Wine, Ebola and Terrorism

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Abstract

We present and compare three models of the Ebola outbreak in Liberia during 2014-2015. We approach the problem from both systematic and agent-based perspectives and compare the results to the actual data as well as between models. We show that if the outbreak is not contained in the early stages and the individuals do not change their behavior as the virus prevails, between 60 and 80 percent of population get the disease.

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1 Introduction

Bacteria growth during wine making, spread of infectious diseases and recruitment to extremists organizations can be modeled in a similar way - either by exponential or logistic growth models. For the purposes of this paper we focus solely on modeling the spread of Ebola through Liberia throughout 2014 - 2015 outbreak. We chose to focus on Liberia because most of the data needed for the model was available in the literature. While the model allows one to consider other countries affected by the outbreak we did not calibrate the associated parameters.

Ebola was first discovered in 1976. Since then, there were 34 records of Ebola reported by the Center for Disease Control and Prevention. However, until 2014 all outbreaks had a reported number of deaths that did not exceed 500; 11 of them did not exceed 10 individuals and 15 records did not exceed 65 individuals [2]. The outbreak of 2014 is considered different. It took thousands of lives over the past two years and received an extensive media coverage.

The current outbreak may be different because it was the first time Ebola was contracted in the West Africa as opposed to Central Africa where it was first discovered. Early symptoms are flu-like: fever, headache, fatigue and joint pain. Diseases like HIV and Malaria, which are common to the region, have the same symptoms. As Ebola progresses, the infected experiences abdominal pain, diarrhea, vomiting and rashes. The virus is contracted through direct contact with bodily fluids and secretion: blood, saliva, urine, fecal matter. Once virus is contracted, the incubation period may last up to two weeks making intervention measures like tracking difficult [1].

A variety of cultural and economic factors have contributed to the spread of the disease: lack of medical centers in some regions and poor sensitization practices in such centers, distrust in the western medicine, poverty and traditional burial ceremony which includes physical contact with the diseased [7].

One may look at the spread of the infectious diseases from two perspectives: system based and agent based. In the system based model the entire population is divided into compartments with a certain proportion of the population in each. As time progresses certain amount of people flow from one compartment into another. Naturally, such relationship is described either by a difference or a differential equation. One of the most well-known equation-based models involves three states: susceptible, infected, recovered. Such model is called an SIR model; each letter in the abbreviation represents one of the compartments in the population. This model has multiple modifications because various compartments can be added. In the case of Ebola, Lekone and Finkenstd [5] consider a four compartment model, inserting an "Exposed" state between "Susceptible" and "Infected". A six-compartment model, presented by Legrand [4] and Rivers[9] differentiates between the modes of transition of the disease, i.e. a virus can be transmitted in the community, at hospitals and medical centers or at funerals.

In contrast to system based models, agent-based models are concerned with the behavior of a typical individual rather than the system as a whole. In such models every individual in the system is assigned certain characteristics, i.e. states. Individual's behavior is probabilistic at each unit of time and causes him either to transition to a different state or stay in his current state. Agent-based models for Ebola include Siettos et al. [10] and Merler et al.[6]. A variety of models examine the effectiveness of intervention measures. Examples include contact tracing by Webb et al. [11] and travel restrictions by Poletto et al. [8].

In this paper we consider a seven-compartment model, both system and agent-based. We show **What did we show?! What about the model with spatial component?**

In section **??** we present our model. Section **??** describes our data and parameters. Section **??** discusses the results of numerical experiments. Section **??** concludes.

It should be written as much as possible in non-technical terms, so that a lay reader can understand the context and the contribution of the paper.

- Describe the problem you are trying to solve, the approach you took, and summarize your contribution and results.
- Review the history of this problem, and existing literature.
- Give an outline of the rest of the paper.

2 Problem Statement

- Give a precise technical description of your problem.
- State and justify all your assumptions.
- Define notation.
- Describe your data, how you collected them, their properties, and whether you did anything to them (removed noise, filled in missing data, applied normalizations).

3 Methods

We examine the problem from two perspectives. We present a system based model first and then discuss an agent-based modification of it. We then consider an agent-based model that incorporates agents' movement through space. Throughout the three models we utilize the same assumptions and compartment-state definitions.

In order to propose a more accurate model and compare the results among different programming languages, the compartment flow model of the Ebola Epidemic in West Africa, 2014, was modeled with a System Dynamics (SD) and Agent Based Model (ABM) approaches. Insight Maker and Mathematica was utilized for the SD, and Insight Maker and Python for the ABM.

- Insight Maker: SD and ABM
- Mathematica: SD
- Python: ABM

We used InsightMaker platform to prototype our model and simulate stepping forward through time. More details about the platform and its functionality can be found in Fortmann-Roe's review [3]. The platform uses fourth order Runge-Kutta differential equation solver for the system dynamics model and first order Euler approximation for the Agent-Based model.

- We consider a model of Ebola Outbreak with parameters calibrated for Liberia.
- We consider two time periods. The first one starts with the announcement of Ebola outbreak in March 2014 and ends the day of the International Intervention in September 2014. The second period covers the time from the International Intervention to July 2015.
- We ignore all the possible births and deaths occurred due to reasons other that Ebola during the chosen time.
- Each individual who dies because of Ebola has a funeral.

3.1 Factors Considered

There are several factors to take into account when analyzing how a virus may spread in a community. First of all the customs and beliefs of a society play an important role, it implies how the individuals interact among themselves, how often they visit their relatives or friends, the amount of travel to other villages, cities or countries to work or buy supplies, as well as the mode of transport.
Having information about the local government and the wealth of the region, would help to determine the capacity of response when facing an epidemic; including the quantity and quality of hospitals and their capacity, as well as the amount of healthcare workers and their expertise.
In the moment of a virus outbreak, governments from other countries may intervene to help to control the disease, possibly decreasing the number of infected people and increased the number of recovered patients, by educating individuals about the virus, the ways of transmission and handling of the deceased family.
Characteristics of the virus itself are also important, having an estimate of the incubation period, the rate of recovery, the time it remains in the deceased would help to predict the behavior of the virus.

3.2 Compartment-State Definition

S - Susceptible. Individuals who have not contracted the disease and have no immunity to it.

E - Exposed. Individuals who have come in contact with the Ebola patient and have contracted the disease but do not yet exhibit sever symptoms and thus, are considered not infectious.

I - Infected. Individuals who experience severe symptoms of Ebola and are contagious.

H - Hospitalized. Individuals who are infectious and are in the hospital because they are experiencing severe symptoms of Ebola.

F - Funeral. Diseased but still contagious victims of Ebola.

D - Dead. Individuals who died because of Ebola, were buried and are currently under ground. They are considered not to be contagious.

R - Recovered. Individuals who had Ebola, survived and now are immune to the disease.

4 Parameter Calibration

The parameter values which represent biological process ($\alpha, \gamma_I, \gamma_D, \delta_1, \delta_2$) or social custom ($\gamma_F$) were discovered in many sources [reference], while the parameters which represent social behavior ($\mathcal{P} = \{\beta_I, \beta_H, \beta_F, \gamma_H, \theta\}$) are site-dependent and unknown. γ_{DH} and γ_{IH} are also unknown, but we assume that they are dependent on other variables ($1/\gamma_{DH}$=$1/\gamma_D$-$1/\gamma_H$ and $1/\gamma_{IH}$=$1/\gamma_I$-$1/\gamma_H$). In this chapter, we calibrated $\mathcal{P}$ based on our systematic model (equation link) and the data of cumulative death in Liberia from March 2014 to July 2015 (reference).

4.1 Bayesian calibration framework

Using Bayesian calibration methodology, we calibrate the unknown parameters ($\mathcal{P}$). The prior distribution of $\mathcal{P}$ is a uniform distribution which ranges are determined based on numerical exploration and previous researches [references] (Table).

Table 1: Range of the prior parameter space

β_I	β_H	β_F	γ_H	θ
$(0, 0.5)$	$(0, 0.5)$	$(0, 1)$	$(2, 7)$	$(0, 0.5)$

To each random choice ($\mathcal{P}_0$) from the prior distribution, we assign likelihood weight by comparing the real world data ($\mathcal{D}_R$) and data simulated with $\mathcal{P}_0$ ($\mathcal{D}_S$). Multiple choices of parameters and their weights will eventually construct the posterior distribution of $\mathcal{P}$. In this methodology, we provide multiple likely parameter sets, rather than a single best fit. Detailed description on the calibration procedure is:

Step 1) Choose a random $\mathcal{P}_0$ from the prior distribution

Step 2) Solve our deterministic system (equation link) with $\mathcal{P}_0$ and given initial value $\{S_0, E_0, I_0, F_0, D_0, R_0\}$, then evaluate $\mathcal{D}_S = \{D(t_i)\}$ for all dates $\{t_i\}$ corresponding to the cumulative death data ($\mathcal{D}_R$).

Step 3) Evaluate likelihood of $\mathcal{P}_0$: $Exp[-Norm(\mathcal{D}_R - \mathcal{D}_S)/Norm(\mathcal{D}_R)]$

Repeat Step 1-3 multiple times and make large number of parameter + likelihood ensembles. Generate posterior distribution with them.

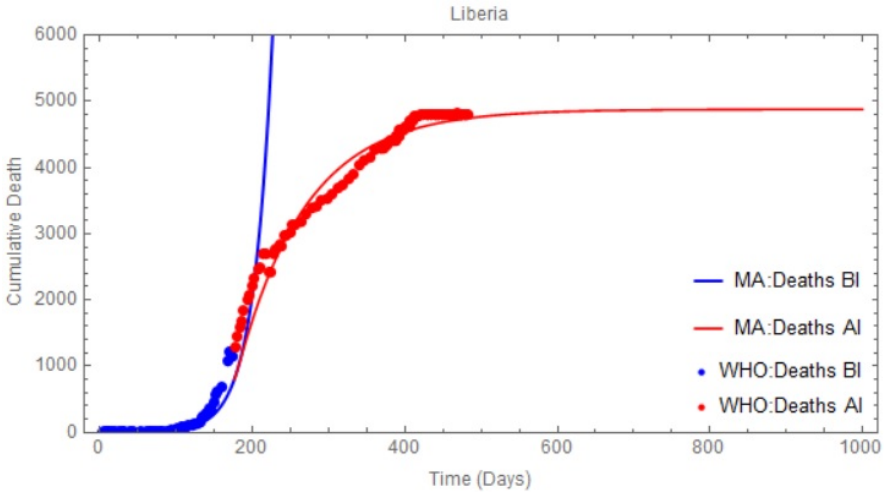

Figure 1: write caption here

4.2 Results and validation

For the calibration of before intervention parameters, we used the data for 176 days (March 14 to September 14), and initial value $\{S_0, E_0, I_0, F_0, D_0, R_0\}$=$\{10^6 - 1, 0, 1, 0, 0, 0\}$ assuming that initial outbreak started from a single infected person in a million population. The calibration of after intervention parameters is based on the data for 306 days (September 14 to July 15), and initial value $\{S[176], E[176], I[176], F[176], D[176], R[176]\}$ which are evaluated from calibrated mean $\mathcal{P}$ for pre intervention. 10000 random samples were used in each calibration. Calibration results and validation are shown in (table) and (figure).
Based on our calibration, the intervention reduce the basic reproduction number of Ebola in Liberia from 1.99 to 0.787, using the formula in (reference). As a result, disease spread is terminated after infecting 0.84% of total population with 0.49% decrease in population, otherwise 92.7% are infected and population decreases by 53.5%.

Table 2: Model Parameters for Ebola Epidemic in Liberia Before and After the International Intervention. Calibrated parameters are written in bold font, and posterior means and standard deviations in parenthesis are notated.

Parameter	Liberia Before Intervention (Mar/14 to Sept/14)	Liberia After Intervention (Sept/14 to Jul/15)
Contact Rate, Community (β_I)	**0.148 (0.0953)**	**0.0446 (0.338)**
Contact Rate, Hospital (β_H)	**0.235 (0.143)**	**0.0877 (0.563)**
Contact Rate, Funeral (β_F)	**0.465 (0.287)**	**0.283 (0.208)**
Incubation Period ($1/\alpha$)	11 days	11 days
Time until Hospitalization ($1/\gamma_H$)	**4.49 (1.44) days**	**4.63 (1.43) days**
Time froml Hospitalization to Death ($1/\gamma_{DH}$)	3.51 days	3.51 days
Duration of Traditional Funeral ($1/\gamma_F$)	2.00 days	2.00 days
Duration of Infection ($1/\gamma_I$)	10.00 days	10.00 days
Time from Infection to Death ($1/\gamma_D$)	8.00 days	8.00 days
Time from Hospitalization to Recovery ($1/\gamma_{IH}$)	5.51 days	5.51 days
Probablity a Case is Hospitalized (θ)	**0.248 (0.142)**	**0.233 (0.145)**
Case Fatality Rate, Unhospitalized (δ_1)	0.500	0.500
Case Fatality Rate, Hospitalized (δ_2)	0.500	0.500

5 System Dynamics

The diagram of the described compartment model is depicted on Figure 2.

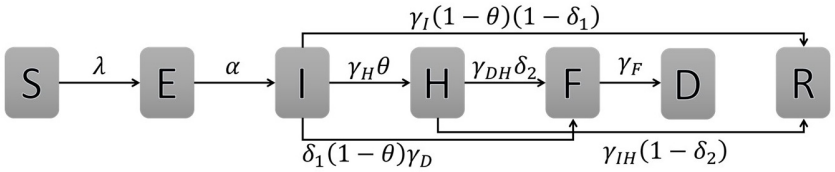

Figure 2: Compartment Model of the Ebola Epidemic in Liberia and Sierra Leone
Being S: Susceptible, E: Exposed, I: Infectious, H: Hospitalized, F: Funeral, R: Recovered and D: Dead. All the possible flows are specified by the arrows and the parameters that direct them. Note that $\lambda = \beta_I I + \beta_H H + \beta_F F$, being a combination of all the β transmission terms shown in Table 4

The governing equations of the system dynamics described on Section **??** are the following:

$$\frac{dS}{dt} = -\frac{\beta_I SI + \beta_H SH + \beta_F SF}{N} \tag{1}$$

$$\frac{dE}{dt} = \frac{\beta_I SI + \beta_H SH + \beta_F SF}{N} - \alpha E \tag{2}$$

$$\frac{dI}{dt} = \alpha E - [\gamma_H\theta + \gamma_I(1-\theta)(1-\delta_1) + \gamma_D(1-\theta)\delta_1]I \tag{3}$$

$$\frac{dH}{dt} = \gamma_H\theta I - [\gamma_{DH}\delta_2 + \gamma_{IH}(1-\delta_2)]H \tag{4}$$

$$\frac{dF}{dt} = \gamma_D(1-\theta)\delta_1 I + \gamma_{DH}\delta_2 H - \gamma_F F \tag{5}$$

$$\frac{dR}{dt} = \gamma_I(1-\theta)(1-\delta_1)I + \gamma_{IH}(1-\delta_2)H - \gamma_F F \tag{6}$$

where each of the parameters are defined on Table 4

5.1 Insight Maker

Insight Maker is a powerful online tool used to model and simulate utilizing different approaches, such as System Dynamics, Agent-Based Modeling and imperative programming. Insight Maker allows to construct a graphical model interface to forecast the system response [3]. We used InsightMaker platform to prototype our model and simulate stepping forward through time. More details about the platform and its functionality can be found in Fortmann-Roe's review [3]. The platform uses fourth order Runge-Kutta differential equation solver for the system dynamics model and first order Euler approximation for the Agent-Based model.
The implemented Insight Maker SD model is depicted in Figure 3 .
A normalized population fraction was simulated. The compartment S was initialized with a value of 999.999/1.000.000, and the compartment I with 1/1.000.000, meaning that there is an infected individual per every million of habitants, the rest of the compartments were set as 0. The flow between the compartments is specified in Figure **??** and all the other parameters were initialized as shown in Table 4. As mention in Section **??**, the parameters were calibrated in two stages, before and after the international intervention. According with the time frame proposed, the change on the parameters was also implemented on Insight Maker. The links to the online models can be found on [12] and [13].
After modeling the system with the parameters before the intervention, it can be observed in Figure 4 how the total population decreases to 46.46% if there is not any type of intervention and the each of the parameters continue to be the same. The number of susceptible individuals exponentially decays, converging to 7% of the population, while exposed, infected, hospitalized and funeral comparments converges to zero; finally, after the system stabilizes, the final proportion of dead people would be 53.53%

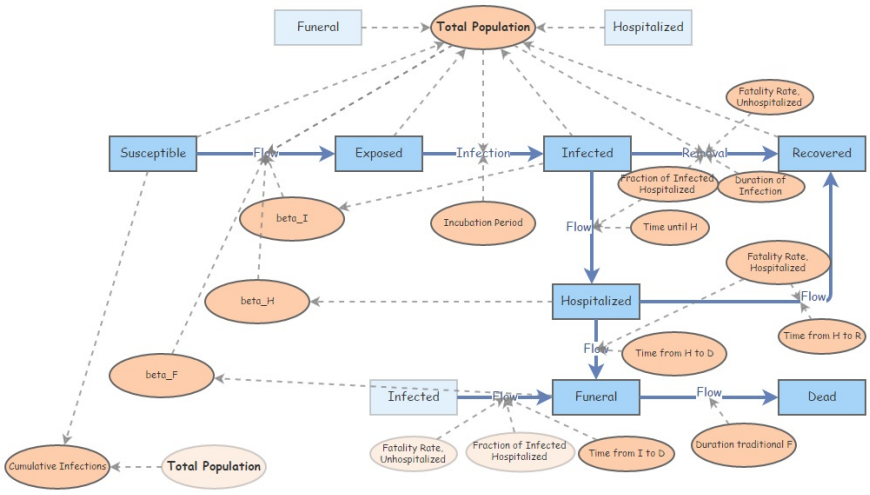

Figure 3: **Compartment model of the system dynamics implemented on Insight Maker**

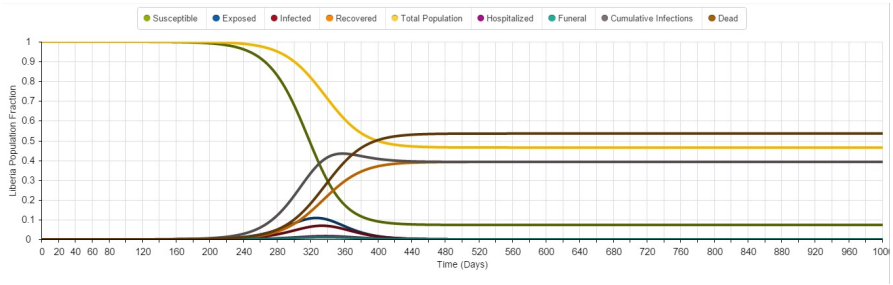

Figure 4: **Insight Maker results using the parameters of the first stage (Mar/14 to Sept/14) and assuming no intervention**

As mentioned before, five parameters were calibrated for the second stage of the Ebola Outbreak, namely, community contact rate (β_I), hospital contact rate (β_H), funeral contact rate (β_F), time until hospitalization (γ_H) and probability a case is hospitalized (θ). Figure 5 A. shows that there is not much change in the Total population and susceptible compartment, meaning that the virus was controlled; Figure 5 B focuses on E, I, R, H , F and D compartments, showing that the international intervention causes a dramatic change in the behavior of such compartments.
Finally, a comparison between the proposed model and World Health Organization data is shown in Figures 6 and 7. As depicted in 6 A and B there is a good fitting of our model with the data reported by WHO. Figure 7 shows the reported WHO data before and after intervention, the results of our model before and after intervention and the forecast for the coming months, predicting that after the system reaches an equilibrium, the proportion of deaths in Liberia product of the EVD would be 5.07% approximately.

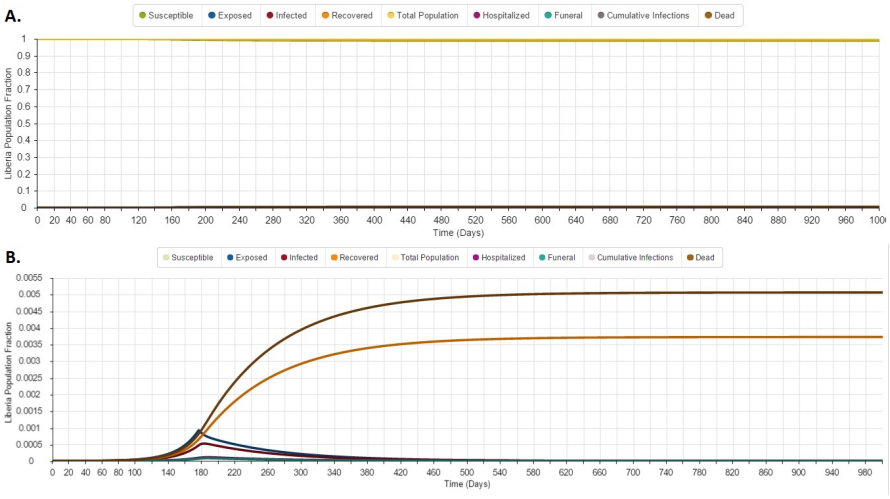

Figure 5: **Insight Maker results using the parameters of the first stage (Mar/14 to Sept/14) and the second stage (Sept/14 to Present)**

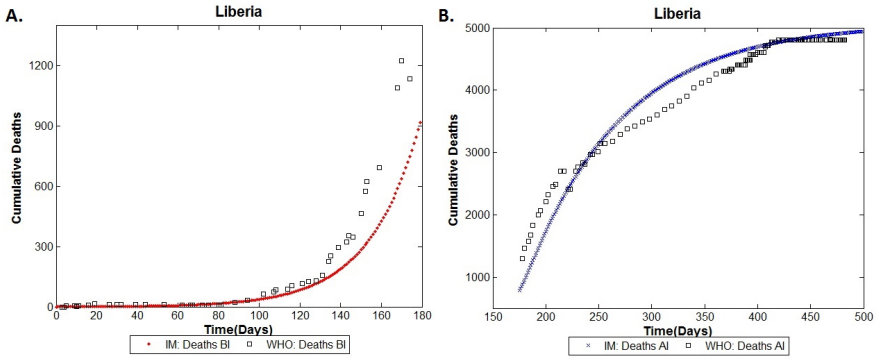

Figure 6: **Comparison between World Health Organization (WHO) data and Insight Maker (IM) results using the parameters of A. the first stage (Mar/14 to Sept/14) and B. the second stage (Sept/14 to July/15) for the cumulative deaths (D).**

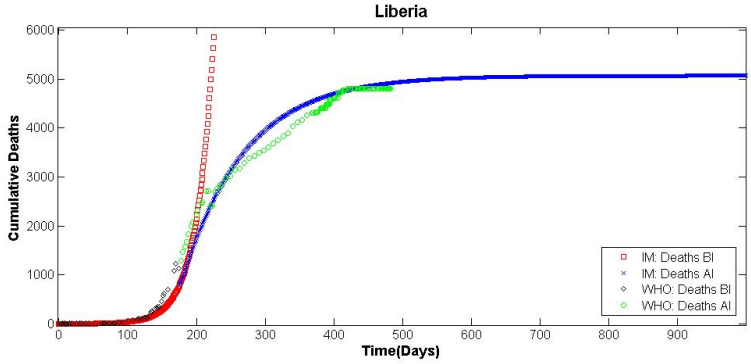

Figure 7: **Comparison between World Health Organization (WHO) data and Insight Maker (IM) results using the parameters before intervention (BI) and after intervention (AI), for the cumulative deaths (D).**

5.2 Mathematica

We drew the plots in the previous section also with Mathematica, and got almost same result. One additional plot we draw in Mathematica is phase portrait of the system (Figure).

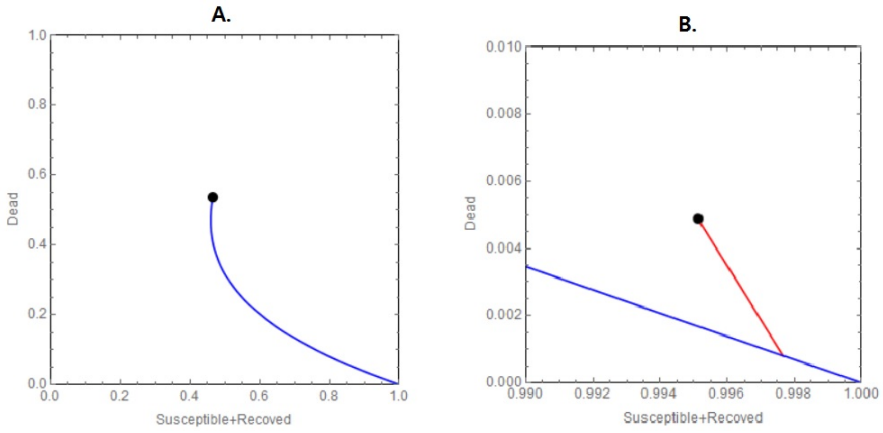

Figure 8: Projection of phase portrait to (Susceptible + Recovered, Dead) space. (Blue) - without intervention, (Red) - with intervention, (Dots) - where the phase converges (equilibrium).

6 Agent-Based Dynamics

The next model we consider is an agent-based model. Each individual in the population can be in either of 7 states discussed above: susceptible, exposed, infected, hospitalized, funeral, recovered or dead. The flow between two states is a probability of transition from one state to another for a typical individual. We represent our model in Figure 9. In each time step a typical individual who is susceptible to contracting a virus can either transition to exposed state with probability p_{SE} or stay susceptible with probability p_{SS}. An individuals in the exposed state transitions to infected with probability p_{EI} and stays exposed with probability p_{EE}. An individual who is infected can stay infected, recover, go to a hospital or die and transition to funeral state with probabilities p_{II}, p_{IR}, p_{IH} and p_{IF} respectively. Recovery is considered a terminal state so individuals in this state stay in it for the remaining duration of the simulation. Hospitalized individuals may stay hospitalized, transition to recovered or funeral with probabilities p_{HH}, p_{HR} and p_{HF}. We assume that the individual who dies from Ebola remains infectious through the duration of the entire burial ceremony and no precautions are taken against disease transmission. Safely buried individuals are considered dead and noninfectious and remain in this state for the remaining time of the simulation.

Let

t_{IP} be the incubation period, i.e. time during which the individual has the virus in his body but does not yet show severe symptoms

t_{ID} infection duration time after the onset of severe symptoms

t_H time to hospitalization after manifestation of severe symptoms

t_{IF} time from the onset of severe symptoms to funeral

t_{HF} time from patient's arrival at the hospital to funeral

t_{HR} time from patient's arrival at the hospital to recovery

t_{DF} duration of traditional funeral

N total number of individuals in a population

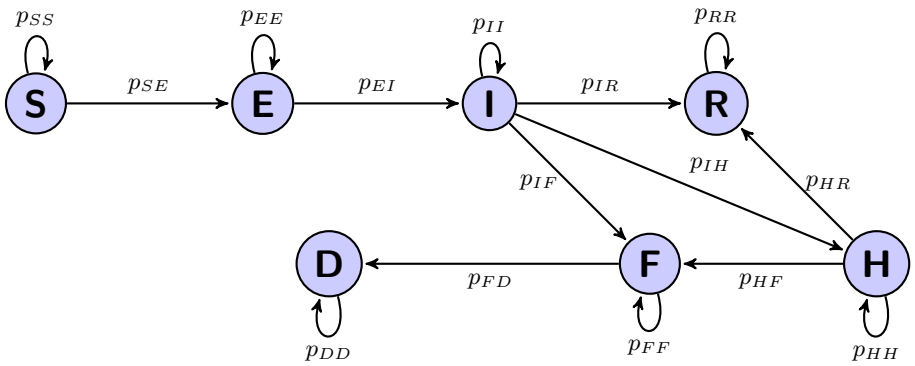

Figure 9: Spread of the disease: Agent-based model. Each node represents a typical individual's state. An individual can transition to a state to which he is connected by a directed arc with a probability specified on an arc

N_I total number of individuals in the infected state

N_H total number of individuals in the hospitalized state

N_F total number of individuals in the funeral state

β_I rate at which the disease spreads during an interaction with an infected person

β_H rate at which the disease spreads during an interaction with a hospitalized person

β_F rate at which the disease spreads during an interaction with a person who is in the funeral state

We define the individual's probability of transition for each state as

$$p_{SE} = \beta_I \cdot \frac{N_I}{N} + \beta_H \cdot \frac{N_H}{N} + \beta_F \cdot \frac{N_F}{N} \tag{7a}$$

$$p_{SS} = 1 - p_{SE} \tag{7b}$$

$$p_{EE} = 1 - \frac{1}{t_{IP}} \tag{7c}$$

$$p_{EI} = \frac{1}{t_{IP}} \tag{7d}$$

$$p_{II} = \frac{1}{t_{ID}} \tag{7e}$$

$$p_{IH} = \frac{1}{t_H} \tag{7f}$$

$$p_{IF} = \frac{1}{t_{IF}} \tag{7g}$$

$$p_{IR} = 1 - p_{II} - p_{IH} - p_{IF} \tag{7h}$$

$$p_{HF} = \frac{1}{t_{HF}} \tag{7i}$$

$$p_{HR} = \frac{1}{t_{HR}} \tag{7j}$$

$$p_{HH} = 1 - p_{HF} - p_{HR} \tag{7k}$$

$$p_{FF} = \frac{1}{t_{DF}} \tag{7l}$$

$$p_{FD} = 1 - p_{FF} \tag{7m}$$

$$p_{RR} = 1 \tag{7n}$$

$$p_{DD} = 1 \tag{7o}$$

6.1 Simulation

We consider a population of size **100** with **99** individuals starting in a susceptible state and **1** individual in the exposed state. Numeric probabilities of an individual transitioning from each state are recorded in Table 3. We simulate **176** days of disease progression without intervention and **306** days of post intervention disease progression. We repeat the process **100** times and record the average outcome.

7 Spatial Agent-Based Dyanmics

Table 3: Agent-Model Parameters for Ebola Epidemic in Liberia Before and After the International Intervention

Parameter	Liberia Before Intervention (Mar/14 to Sept/14)	Liberia After Intervention (Sept/14 to Jul/15)
p_{SE}	**DYNAMIC**	**DYNAMIC**
p_{SS}	**COMPUTE**8	**COMPUTE**
p_{EE}	0.9091	0.9091
p_{EI}	0.0909	0.0909
p_{II}	0.1	0.1
p_{IH}	0.2227	0.2160
p_{IF}	0.125	0.125
p_{IR}	0.5523	0.559
p_{HF}	0.2849	0.2849
p_{HR}	0.1815	0.1815
p_{HH}	0.5336	0.5336
p_{FF}	0.5	0.5
p_{FD}	0.5	0.5
p_{RR}	1	1
p_{DD}	1	1

fd

We next look at an agent-based model where agents are allowed to move within and between cities. Incorporating spatial movement requires making additional assumptions about the map on which movement is allowed and the movement of individuals. The model is coded in `Python` and propagates the infection and spatial information in discrete days.

7.1 Spatial Assumptions

We restrict the space (on which cities and individuals are located) to a specified width and height and generate cities randomly within the space with specified variance and relative density. For example, a model may have one city with variance 30 and density 0.9 and a village with variance 5 and density 0.1. Locations of individuals and cities are real numbers stored as `floats`. We also create a grid, which partitions the individuals based on their location and is used to determine the closest neighbors for community infection and funeral attendance. A family is assumed to have $3-6$ members (randomly chosen) all of which live in the same exact location. Upon initialization (and later travel), families are place based on the specified city densities, normally distributed around the city's center location using the city's variance. We define an individual's *home* as their initial location.

An individual is *movable* if he is susceptible, exposed, or recovered. All other individuals remain stationary. Movable individuals travel each timestep with probability p_{trav}. If they are away from home, they will travel home with probability p_{home}. Otherwise, they will travel locally (within their current city or village) or non-locally (to another city) based on the density of their current city. It is assumed that when an individual is in a density with higher density they are less likely to leave. If individual i's current city density (percentage of the total population) is $d[i]$, then the non-local travel probability is $(1 - d[i])/2$.

7.2 Agent Behavior

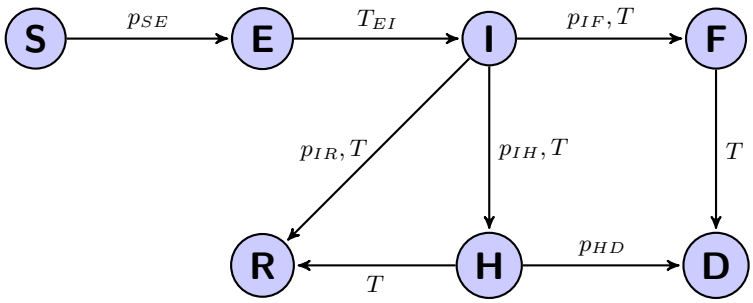

Figure 10: Available states for individuals and the transitions between them. Probabilistic transitions are denoted be p and timeouts between states by T. If both are present, once it is decided that the individual will transition, the timeout is calculated and counted down.

The model uses the same states as the previous models, but some of the transitions and probabilities have been modified. Specifically, hospitalized individuals are assumed to be quarantined, and thus no longer infect others or have funerals. Instead, hospitalized individuals move straight to the *Dead* state upon death. See Figure 9 vs Figure 10 for a comparison between the two agent-based models. Figure 10 denotes the probabilistic and timeout transitions between states. We define a *timeout* to be an integer number of days to wait before transitioning to another state, either uniformly randomly generated between two in or equal to a specified constant. Whenever a range of integers is listed, the number used in simulation is uniformly drawn from that range.

The spatial movement and transitions between states is dependent on the individual's current state. Following are a description of the behavior of each type of individual.

Susceptible individuals travel randomly and may only transition to the exposed state.

Exposed individuals may also travel randomly. Upon initial transition, they generate a timeout of ?? days until they will transition to the infected state.

Infected individuals are assumed to be too sick to travel. Upon initial transition, it is decided whether they will go to the hospital (with probability ??, generating a timeout of ?? until transitioning to hospitalization), die and be buried at a funeral (with probability ???, generating a timeout of ?? until transitioning to the funeralized state), or recover (generating a timeout of ?? until transitioning to the recovered state). While in the infected state, the individual infects people in the surrounding grid each with probability ?? if they are a family member or *sdf* otherwise.

Hospitalized individuals are quarantined and no longer infect anyone. Upon initial transition, it is decided whether they will die in the hospital (with probability *sdf*, generating a timeout of *sdf* until death) or recover (generating a timeout of sf until recovery). Because they are quarantined, traditional funerals with high infection rates are not held upon death.

Funeralized individuals spend 2 days in the funeralized state before transitioning to the *dead* state, but only infect people on the initial entrance to the *funeralized* state. Upon initial transition, the individual and all of his movable relatives return home. All susceptible people in his home grid cell who were also in that grid cell at initialization (family and initial neighbors not currently away) are then infected with probability β_{fun}.

Recovered individuals do not affect the model but can continue traveling.

Dead individuals remain stationary and do not affect the model.

insert picture of grid

7.3 Parameters

Table 4: Model Parameters for Ebola Epidemic in Liberia Before and After the International Intervention

Parameter	Liberia Before Intervention (Mar/14 to Sept/14)	Liberia After Intervention (Sept/14 to Jul/15)
Contact Rate, Community (β_I)	0.148	0.0446
Contact Rate, Hospital (β_H)	0.235	0.0877
Contact Rate, Funeral (β_F)	0.465	0.283
Incubation Period ($1/\alpha$)	11 days	11 days
Time until Hospitalization ($1/\gamma_H$)	4.49 days	4.63 days
Time from Hospitalization to Death ($1/\gamma_{DH}$)	3.51 days	3.51 days
Duration of Traditional Funeral ($1/\gamma_F$)	2.00 days	2.00 days
Duration of Infection ($1/\gamma_I$)	10.00 days	10.00 days
Time from Infection to Death ($1/\gamma_D$)	8.00 days	8.00 days
Time from Hospitalization to Recovery ($1/\gamma_{IH}$)	5.51 days	5.51 days
Probability a Case is Hospitalized (θ)	0.248	0.233
Case Fatality Rate, Unhospitalized (δ_1)	0.500	0.500
Case Fatality Rate, Hospitalized (δ_2)	0.500	0.500

For the first group of parameters, each individual has a 20% chance of traveling per timestep. If he travels and is not home, there is a 50% chance he travels home. Otherwise, he travels non-locally (to another city or village) with probability .... This incorporates the lower probability of non-local travel from large cities and higher non-local travel from small villages, but still leaves at least a 50% chance to travel locally instead.

Other parameters for the simulations included map width (100) and height (50), city densities $(80\%, 10\%, 10\%)$ and variance $(20, 5, 5)$, and population size (500).

Although the values may not precisely match those from the Ebola outbreaks, they still provide some insight into the spread of a disease through a spatial model.

Parameter	Value
Travel probability	0.2
Travel home probability	0.5
Travel non-locally probability	$(1 - \text{current city density})/2$
Family size	3-6
Family infection probability	?
-Community infection probability	?
-Funeral infection probability	?
Funeral length	?
Funeral attendance size	?
*Incubation time	?
Infected mortality (does this include hospital?)	?
*Time from infection to death	?
*Time from infection to recovery	?
*Hospitalization probability	?
*Time until hospitalization	?
*Hospital death probability	?
*Time from hospitalization to death	?
*Time from hospitalization to recovery	?

8 Results

We initialize the model with one infected individual who does not go to a hospital and does not recover.

9 Model Comparison

10 Summary and Future Work

- Briefly summarize your contributions, and their possible impact on the field (but don't just repeat the abstract or introduction).
- Identify the limitations of your approach.
- Suggest improvements for future work.
- Outline open problems.

A MATLAB Pseudocode for Agent-Based Dynamics

```
clear;
clc;

SimulationNUM = 100;
population = 200;
timestep = 500;

beta_I = 0.16;
beta_H = 0.062;
beta_F = 0.489;
Incubation = 12;
InfDur = 15;
TimeToHosp = 3.24;
```

```
TimeInfDeath = 13.31;
TimeHospDeath = 10.07;
TimeHospRec = 15.88;
DurFun = 2.01;

% Transition matrix [S E I H F R D]
Tran = [0.5 0.5 0 0 0 0 0;
      0 1-1/Incubation 1/Incubation 0 0 0 0
      0 0 1/InfDur 1/TimeToHosp 1/TimeInfDeath 1-1/InfDur-1/TimeToHosp-1/TimeInfDeath 0;
      0 0 0 1-1/TimeHospDeath-1/TimeHospRec 1/TimeHospDeath 1/TimeHospRec 0;
      0 0 0 0 1/DurFun 0 1-1/DurFun;
      0 0 0 0 0 1 0;
      0 0 0 0 0 0 1];

final_S = zeros(1,SimulationNUM);
final_R = zeros(1,SimulationNUM);
final_D = zeros(1,SimulationNUM);


for s = 1:SimulationNUM

people = [1 zeros(1,population-1)]; % initialization

c0=zeros(1,timestep);
c1=zeros(1,timestep);
c2=zeros(1,timestep);
c3=zeros(1,timestep);
c4=zeros(1,timestep);
c5=zeros(1,timestep);
c6=zeros(1,timestep);

a0 = sum(people == 0); %compute how many people are 0 at timestep 1
a1 = sum(people == 1); %compute how many people are 1 at timestep 1
a2 = sum(people == 2); %compute how many people are 2 at timestep 1
a3 = sum(people == 3); %compute how many people are 3 at timestep 1
a4 = sum(people == 4); %compute how many people are 4 at timestep 1
a5 = sum(people == 5); %compute how many people are 5 at timestep 1
a6 = sum(people == 6); %compute how many people are 6 at timestep 1

c0(1)=a0;
c1(1)=a1;
c2(1)=a2;
c3(1)=a3;
c4(1)=a4;
c5(1)=a5;
c6(1)=a6;

SroE = zeros(1,timestep);

for t=2:timestep

d0=0; %change of amount
d1=0;
d2=0;
```

```
d3=0;
d4=0;
d5=0;
d6=0;

StoE(t) = (beta_I*c2(t-1)+beta_H*c3(t-1)+beta_F*c4(t-1))/population;

for i=1:population

r=rand(1,population); %comparison vector


    if people(i)==0     % S goes to S or E
        if r(i)<=StoE(t)
            people(i)=1;
            d1=d1+1;
            d0=d0-1;
        end
    elseif people(i)==1 % E goes to E or I
        if r(i)<=Tran(2,3)
            people(i)=2;
            d2=d2+1;
            d1=d1-1;
        end
    elseif people(i)==2 % I goes to I, H, F or R
        if r(i)<=Tran(3,4)
            people(i)=3;
            d3=d3+1;
            d2=d2-1;
        elseif Tran(3,4)<r(i)<=Tran(3,4)+Tran(3,5)
            people(i)=4;
            d4=d4+1;
            d2=d2-1;
        elseif Tran(3,4)+Tran(3,5)<r(i)<=Tran(3,4)+Tran(3,5)+Tran(3,6)
            people(i)=5;
            d5=d5+1;
            d2=d2-1;
        end
    elseif people(i)==3 % H goes to H, F or R
        if r(i)<=Tran(4,5)
            people(i)=4;
            d4=d4+1;
            d3=d3-1;
        elseif Tran(4,5)<r(i)<=Tran(4,5)+Tran(4,6)
            people(i)=5;
            d5=d5+1;
            d3=d3-1;
        end
    elseif people(i)==4 % F goes to F or D
        if r(i)<=Tran(5,7)
            people(i)=6;
            d6=d6+1;
            d4=d4-1;
        end
```

```
    end

    c0(1,t) = c0(1,t-1) + d0;
    c1(1,t) = c1(1,t-1) + d1;
    c2(1,t) = c2(1,t-1) + d2;
    c3(1,t) = c3(1,t-1) + d3;
    c4(1,t) = c4(1,t-1) + d4;
    c5(1,t) = c5(1,t-1) + d5;
    c6(1,t) = c6(1,t-1) + d6;

end
people;
end

people;
SUM_OF_PEOPLE = sum(c0(1,timestep)+c1(1,timestep)+c2(1,timestep)+c3(1,timestep)
              +c4(1,timestep)+c5(1,timestep)+c6(1,timestep));


 figure
 subplot(4,2,[1,2]);
 plot(c0/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of S State')

 subplot(4,2,3);
 plot(c1/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of E State')

 subplot(4,2,4);
 plot(c2/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of I State')

 subplot(4,2,5);
 plot(c3/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of H State')

 subplot(4,2,6);
 plot(c4/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of F State')

 subplot(4,2,7);
 plot(c5/population,'LineWidth',2)
 axis([1 timestep 0 1])
 title('Proportion of R State')

 subplot(4,2,8);
 plot(c6/population,'LineWidth',2)
 axis([1 timestep 0 1])
```

```
 title('Proportion of D State')


final_S(s) = c0(timestep)/population;
final_R(s) = c5(timestep)/population;
final_D(s) = c6(timestep)/population;

end

final_S
final_R
final_D

% to compute the mean
% A = 1 - final_S
% for i = 1:100
%     if A(i) < 0.1
%         A(i)=0
%     end
% end
% A(A==0) = [];
% mean(A)
```

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