Developing the Logical Method for Converting the Multiple-transmission-pathway System Dynamics Model to the Agent-based Modeling and Simulation

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ABSTRACT

This paper specifically shows how to translate a system dynamics model—the epidemiological model of SIWR (Susceptible-Infected-Water-Recovered)—into a corresponding agent-based model (ABM). Based off of the existing ABM of SIR (Susceptible-Infected-Recovered), a logical method for updating the agent state has been developed. To gain deeper understanding of disease dynamics and emergence, the influence of the water compartment has been analysed. Due to the added water compartment in the SIR model, an additional agent class, the pathogens have been added to the existing class of humans. Pathogens in water allow an additional transmission pathway through the water compartment. The results indicate that there is a significant impact of the added water compartment on the spread of the disease and the number of infected individuals. However, the impact decreases with an increase in the size of population.

1. INTRODUCTION

The two main computational models effectively used in epidemiology to gain insights of dynamic behavior of diseases are system dynamics and agent-based models. The two models originate from the two opposing perspectives. System dynamics (SD) model has long been applied to social systems (Forrester, 1961; Forrester, 1971; Roberts et al., 1983; Sterman, 2000). The SD model consists of a set of difference equations that are recursively solved forward through time. A rate of change is assigned to each state variable depending on the previous system state. It simulates changes of the whole system, and puts an emphasis on the importance of feedback between different components of the system. The effects of feedback then determine the system behavior. On the contrary, agent-based model (ABM) simulates actions and interactions among "agents," as well as the interactions of agents with their environment (Epstein and Axtell, 1996; Bonabeau, 2001; North and Macal, 2007; Macal and North, 2009). Agents may be organisms, humans or any other entity that acts independently and pursues its own objectives. The agents' behaviors are conditioned on their states and varied over time—adaptive behaviors. The behavior of a system can be observed and understood through those interactions. In other words, an agent-based model looks at what happens to a system because of what each individual does, and simultaneously what happens to each individual because of what the system does—emergent behaviors. The ABM is widely used to model complex systems composed of unique, autonomous agents. It is thus characterized as a bottom-up approach, while, system dynamics model is characterized as a top-down approach. Many researchers compare and contrast SD and ABM model by applying them in the area such as supply chain networks (Parunak et al., 1998) and infectious disease (Rahmandad and Sterman, 2008).

In epidemiology, agent-based simulation has become popular over the past years since it allows high fidelity of modeling disease outbreaks and is a flexible approach in evaluating realistic scenarios (Skvortsov et al., 2007). Consequently, system dynamics models theoretically developed and proved have been converted to agent-based models. For example, SIR (Susceptible-Infected-Recovered) model was used to develop the ABM for influenza epidemic (Lawniczak et al., 2006). SEIR (Susceptible-Exposed-Infectious-Recovered) was used to develop the ABM for Ebola virus epidemic (Siettos et al., 2015) and influenza pandemic (Khalil et al., 2012). Many researchers chose to convert SD models to ABMs presumably because they did not have to start from scratch and did extra calibration and validation of the created model (Giabbanelli & Crutzen, 2017).

The transformation process is a general one and can be applied to any SD model that has strong agent interactions (Macal, 2010). Agent-based simulation provides the opportunities to extend or change the SIR model to include some properties of a disease that are of interest. This is because the ABM is stochastic, while the SD model is deterministic. In this paper, the logical method of transforming SD models to ABMs, which interact with environment and have multiple transmission pathways, is developed. We use the SIWR (Susceptible-Infected-Water-Recovered) from Tien and Earn (2010) to demonstrate our logical method. The SIWR model is a simple extension of the classical SIR model. We added a water compartment *W*, and allow both person-person and person-water-person transmissions. Then, we converted the SIWR model, a SD model, to an ABM. We aim to study the spread of waterborne diseases, which currently remain a serious health concern, resulting in more than 3.5 million deaths per year according to the WHO Global Health estimates (Prüss-Üstün et al., 2008).

2. METHODOLOGY

The SIR (Susceptible-Infected-Recovered) model was first proposed by Kermack and McKendrick (1927), and has been used widely to predict the spread of diseases (Bjørnstad et al., 2002; Tiing & Labadin, 2008; Side & Noorani, 2013). In the model, the whole population is divided into three groups: susceptible individuals (S), infected individuals (I) and recovered individuals (R). With the constant total population (N), the model determines the number of susceptible, infected and recovered population at each time point. This constant total population implies that birth and death rates are not considered in this model. The SIR model is represented by a nonlinear system of three equations:

$$dS/dt = -\beta \cdot S \cdot I \quad (1)$$

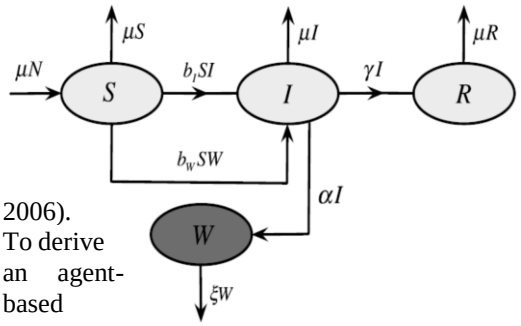
$$dI/dt = \beta \cdot S \cdot I - \gamma \cdot I \quad (2)$$

$$dR/dt = \gamma \cdot I \quad (3)$$

The parameter β is defined as the number of contacts that an individual has with other individuals, or the probability that an infected individual transmits the infection to a susceptible individual through contacts. The parameter γ is the rate at which an infected individual recover from an infection. The SIR model assumes that there is homogenous mixing of the population. This means each individual has the same chance of interacting

with other individuals, and thus, the same chance of becoming infected in this mixed population.

Next is converting the SIR model to the ABM. For instance, the SIR model, which is formulated from differential equations, has a corresponding system dynamics representation known as difference equations. According to the Equivalence Theorem, the set of all SD model is a subset of the set of all ABMs. That is, every well-formulated SD model has an equivalent formulation in an ABM (Macal, 2006). To derive an agent-based model (ABM) from a system dynamics (SD) model of the SIR model, the first step is to disaggregate the state of the system in order to generate agents. An agent class is then defined to cover all individuals in the population. The three states of the system (i.e., S, I, and R) are replaced by the state of an agent. The state of an agent is its particular disease state, which is the only information in the model to be dynamically updated. All other parameters are static. Hence, since the population size is N, there are N agents in various disease states of S, I and R and each agent's disease state is updated through a logical method at each time step. The next step is to identify, isolate, and translate probabilistic elements in the SD model into probabilities in the ABM. The two probabilities considered in the SIR model refers to the chance of contacting infected individuals, and the chance of recovering from infectious diseases, respectively.



2.1 Logical method for updating an agent state

We select the Tien and Earn (2010)'s SIWR model. This model describes the disease states as differential equations, which depend on time, as well as the transmission and recovery parameters seen in Figure 1 and a system of four equations below.

$$dS/dt = \mu \cdot N - b_W \cdot W \cdot S - b_I \cdot S \cdot I - \mu \cdot S, \quad (4)$$

$$dI/dt = b_W \cdot W \cdot S + b_I \cdot S \cdot I - \gamma \cdot I - \mu \cdot I, \quad (5)$$

$$dW/dt = \alpha \cdot I - \xi \cdot W, \quad (6)$$

$$dR/dt = \gamma \cdot I - \mu \cdot R \quad (7)$$

Deriving an agent-based model: We first identified agents of the system, their states and variables. Agents are individuals whose states are either Susceptible (S), Infected (I), or Recovered (R). Their interactions change outcomes of the whole system. In Figure 1, $\beta \cdot S \cdot I$ is the first disease transmission pathway through person-to-person contacts. At this transition, the number of susceptible individuals would decrease, while the number of infected individuals increase. The chance or probability of being infected by contacting infected individuals, b_I, is unique for each specific disease. This value increases with the number of infected individuals. The function $\gamma \cdot I$ is the rate at which the infected individuals recover from a disease. At the change of states from I to R, infected individuals cannot infect others through person-to-person contacts even though the individuals may still have signs and symptoms of the disease. Water compartment, W, was added to the model and it is contaminated by infected individuals.

Figure 1. Flow diagram for the SIWR model (Tien and Earn, 2010).

The $\alpha \cdot I$ describes the transmission pathway through person-to-water contacts. In the equation (Figure 1), W represents the number of pathogens, and this numerical data vary over time. Here we introduced another pathogen or infectious agent, in addition to human agent. Pathogens are microorganisms such as bacteria and viruses, which in this case, reside in the water compartment and can cause disease in humans. Here, the $\alpha \cdot I$ variable describes the spread of the disease from infected people coming into contact with the water source. Lastly, $b_W \cdot W \cdot S$ refers to the disease transmission pathway through water-to-person contacts, or rather pathogen-to-person contact. Susceptible individuals get infected through coming into contact with infected water. This water, however, can return to its original clean state through $\xi \cdot W$ (e.g., adding chemicals, passing current to the water, and adding large amount of fresh water). Each pathogen also has its lifetime. When its lifetime ends, the pathogen dies causing the water to become uninfected.

In sum, in converting the system dynamics SIWR model to the agent-based model, the states of the system are converted to the states of agents—humans and pathogens—in the system. These agents act according to their states.

On each step of the simulation, each agent would update its disease state as shown below in Figure 2. During the simulation, every human agent moves

around randomly and updates its disease state with every time step. If an agent is in the infected state, it will either contaminate the water source or recover depending on the location and time period at that state. Susceptible agents can either change their state to Infected (I) when coming into contact with infected people or contaminated water, or remain in the same state. In the simulation, the infected people are separated into ordinary Infected (I), Waterinfected (WI) and Secondary-Waterinfected (SWI). The ordinary infected are infected through person-to-person contacts. The Waterinfected are infected by contacting contaminated water. Secondary-Waterinfected are those who got the infection from the WI or from those who categorized in the SWI. However, all infected people behave similarly and have the same potential to infect other individuals or contaminate the water. Each type of infected people is classified because we will use this classification to analyse the impact of water compartment in the results and discussion section. Agents who recover from disease stay until simulation is terminated without changing their state. The simulation ends when no infections can occur—when all pathogens die and all infected individuals are recovered from the disease.

2.2 Translation from Tien and Earn (2010)'s system dynamics (SD) model to an agent-based model (ABM) in NetLogo

We started with the NetLogo Epidemic Basic model (Wilensky, 2011). This is an agent-based model converted from the SIR model. We utilized the Netlogo as it is a simple tool to simulate update rules in an ABM. In the Epidemic Basic Model, there exists three variables: Susceptible (S), Infected (I) and Recovered (R). At the beginning of the simulation, each human agent has a specific chance (5%) of getting infected. The initial number of people can be varied. Each human agent has its own value of transmission and recovery rate based on the probability defined in the model. The rate at which individuals contact with infected ones, b_I, can be viewed as chance or probability of being infected by contacting infected individuals. This depends on the disease in focus. In the NetLogo model, each individual meet infected ones by random, and this chance is named "infection-chance."

In the Epidemic Basic model, the parameter γ, or the rate at which an infected individual recover from an infection (recovery chance), is included. This value can be varied. The model keeps track the time each agent is infected.

To develop the SIWR model in NetLogo, we made a few changes to the Epidem Basic model from the library in Netlogo. We differentiate the agents by

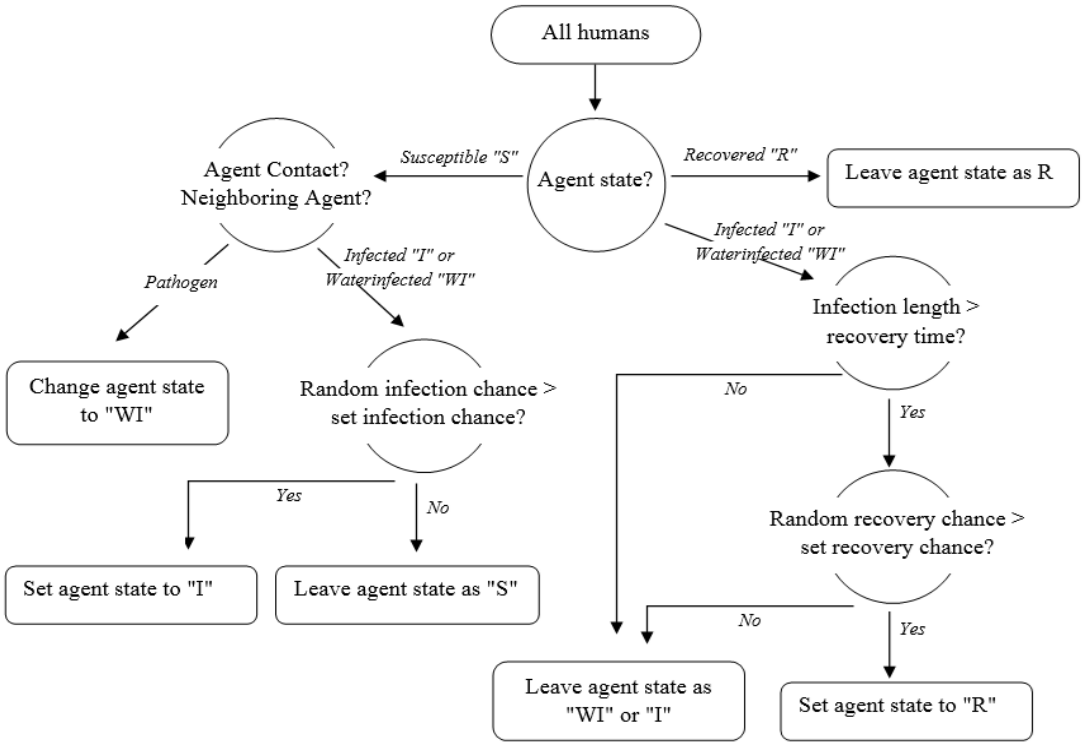


Figure 2. The logic of updating—modified from the logic of the Macal's SIR model (Macal, 2010).

introducing two types of agents which are *humans* and *pathogens*. These two types of agents have different appearances in the simulation. The shape of *humans* looks like persons and *pathogens* are represented as arrows. Furthermore, we introduce two new disease states: *WI* and *SWI* for visualization purpose and analysis of the number of people who have been directly infected by water and who have been secondary infected by people who infected by the water. In order to visualize the differences, *WI* and *SWI* are color-coded in orange and yellow respectively. *I* is color-coded in red, *R* is color-coded in green and initial people is color-coded in white.

When using the term "infected" outside of the code, *WI* and *SWI* are included in the infected population. In further description, we use humans and pathogens rather than agents in order to differentiate them clearly. To describe their attributes and states, *pathogens-own* and *humans-own* are used to define the variables belonging to each agent.

The water compartment is represented as blue patches. Each patch in the model has the same probability of being reached by any *human*; therefore, the size of the *waterpatch* serves as an equivalent to the chance of a *human* coming into contact with water which could be contaminated by infected population. In order to be able to change the size of the water compartment, the variable *watersize* is introduced in the code. The water can represent various types of water sources such as lakes, rivers, etc.

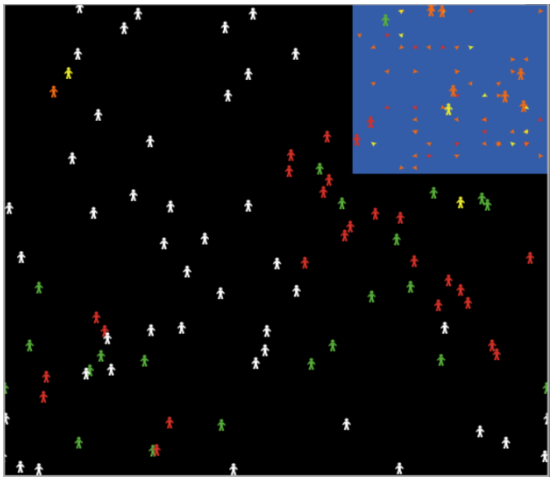


Figure 3. The example of simulation run with a little water compartment.

Besides coming into contact with infected individuals, susceptible individuals have a chance of getting infected when coming into contact with contaminated water. The water in our model is not contaminated in the beginning. It has to get infected by infected individuals. The infected individuals

spread pathogens when they come into contact with the water compartment. Based on the parameter ?? of Tien and Earn equation based model (Tien and Earn, 2010), *waterpolution* is developed to represent the likelihood of spreading pathogens when infected individuals come into contact with water. Whenever any of the infected people (*I, WI* or *SWI)* moves onto the blue patch representing the water, that agent has the chance of contaminating the water. The pathogens are only inside of the water, therefore the movement of those pathogens are restricted inside of the *waterpatch*. Pathogens move randomly in the water compartment.

In Tien and Earn model, they describe the rate that susceptible individuals come into contact with contaminated water as "reservoir – person contact rate" (Tien and Earn, 2010). If an infected individual stays at the *waterpatch* for a longer period of time or multiple infected individuals are within the patch, more pathogens are being spread. Therefore, high amount of pathogens or density of pathogens inside of the *waterpatch* indicates high risk of susceptible individuals getting infected when coming into contact with the water. The new infected individuals are called Waterinfected (*WI*) for analytical purposes.

Those *WI* infect susceptible individuals through the same logic as the Infected (*I*). The only difference is that the new infected are called Secondary-Waterinfected *(SWI*). The lifetime of each pathogen can be set in the model. After this lifetime the pathogens die and simply disappear in the simulation. Therefore, contaminated water can be cleaned. The lifetime of the pathogens can also be easily changed in order to accurately represent the realistic situation.

3. RESULTS AND DISCUSSION

By adding the water compartment, we observed what happened to the disease dynamics and emergence in several scenarios by looking at the peak number of infected individuals, and the time at which the peak occurs. The scenarios vary by the size of water compartments. The remaining number of susceptible individuals who never get infected after the simulation indicates the severity of a disease. If this number is high, it means that the disease severity is low.

The initial conditions for this simulation are as follows: the number of the initial people (*N*) is 100. The infection chance is 50%. The recovery chance is 80%, and the average-recovery time is 100. The chance that infected people shedding pathogens into the water is 20%. The pathogen has a lifetime of 30. The big water compartment means 25% of the simulated area are water patches. The small water compartment means 13.6% of the simulated area are water patches. For every analysis, the initial conditions remain the same unless mentioned otherwise. We ran the simulation 100 times and compute the average number of infected people and average percentage of susceptible people who are not infected. A simulation ends when the number of infected individuals and pathogens declines to zero—no further infections are possible.

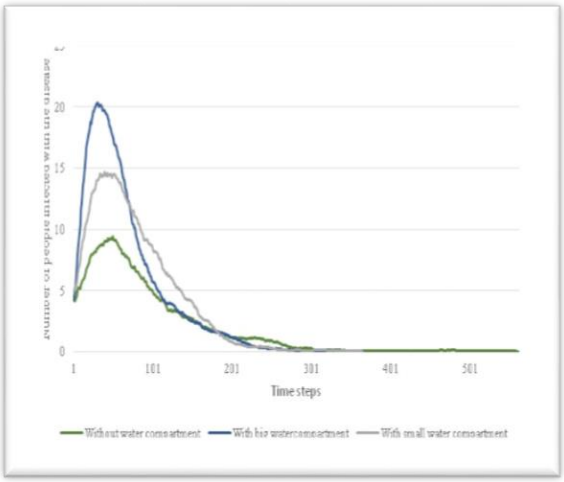


Figure 4. The graph of disease dynamics and emergence without water compartment, with big, and with small water compartment.

The analysis presented here compares the SIR model with the extended SIWR model. The varying size of the water compartment represents different environmental conditions, such as tropical/dry areas and wet areas. Hence, the size of the water compartment indicates the likelihood of humans come into contact with water. Figure 6 shows the number of infected individuals over time for various scenarios. The shapes of the graphs represent the disease dynamics, which are similar across scenarios. However, the peak number of infected individuals are significantly different. For the simulation run with the classical SIR model with no water compartment, the peak number of infected individuals is 9.40 and occurs at time 50. For the simulation run with a water compartment, the peak number of infected individuals are significantly higher. With a small water compartment, the peak number of infected individuals is 14.68 and occurs at time 40. With a large water compartment, the peak number of infected individuals is 20.30 and occurs at time 31. The water compartment has a significant effect on disease dynamics and emergence. Hence, in an environment where people have a higher chance of getting into contact with water, the disease spreads faster and at the same time more individuals are infected. An additional

transmission pathway that passes through water accelerates the spread of the disease, and shortens the time the graph reaches its maximum number of infected people. Thus, it is important to know the exact value of the parameter, b_W, which is the rate at which an individual gets infected when contacting the contaminated water.

Next, we focused on the big water compartment scenario and splits the infected individuals into three groups: ordinary Infected (*I*), Waterinfected (*WI*), and Secondary-Waterinfected (*SWI*). The results are shown below in Figure 5.

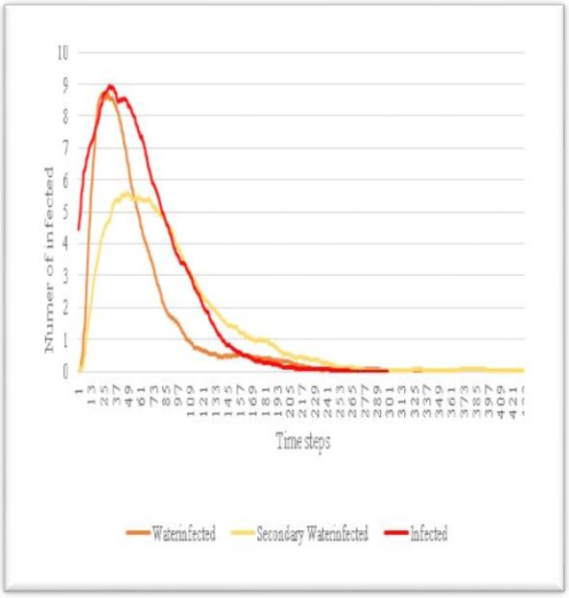


Figure 5. The graph of disease dynamics and emergence with big water compartment classified into the ordinary Infected (I), Waterinfected (WI), and Secondary-Waterinfected (SWI).

It is clearly seen that the sum of each graph in Figure 5 can be added up to the blue curve, the total number of infected individuals with big water compartment, in Figure 6. The number of people directly infected through water quickly reaches its peak of 8.70, at time step 27. However, it takes more time for the Secondary-water infected to reach its peak of 5.59, at time step 47. This indicates the importance of isolating infected people from not-infected ones.

The peak occurs when either the infected individuals or the susceptible individuals are not large enough to cause an increasing number of infected individuals. Alternatively, we can observe the remaining number of susceptible individuals seen in Figure 8. We can see that the susceptible individuals is highest with no water compartment and small number of total people.

The outcome of each simulation is highly sensitive towards changes in the initial conditions. Higher infection chances, higher number of initial people lead to a larger number of infected people and a decreasing number of people who remain susceptible throughout the simulation. We intend to simulate various conditions shown in Figure 7. Within each infection chance, the number of people remaining susceptible decreases with the increasing size of the water compartment. Depending on the disease, the risk of getting infected when coming into contact with an infected person or contaminated water varies vastly. A higher infection chance leads to a higher infection rate and therefore less people who do not contract the disease. The combination in our case shows the impact of initial conditions. A disease which can be transmitted through water with a low infection chance (25%) can have the same outcome as a disease which is able to be transmitted through water with a high infection chance (75%). Therefore, a clear knowledge of a particular disease's transmission and initial condition are important in the simulation.

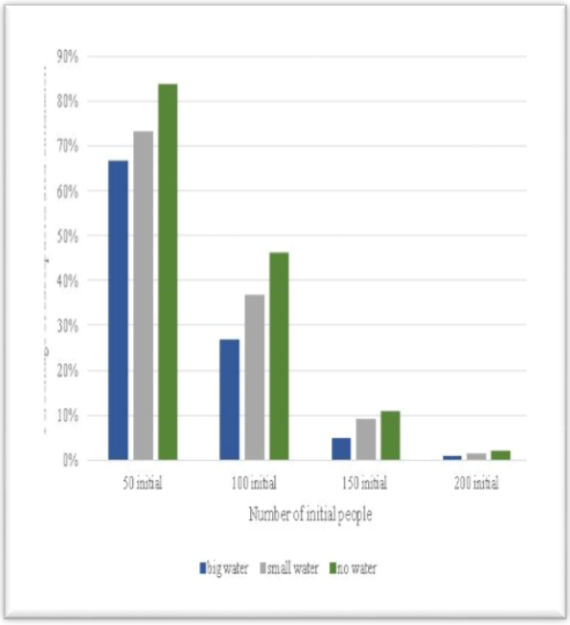


Figure 6. Comparison of percentage of susceptible people by varying initial population and water compartment size.

In addition, we observe the impact between number of initial people and the percentage of susceptible individuals. The output of Figure 7 shows the percentage of susceptible individuals after the simulation related to the number of initial people. Cases with initial people of 50, 100, 150 and 200 are considered, while the other initial conditions remain the same.

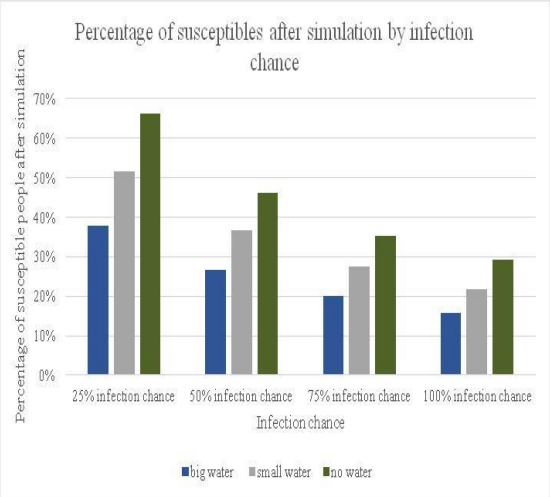


Figure7. Comparison of percentage of susceptible people by varying infection chance and water compartment size.

The output for every case is similar. For every case, the percentage of susceptible after the simulation with no water compartment is greater than in simulations with a water compartment. In the case with initial people of 50, the percentage of Susceptible after the simulation with no water compartment is 83.80%, with a small water compartment is 73.32%, and with a big water compartment is 66.58%. In the case of 100 initial people, the percentage of Susceptible after the simulation with no water compartment is 46.20%, with a small water compartment is 36.76%, and with a big water compartment is 26.77%. Hence, the results support the assumption that more individuals become infected if they live in an environment with water. Nevertheless, with the increasing number of initial people, the difference between the percentage of remaining susceptible after the simulation with and without a water compartment decreases. In the case with initial people of 200, the percentage of susceptible after the simulation with no water compartment is 1.97%, with a small water compartment is 1.41%, and with a big water compartment is 1.08%. Almost the entire population becomes infected and the number of susceptible individuals declines nearly to zero over the course of the simulation. Therefore, we can conclude that the influence of the water compartment decreases with an increasing number of initial people. That is, if the population is large enough, the occurrence of an epidemic is independent of water.

4. CONCLUSION

Agent-based modeling and simulation have been used to predict spread of infectious diseases, its severity, and to analyze given prevention mechanisms. This paper converts the SIWR (Susceptible-Infected-Water-Recovered) model—a system dynamics model—into an agent-based model. This is an extension of the existing agent-based model converted from the SIR (Susceptible-Infected-Recovered) model. That is, an additional water compartment is added to determine the pathogen concentration in the water source. We first formulated the SIWR model, with its corresponding difference equations model, and finally the agent-based model by developing a logical method of updating the agent state. We also examined the impacts of the size of water compartment, pathogen lifetime, pathogen recovery time on disease dynamics. We presented an example analysis of transmission pathway of waterborne diseases that can be useful for public health officials in selecting appropriate intervention strategies.

The logical method proposed in this paper might be applied to other diseases. Most importantly, this study suggests a new way of predicting spread of the diseases and its severity by categorizing infected people into the ordinary Infected (I), Waterinfected (WI) and Secondary-Waterinfected (SWI).

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