Modelling Infectious Disease Spread and Control Strategies Using Agent-Based Models

Done by: Daniel Tan (22684196), Melo Xue (23955182)

1. Background

1.1 Problem statement:

There has been an increasing number of infectious diseases and growing threats of further variants and new viruses in the 21st century. Despite the vast number of viruses known to man, the spread of these diseases exhibits similar patterns. Hence, in this project, an Agent-Based Model (ABM) is implemented to study and simulate the spread of infectious diseases in a specific area across individuals over time. The aim of the study is to create a computational model that represents the pattern of disease transmission and then moving to an endemic state (herd immunity), considering some factors such as recovery rates, infection rates, and population movement.

1.2 Importance discussion

Over the past 10 years, the infectious diseases, such as COVID-19, Zika virus and Ebola virus, have caused pandemics or epidemics, posing a serious threat to the health and security of people. The pandemic not only led to widespread illness but also economic disruptions especially in densely populated cities or developing countries, where the healthcare infrastructure could be severely stressed (Fauci, 2014). Hence, it is critical to find the pattern of the spread of infectious diseases to understand the causes, sources, and risk factors of the disease, and to design relative and effective control measures. ABM can therefore provide a more comprehensive and realistic picture of the disease dynamics and the impact of policies than other models, such as equation-based models, that rely on simplifying assumptions and aggregate variables (Hunter et al, 2018). These variables although simple, can show emergent and complex patterns in the grid space over time. Understanding the spread of disease dynamics can be beneficial to evaluate the uncertainty and the effects of various interventions in place.

1.3 Overview

As we embark on this research journey, our primary objectives include understanding the dynamics of disease spread and pinpointing causal factors. The project unfolds in a structured manner, with subsequent sections delving into the methodology, data sources, model development and simulation results. The results of ABM model may show that from the individual and holistic system behaviour, that infections amongst the agent population gradually focuses on a certain area. Hence, the application and results of this model of infectious diseases may illuminate the future control of the epidemics.

2. Model description

2.1 Reasons for model selection

There are several advantages of Agent-based models (ABM) that can mimic and imitate how diverse people and groups act and interact with each other and discover the patterns that rule their actions. Firstly, ABMs simulation models can represent the interactions between individual agents and their environment and capture the dynamics and heterogeneity of disease transmission and behaviour (Steinbacher et al, 2021). Secondly, Pitman et al (2012) concluded that Agent-based models are a more flexible alternative approach for dynamic transmission modelling since ABMs are modelling individuals instead of compartments. Thirdly, Steinbacher et al. (2021) used the modular ABM to simulate persons and mosquitoes over a year considering daily time steps and validated that ABM is a practical approach that is capable to reproduce direct and indirect effects of interventions for dengue.

Moreover, we apply an ABM model with a 100x100 grid space to analyze the trend of infectious disease because William et al. (2015) proved that a 100x100 grid space can reach a balance between model

accuracy and computational efficiency. Smith et al. (2018) represented that it allowed to capture the spatial heterogeneity and the influence of geographical factors on disease transmission. Agents can move from and from one cell to another based on rules so that it can mimic real-world behaviors and the movement can lead to interactions between agents from different locations, which could capture the pattern of diseases spread.

2.2 Assumptions and rules

Within this project, the agents' behaviours are based on three location rules and three infection rules. The assumptions and rules for this project outline the behavior and interactions of agents in a simulation. The location rules are: (1) that an agent can choose one of two choices, stay where they are (s.t infection), or move to another grid space. (2) Agents can move freely from one grid space to any other at one timestep, where there are no hinderances besides capacity in (3) If the grid space is already occupied by an agent, randomly select another space in the node.

The infection rules are: (1) An agent can be infected at a timestep if they are within a 3x3 grid space vicinity of an infected individual, dependent on their transmission rate; (2) The probability of the agent recovering from the infection depends on the recovery rate; and (3) An individual who is infected has should not move from their location. Once an agent is infected, they are expected to remain in the same grid space and not move to other locations within the simulation. Upon recovery, the agent gains immunity, and then also decides on whether to get vaccinated. Finally, if an agent dies, then another agent with completely different attributes will replace them in the same grid space. These assumptions and rules provide a framework for the behavior and interactions of agents within the simulation, governing aspects such as movement, infection, and recovery.

2.3 Configuration and parameters

The model consists of two main components, the agent, and the disease. The disease parameters determine the strength and the variability of the disease overall. This is controlled by 5 parameters – (1) the scan space, which is the variable of the area around an agent that infected agents can infect them, (2) the minimum number of infected days before recovery can occur, (3) the minimum number of days before death can occur, (4) the multiplier factor, meaning for an increased number of infected around the agent, this factor increases the chance of them getting infected. Finally, (5) the chance of death given by a small probability.

In the case of the agent, they have the following random attributes that are unique to them: (1) transmission rate (how easily they catch the disease) and (2) the recovery rate (how easily they recover from the disease). At any point in time, they can either be infected or not, and the amount of time that they have been infected is also recorded. Given the 2 parameters, they can be manipulated by 2 key components, the vaccine and immunity multipliers, which controls the effectiveness on the disease and the variability of them across agents are defined over a normal distribution given mean (multiplier) and variance (randomness) that impact their recovery and infection chance.

The number of agents within the environment can be chosen with the constraint: number of agents < number of grid spaces, which can be configured by defining the length and breadth of the space. The number of steps can be tuned to track.

3. Results

3.1 Results visualization and discussion

Our aim is to collect three parameters of interest, which will help us to understand the results of the varying attributes in the model and how they contribute to the study of the spread of the disease. First, infection rate sets the overall infection rate over time, determining the percentage of the population that is infected at each step. Second, the percentage of infected at each time step and lastly, the death rate over time. In our infectious disease simulation model, several key hyperparameters dictate the initial conditions and dynamics of the simulation. It starts with an infection rate of 0.01 and a vaccination rate of 0.2 in a population of 1000 individuals on a 100x100 grid over 100 time steps. The transmission space (3) controls disease contagiousness. Infections occur after 7 days, and a death chance of 0.05 can occur after 14 days. Vaccine and immunity multipliers (0.3 and 0.2) affect their effectiveness, with variability introduced by vaccine and immunity randomness (0.2 and 0.05). Individuals may choose to get vaccinated (probability of 0.3) after recovery, and the multiplier factor (1.1) influences the disease's spread based on the number of infected individuals. Simulations are run for a total of 10 iterations, and the values are averaged.

Finally, by running the model the emergent patterns can be observed in the Figure 2. The red points represent infected people, while the grey points represent healthy people. The initial figure is constructed and fixed to show that the initial infected population is randomly distributed in the appropriate area.

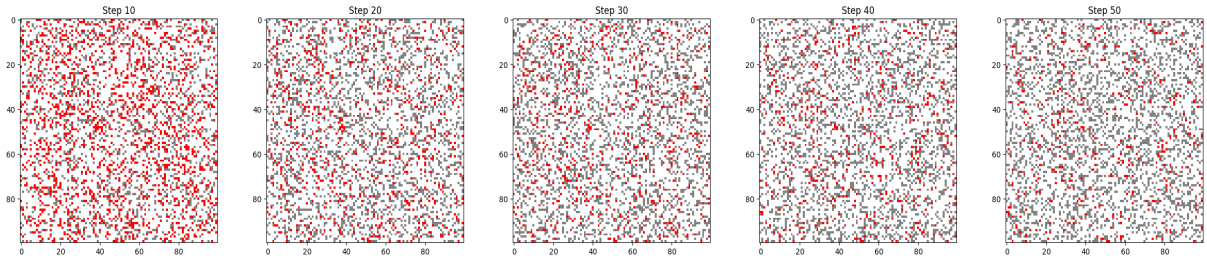


Figure 1:

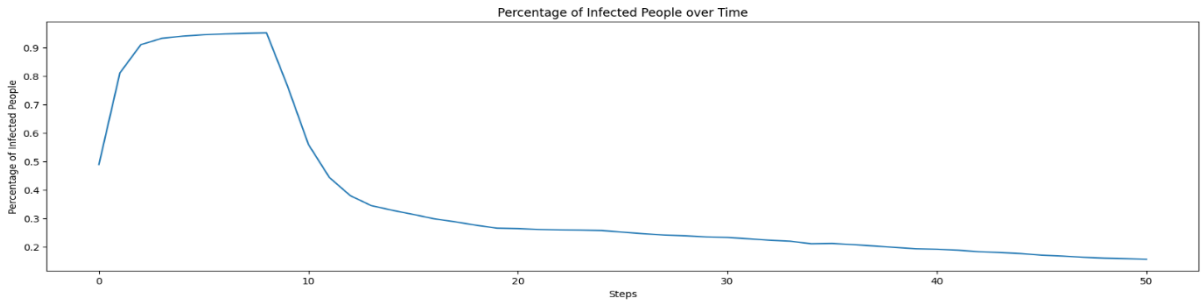


Figure 2: Percentage of Infected over time

The graphs depict the progression of an infection over time, with the number of infected (red) individuals increasing and then decreasing. The peak of infected population is reached at step 10, it can be observed that infected people are around the area. After 50 steps, there are less infected people and several disease hotspots. Disease hotspots are localized areas where the disease is spreading at a higher rate compared to surrounding regions. Identifying these hotspots can help public health officials gain insights into how the disease is spreading and which areas are most affected.

3.2 Parameter comparison and analysis

For the purposes of this assignment, we dedicate the focus on the different (1) vaccine multipliers, (2) initial percentage of population that are vaccinated and (3) scan space size. To observe the isolated effects of each parameter, all other ones are kept constant throughout the experiment.

First, the initial vaccine multipliers are adjusted in a list that encapsulates three distinct values: 0.2, 0.5, 0.8. These values represent how strong the vaccine is to resistance of the disease, allowing for the exploration different experiments when producing vaccines. The figure 3 displays that a higher vaccine strength (lower multiplier) will mean that there will be less people who get infected. More graphs related to initial infection are in the appendix. Additionally, in the experiment, initial vaccination percentage of the population can also be varied to see the impacts of the vaccine in the early stages of the spread. For the immunity multiplier, we observe the same phenomena, and hence, both these parameters can be tweaked in tandem to retrieve an optimal outcome to fight against the spread.

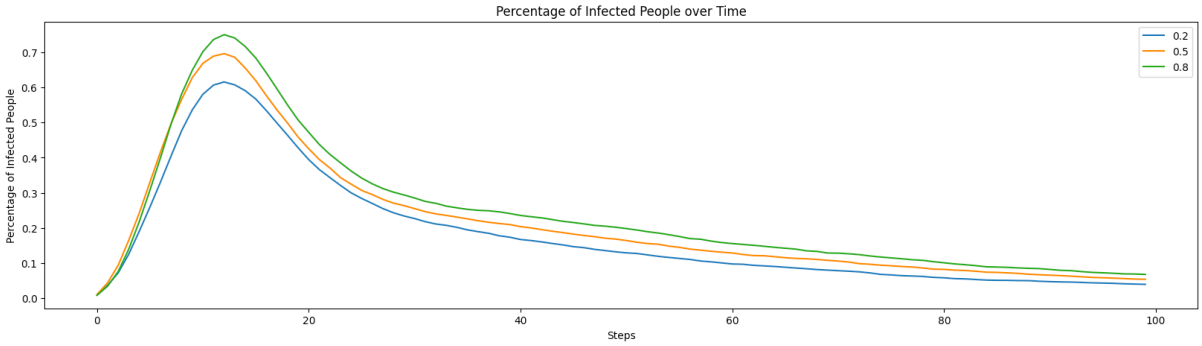


Figure 3: Percentage of Infected people over time, varying vaccine strengths

Under the set environment and population, the infection rate shows a sharp increase first to a peak and then decreases to a flat line. The sharp increase to a peak could represent the rapid spread of an infection in a population, where the number of infected individuals increases quickly. The subsequent decrease and flattening of the curve could represent the point at which interventions have been put in place.

Secondly, we want to look at the how the disease spreads given different percentages of the population being vaccinated. This is observable in Figure 4, when more of the population are vaccinated before the onset of the disease, the peak and recovery is more gentle. However, we do observe that because less of the population gets the disease, they do not build up immunity or choose to get the vaccine, and thus, the level of infection still remains high. Figure 5 shows us the infection rate over time, which perhaps cements our understanding of how the disease spreads.

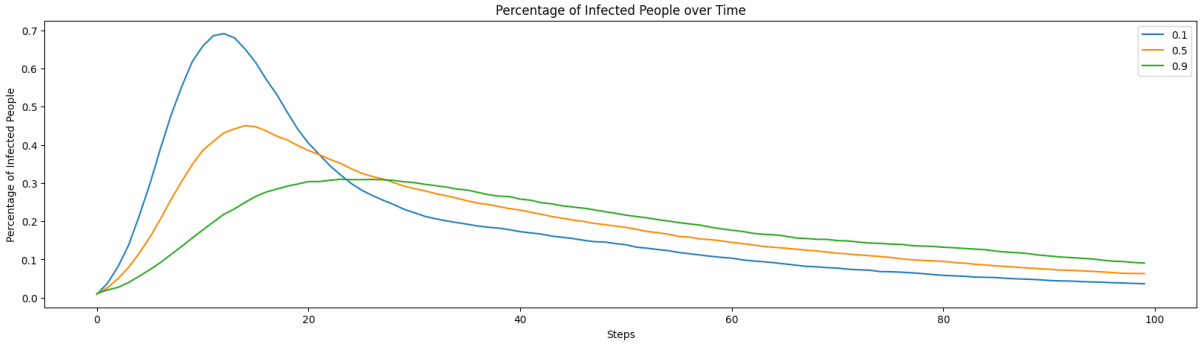


Figure 4: Percentage of Infected people over time, varying initial vaccinated population

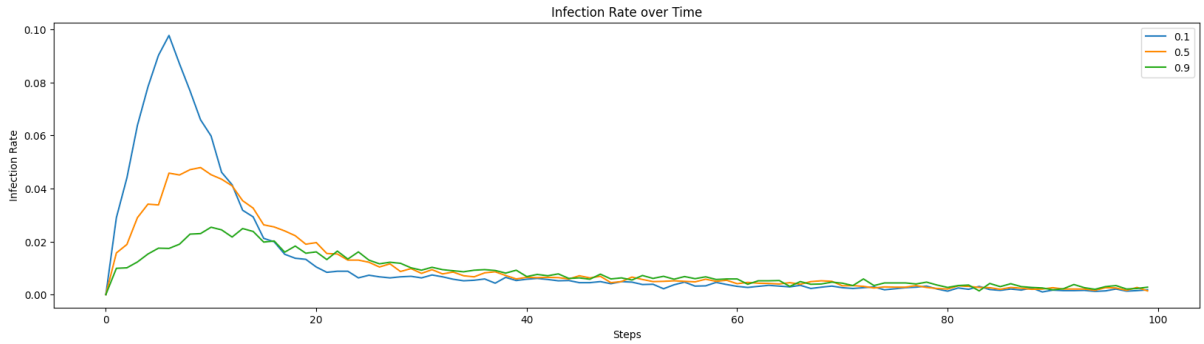


Figure 5: Infection rate over time, varying initial vaccinated population.

At last, the scan space parameter is being varied to observe its impact on disease spread and control measures. The scan space represents the area around an individual where they can get infected. A larger scan space can simulate diseases with a wider transmission range, such as airborne diseases, while a smaller value simulates diseases with limited transmission, like contact-based infections. In this specific case, three different scan space values are being tested: 1, 2, and 3. These values control the extent to which an individual can infect or get infected by others. A scan space of 1 means a very limited interaction range, while a scan space of 3 allows for a broader area of potential transmission. The results are shown in the figure 6, where a 1x1, smaller window of possible infections will see lower peaks, while a larger scan area will see more people infected at the start.

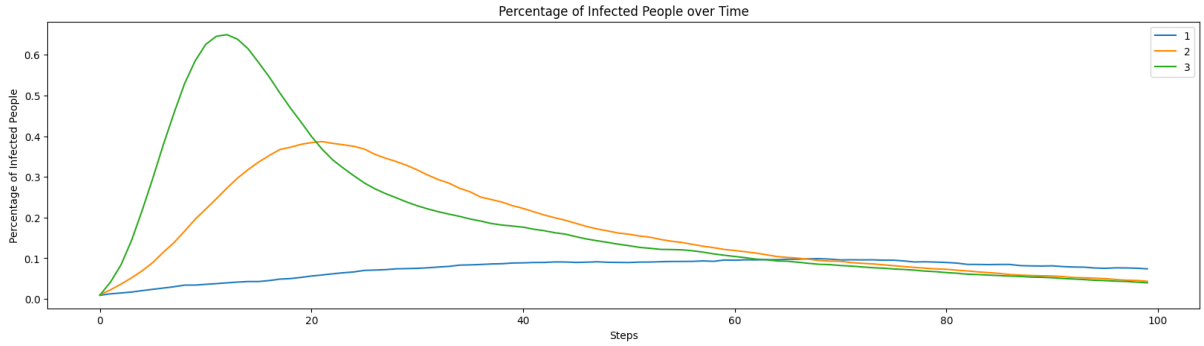


Figure 6: Percentage of Infected people over time, varying initial vaccinated population

Further results of the other parameters we have discussed and experimented in can be found in the appendix.

4. Conclusion

In conclusion, the ABM model is suitable for simulating the spread of an infectious disease in a population. Under the defined environment and population settings, our simulation revealed intriguing patterns in disease spread. The infection rate exhibited a characteristic trajectory, initially rising sharply to a peak and then gradually decreasing to a stable level, exhibiting an equilibrium state. This initial surge in infections reflects the rapid transmission of the disease within the population. Subsequently, the curve flattened, indicative of the implementation of effective interventions and containment measures. The findings also suggest that the disease spreads rapidly initially but gradually slows down as immunity develops among the population. Moreover, these findings emphasize the importance of vaccination campaigns as a critical strategy for controlling and mitigating infectious disease outbreaks. In the further research and refinement of the model, more parameters may be included, such as healing ability and weather condition, to increase the accuracy and utility in addressing real-world infectious disease challenges.

References

Fauci, A.S. (2014). Ebola-underscoring the global disparities in health care resources. *New England Journal of Medicine*, 371(12), 1084-1086.

Hunter, E., Mac Namee, B., & Kelleher, J. (2018). A comparison of agent-based models and equation-based models for infectious disease epidemiology. In D. Lillis, F. Toolan, R. Walshe, M. Abgaz, & B. Mac Namee (Eds.), *Proceedings of the 29th Irish Conference on Artificial Intelligence and Cognitive Science* (pp. 31-42). CEUR Workshop Proceedings.

Steinbacher, M., Raddant, M., Karimi, F., Camacho Cuena, E., Alfarano, S., Iori, G., & Lux, T. (2021). Advances in the agent-based modeling of economic and social behavior. *SN Business & Economics*, 1(7), 99.

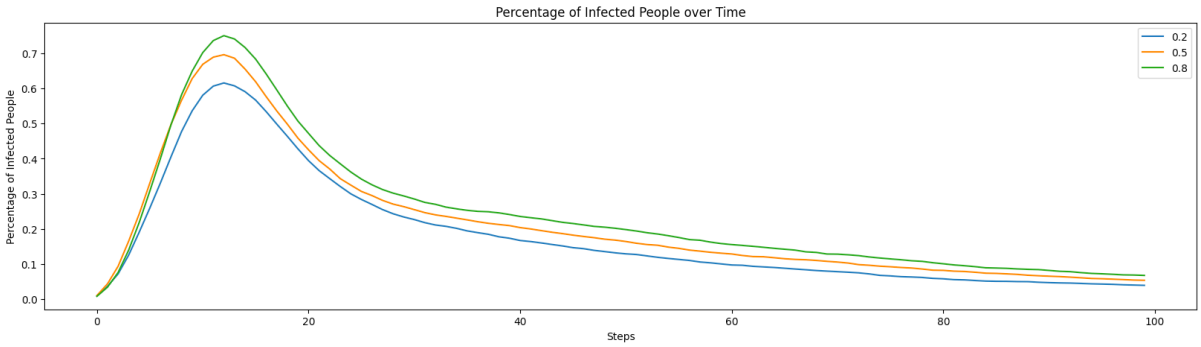
Miksch, F., Jahn, B., Espinosa, K.J., Chhatwal, J., Siebert, U., & Popper, N. (2019). Why should we apply ABM for decision analysis for infectious diseases? —An example for dengue interventions. *PLOS ONE*, 14(8), e0221564.

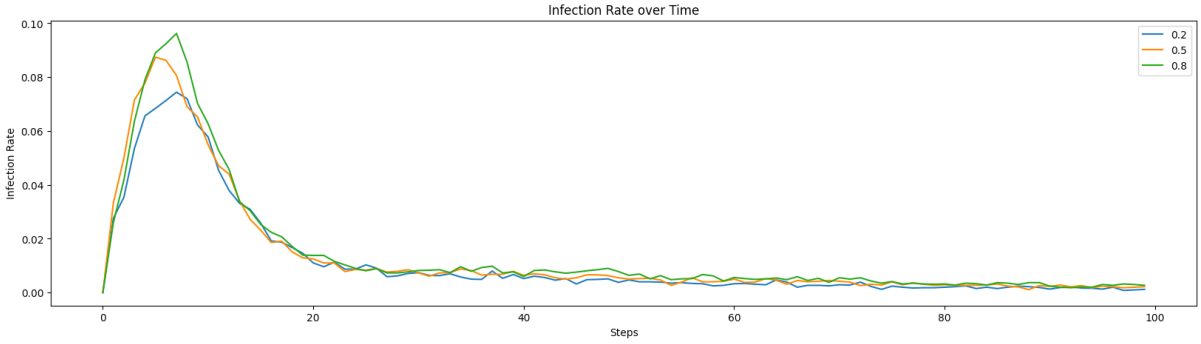
Smith, N.R., Trauer, J.M., Gambhir, M., & et al. (2018). Agent-based models of malaria transmission: a systematic review. *Malar J*, 17, 299.

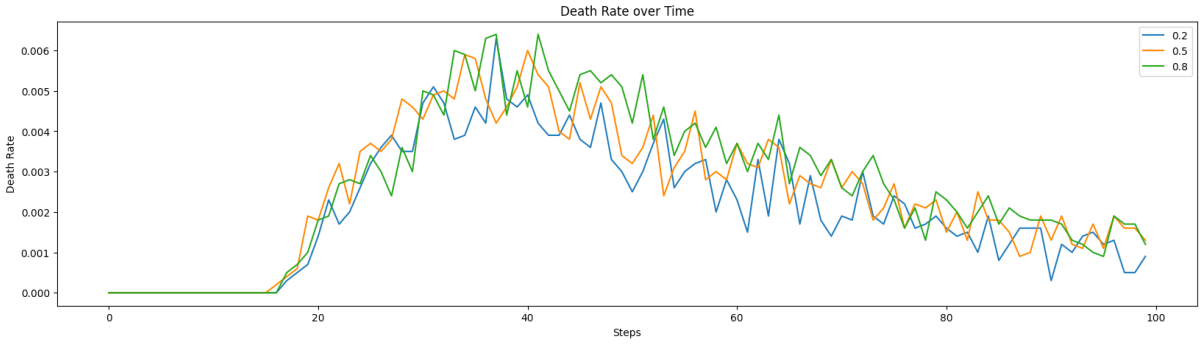
Willem, L., Stijven, S., Tijskens, E., & et al. (2015). Optimizing agent-based transmission models for infectious diseases. *BMC Bioinformatics*, 16, 183.

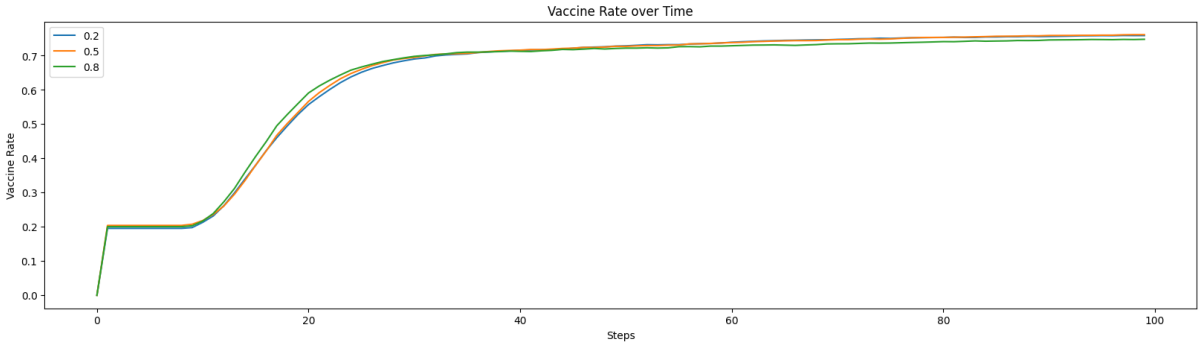
Appendix

The vaccine multiplier hyperparameter between (0, 1) controls the effectiveness of the vaccine. There are infected population over time, infection rate over time, death rate over time and vaccine rate over time based on three different values of vaccine multiplier.

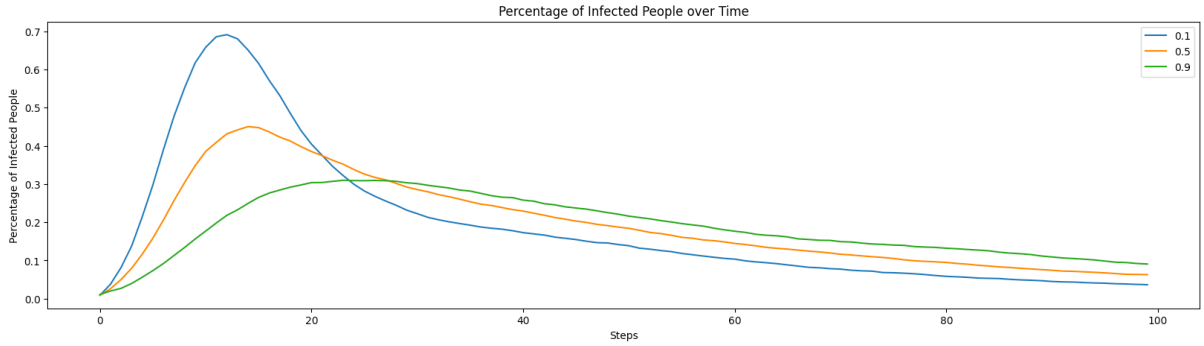


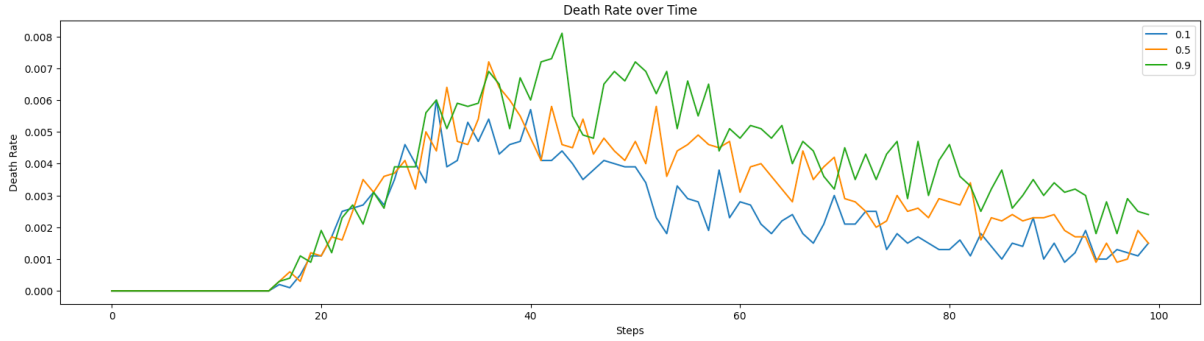


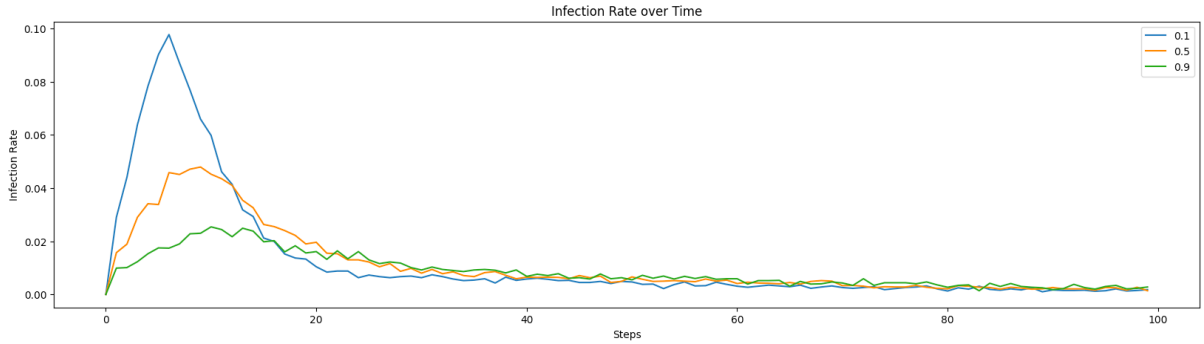


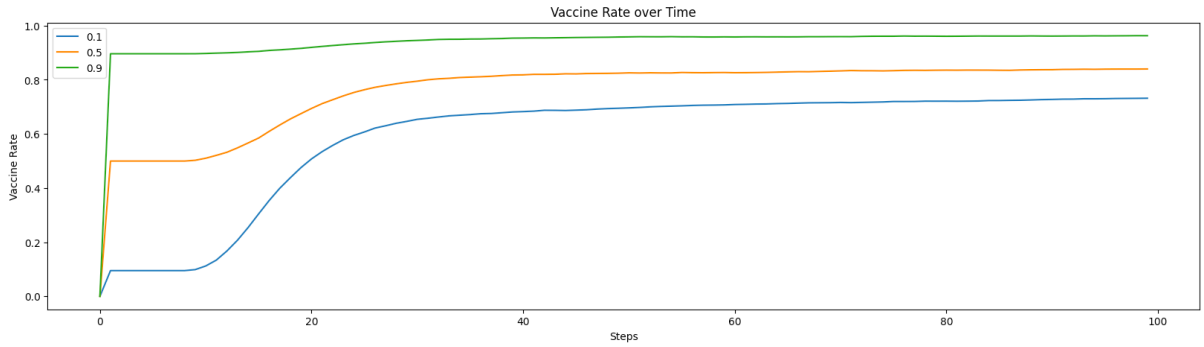


The initial vaccine rate is the percentage of the population that is vaccinated at the start of the simulation. This is a constant value between (0, 1). There are infected population over time, infection rate over time, death rate over time and vaccine rate over time based on three different values of vaccine rate.









The scan space size is the size of the grid space that the agents can get infected around in. This is a value that determines the area that they are around. There are infected population over time, infection rate over time, death rate over time and vaccine rate over time based on three different sizes of scan space.