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# Modeling the Effect of Contact Rates on Infectious Diseases in Contact Networks

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***Abstract*— Infectious diseases have been modeled over the past centuries using equation-based modeling. Ordinary differential equations have been used in these models to represent the rate of flow of individuals among compartments in the modeling process. These equations have been quite useful but over the past few decades, two different models that have also proved a lot powerful and very useful are the agent-based model and the contact network-based model. In Agent-Based Modeling (ABM), the movements of individuals are simulated over time and space to model the spread of an infection. Similarly in contact Network-Based Modeling (NBM), the spread of an infection is modeled as a diffusion process on graphs. Our sole aim in this paper is to investigate how contact rates in a network based model influence infection spread within populations. We use susceptible-; infected-; and recovered epidemic models consisting of ordinary differential equations for our equation based model. For our contact based network model, we simulate the infection spread on a network following a Poisson degree distribution. The epidemic spread on the network uses bond percolation whereas in the agent based model, we use NetLogo to simulate the infection spread process. Using the network based model, we investigate how different contact rates contribute to epidemic spread within populations.**

***Keywords—epidemiology; emerging infectious diseases; bond perclation; contact network.***

## I. INTRODUCTION

Infectious diseases have caused devastating effects on the human race for centuries. From the 1918 Spanish Flu pandemic which claimed about 20 to 100 million lives [1-4] to the recent 2019 measles outbreaks in the United States of America which the CDC has warned is the highest measles outbreak since 1992, infectious diseases have affected many populations and countries. The CDC has estimated 1215 cases for the outbreak as at August 2019. Measles is highly contagious with high infection rate and basic reproductive number [5, 6]. One other infectious disease that has also been so devastating is the Ebola virus. It has been a great threat to some parts of West Africa with a mortality rate of 70 percent at one point. Liberia recorded about 10,666 cases with close to 3,200 deaths. In spite of control measures like quarantine, Sierra Leone at some point recorded 13,379 total infections with close to 9,000 deaths. Infected individuals were quarantined since it was observed that one key factor that resulted in the fast spread of the infection was contact with infected people. Contacts between infected and susceptible individuals in populations result in the transmission of infectious diseases. There is therefore the need to investigate how contact rates within populations result in the spread of infections and their influence in the occurrence of large scale epidemics. Conditions that result in outbreak of epidemics and the percentage of population that is infected are among issues that are of keen interest to researchers. Thus, resources such as isolation, influence, vaccination and anti-virus have been modeled to investigate their effect on infection spread [7]. Zhilan et al [7] in 2011 investigated how vaccination and antiviral drug treatment could help with the spread and control of the influenza disease. Lisa et al [8] investigated the effect of quarantine on the spread of the 1918-19 Spanish flu in central Canada and Troy et al [9] also looked at quarantine as a control strategy for emerging infectious diseases in general.

In this paper, we consider the contact rates within a network and its influence in determining whether a large scale epidemic is possible within a population. We first simulate the spread of infectious diseases in agent based; network based; and equation based models. For the agent based model, we use NetLogo, computer software that is used to build models; run experiments; produce, store and analyze simulated data [2, 10, 11]. Here, we use it to simulate the interaction between individuals in a population as a system of interacting agents. For the network model, we consider how contact rates influence the likelihood of epidemics. How frequent or scarce people within the population of interest have disease causing contacts determines the rate at which infection will be transmitted within the population. The disease causing contacts from node $i$ to node $j$ are denoted by $s_{ij}$ [1, 12] and it is used in computing the transmissibility, $T_{ij}$- : the probability that node $j$ will be infected by node $i$ [12, 13].

In the agent based and equation based models, we briefly simulate how infection spreads within those models and when large scale epidemics are possible. For the network model, we particularly examine the impact of contact rates on epidemic spread from a bond percolation perspective in Poisson networks. We simulate how varying contact rates affect infection

spread. We use data from past infectious disease outbreaks to simulate the contact rates and relate this to the recent 2019 measles outbreaks in the United States. The results show the high influence of contact rates on large scale epidemics. We present our methodology in Section 2 and the experiments with their results in Section 3. Section 4 contains the discussions and the conclusions from the investigation.

## II. METHODOLOGY

In this section, the models used in the paper are discussed. Information on how the SIR equation based model is used is provided as well as the network model. Finally, an introductory model in the curricular unit section of NetLogo, called epiDEM (Epidemiology: Understanding Disease Dynamics and Emergence through Modeling) [2] will be looked at for Agent-Based modeling.

### *A. Equation-Based Model*

**Susceptible, Infected and Recovered Model:** A system of Ordinary differential equations is considered for our initial simulation where we show infection transmission within populations from different modeling paradigms. We solve the system of ordinary differential equations in eqn. (1) in MATLAB to simulate the infection spread process.

$$\frac{dS}{dt} = \frac{-\beta \mathrm{IS}}{\mathrm{N}}$$
$$\frac{dI}{dt} = \frac{\beta \mathrm{IS}}{\mathrm{N}} - \gamma I$$
$$\frac{dR}{dt} = \gamma I \quad (1)$$

S, I and R are the number of susceptible, infected and recovered individual. These change with time, thus, can be represented by S(t), I(t) and R(t). The rate of movement of individuals from compartment S(t) to I(t) is denoted as $\beta$, the infection rate, whereas $\gamma$ is the recovery rate-: the rate of transitioning of individuals from the infected compartment to the recovered group. The infection and recovery rates are estimated from epidemiological data and for each infection being modeled, these parameters will be provided. The population is considered a closed one, hence, there are no births or deaths. The total population size (N) is therefore given by:

$$\mathrm{N} = S(t) + I(t) + R(t) \quad (2)$$

### *B. Agent-Based Model*

epiDEM (Epidemiology: Understanding Disease Dynamics and Emergence through Modeling), an introductory [2] model in curricular unit in NetLogo is the model to be considered for agent-based models. This agent-based model follows the concept of SIR model thus individuals are classified into susceptible, infected and recovered. In NetLogo, the agents are the individuals in the population under consideration. NetLogo has two types of agents, 'turtles', which move about and 'patches' which are stationary [2, 10, 14]. The agents have contact with each other according to a Poisson distribution and in the course of contact; infected agents transmit infection to susceptible agents.

In order to model the spread of an infection in the agent-based model, an infected agent (turtle) is introduced into the model. This agent has a color red while all other agents are white. Disease spread in this model is based on the proximity of other agents to the infected agent and the infection spread chance. The turtles move about and when a susceptible turtle and an infected turtle occupy the same patch, the program tests whether there has been an infection spread using the infection spread chance. Once a turtle becomes infected, it is infectious thus transmits the infection to other turtles. When an infected turtle reaches its recovery time period, it recovers based on its recovery chance. The infection spread chance and the recovery chance are both probabilities. With the recovery chance, the program tests if an infected turtle could become recovered. Once the turtle recovers, it becomes green and is eliminated from the disease spread. The recovery chance, the infection spread chance, the initial number of people and the average recovery time are all determined by the user.

### *C. Network-Based Model*

Contact networks are used based on compartmental models to model an infection spread. This model uses bond percolation theory in modeling the spread of infections [15, 16] and the simulations are done in MATLAB. Populations under consideration are considered as the network and the individuals are the nodes.

Contacts between individuals are represented by edges and infections are transmitted from one node to the other through these vertexes. Previously derived relations from Lauren and Newman [1, 3, 4, 12, 17] are used here. From Edoh et al [1], based on the disease causing contacts, $s_{ij}$, an infection is transmitted with the probability $T_{ij}$ which is given in equation 3 below. More so, the infection spread depends on the mean disease transmission probability, T, which is also referred to by Newman as average transmissibility [13].

$$T_{ij} = 1 - (1 - s_{ij})^{\tau} \quad (3)$$

$T_{ij}$ is the probability of an infection being transmitted after $\tau$ time [1]. We see from (3), that this is dependent on the contact rate. We show in this paper from our simulations how the contact rate influences $T_{ij}$ and the infection spread.

## III. RESULTS AND DISCUSSION

In the first part of our results, we show briefly how infection spread is modeled through the agent based, network based and equation based models. Our previous work in Edoh et al [1] has more details on infection spread in Network and Equation based models for your reference. We simulate how infection spreads in the agent based model using the epiDEM model described in Section 2. Contact patterns in the network and agent based models follow a Poisson distribution which is the assumption upon which the equation based model is built.

1000 agents are considered in the agent based model to represent a small town and the infection spread is modeled for 100 days in the population by introducing three infected agents into the population. The network based model also has three infected nodes placed within the network. For the equation based model, we set the infection rate as $\beta$ = 0.5 and the recovery rate as $\gamma$ = 5days based on past epidemiological data. The initial conditions are set as below:

I(0) = 3 ;R(0) =0; S(0) = 997.

In our simulation, we consider two cases of networks, one with varying contact rates and another with fixed contact rates. Equation based models assume individuals in a population are equally likely of being infected when an infected individual is introduced into the population, thus, we consider such a case on the network model by fixing contact rates between nodes. The results for the varying contact rates is shown in Fig. 1 whereas that for the fixed contact rates is shown in Fig. 2.

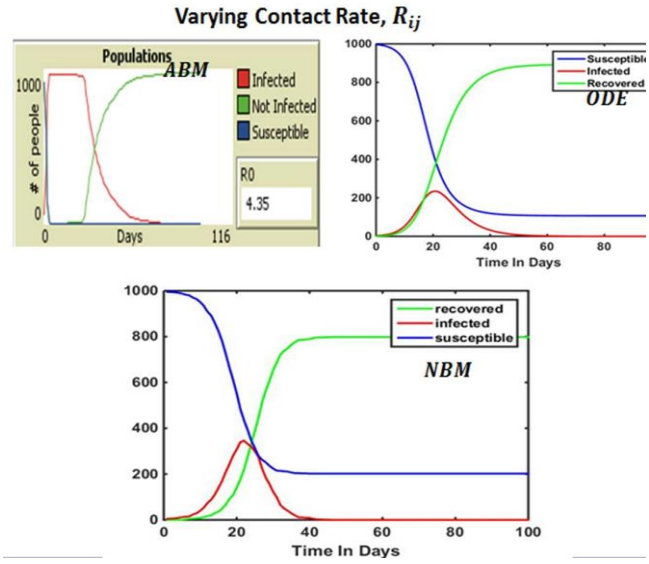


Fig.1: varying contact rates, $s_{ij}$ as in regular network models.

The results in Fig. 1 indicate that about 90% of the population was infected considering the equation based model, 80% with the network model with varying contact rates and the entire population from the agent based model.

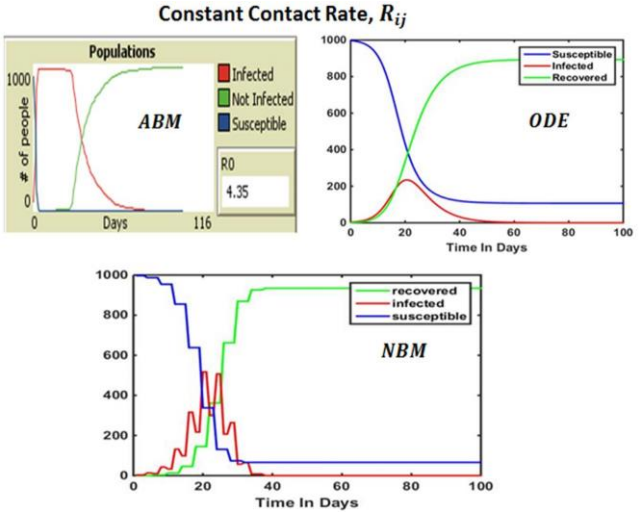


Fig. 2: contact rates, $s_{ij}$ fixed for simulation based on assumption of equation based models.

In Fig. 2, we see the network model with fixed contact rates resulting in about 95% infected cases in the lifespan of the infectious disease.

After showing how infection spread is simulated in the different models, we investigate how the contact rates influence infection spread. The results are shown in Fig. 3 and 4 for the varying and fixed contact rates respectively.

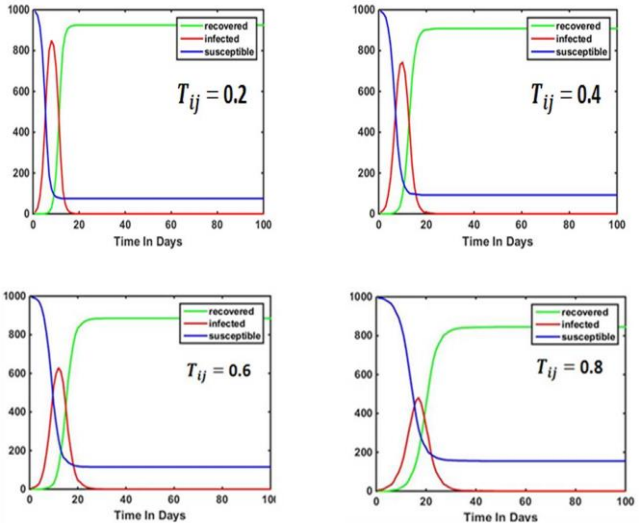


Fig. 3: Effect of contact rates on infection spread. Varying contact rates

From Fig. 3, we notice as $T_{ij}$ increases, the number of infected cases reduces and as $T_{ij}$ decreases, the number of infected cases increases. From Eqn. (3), $T_{ij}$ is influenced by contact rates in the period of infectiousness of an infectious disease. Our simulation therefore shows that an increase in the contact rate, $s_{ij}$, results in a decrease in $T_{ij}$, which in turn, leads to a rise in infected cases. In the first case in Fig. 4, we see $T_{ij}$ =0.2 with almost 100% of the population being

infected in the long run and then $T_{ij}$ =0.8, we see about 85% of the population being infected.

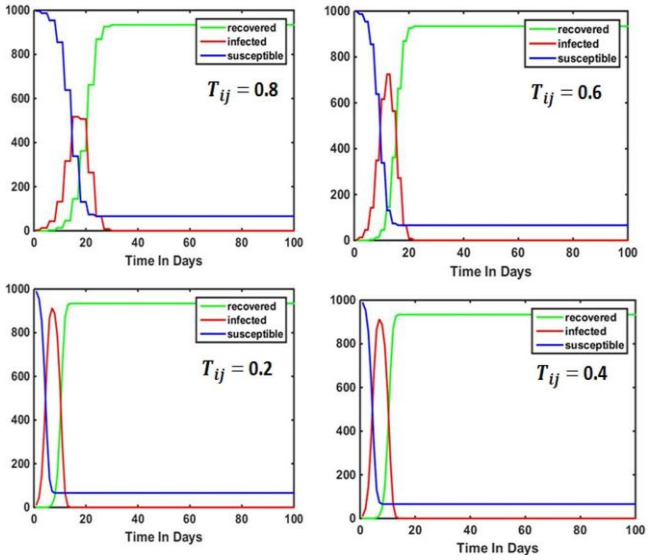


Fig. 4: Effect of contact rates on infection spread. Fixed contact rate.

For the fixed contact rates in Fig. 4, we see the same relationship between $s_{ij}$ and the possibility of large scale epidemic as in Fig. 3. Thus from our simulations, we have been able to show how increasing contact rates influence the occurrence of large scale epidemic.

Reducing contact rates in a population will reduce to a great extent the possibilities of a large scale epidemic, notwithstanding; it is worth noting that factors like the pathogen strength and vaccination status also have influence on the chances of an epidemic. However, since individuals need to come in contact before pathogen strength and vaccination status influence infection transmission, the contact rates are very important. We therefore see the reason for the concept of quarantine as a control strategy, implemented by public health.

While reducing the contact rates play a significant role, it might be difficult in some cases. In big cities where there are crowds of people that need to use health facilities, schools and public transportations, contact reduction can only be applied to the minimum except in the worse outbreak cases (like in Liberia during Ebola outbreak). Vaccination and other control strategies are implemented in most cases: as in the case of the New York City making vaccination a requirement in 2019 for individuals within specific zip-codes.

## IV. Conclusions

We showed how contact rates in a network influence infection spread within populations. For the initial part, we illustrated how infectious diseases are simulated within different modeling frameworks: considering agent based; network based and equation based models. For our main aim, the effect of contact rates on the infection spread, we observe that for higher contact rates in the network, the $T_{ij}$is low, resulting in a higher infection spread and vice versa. Thus, for an infection spread to be contained in a population, the contact rates within the population play a significant role-: the contact rates need to be reduced significantly.

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