Lizzie Healy
Professor Everett
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Cutting the Cheese: Simulating Infectious Disease Spread with Fiction

I. Introduction

In general, Susceptible-Infected-Recovered (SIR) models are used to model how a disease spreads throughout a population using a system of differential equations. The basic model includes three populations that are separated into compartments: susceptible, infected, and recovered, and provides a framework for how the populations interact with each other and how the disease flows through them. Generally, the flow is expected to be susceptible to infected to recovered. The overarching assumptions are that there is a mixing of the infected and susceptible populations that allows the disease to spread and that the population is constant over time. It is assumed that the spread of the disease is based on how infectious the disease is and how many people are in the population. With different diseases, these assumptions can be altered to show vaccines, infection-slowing tactics (masks, isolation, etc.), and exiting of the population through death by disease [1]. The model has been applied to many different diseases both to understand how diseases spread and to find ways to eliminate and slow the spread of cases for pandemics and epidemics.

In terms of background for this particular research, the idea stems from the game played in the book series “Diary of a Wimpy Kid” [2]. In the books, a piece of cheese ends up molding on the basketball courts at their school until one of the students is forced to touch it and he immediately becomes known as the kid with “the cheese touch.” From then on, the students continue the game passing the cheese touch onto their unsuspecting peers. The rules are simple: if the person with the cheese touch touches you, you have the cheese touch. There is no limit to how long you can have the cheese touch or how many times you get it, but you no longer have it once you pass it on. Any person can start the cheese touch by touching the piece of cheese. The other important stipulation is that a person can have their fingers crossed when being given the cheese touch to block the infected person from passing it on. In addition, some characters move away while having the cheese touch and one character even eats the moldy cheese, both of which end the cheese touch spread [3].

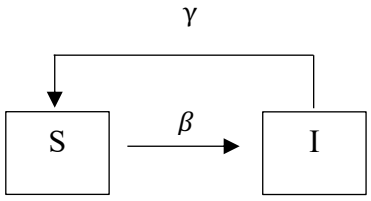
For this project, I aim to create my own model of the cheese touch and have it mirror an infectious disease (based [4]). The cheese touch acts differently than most common diseases, so I will alter the rules somewhat to better represent disease spread. My idea is to use the basic model of the cheese touch game as a control experiment and then change the parameters and the rules slightly to investigate how different factors affect the spread of disease. I will seek to answer the research question: is it possible to model the made-up cheese touch in a way that mirrors a basic SIR model of disease? Section II will explain the creation of the mathematical model as well as the parameters and general assumptions. Section III will provide results from simulating the model as well as estimating parameters. Section IV will explain the calculations needed to model in MATLAB. Section V will provide results and Section VI will conclude and provide commentary on the future direction of this research.

II. Mathematical Model

The basic model will be the cheese touch beginning with any person who encounters the cheese (disease origin), and that person can only spread to one person at a time. I will then allow any person to begin the disease again but with the inclusion of a new infection every three hours. I will include one run where the infected person can spread the disease to as many people as possible, however, they are only infectious for a specific period of time. In the fourth iteration, the disease can be spread to as many people as possible in the infection period and new infections are added at time intervals, however, an individual can block the spread of the disease by crossing their fingers. The finger-crossing rule will be a proxy for tactics that slow the spread of disease. In each iteration, S represents the susceptible, I is the infected population, and F is the finger-crossing population.

In the first iteration, one person will get the cheese touch and can then give it to one person passing it on to them. In this basic scenario, the only way to get the disease is by being touched by an infected individual. Once you have passed on the disease, you are immediately susceptible again. The basic assumptions are that the cheese can only be enacted once to begin the game and that a person immediately becomes susceptible again once they pass the cheese touch to the next person. In Figure 1, we see the term βSI, which represents the susceptible population getting infected through an interaction with the infected population and γI represents the infected population re-entering the susceptible population. In addition, the S' equation is the

rate of change of the susceptible population and I' is the rate of change of the infected population.



$$\begin{cases} S' = -\beta SI + \gamma I \\ I' = \beta SI - \gamma I \end{cases}$$

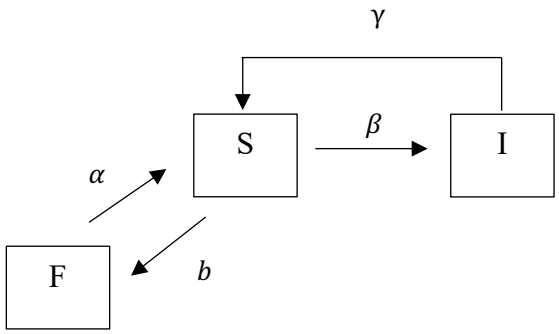
Figure 1: Schematic of the first, second, and third iteration as well as the system of differential equations. S' and I' are in units of $\frac{ppl}{t}$, S and I are in terms of people (ppl) and β and γ are both in terms of $\frac{1}{t}$.

In the second iteration of the model, the rules are generally the same, however, the cheese continues to remain in play with stipulations. This means every three hours a new person will touch the cheese, increasing the number of infected people by one. Thus, there are now two ways of contracting the disease: touching the cheese or by being touched by an infected individual. The assumptions are as follows: the cheese remained in play and caused a new infection every three hours, a person recovered once they passed the cheese touch to someone else, and the only cure was to infect another person with the cheese touch.

In the third iteration, a person with the cheese touch disease could give it to as many people as possible by touching them. In addition, a person was no longer infected after three hours. The general assumptions are that a person was permitted to infect as many people as possible, an infected person recovered after three hours, and returned to the susceptible population, and the cheese did not remain in play.

In the fourth and final iteration of the model, a person with the cheese touch disease could still infect as many people as possible by touching them. In addition, a new infection was added every three hours, and an infected person returned to the susceptible population every 3 hours. However, this iteration implements the finger-crossing rule, which states that if a susceptible person is crossing their fingers at the time of being touched by an infected person, they will not become infected. This, therefore, adds a third compartment to the model as well as

a third differential equation. The assumptions here are that a person could infect as many people as possible, an infected person recovered every three hours, the cheese remained in play and a new infection occurred every three hours, if a person had their fingers crossed when they were touched by an infected person, they did not become infected, and a person was allowed to have their fingers crossed for 0.5 hours at a time. In Figure 2, βSI and γI are again the susceptible population getting infected and the infected population re-entered into the susceptible population, respectively. However, bS is the susceptible population becoming safe from infection by entering the fingers crossed population and aF is the fingers crossed population becoming susceptible to infection. In addition, F' is the rate of change of the fingers crossed population.



$$\begin{cases} S' = -\beta SI + \gamma I + aF - bS \\ I' = \beta SI - \gamma I \\ F' = bS - aF \end{cases}$$

Figure 2: Schematic and system of equations for iteration four of the model. S' and I' are in units of $\frac{ppl}{t}$, S and I are in terms of people (ppl), β and γ are both in terms of $\frac{1}{t}$, and β , γ, a, and b are all in terms of $\frac{1}{t}$.

III. Mathematical Calculations

Preliminary results are depicted below for both iterations one and two. These graphics and calculations are based on MATLAB code that mirrors the equations, assumptions, and parameters described in detail above. In each of the iterations the R naught value is calculated as $R_0 = \frac{\beta N}{\gamma}$, where N is the size of the total population. This value is a measure of the number of infections caused by introducing an infected individual assuming that the whole population is susceptible and was developed utilizing the Next Generation Matrix Model Method. To do this,

we assumed the total population to be twenty individuals and the population equilibrium to be nineteen susceptible and one infected. From this, the F vector representing new infectants entering the compartment and the ν vector representing the transfer out the compartment minus the transfer into the compartment were calculated as βSI and γI, respectively, which were simplified to βN and γ. The Jacobians matrices were then calculated as J = $\begin{bmatrix} -\beta I^* & 0 \\ \beta^* & 0 \end{bmatrix}$ and J = $\begin{bmatrix} -\beta I & -\beta S + \gamma \\ \beta I & \beta S + \gamma \end{bmatrix}$. FV^{-1} was calculated as $\frac{\beta N}{\gamma}$, which is interpreted as the R_0. The main assumptions entered into MATLAB were that twenty people in the population and this number stayed constant, the timespan of the disease was twelve hours, and the initial conditions are that one person infected and nineteen people were susceptible.

In the first two iterations, the parameters of gamma and beta are fixed such that the equilibriums are forced to a specific number. In the first iteration, we solved for the equilibrium value of S* using the results found when solving for the R_0, to get a relationship between beta, S, and gamma as $\beta S^* = \gamma$. From this, S* = $\frac{\gamma}{\beta}$ and because in this iteration, only one person can be infected at any time, we know the value of S* is 19 and the value of I* is 1. Thus, gamma is calculated as 19*β and $\beta = \frac{1}{19}$. In iteration two, due to an additional infected person being added every three hours, beta and gamma are changing every three hours, thus these are calculated for each timeframe. Beta remains at $\frac{1}{19}$ as above and gamma starts as 19* β, but changes to 18* β, 17* β, and finally 16* β to account for the steady state adding an additional infectious person and thus increasing by one every three hours. To accommodate these different parameter values, t-span is split into three-hour increments and the system of differential equations is solved separately for each timespan and then compiled to create a continuous function.

In the third iteration, the main assumption is that a person is infectious with the disease for three hours at a time, which means that the gamma coefficient, which represents the rate at which the infected population becomes susceptible again and is measured in 1/time, is fixed at $\frac{1}{3}$. Additionally, the steady states are set as six infected and fourteen susceptible based on the oscillations seen around these numbers when collecting data for the fourth iteration (see Figure 6). Thus, S* is equal to 6 and beta is calculated as $6\beta = \frac{1}{3}$, so $\beta = \frac{1}{18}$.

In the fourth iteration, data is collected through running a real-life cheese touch simulation following these rules:

1. The game began at 8am (t=0) and ended at 8pm (t=12) with 14 participants total.
2. A person was randomly chosen to begin with the cheese touch and could infect as many people as possible by touching them.
3. Each person was able to spread the disease for three hours after the beginning of their infection, and then re-enters the susceptible population.
4. At hour 3, 6, and 9 a person is randomly chosen to be infected.
5. Each individual reported who they tagged and at exactly what time.

The data was collected and normalized to decimal points on a twelve-hour scale and then uploaded into MATLAB. For the parameters, gamma was still set at $\frac{1}{3}$, but beta was allowed to be estimated. In order to fit the model to data, an initial guess was entered as S* = 5, I* = 15, and $\beta = \frac{1}{15}$ based on the shape of the initial preliminary figure (see Figure 6) that graphed the collected data. From here, fminsearch was used to estimate the beta parameter to minimize the distance between the actual data and the model data [5].

The final iteration was the fourth iteration including the fingers crossed compartment. For these parameters, the same calculations applied where gamma and beta are found based on setting the steady states to S*=6 and I*=14. In addition, the new parameters b and a are both set to 2 to simulated people crossing and un-crossing their fingers at a rate of 0.5 hours. The initial conditions are set to 14 susceptible, 1 infected, and 5 fingers crossed.

IV. Results

In Figure 3, it is clear that the populations of both the susceptible and infected will remain at constant levels of 19 people and 1 person, respectively. This is a direct result of the assumptions made in the first iteration that a person fully recovers once they pass on the disease and that new infections cannot arise. The calculated R_0 value is 1.0526.

In Figure 4, we can see that both populations are acting like step functions. The infected population remains constant for a time of three hours and then instantaneously jumps to add a member to the population. The susceptible population, conversely, remains constant for three hours and then instantaneously loses a member of the population. Again, these reflect the assumptions made in this iteration. In this iteration, however, the calculated R_0 value changes with each different time range (every three hours). For t=0 to t=3 the R_0 value is again 1.0526,

but from t=3 to t=6 it changes to 1.1111, then to 1.1765 during the t=6 to t=9 frame, and finally to 1.2500 during the t=9 to t=12 portion. These changes in R_0 are due to the code changing the parameters in each time step, in order to force the populations to approach the specific equilibriums pairs of S*=19 and I*=1, S*=18 and I*=2, S*=17 and I=*3, and S*=16 and I*=4.

In the third iteration, the R_0 value increases once again to a value of 3.33. Figure 5 shows the dynamics of the two populations before they reach the designated steady states of S* = 14 and I* = 6. These steady states can be adjusted to look at how the beta and gamma values change as well as vice versa to investigate the population dynamics graphically. Similarly, in iteration four where the fingers crossing rule applies, we find an R_0 value of 3.33, which is because this value is still based on beta and gamma and not on the a and b parameter values, which are different in this iteration. As Figure 11 shows, the susceptible population is approaching 7.19, the infected population is approaching 5.52, and the fingers crossed population is approaching 7.28. These steady-state equilibriums are also independent of the initial conditions and solely based on the parameter values.

The fourth iteration where data was collected, yielded the highest R_0 value of 3.708. It also calculated the best fit for beta to be 0.0618. Figures 8 and 9 show the dynamics of the susceptible and infected population based on the initial guess of the beta value compared to the collected data. Comparatively, the estimated beta was a better fit for the data as shown by the decreased distances between the actual data and the model data in Figures 10 and 11.

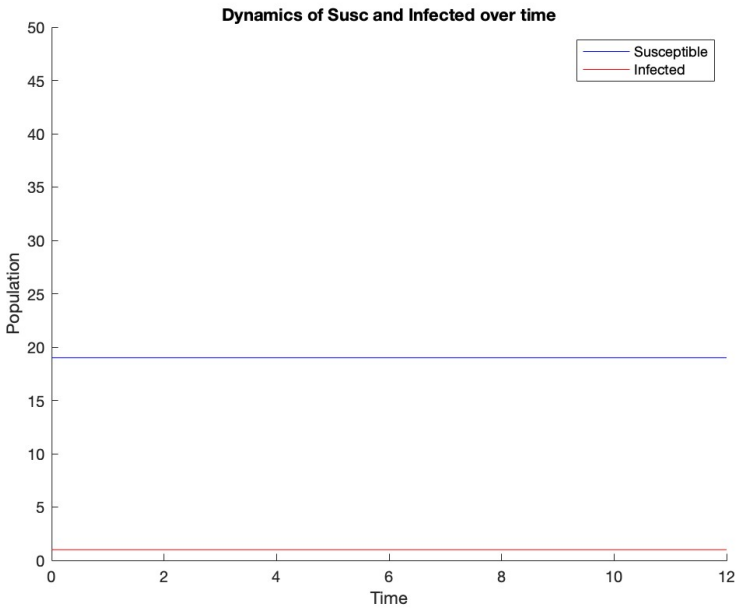


Figure 3: Depicting the dynamics of the susceptible and infection population over a twelve-hour period and utilizing the assumptions of Iteration 1.

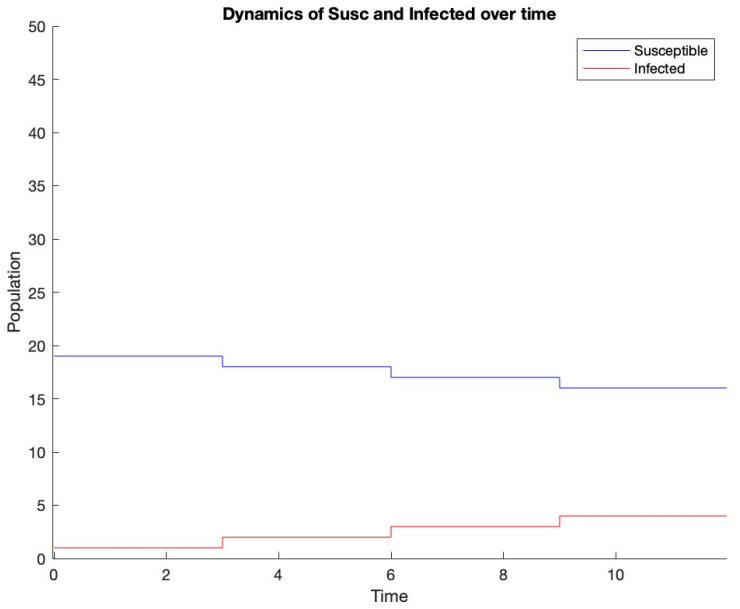


Figure 4: Depicting the dynamics of the susceptible and infection population over a twelve-hour period and utilizing the assumptions of Iteration 2.

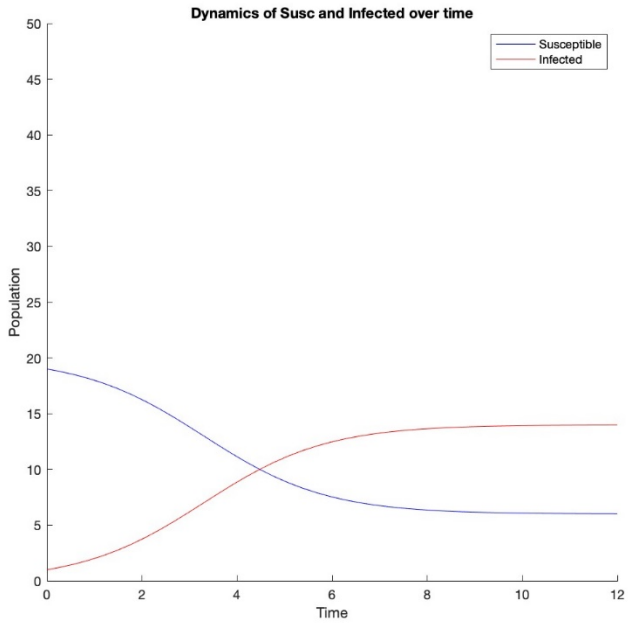


Figure 5: Dynamics of the susceptible population and infected population with the assumptions of the third iteration over twelve-hour time.

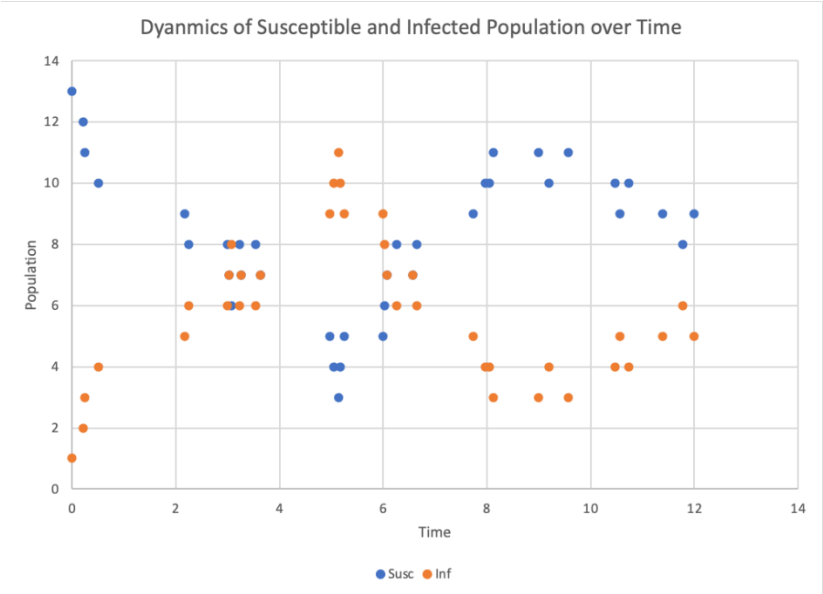


Figure 6: Preliminary graph of the raw data collected from the cheese touch simulation over the twelve-hour time period.

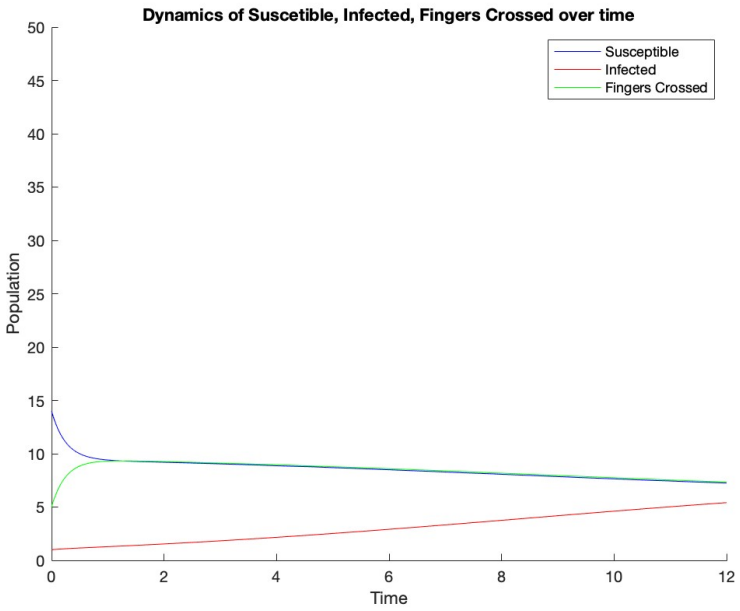


Figure 7: The susceptible, infected, and fingers crossed population over time with the listed assumptions from the fourth iteration model.

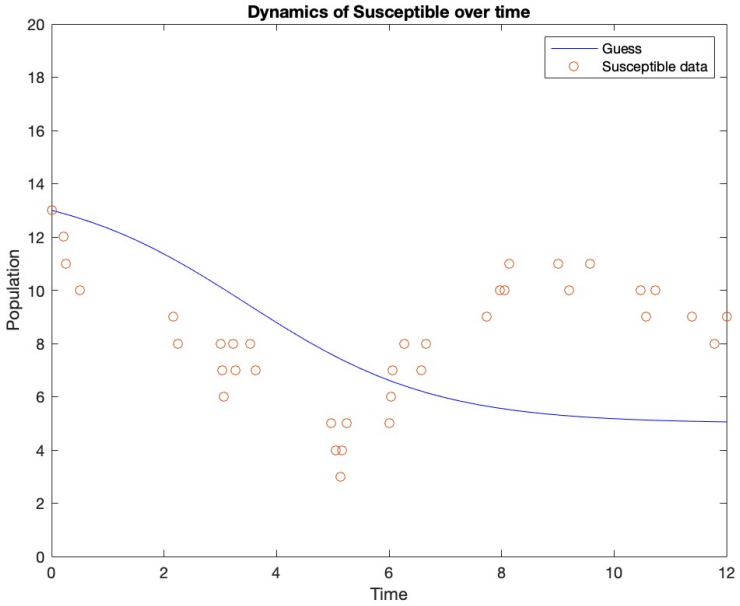


Figure 8: The initial susceptible population against the actual collected susceptible population data from the simulation over time.

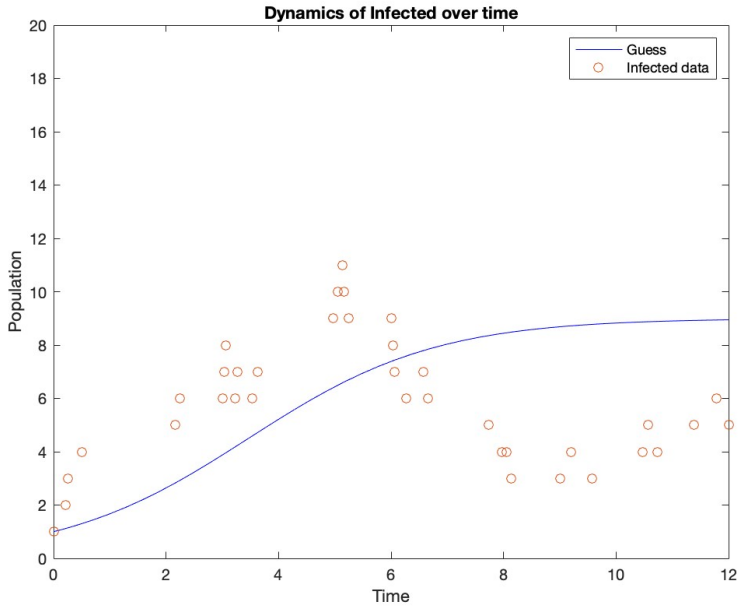


Figure 9: The initial guess infected population against the actual collected infected population data from the simulation over time.

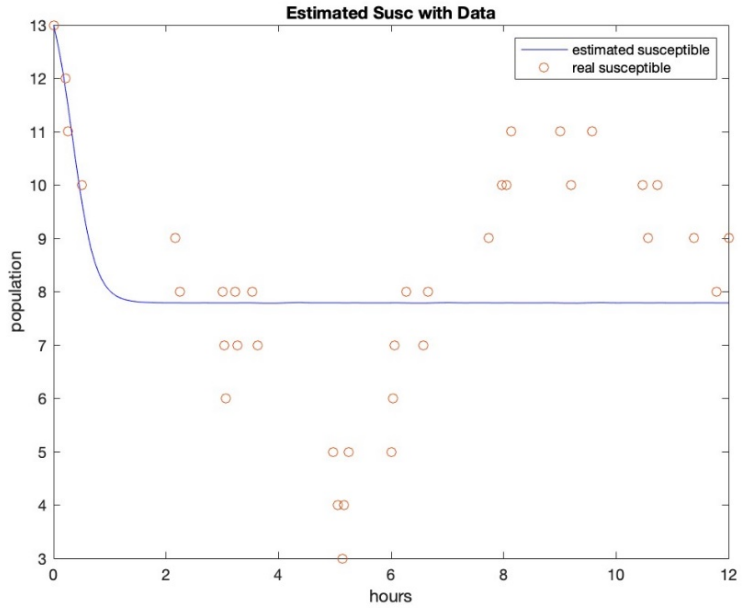


Figure 10: The estimated susceptible population against the actual collected susceptible population data from the simulation over time.

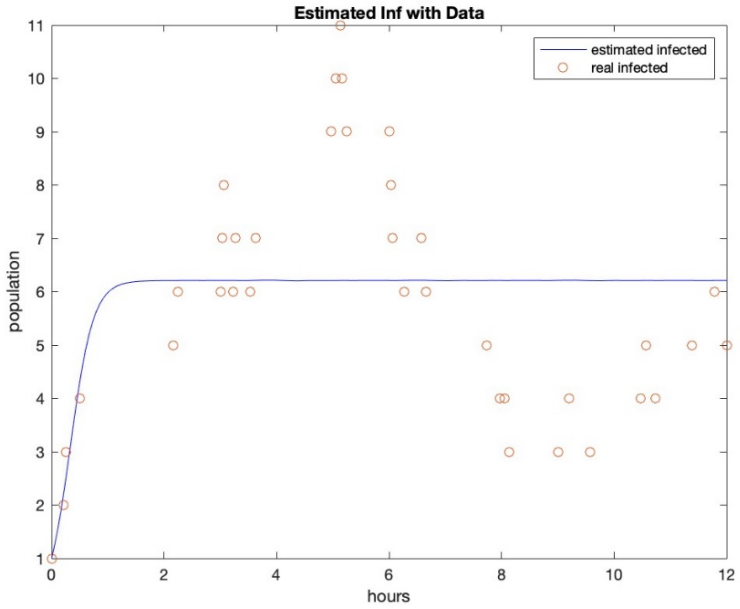


Figure 11: The estimated infected population against the actual collected infected population data from the simulation over time.

V. Conclusion

The main conclusion is that the model is not truly fitting the cheese touch design. This is most likely because the cheese touch acts in a way unlike any known infectious disease, thus the SIR model is unable to capture the exact dynamics of the cheese touch. I would probably need to use a non-disease model to find a better fit. This point is best exemplified by Figure 6, which is the data-collection graph because here we see the oscillating shape of the data, which is not truly how a disease would act. In addition, the R_0 value is not the most accurate and descriptive measure to use because it does not truly capture the level of infectiousness of the disease. The second iteration exemplified this because, in reality, the R_0 value should not be changing. After all, each individual person is not truly more infectious. These issues are due to the dynamics of only being able to spread the disease to one individual, which makes the cheese touch not an infectious disease.

For the future direction of this work, I would suggest adjusting the model or using a different design than that of the SIR model. In addition, more data should be collected on the fourth iteration with the fingers crossed stipulation and without it to decrease the level of error

and find the best fit for the parameters. This data should also be collected in a more controlled environment with a more randomized set of subjects.

Overall, the cheese touch does not mirror an infectious disease, but, interestingly, if we were to accept this R_0 value as a measure of the infectiousness of the cheese touch, we find that it is more infectious than Ebola, less infectious than smallpox, and about in the range of Covid-19 [6].

VI. Bibliography

1. Smith, D., & Moore, L. (n.d.). *The sir model for spread of disease - the differential equation model*. The SIR Model for Spread of Disease - The Differential Equation Model | Mathematical Association of America. https://maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model
2. Kinney, J. (2007). *Diary of a Wimpy Kid.* Harry N. Abrams.
3. Contributors to Diary of a Wimpy Kid Wiki. (n.d.). *Cheese touch*. Diary of a Wimpy Kid Wiki. https://diary-of-a-wimpy-kid.fandom.com/wiki/Cheese_Touch
4. Munz, P., Hudea, I., Imad, J., & Smith?, R. J. (2009). When Zombies Attack!: Mathematical Modelling of an Outbreak of Zombie Infection. *Infectious Disease Modelling Research Progress*, 133–150. https://mysite.science.uottawa.ca/rsmith43/Zombies.pdf
5. Prodanov, D. (2021). Analytical solutions and parameter estimation of the SIR epidemic model. *Mathematical Analysis of Infectious Diseases*, 163-189. https://mysite.science.uottawa.ca/rsmith43/Zombies.pdf
6. Mohajan, H. (2023). Mathematical Analysis of SIR Model for Covid-19 Transmission. *Journal of Innovations in Medical Research*, *1*(2), 1–18. https://mpra.ub.uni-muenchen.de/114390/