx of new refugees coming from Somalia due to drought, famine, and violence. The camp has poor sanitation and housing conditions with frequent incidences of cholera outbreaks (see UNHCR, 2011b) along with other diseases (e.g. measles). In the remainder of this paper, we first review past attempts to model cholera and the utility of agent-based models to explore such an issue (Section 2). In Section 3, we present our conceptual model before presenting some model results in Section 4. Finally we summarize the paper and identify areas of further work.

2. Background

Our understanding of how cholera spreads and infects people relates to some of earliest work with respect to the spatial analysis and disease outbreaks. Snow (1855) used mapping to explore the association between water contamination and the risk of cholera in

the 1854 London cholera outbreak. This analysis not only led to the foundation of modern epidemiology (Longley et al., 2010) but also showed the importance of space when exploring the spread of the disease. Snow's work has proved to be an inspiration of other studies of cholera, all of which extends his basic research. For example, Geographical Information Systems (GIS) have been used to identify the environmental preconditions (e.g. rainfall and temperature) leading to the outbreak of cholera (e.g. Fleming et al., 2007) or developing cholera prediction models with several months lead time from remote sensed images and climate models (e.g. Lobitz et al., 2000; Pascual et al., 2008; Reiner et al., 2012; Jutla et al., 2013).

Although cholera has a long tradition of being mapped and modeled using spatial analysis techniques (e.g. Oseia et al., 2010), modeling the propagation and the spread of the disease on the human population has had a much briefer history. Several cholera models exist, which use aggregate mathematical models utilizing differential equations (e.g. Capasso and Paveri-Fontana, 1979; Codeço, 2001; Longini et al., 2007; Bertuzzo et al., 2010, 2011; Chao et al., 2011; Tuite et al., 2011). Many of the more recent cholera models have been spurred on by the recent outbreaks of cholera in Haiti. For example Tuite et al. (2011) developed a spatial interaction model on the probability of cholera transmission using the Susceptible-Infected-Recovered (SIR) model at the meta-population level in order to calculate what percentage of the population needed to be vaccinated to stop the spread of cholera. The notion behind such models is that if one can detect the rate in the number of infections at the start of a cholera outbreak, one could provide information with respect to the spread of cholera in the future (Mukandavire et al., 2013).

While such styles of models have proved useful, they have also been criticized by researchers. For example, Epstein (2009) writes that such models are ill-suited to model complex natural-human systems. This relates to the notion that such models do not incorporate direct contact between individuals or their environment, and too often assume uniform mixing (Eubank et al., 2004), which is not the case as people interact with each other in many different ways (Crooks and Heppenstall, 2012; Filatova et al., 2013). Moreover, they treat people as aggregate individuals, missing the heterogeneity of the human population and key individual based behaviors. By focusing on heterogeneous individuals operating over different social and geographical spaces, we can capture a fundamentally different view of the disease dynamics (Levin et al., 1997).

Agent-based models (ABMs) therefore offer an alternative to classical mathematical models or discrete choice models (Bithell et al., 2008) as compared to other modeling approaches (e.g. system dynamics, bayesian networks) ABMs allow us to focus on the dynamic interactions between individuals and their impact on the system under study (Kelly et al., 2013). Moreover, Kelly et al. (2013) note that ABMs are particularly suitable when the purpose of the model is for developing an understanding of the system under investigation, where assumptions about processes and interactions can be explored through simulation. Also by linking agent-based models to GIS allows us to explore and understand the complexity of disease transmission over space (Perez and Dragicevic, 2009). It has already been shown that the landscape and the sharing of resources have an impact on disease transmission (e.g. Nunn et al., 2014). For these reasons, ABM within epidemiology has been growing, and applications range from studying dengue fever (Lourenço and Recker, 2013), foot-and-mouth (Dion et al., 2011), hepatitis (Ajelli and Merler, 2009), influenza (Rao et al., 2009), malaria (Linard et al., 2008), measles (Perez and Dragicevic, 2009), mumps (Simoes, 2012), smallpox (Epstein et al., 2002), swine flu (H1N1, Epstein, 2009), tuberculosis (Patolla et al., 2006) etc. Little attention however, has been focused

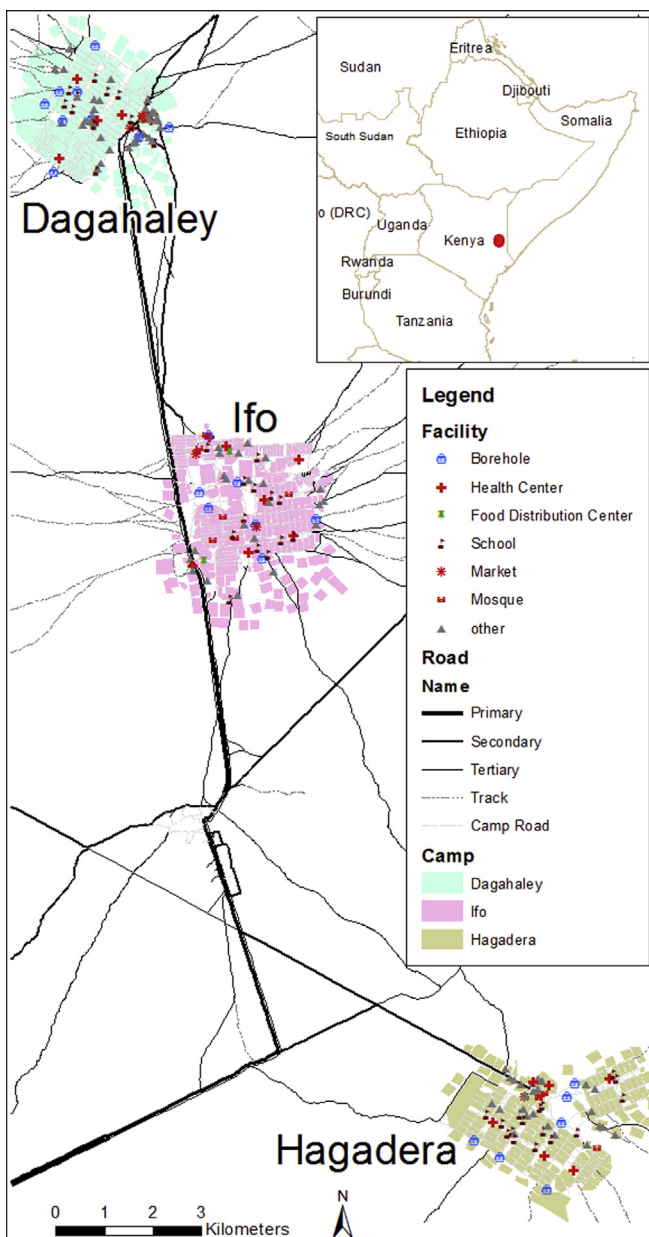


Fig. 1. The Dadaab refugee camp and its physical infrastructure.

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