Agent-Based Modelling and Disease: Demonstrating the Role of Human Remains in Epidemic Outbreaks

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Abstract

Hemorrhagic fever viruses present a high risk to humans, given their associated high fatality rates, extensive care requirements, and few relevant vaccines. One of the most famous such viruses is the Ebola virus, which first came to international attention during an outbreak in 1976. Another is Marburg virus, cases of which are being reported in Equatorial Guinea at the time of writing. Researchers and governments all over the world share a goal in seeking effective ways to reduce or prevent the influence or spreading of such diseases. This study introduces a prototype agent-based model to explore the epidemic infectious progression of a simulated fever virus. More specifically, this work seeks to recreate the role of human remains in the progression of such an epidemic, and to help gauge the influence of different environmental conditions on this dynamic.

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Supplementary Material
Software: `https://github.com/Huixin-coder/Huixin--Giscience-2023.git`

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1 Introduction

Viral hemorrhagic fevers (VHFs) represent a growing threat to human health, even as recent events reflect the challenges and costs of widespread pandemics. The 2014-16 Ebola outbreak occurred primarily in West Africa killed over 11,000 people, with the World Health Organization reporting new outbreaks every single year; Marburg disease, too, has been detected with increasing frequency.[2] The main form of transmission for VHFs that spread from human to human are blood or body fluids from a human infected with Ebola.[5] It is known that in certain cases, human remains continue to be infectious; through unsafe handling of human remains or funeral ceremonies, people may infect others even after death. While well known to practitioners as a pillar of outbreak control, this dynamic has received less attention than living human-to-human contact in the simulation literature. This is unfortunate, as funeral customs in some of the areas where these diseases are endemic involve extensive contact between mourners and the body of the deceased; it is thought that this may have been a significant driver of certain outbreaks.[1][3] Thus, this paper will explore how adding corpse-to-human transmission influences an existing human-to-human model, developing a prototype agent-based model to explore the epidemic infectious progression of a theoretical hemorrhagic fever virus.

2 Background

The outbreak of Covid-19 prompted many researchers to turn their hand to the problem of epidemics, resulting in an explosion in the creation of agent-based models (ABMs) of disease (see for example [9]; [17]). The popularity of SIR (Susceptible, Infectious, and Recovered) models and its close cousins (those with states such as exposed, vaccinated, or immune) meant that researchers could track the development of disease in individual simulated persons. Agent-based models made it possible for researchers to vary the specific qualities of the individuals being exposed to disease, to control contact through social networks, and to impose non-pharmaceutical interventions on the world which had varying impacts on different groups (eg school closures versus general travel bans). Given the pressure to respond to the crisis, these simulations were naturally targeted at Covid-19 specifically - and perhaps therefore tended to deprioritise the role of the deceased in the spread of disease.

To take a more general example, [7] present nosoi, an open-source r package that offers a agent-based framework for simulating infectious disease events. Agents are removed from the nosoi model when they die - meaning that their bodies do not remain in the model to infect others. This appears to be a widespread practice across the discipline. Even when modelling Ebola specifically, [8] remove bodies upon death. [14] apply an SIR system dynamics model to Ebola, using Bayesian inference to calculate the flow among compartments representing different statuses; they add an extra compartment they call 'X' to allow them to track deaths more easily and vary the R_0 to reflect local care and funeral practices. The deterministic numerical simulation of [2] does include the role of funerals and the un/safe handling of infectious human remains. Finally, [11] builds upon the work of [6], with the former expanding upon the latter's basic compartmental model to apply the transmission process to a spatial agent-based model. The model of [11] takes into account the role of contact with the deceased during unsafe funerals; it is the only simulation we have been able to identify that considers the impact of human remains on transmission.

This work is focused on exploring the role of the human remains in the growth of an epidemic. We seek to demonstrate the significance of including or ignoring this process, investigating how the presence of human remains influences the infectious progression under different environmental conditions. Thus, this study utilises a simple agent-based model to present a series of counterfactuals. This method is computationally inexpensive enough to execute a large number of simulations and for us to pinpoint the exact role of the changing variables.

3 Methods

As this research aims to explore the impact of traditional burial practices on the spread of VHFs, we developed a basic simulation framework[1] using the Python Mesa module [10]. In the model, individual humans move randomly around the environment, potentially infecting those immediately around them with the theoretical VHF. Susceptible individuals may sicken and die, and their remains will eventually - but not immediately - be removed from the simulation.

In order to focus on the impact of time to interment - which we considered in the experiments in the following chapter, we generate an empty, theoretical environment which allows us to experiment without concern for confounding factors. Agents are randomly moving and interacting with each other on the grid. The default model parameters are as

[1] Available on GitHub at `https://github.com/Huixin-coder/Huixin--Giscience-2023`

Table 1 Default Model parameters.

Parameter	Default Value	Reference/Assumption
Multigrid	150 x 150	—
Step	100	—
Population	5000	See the determination below
Initial infected rate	0.11	Initial infection rate is 1/9 [15]
Transmission probability	0.44	From 0.44 to 0.9 [13]
Progression period mean	8	The incubation period of 2–21 days (mean 4–10 days) [4]
Recover days mean	7	7-14 days after first symptoms [16]
Eliminated days mean	3	The virus is infectious for 7 days [12]

shown in Table 1. Similarly, the susceptible human population is held constant and will not be supplemented, as the time period being simulated is not long enough for births or natural deaths to play a significant role. The model's step represents the a single day in the simulation.

Individuals in the population behave as visualised in Figure 1. At the beginning of the simulation, a small number of human individuals will be selected from the susceptible population S to be infected based on the initial infection rate I_0. Susceptible individuals may acquire the infection after contact with infectious individuals (with chance β_1) or infectious human remains (with chance β_2). Infectious individuals I may recover at rate γ or die at rate μ. Deceased individuals remain temporarily in the simulation, potentially infecting others around them as controlled by the β_2 parameter. After some number of days defined by the eliminated days parameter, the human remains are removed from the environment. The parameters used in this paper are roughly based on the Ebola virus, but can easily be varied to explore other VHFs.

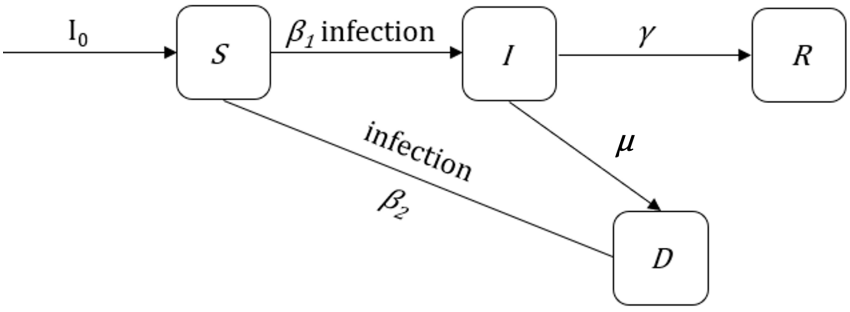

Figure 1 VHF status flowchart (SIRD): individual agents exposed to the virus may progress from susceptible (S) to infectious (I) with probability β_1. Eventually they will experience either recovery (R) or death (D), with probabilities γ or the "death rate" respectively. Deceased agents remaining in the simulation may come into contact with other, living, susceptible agents and transmit the disease to them (with probability β_2).

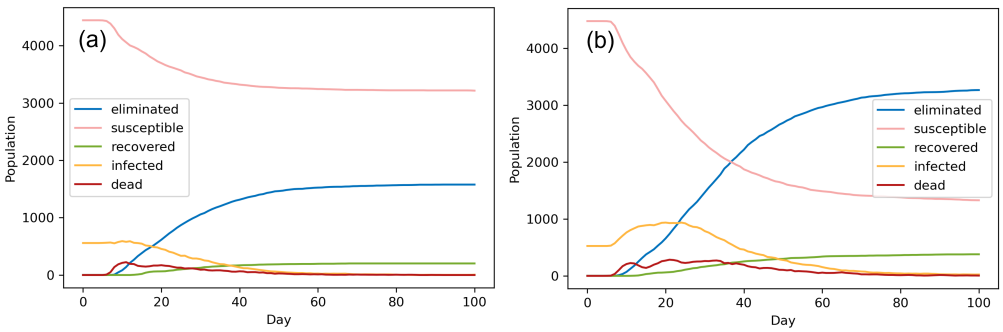

Figure 2 Typical sample instances of simulation results for Model 1 (a): human remains are not infectious, and Model 2 (b): human remains are infectious and can transmit the virus to living persons. Parameter values are the same in Models 1 and 2.

4 Results

In this section, we will first present a comparison of two versions of the model. In Model 1, human remains are not infectious. In Model 2, human remains **are** infectious and can transmit the virus to living persons. Building on this, we present two further experiments, exploring the impact of time to interment (called 'eliminated days') relative to different population densities (Experiment 1) or virus fatality rates (Experiment 2). All other parameters are held constant throughout.

4.1 Infectious versus Noninfectious Remains

Models 1 and 2 are run until the 100th timestep, at which point experimentation shows they usually equilibrate. The results do not show large deviations across either set of simulations. Figure 2 shows a comparison of the different model outcomes.

In Model 1, the R_0 typically stabilises around time 60, levelling out at 0.258, meaning that the outbreak will gradually disappear and be well controlled. Notably, such an R_0 is far from the R_0 of, say, the real-world Ebola virus which lie in the range of 1.56 to 1.9. In contrast, Model 2 with its infectious remains sees the measurements stabilise around time 70, with many more fatalities. Its R_0 value reaches about 1.6, suggesting that the disease has the potential to create an epidemic. The average final number of deceased persons are 1587.3 in Model 1, and 3161.2 in Model 2, reflecting the increased mortality associated with infectious remains.

4.2 Experiment 1: Population Density relative to Eliminated Days

As described above, Experiment 1 involves varying the population and eliminated days (2 to 7 days [12]) relative to one another, holding all other parameters as in the default model. This is meant to explore the sensitivity of the process to population density, and to better understand how significantly the timely handling of human remains impacts the spread of disease.

The model tracks the number of agents which are alive at the end of the simulation, referred to here as the "alive rate". This is calculated by the following equation:

$$AliveRate = \frac{Susceptible + Recovered}{population}$$

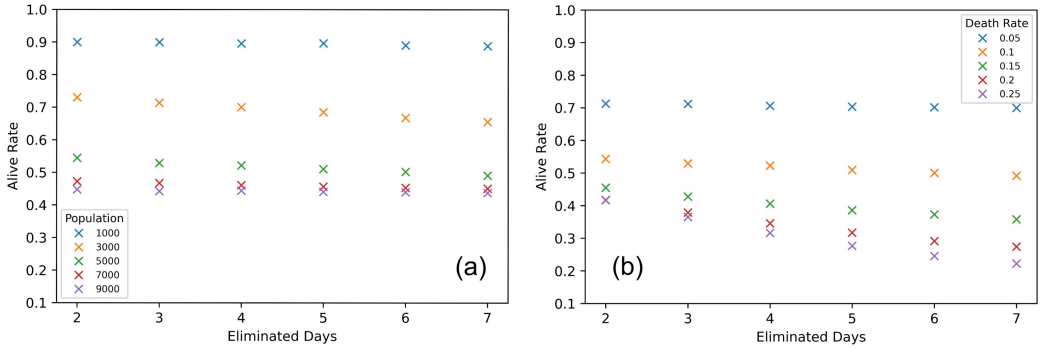

Figure 3 Average measures of the "Alive Rate" across 50 repetitions of (a) Experiment 1: varying population densities and number of days until human remains are eliminated from the model, and (b) Experiment 2: varying death rates and number of days until human remains are eliminated from the model.

Results are taken at the end of the 100th step. The population is set at 1000, 3000, 5000, 7000 and 9000, while the eliminated days range from 2 to 7 days. Each combination of parameters is repeated 50 times.

Figure 3(a) tracks the average "alive rate" of each combination of parameters as population and eliminated days are varied. The different population levels are clearly distinguishable, and as expected the alive rate decreases as either eliminated days or population density increases. Interestingly, the most extreme population values appear to be less affected by the speed with which remains are handled. In contrast, the sensitivity of the population of 3000 to the number of eliminated days is related to the size of the population relative to the size of the grid. The uneven distribution of alive rates relative to population size at any given value of eliminated days suggests that there may be critical points of inflection in model behaviour.

What the graph suggests is that in situations of medium population density when a susceptible person might not otherwise encounter an infectious living person, the long-term presence of infectious remains represents a noticeable peril.

4.3 Experiment 2: Change daily death rate and eliminated days

Experiment 2 holds population constant (size 5000) and instead varies the fatality of the infection relative to the eliminated days. The daily death rate increases from 0.05 to 0.25 in increments of 0.05, while the eliminated days again range from 2 to 7. Once more, each parameter combination is run 50 times.

Figure 3 (b) shows the relationship between the daily death rate and eliminated days as defined by the average alive rate. Again, as expected the alive rate decreases with the increase in number of eliminated days, regardless of daily death rate level. In certain situations, infections are known to "burn themselves out" by killing off hosts before a virus has the opportunity to spread to new hosts. If human remains are infectious, however, the highly virulent strains of disease are still able to spread, especially when these deceased hosts remain in the environment.

5 Discussion and Conclusion

This article demonstrates a simple example of how improperly handled infectious human remains can propagate and worsen epidemics. Many extant modelling frameworks remove deceased agents immediately; our goal is to show the impact that such a modelling choice may have. There are of course often reasons for such coding decisions. For example, in extremely large-scale models being run on suboptimal hardware setups, recovering memory may be a priority. However, we would caution against adopting such a framework without careful consideration. At a minimum, modellers should be aware of the impact such decisions have on the ultimate course of an epidemic.

Simulation as a tool showed a great deal of promise during the recent Covid-19 pandemic. It is crucial, however, that researchers ensure that models not sacrifice essential functionality in the name of parsimony. This paper presents a simple example drawn from a well-known principle of infectious suppression. It is important that modellers engage proactively with subject matter experts to ensure that we incorporate such dynamics into our work in the future.

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