Modeling a Zombie Infection using Agent-Based Modeling

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Abstract

This study investigates the dynamics of a Zombie Infection using Agent-based Modeling (ABM), adapting the classical SIR model to include two additional states: zombies and deceased individuals, forming the SIZRD model. By simulating interactions between agents in a confined environment, the research explores the spread, recovery, and mortality dynamics associated with zombie outbreaks. Parameters such as infection probability, transformation likelihood, and recovery time are examined. Monte Carlo simulations yield insights into infection trajectories and relationships between critical parameters. Results reveal that higher probabilities of zombie transformation lead to a reduction in maximum infections, with a quantified slope indicating a rate of 43.84.

1 Overview

Zombies, often portrayed as reanimated corpses driven by an insatiable hunger for human flesh which eventually leads to the spread of more zombies, have become a very popular genre in today's popular culture and movies. Even though the first record of the use of the word "Zombie" is from the year 1819 in the history of Brazil by the poet Robert Southey, the dictionaries trace the word's origin back to African Languages. In Haitian folklore, Zombies are dead individuals revived by a bokor, a sorcerer, through necromancy which is an act of magic. These zombies are controlled by the sorcerer and serve without free will.

Modern zombies, as depicted in movies, video games, and pop culture differ significantly from their folklore origins. These contemporary zombies are largely defined by the model established in the movie, "Night of the Living Dead" (1968). They are mindless, pain-insensitive creatures with an insatiable hunger for human flesh. Their primary goals are to kill, devour, or infect others. Characteristically, these "undead" move in slow, erratic motions and display signs of decay, including rotting skin, discolored eyes, and open wounds. Often linked to apocalyptic scenarios, modern zombies are central to stories of civilization's collapse due to a deadly undead outbreak.

In this project, we will try to use Agent-Based Modeling to model a scenario of a Zombie Infection. The model zombie is of the classical pop-culture zombie: slow-moving, cannibalistic, and undead.

2 The Model

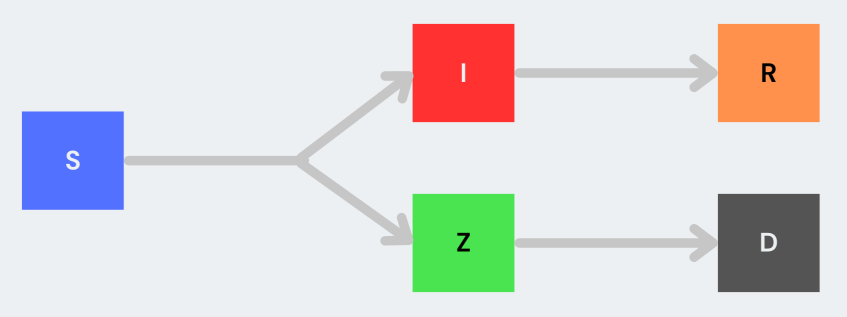


Figure 1: The flow of the SIZRD Model.

To investigate this zombie infection we develop a new model using the famous and basic SIR Model. Thus, we changed the previous model to include two new groups, Zombie(Z) and Deceased(D). We will call this new model the SIZRD Model.
Then our new model contains 5 groups:

- **Susceptible (S)** Susceptible individuals are those who are at risk of contracting the infection or becoming a zombie.
- **Infected (I)** Infected people are the ones who either had the disease at the start or the ones who get infected later.
- **Zombie (Z)** This is the special group that we use to mimic the behavior of the zombies. Having in mind that the zombies only have a craving for human flesh without any impurities, we assume that the Zombie group will only interact with the susceptible group.
- **Recovered (R)** The recovered group contains the people who have developed an immunity against the infection.
- **Deceased (D)** The Deceased class consists of individuals who have died after being a Zombie.

2.1 Interactions between Species

We build up a certain set of rules to properly manage our model.

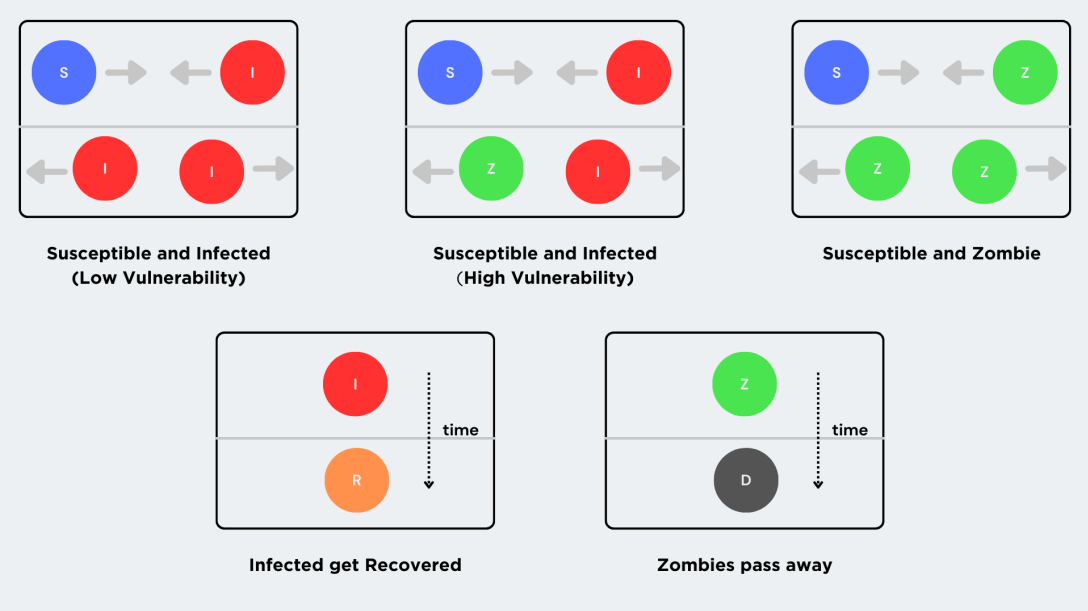


Figure 2: Interactions between Species

1. When a Susceptible person meets an Infected person, there are two possibilities that can happen.
   - If the vulnerability is low, there is a probability of β_i where the susceptible person becomes Infected.
   - If the vulnerability is high, there is a probability of β_z where the susceptible person becomes a Zombie.
2. When a susceptible person meets a zombie, there is a probability of z where the susceptible person becomes a zombie.
3. After some time $\Delta t = gamma_i$, the infected person recovers and become a Recovered.
4. After being a Zombie, they pass away in $\Delta t = gamma_z$ time period.

We also make some assumptions regarding this model to control the model.

- There are no interactions between the species and the environment.
- There are no other interactions between the species than the ones described above.
- There are I_0 infected people at the beginning.
- The probability of a susceptible becoming a zombie β_z, is a really low value compared to the probability of a susceptible becoming an infected β_i.

3 Methodology

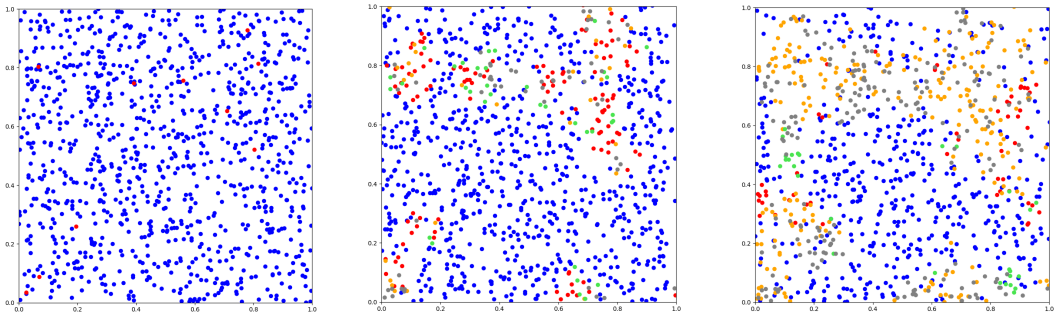
To simulate our model, we employed Agent-Based Modeling (ABM), a technique that focuses on modeling individual agents and their interactions. In an ABM, a fixed number of agents is created, each with specific properties. As the simulation progresses, the agents interact with one another, and these interactions influence the agent's properties and behaviors over time. This approach allows us to observe how individual actions and decisions collectively shape the system's evolution. In our disease spread simulation, each agent corresponds to an individual person. We will monitor their location, species type, and all the other attributes throughout the simulation to track how their interactions and movement impact the spread of the disease.

To effectively model our agents, we must define their interactions and how these interactions affect their properties. This involves calculating the distance between agents, considering them to have encountered each other if they come within a certain proximity. Based on the set of predefined rules, we allow the agents' attributes to evolve as they interact. By repeatedly iterating this process as the agents move through the environment, we gather the necessary data to drive the simulation and observe the dynamics of disease spread.

We used Python as our programming language to run our ABM algorithm. It is often convenient and customary to define both agents' attributes and behaviors using a class in object-oriented programming languages. Classes combine data and functionality into a single unit, allowing the creation of objects with attributes and methods to manage and modify their state.

Defining a new class introduces a new object type, enabling the creation of multiple instances of that type. Each instance can hold specific attributes that represent its state, and these attributes can be modified using methods defined within the class. In our case, we will use classes to create our agents since classes allow us to create data structures that store the same kind of information over and over again. Therefore we use Python's dynamic class as a pure data structure to store agents' attributes in a concise manner.

The Environment We consider a square area of size 1×1 with connected top and bottom margins as well as connected left and right margins. We used 1000 agents as the total population of our model. There are no interactions between the agents and the boundaries and also there won't be any changes to the environment once the simulation begins.



(a) at $t = 0$ (b) at $t = 50$ (c) at $t = 150$

Figure 3: Graphical representation of the simulation

In the beginning, we assign random locations to our agents. We assume that there are I_0 number of initially infected agents in the model, who will be assigned randomly.

Moving criteria We assign random movement to each agent at each iteration of the simulation which will make them move around the environment randomly. Here we need to address our boundary conditions as well (what our agents do when they get to the edge of our simulation); If an agent crosses the upper boundary they will come up from the bottom boundary. If they cross the bottom boundary they will come down from the upper boundary. Similarly, if an agent crosses the left boundary it will pop u from the left boundary and vice versa. We will have a parameter called **step size** which is the longest distance they can travel during an iteration.

Encounters between the species We will introduce a new parameter called **disease spreading radius**. This will be a neighborhood around the Infected and Zombie Species. If a susceptible person enters that neighborhood we will consider that as an encounter.

We will introduce some more parameters to the algorithm to model the spread of the disease and to model the recovery and passing away of zombies. The parameters that we introduce are as follows,

- Probability of being infected - β_i
- Probability of being a zombie - β_z
- Time it takes for an infected to recover - γ_i
- Time it takes for a zombie to pass away - γ_z
- Probability of a susceptible person becoming a zombie after an encounter with a zombie - z

4 Results and Analysis

First, we built a simulation using the `pycxsimulator`. When we ran the simulation for the following parameter values and obtained the following graph.

Parameter Values

- $\beta_i = 0.1$
- $\beta_z = 0.8$
- $\gamma_i = 50$
- $\gamma_z = 20$
- $z = 0.6$

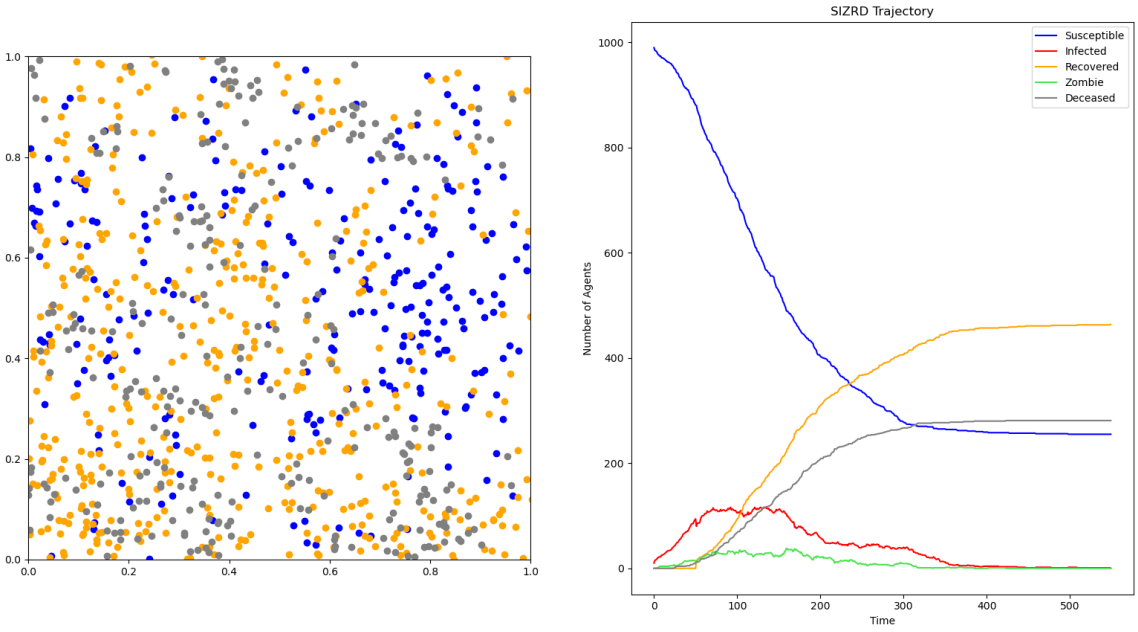


Figure 4: Graph of the SIZRD Trajectory and the Graphical representation of the model

Then we used the Monte Carlo Method to obtain a smoother graph using the averages of each simulation together with the Standard Deviations as the error. We conducted 50 simulated runs to obtain the following plot. The shaded region indicates the error.

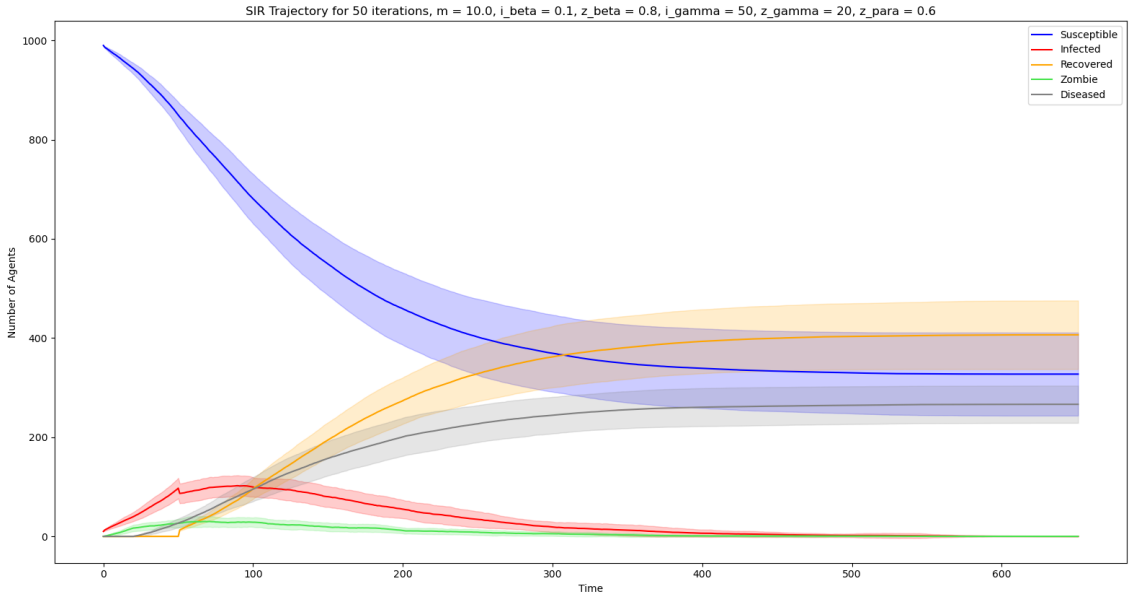


Figure 5: Graph of the SIZRD Trajectory for 50 iterations (Monte Carlo Method)

We can see that there is a sudden spike at $t = 50$ in both Infected and Recovered curves. That is due to the recovery of all the initial infected people, I_0 at $t = 50$.

4.1 Infection Curve

Next, we were interested to know the connection between the **Total number of infected people** and the z **values**. To get an idea we plotted the Infection curve for different values of z to obtain the graph below.

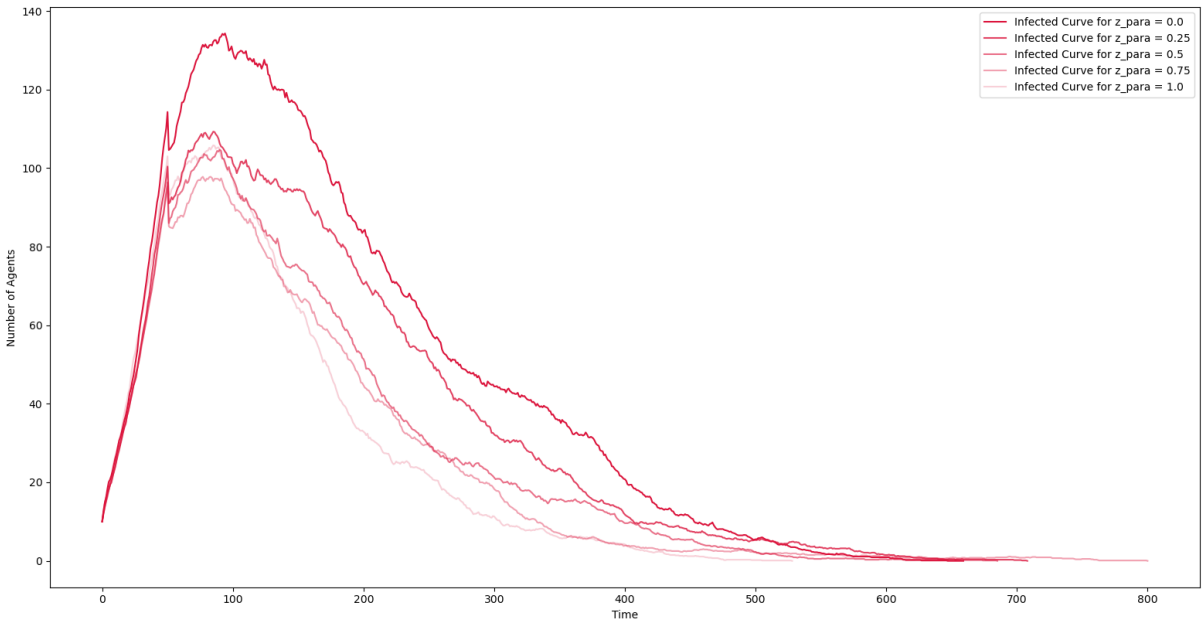


Figure 6: Change in the Infection Curve as the z parameter changes

We can see that there is a direct connection between the **Maximum number of infected people** and **z**. Therefore, to further investigate this relationship we plotted the **Maximum Number of Infected People** as a function of **z** and obtained the following graph.

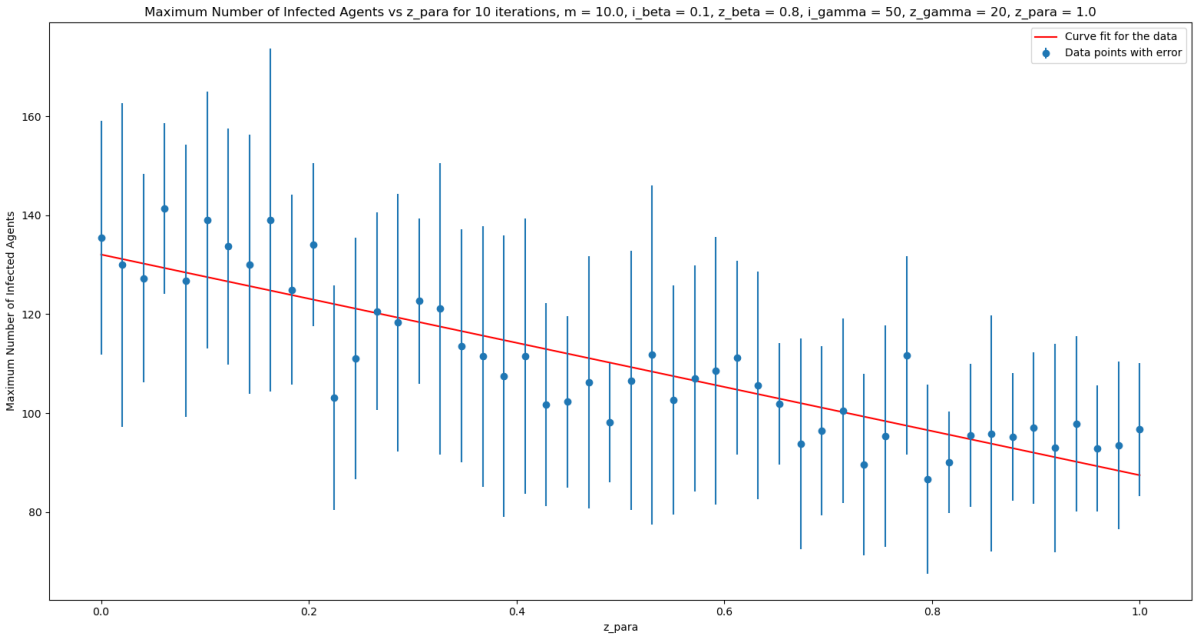


Figure 7: Graph of Maximum number of Infected Agents vs z parameter (Number of z values = 50)

We fitted a line for these data points using polynomial curve fitting. Note that if we increase the number of points in the graph we can get a better fit for the data which in return gives a a line with a far more accurate slope. Therefore we increase the number of z values in $[0, 1]$ interval.

5 Conclusions

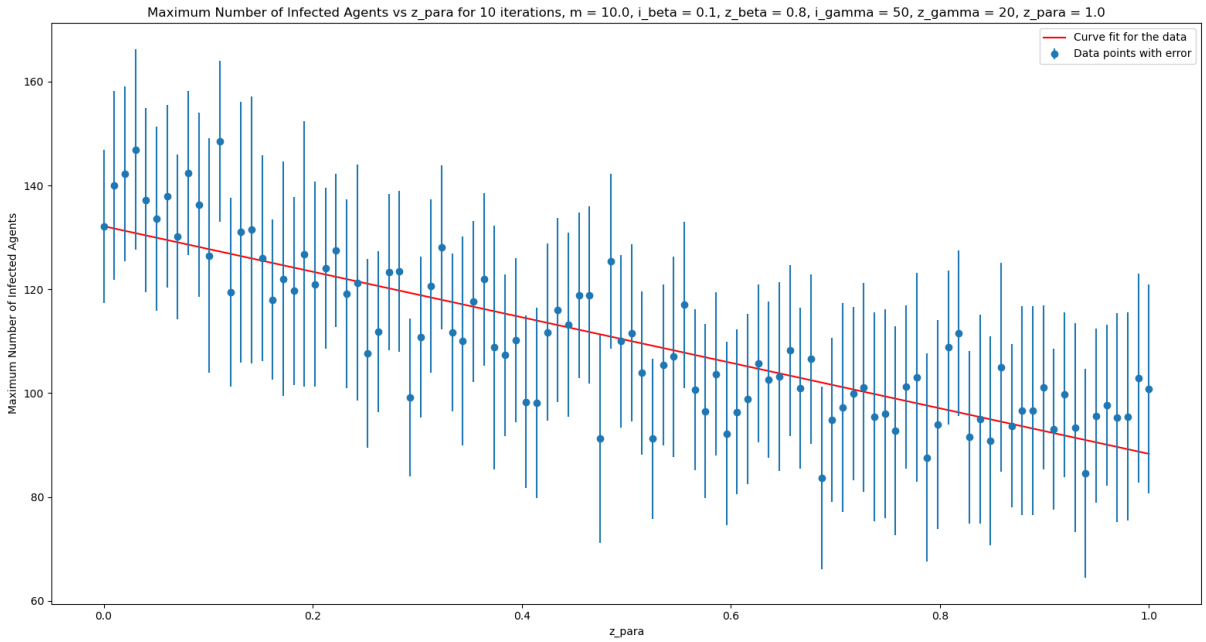


Figure 8: Graph of Maximum number of Infected Agents vs z parameter (Number of z values = 100)

We observe that if we take, $z = 0$ which is the case where there is no chance for a zombie to catch a susceptible then the Maximum number of Infected people is at an average highest of 132.

We can also note that even if we increase the z parameter to a highest where every zombie susceptible encounter leads to a guaranteed win for the zombies, the Maximum number of Infected people is at an average lowest of 91. This means that when z is increased from 0 to 1, the Average Maximum number of Infected people decreases and settles down at the low value.

Another thing we can observe is that even though we used a linear fit for this data set, it could have been better if we used an exponential fit for this given data.

Relationship between Maximum Number of Infected vs Z

From the curve fitting data, we obtained that the fitted line has a slope of $-\mathbf{43.84}$. This means that during the encounters between the zombie and susceptible groups, as the **Probability of a susceptible person becoming a zombie** (**Z**) increases the **Maximum number of Infected** decrease at a rate of **43.84**.

References

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Supplementary Files (Jupyter Notebook Files)

https://github.com/Mahagedara/MTH555_Project.git