Spread of Disease

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Contents

1 Introduction

Due to the extremity of the COVID-19 epidemic, a large portion of humanity has now realized the extreme consequences of a spread of infectious disease. Many have been left with trauma, anxiety, and other mental and physical health concerns [3]. One of the only ways in which such infectious diseases can be monitored is with the use of mathematical models.

In this report, a mathematical model is developed which investigates the manner at which diseases spread with regards to a fixed population. The model will be created by exploring different simplified scenarios. First, the case where there is no recovery from the disease is considered. Thus once an individual is infected, they remain infected. Next, the case where all individuals are infected and eventually recover is studied. In this case, the disease no longer spreads, thus a recovery model is built. Furthermore, these two cases are considered together as both the infection and recovery models are joined into one model. Additionally, an introduction will be made to the different scales of diseases, specifically investigating the conditions of an epidemic. Furthermore, an immunity model is created where once individuals recover, the become resistant to the infection. With these three variables, the long-term results of the infection will be analysed with regards to varying parameters, and a selection of possible equilibrium states are investigated. Finally, conclusions are drawn based on which parameters would effect the spread and long term results of the infectious disease.

1.1 Assumptions

To create a model of the spread of disease, some initial assumptions must be made.

1. The disease can only be transmitted through mutual contact.
2. The individuals of the population are, and remain, well mixed so that spatial aspects do not play a role.
3. Individuals are independent of one another, and every individual has the same expected number of contacts per unit of time with any other individuals.
4. There is a fixed probability that the disease is transmitted per contact between a susceptible and an infected.

1.2 Variables and Parameters

The variables and parameters plus their units that will be referenced throughout the report are defined as,

$S(t)$ = the number of susceptible individuals at a certain time (people)
$I(t)$ = the number of infected individuals at a certain time (people)
$s(t) = \frac{S(t)}{N}$ = the ratio of susceptible individuals of the total population at a certain time $\left(\frac{\text{people}}{\text{person}} = \text{unitless}\right)$
$i(t) = \frac{I(t)}{N}$ = the ratio of infected individuals of the total population at a certain time $\left(\frac{\text{people}}{\text{person}} = \text{unitless}\right)$
N = the fixed total population (people)

c = the total expected number of contacts per unit time within the whole population N $\left(\frac{1}{\text{unit time}}\right)$
p = the fixed probability that the disease is transmitted once interpersonal contact is made (unitless)
t = time (unit time)

2 Construction of the Model

In this section, the focus lies on the use of differential equations to model varying sizes of the number of susceptible and infected individuals. This is done in a few stages. First, some basic conditions which hold for all of the different simplified models are introduced.

Note that the total population of people, N is fixed. Therefore, the number of susceptible people, $S(t)$, at a certain time t, and the number of infected people, $I(t)$, at a certain time t always add up to the total N. Due to this,

$$S(t) + I(t) = N. \tag{1}$$

Furthermore, the rate of change of infected people over time is negatively proportional to the rate of change of susceptible people over time. This is found by differentiating both sides of equation (1) with respect to t. This generates the differential equation

$$\frac{dI(t)}{dt} = -\frac{dS(t)}{dt}. \tag{2}$$

Additionally, the ratio of the population that is susceptible, $s(t) = \frac{S(t)}{N}$, and the ratio of the population that is infected, $i(t) = \frac{I(t)}{N}$ adds up to one due to basic axioms of probability. These ratios are dimensionless. Therefore,

$$s(t) + i(t) = 1. \tag{3}$$

The individual cases of an infected and a susceptible individual being somewhere is independent as stated by assumption (3). This can be estimated using probabilities. In probability terms, this means that the probability of an infected and a susceptible person meeting is equal to

$$i(t) \cap s(t) = i(t) \cdot s(t). \tag{4}$$

2.1 Infection Model

In this section, an initial model is built based on a new assumption.

5. Once infected, a person remains infected indefinitely.

To construct the transmission rate of the infection, multiple parameters must be considered.

(a) c = the total expected number of contacts per unit time within the entire population, N.

(b) p = the probability that the disease is transmitted through contact.

Thus, the transmission rate is $c \cdot p$. Note that for this model, the transmission rate is considered to be constant due to assumptions (3) and (4). However, in situations of social distancing or if the disease is less infectious, this rate will be lower. From this, the rate of change of the ratio of infected individuals, $i(t)$ per unit time t, is equal to

$$\frac{di(t)}{dt} = cp\ s(t)i(t). \tag{5}$$

Note that the dimensionless equation (5) can be rewritten in terms of the physical numbers of susceptible, $S(t)$, and infected people, $I(t)$ by multiplying both sides by the total population N. Thus for equation (5), this results in

$$\frac{dI(t)}{dt} = \frac{cp}{N}\ S(t)I(t). \tag{6}$$

Note that both sides of equation (6) have the same dimension $\left(\frac{\text{people}}{\text{unit time}}\right)$.

With this equation, it can be concluded that the rate of change of the number of infected individuals, $I(t)$, per unit time t, is dependent on the number of infected people at a certain time, the number of susceptible individuals at a certain time, and a new proportionality constant $\frac{cp}{N}$. This proportionality constant varies from the previous one by a factor of N. Thus, instead of being dependent on the average total amount of contacts the whole population has, the rate of change over time is dependent on the average contact any individual would have. Therefore the proportionality constant $\frac{cp}{N}$ signifies the expected transmission of disease through interpersonal contacts per person per unit time.

By combining this equation with equation (2), the differential equation

$$\frac{dS(t)}{dt} = -\frac{dI(t)}{dt} = -\frac{cp}{N}\ S(t)I(t). \tag{7}$$

is created. Hence, the system of differential equations describing $S(t)$ and $I(t)$ is

$$\begin{cases} S(t) + I(t) = N \\ \dfrac{dI(t)}{dt} = -\dfrac{dS(t)}{dt} = \dfrac{cp}{N}\ S(t)I(t). \end{cases} \tag{8}$$

To reduce this system into a single differential equation, the number of susceptible people, $S(t)$ can be expressed as

$$S(t) = N - I(t).$$

Substituting this into equation (6) generates

$$\frac{dI(t)}{dt} = \frac{cp}{N}\big(N - I(t)\big)I(t). \tag{9}$$

From the assumptions, it is known that once an individual is infected, they remain infected.

Note that c, p, $N - I(t)$ and $I(t)$ are all non-negative and $N > 0$. Therefore, the amount of infected individuals increases unless c, p, $N - I(t)$, or $I(t)$ is equal to zero. Once the disease breaks out, c, p, and $I(t)$ are strictly positive. The increase of infected individuals stops only when the whole population is infected.

It can be concluded that in the long term, the number of infected people, $I(t)$ tends to the full population N where there are no remaining individuals who are susceptible, and thus the rate of infection, $\frac{dI(t)}{dt}$, tends to 0. This is when $N - I(t) = 0$. In biological terms, the entire population eventually becomes infected, and then the spread of the disease stops.

2.2 Recovery Model

In realistic terms, assumption (5), where once an individual is infected, they remain infected is not plausible. Therefore, in this next scenario, this assumption is disregarded.

To model the recovery process of these individuals, the situation is first simplified. In this specific situation at time t_N, the total population is expressed as

$$I(t_N) = N$$

and thus the full population is infected at this time. To further simplify the model, an additional assumption is made.

6. The disease no longer spreads.

Therefore, confusion is avoided over susceptible individuals becoming infected while monitoring recovery. Furthermore, a new parameter is introduced. The probability that an individual recovers over a time period Δt is given by $\gamma \Delta t$. Due to these simplifications, the amount of recovered people over a time period is $-\Delta I(t)$. Note that with this new parameter, the net growth of the number of recovered individuals during a time period Δt where $t_N \leq t$ is

$$\Delta I(t) = -\gamma \Delta t \; I(t). \tag{10}$$

Thus, by dividing equation (10) by the time period, Δt, the growth rate of recovered individuals over a time period is found. Additionally, as $\Delta t \to 0$, the momentary growth rate of recovered individuals can be found. This generates the equation

$$\lim_{\Delta t \to 0} \left(\frac{\Delta I(t)}{\Delta t} \right) = \frac{dI(t)}{dt} = -\gamma \; I(t). \tag{11}$$

Note that the variables in equation (11) have the dimension $\left(\frac{\text{people}}{\text{unit time}}\right)$. Thus, the change in the number of recovered individuals over time is solely dependent on this parameter, γ, and the number of infected individuals at that specific time.

Now, to estimate this parameter, γ, the average time it takes for an individual to recover will be considered. From equation (10) it can be concluded that the time period Δt is expressed as

$$\Delta t = -\frac{1}{\gamma} \cdot \frac{\Delta I(t)}{I(t)}. \tag{12}$$

The average time of recovery will be denoted by $\Delta t = t_a$. Once this amount of time has passed, half of the population would be recovered. This is when the net growth of recovered individuals for $t_N \leq t_a$ is $-\Delta I(t_a) = I(t_a) = \frac{N}{2}$. Thus, substituting this equality into equation (12), the average time for an individual to recover is $t_a = 1/\gamma$. Therefore, $\gamma = 1/t_a \left(\frac{1}{\text{unit time}}\right)$. Note that since time is always positive, it follows that γ is also positive. Thus, this parameter, γ, can be estimated using the average recovery time, t_a.

2.3 Combined Model

To model the spread of disease more realistically, both the infection and recovery models must be combined. Assumption (5), where individuals remain infected once they are

infected, is still disregarded. Furthermore, in this case, assumption (6) is disregarded and once again the disease spreads through contact between infected and susceptible individuals. An additional assumption is made.

7. Once an individual recovers from the disease, they immediately become susceptible.

Thus, immunity is disregarded. Two main equations will be utilized within this model. The first is equation (6), which describes the increase of the number of infected individuals with respect to unit time. The second equation, (11), describes the decrease in number of infected individuals with respect to unit time. Combining both equations describes the total change in the number of infected people with respect to unit time as

$$\frac{dI(t)}{dt} = \frac{cp}{N}\, I(t)S(t) - \gamma I(t). \tag{13}$$

Furthermore, a new time variable $\tau = \gamma t$ is introduced. Note that τ is unitless $\big(\frac{1}{\text{unit time}} \cdot \text{unit time}\big)$. This variable will describe the proportions of susceptible and infected individuals of the population at time $t = \frac{\tau}{\gamma}$ as a function of τ. Let $\bar{i}(\tau) = i(t) = \frac{I(t)}{N}$ and $\bar{s}(\tau) = s(t) = \frac{S(t)}{N}$. Since both $\bar{i}(\tau)$ and $\bar{s}(\tau)$ are dependent on τ, it follows that they are also unitless. Observe that by taking the derivative of τ with respect to t

$$\frac{d\tau}{dt} = \gamma$$

$$d\tau = \gamma dt$$

Additionally, note that

$$\frac{d\bar{i}(\tau)}{d\tau} = \frac{1}{N} \cdot \frac{dI(t)}{d\tau} = \frac{1}{N\gamma} \cdot \frac{dI(t)}{dt}.$$

Substituting this into the combined differential equation (13) generates

$$\begin{aligned}
\frac{d\bar{i}(\tau)}{d\tau} &= \frac{1}{N\gamma} \cdot \frac{dI(t)}{dt} \\
&= \frac{1}{N\gamma} \cdot \Big(\frac{cp}{N}\, I(t)S(t) - \gamma I(t)\Big) \\
&= \frac{cp}{\gamma}\Big(\frac{I(t)}{N}\Big)\Big(\frac{S(t)}{N}\Big) - \frac{I(t)}{N} \\
&= \frac{cp}{\gamma}\, \bar{i}(\tau)\bar{s}(\tau) - \bar{i}(\tau) \\
&= \Big(\frac{cp}{\gamma}\, \bar{s}(\tau) - 1\Big)\bar{i}(\tau).
\end{aligned} \tag{14}$$

Next, the parameter, $R_0 = cp/\gamma$, is reintroduced to further simplify the model. R_0 is linearly proportional to the total expected contact within the population N, the probability that the disease gets transferred, and the average time it will take for an individual to recover, $t_a = \frac{1}{\gamma}$. This is a unitless and non-negative parameter. Due to this, equation (14) becomes

$$\frac{d\bar{i}(\tau)}{d\tau} = \big(R_0\, \bar{s}(\tau) - 1\big)\bar{i}(\tau). \tag{15}$$

Moreover, utilizing equation (3), a condition is made on the new variables where

$$\bar{i}(\tau) + \bar{s}(\tau) = i(t) + s(t) = 1.$$

Thus the adapted system of differential equations used to model the spread of disease is

$$\begin{cases} \bar{i}(\tau) + \bar{s}(\tau) = 1 \\ \dfrac{d\bar{i}(\tau)}{d\tau} = \big(R_0\ \bar{s}(\tau) - 1\big)\bar{i}(\tau). \end{cases} \tag{16}$$

Once again, this system can be summarized into a single differential equation where $\bar{s}(\tau) = 1 - \bar{i}(\tau)$ and thus

$$\frac{d\bar{i}(\tau)}{d\tau} = \big(R_0 - 1 - R_0\ \bar{i}(\tau)\big)\bar{i}(\tau) \tag{17}$$

$$= R_0\ \bar{i}(\tau)\left(\left(1 - \frac{1}{R_0}\right) - \bar{i}(\tau)\right) \quad (\text{for } R_0 \neq 0). \tag{18}$$

From these differential equations, there are four possible cases for which R_0 can be defined.

(a) From equation (17), if $R_0 = 0$, it implies that $c = 0$ or $p = 0$. By definition of these parameters, there would be no interpersonal contact, or the disease itself is not transmittable.

(b) From equation (18), if $0 < R_0 < 1$, it implies $\frac{1}{R_0} > 1$. Due to this,

$$\big(1 - \frac{1}{R_0}\big) - \bar{i}(\tau) \leq 1 - \frac{1}{R_0} < 0.$$

It can then be concluded that $\frac{d\bar{i}(\tau)}{d\tau}$ is always negative and thus the disease does not spread.

(c) If $R_0 = 1$, it implies that

$$\frac{d\bar{i}(\tau)}{d\tau} = -\big(\bar{i}(\tau)\big)^2 \leq 0$$

and the disease does not spread.

(d) Let $R_0 > 1$. There a three possible sub-cases.

- If $0 \leq \bar{i}(\tau) < 1 - \frac{1}{R_0}$,
  then $\frac{d\bar{i}(\tau)}{d\tau} > 0$ so the number of infected individuals grows.
- If $\bar{i}(\tau) = 1 - \frac{1}{R_0}$,
  then $\frac{d\bar{i}(\tau)}{d\tau} = 0$ and it is at an equilibrium where the ratios of infected and susceptible people do not change.
- If $1 - \frac{1}{R_0} < \bar{i}(\tau) \leq 1$,
  then $\frac{d\bar{i}(\tau)}{d\tau} < 0$ which means that the number of infected individuals decreases until it reaches the equilibrium where $\bar{i}(\tau) = 1 - \frac{1}{R_0}$.

Furthermore, the derivative $\frac{d\bar{i}(\tau)}{d\tau}$ can be expressed as

$$\frac{d\bar{i}(\tau)}{d\tau} = \Big(R_0\big(1-\bar{i}(\tau)\big)-1\Big)\bar{i}(\tau). \tag{19}$$

From this differential equation, it can be concluded that for any fixed $\bar{i}(\tau)$, the greater R_0 is, the greater the derivative is. Thus, the derivative of the ratio of infected individuals is directly proportional to the parameter R_0. It follows that the disease is more infectious with a greater R_0.

2.4 Analysis Around the Trivial Equilibrium

The equilibrium of the model describes the situation when all individuals are susceptible and no one is infected. Thus there is no opportunity for the infection to spread and all of the ratios stay constant. Therefore the model is at a stable equilibrium when $\bar{i}(\tau) = 0$ and $\bar{s}(\tau) = 1$. It starts to deviate from this equilibrium as soon as a small change is made in this ratio, such as when

$$\begin{cases} \bar{i}(\tau) &= 0 + \epsilon(\tau) \\ \bar{s}(\tau) &= 1 - \delta(\tau) \end{cases} \tag{20}$$

for small-scale positive $\epsilon(\tau)$ and $\delta(\tau)$. Note that (when taking the derivative of the first equation of system (20)), it is found that $\frac{d\bar{i}(\tau)}{d\tau} = \frac{d\epsilon(\tau)}{d\tau}$. Substituting this into equation (15) generates the equation

$$\begin{aligned} \frac{d\bar{i}(\tau)}{d\tau} = \frac{d\epsilon(\tau)}{d\tau} &= \Big(R_0\,\big(1-\delta(\tau)\big)-1\Big)\epsilon(\tau) \\ &= \big(R_0-1\big)\epsilon(\tau) - R_0\,\delta(\tau)\epsilon(\tau) \\ &\approx \big(R_0-1\big)\epsilon(\tau). \end{aligned} \tag{21}$$

This approximation is made due to the small and insignificant nature of the term $R_0\,\delta(\tau)\epsilon(\tau)$. Note that equation (21) is constructed similarly to that of the derivative of an exponential function. Thus by taking its integral, the solution of the linear system derived from the approximation is found to be

$$\epsilon(\tau) \approx \epsilon_0\, e^{(R_0-1)\tau} \quad (\epsilon_0 \in \mathbb{R} > 0) \tag{22}$$

where ϵ_0 describes the constant of integration and the value of the equation when $\tau = 0$.

From the approximation of equation (21), it can be concluded that the nature of $\frac{d\epsilon(\tau)}{d\tau}$ is dependent on $R_0 - 1$. This is because $\epsilon(\tau)$ is positive. To further investigate the behavior of the transmission of the infectious disease around the predetermined equilibrium, three cases are addressed, varying the value of R_0.

(a) If $0 \leq R_0 < 1$, it implies that $\frac{d\epsilon(\tau)}{d\tau} < 0$ and thus, the number of infected individuals decreases.

(b) If $R_0 = 1$, it implies that $\frac{d\epsilon(\tau)}{d\tau} = 0$ and thus, a new equilibrium is established where the ratio of infected and susceptible individuals remains constant. Therefore, as the disease spreads to new individuals, the same amount recover from their infection. For any possible value of τ, there will be a ratio of $\epsilon(\tau)$ infected individuals.

(c) If $R_0 > 1$, it implies that $\frac{d\epsilon(\tau)}{d\tau} > 0$ which signifies that the number of infected individuals grows, ultimately causing an epidemic to break out.

Hence, around the equilibrium of the system, the sole influence on the derivatives of the ratios of infected and susceptible people is the parameter R_0.

2.5 Immunity Model

Furthermore, in realistic terms, once an individual recovers from the infection, their immune system retains a memory of it [4]. Thus the individual becomes resistant to the disease. Therefore, an additional variable is added to the model, $R(t)$, which counts the number of resistant individuals (people). Thus, the total population is now described as a sum of susceptible, infected, and resistant individuals at any point in time, t. Due to this,

$$S(t) + I(t) + R(t) = N. \tag{23}$$

Differentiating this equation with respect to t generates

$$\frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0. \tag{24}$$

Additionally, the growth rate of each individual variable over time consistent with equations used previously where

$$\frac{dS(t)}{dt} = -\frac{cp}{N}\, S(t)I(t) \tag{25}$$

$$\frac{dI(t)}{dt} = \frac{cp}{N}\, S(t)I(t) - \gamma\, I(t). \tag{26}$$

However, note that within the Recovery model, the rate of change of recovered individuals in equation (10) is now written with respect to $R(t)$ where

$$\frac{dR(t)}{dt} = \gamma\, I(t) \tag{27}$$

Similarly to before, a re-scaling takes place to create dimensionless variables and equations. This is done by once again letting $\tau = \gamma t$ where $d\tau = \gamma dt$ where $\overline{s}(\tau)$ and $\overline{i}(\tau)$ are defined as before. Moreover, the new dimensionless variable of the ratio of recovered individuals is

$$\overline{r}(\tau) = r(t) = \frac{R(t)}{N}.$$

With these dimensionless variables, the equations that make up system describing the spread of disease with respect to τ are found. Firstly, since the variables are all ratios,

$$\overline{s}(\tau) + \overline{i}(\tau) + \overline{r}(\tau) = 1. \tag{28}$$

Next, equation (14) which describes the rate of change of $\overline{i}(\tau)$ will still be used within this system since equations (13) and (26) coincide. Furthermore, the rate of change of $\overline{s}(\tau)$ is found by first noting that

$$\frac{d\overline{s}(\tau)}{d\tau} = \frac{1}{N} \cdot \frac{dS(t)}{d\tau} = \frac{1}{N\gamma} \cdot \frac{dS(t)}{dt}.$$

With this and utilizing equation (25), the rate of change is found to be

$$\begin{aligned}\frac{d\overline{s}(\tau)}{d\tau} &= \frac{1}{N\gamma}\cdot\frac{dS(t)}{dt}\\ &= \frac{1}{N\gamma}\cdot\Big(-\frac{cp}{N}\,I(t)S(t)\Big)\\ &= -\frac{cp}{\gamma}\Big(\frac{I(t)}{N}\Big)\Big(\frac{S(t)}{N}\Big)\\ &= -\frac{cp}{\gamma}\,\bar{i}(\tau)\overline{s}(\tau). \end{aligned} \tag{29}$$

Lastly, using the same logic where

$$\frac{d\overline{r}(\tau)}{d\tau} = \frac{1}{N\gamma}\cdot\frac{dR(t)}{dt},$$

the rate of change of the ratio $\overline{r}(\tau)$ using equation(27) is found to be

$$\begin{aligned}\frac{d\overline{r}(\tau)}{d\tau} &= \frac{1}{N\gamma}\cdot\frac{dR(t)}{dt}\\ &= \frac{1}{N\gamma}\cdot\Big(\gamma I(t)\Big)\\ &= \frac{I(t)}{N} = \bar{i}(\tau). \end{aligned} \tag{30}$$

By once again defining the parameter $R_0 = \frac{cp}{\gamma}$, the system of differential equations describing the spread of disease with the new recovery variable is

$$\begin{cases} \overline{s}(\tau) + \bar{i}(\tau) + \overline{r}(\tau) = 1\\[2ex] \dfrac{d\overline{s}(\tau)}{d\tau} = -R_0\,\bar{i}(\tau)\overline{s}(\tau)\\[2ex] \dfrac{d\bar{i}(\tau)}{d\tau} = \Big(R_0\,\overline{s}(\tau) - 1\Big)\bar{i}(\tau)\\[2ex] \dfrac{d\overline{r}(\tau)}{d\tau} = \bar{i}(\tau). \end{cases} \tag{31}$$

2.6 Long-Term Results

Next, with the addition of this new resistance factor, the relation between the ratios of infected and susceptible individuals gets blurred. Thus to rectify this, the variable $\overline{r}(\tau)$ will be described with regards to both $\overline{s}(\tau)$ and $\bar{i}(\tau)$, allowing further analysis of the main two variables and their relation. The purpose of studying the relation between $\overline{s}(\tau)$ and $\bar{i}(\tau)$ is to analyse the behaviours of the disease in differing conditions. In the case of this model, this is varied with the use of the parameter R_0. Furthermore, the full influence of

the disease will be monitored with regards to this parameter. To do this, first note that from equation (28),

$$\overline{r}(\tau) = 1 - \overline{s}(\tau) - \overline{i}(\tau). \tag{32}$$

Due to the fact that all three relevant variables are ratios, $0 \leq \overline{r}(\tau),\ \overline{s}(\tau),\ \overline{i}(\tau) \leq 1$. Thus as a consequence, $\overline{s} + \overline{i}$ is bounded such that

$$0 \leq \overline{s}(\tau) + \overline{i}(\tau) \leq 1$$

From this information, the phase space of the dynamics where all possible states of the system are presented is illustrated as the blue-colored area in Fig.1

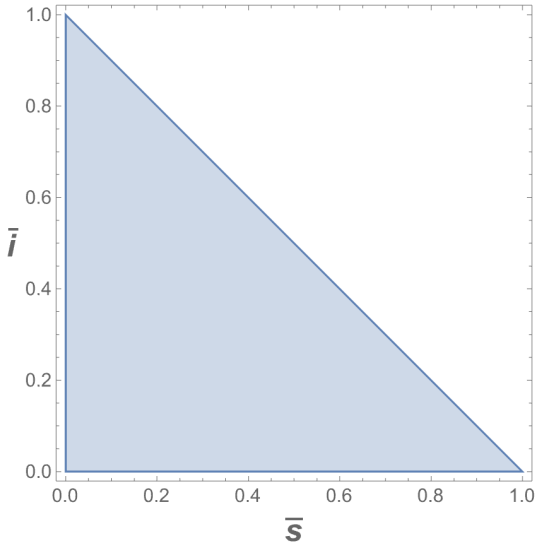

Figure 1: Phase Space of $\overline{s}$ and $\overline{i}$

To study the relation of two quantities, $\overline{s}(\tau)$ and $\overline{i}(\tau)$ in all possible τ, numerical analysis of the two-dimensional system is introduced. By the chain rule, the proportion of the rate of change of $\overline{s}(\tau)$ to the rate of change of $\overline{i}(\tau)$ is given by dividing $\dfrac{d\overline{s}}{d\tau}$ by $\dfrac{d\overline{i}}{d\tau}$. This is done with the use of the equations in system (31) where it is found that

$$\frac{d\overline{s}(\tau)/d\tau}{d\overline{i}(\tau)/d\tau} = \frac{d\overline{s}(\tau)}{d\overline{i}(\tau)} = \frac{-R_0\ \overline{s}(\tau)\overline{i}(\tau)}{R_0\ \overline{s}(\tau)\overline{i}(\tau) - \overline{i}(\tau)} = \frac{R_0\overline{s}(\tau)}{1 - R_0\overline{s}(\tau)}. \tag{33}$$

Considering the equilibrium initial condition discussed prior where $\tau = \tau_0$ and $\overline{i}(\tau_0) = 0$ when $\overline{s}(\tau_0) = 1$, integrating $\dfrac{d\overline{s}(\tau)}{d\overline{i}(\tau)}$ from equation (33) with respect to $\overline{i}(\tau)$ gives

$$\overline{s}(\tau) = \frac{R_0\ \overline{s}(\tau)\overline{i}(\tau)}{1 - R_0\overline{s}(\tau)} + 1. \tag{34}$$

To examine the full influence of the disease, the long-term behavior of $\overline{s}(\tau)$ and $\overline{i}(\tau)$ are examined and compared to the initial value. This is done by examining the vector trajectories of the variables with regards to three possible, different values of R_0. Recall that from section 2.4, the most notable R_0 around the initial equilibrium were

- $0 < R_0 < 1$ pictured in Fig. (2) with arbitrary $R_0 = 0.2$,
- $R_0 = 1$ pictured in Fig. (3),
- $R_0 > 1$ pictured in Fig. (4) with arbitrary $R_0 = 5$ below which was identified as an epidemic disease from subsection 2.4.

These R_0 values influenced the manner at which the disease spread.

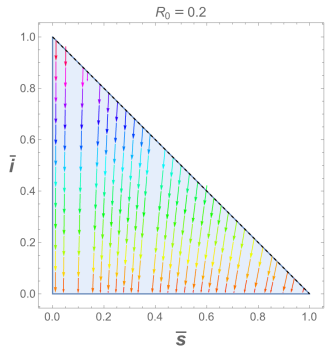

Figure 2: $0 < R_0 < 1$

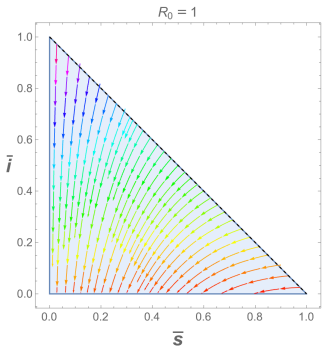

Figure 3: $R_0 = 1$

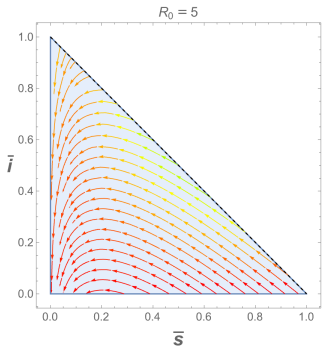

Figure 4: $R_0 > 1$

From the figures above, it can be seen that starting from any point in the phase space, regardless of the value of R_0, the long-term behavior shows that $\bar{i} \to 0$. This can be seen as the arrows per trajectory lead to the bottom of the triangles. Let the limits of each variable be defined as

$$\begin{aligned} \bar{s} &\to S_\infty \\ \bar{i} &\to I_\infty \\ \bar{r} &\to R_\infty \end{aligned}$$

to describe the long-term behavior of the dynamic. From the figures, it could be concluded that for all R_0 values, $I_\infty = 0$. Moreover, by equation (32), $S_\infty + R_\infty = 1$. In other words, the infection becomes extinct and the remainder of the population is made up of susceptible and recovered individuals in the long term for all cases. The ratios of these are dependent on the number of people that became infected throughout the spread of the disease. Note that the ratio of individuals who were infected throughout the disease is equivalent to R_∞. Later in the report, this becomes an important factor within the model.

When studying the three figures, (2), (3), and (4), it can be noted that as R_0 increases, the resultant change in the ratio of susceptible individuals increases. This can be seen as the arrows of the trajectories travel more to the left as the parameter grows. Thus the higher the R_0 value, the more the number of susceptible individuals seems to eventually differ from the initial condition. In biological terms, this means that there is a larger percentage of the population that is infected due to the epidemic qualities of the disease. Due to the fact that once an individual recovers from the infection they become resistant, the only susceptible individuals left are those who never once had the infection. Thus there is a smaller number of people who are not affected by the disease at all.

Additionally, in the case that $0 < R_0 < 1$, the arrows on Fig.(2) can be seen going only downwards for all τ. Thus, in this case, the ratio of the infected population only decreases. This is concurrent with the numerical information from subsection 2.4. The

ratio of susceptible individuals does not change much, due to the rapid rate that the infection dies out. The infected individuals then become resistant.

On the contrary, if $R_0 > 1$, the arrows of the trajectory on Fig.(4) first go upwards, reaching a peak, and then tending downwards. This signifies that at first, the ratio of infected individuals grows, yet eventually starts to decrease as the disease becomes extinct. This decrease has a steeper slope, thus the change in the ratio is more drastic than when the infection seems to be growing. It seemingly comes to a crashing halt. This sudden extinction of the infection happens due to the fact that individuals can now become resistant after they have recovered from their infection. Thus eventually, there will be a limited number of susceptible people within the population, leaving no room for the infection to spread.

2.7 Analysis around the Disease-Free Equilibrium

The next point to investigate is the condition on R_0 which would enable a disease-free stable equilibrium. By the definition of an equilibrium, all three variables $\overline{s}$, $\overline{i}$, and $\overline{r}$ are static. Thus their respective rates of change with respect to τ are zero. From system (31), recall that $\frac{d\overline{r}(\tau)}{d\tau} = 0$ if and only if $\overline{i}(\tau) = 0$. This is what makes the equilibrium disease-free. The ratio of infected individuals is zero. Additionally, if $\overline{i}(\tau) = 0$, $\dfrac{d\overline{s}(\tau)}{d\tau}$ and $\dfrac{d\overline{i}(\tau)}{d\tau}$ are zero as well due to it being a component of the product. Thus in this equilibrium, the entire population is made up of susceptible or resistant individuals. In the case that it is a new disease, the population will all be susceptible as no one has had a chance to build up their immunity to it.

This equilibrium may not be entirely stable. To investigate the stability of this disease-free equilibrium, it is assumed that the majority of the population is susceptible. Thus, only a few select individuals are newly infected. In this case $\overline{r}(\tau) = 0$ and $\overline{s}(\tau) + \overline{i}(\tau) = 1$ by the restriction on ratios. Based on system (31) from the immunity model, it is known that $\overline{s}(\tau)$ is a decreasing function where $\dfrac{d\overline{s}(\tau)}{d\tau} \leq 0$ for all τ. However, the sign of $\dfrac{d\overline{i}(\tau)}{d\tau}$ is not as simple. Note that when using the substitution $\overline{s}(\tau) = 1 - \overline{i}(\tau)$ due to the fact that there are no resistant individuals by assumption,

$$\begin{aligned} \frac{d\overline{i}(\tau)}{d\tau} &= \overline{i}(\tau)(R_0\overline{s}(\tau) - 1) \\ &= \overline{i}(\tau)(R_0 - 1 - R_0\overline{i}(\tau)). \end{aligned} \tag{35}$$

Thus the ratio of infected individuals will either increase or decrease around the disease-free equilibrium depending on the value of R_0. If $R_0 > \dfrac{1}{1 - \overline{i}(\tau)}$, then $\overline{i}(\tau)$ will increase and the disease will therefore spread. Thus even with a small outbreak of the disease, the R_0 parameter will influence whether the disease survives or eventually goes extinct.

2.8 Analysis around the Post-Epidemic Equilibrium

In the case of a post-epidemic disease, it is assumed that the disease has already gone extinct, thus $I_\infty = 0$. From subsection 2.6 it was found that at all varying R_0 values, the disease eventually died out. Due to this, $S_\infty + R_\infty = 1$. Note that in this case R_∞ is equivalent to the ratio of individuals who have been infected by the disease. This ratio will be compared to the initial ratio of susceptible individuals, and conclusions will be drawn.

To analyse this equilibrium, first, the relation between the variables $\overline{r}(\tau)$ and $\overline{s}(\tau)$ is established. Thus two-dimensional system is once again introduced. By the chain rule, the proportion of the rate of change of $\overline{r}(\tau)$ to the rate of change of $\overline{s}(\tau)$ is given by dividing $\frac{d\overline{r}}{d\tau}$ by $\frac{d\overline{s}}{d\tau}$. This is done with the use of the equations in system (31) where it is found that

$$\frac{d\overline{r}(\tau)/d\tau}{d\overline{s}(\tau)/d\tau} = \frac{d\overline{r}(\tau)}{d\overline{s}(\tau)} = \frac{\overline{i}(\tau)}{-R_0\,\overline{s}(\tau)\overline{i}(\tau)} = -\frac{1}{R_0\,\overline{s}(\tau)}. \tag{36}$$

Next, $\frac{d\overline{r}(\tau)}{d\overline{s}(\tau)}$ is integrated with respect to $\overline{s}(\tau)$ to derive the equation of $\overline{r}(\tau)$ in terms of $\overline{s}(\tau)$. To find the integration constant, an initial condition is established where $\tau = \tau_0$ and where $\overline{r}(\tau_0) = \overline{r}_0 = 0$. Thus initially, there are no resistant individuals initially and all are susceptible. Thus by the restriction on ratios, initially, $\overline{s}(\tau_0) + \overline{r}(\tau_0) = \overline{s}_0 + \overline{r}_0 = 1$. The resultant integration with substitution of the initial values generates

$$\overline{r}(\tau) = \frac{1}{R_0} \ln \frac{\overline{s}_0}{\overline{s}(\tau)}. \tag{37}$$

Equivalently, $\overline{s}(\tau)$ can also be expressed in terms of $\overline{r}(\tau)$ where

$$\overline{s}(\tau) = \overline{s}_0 \cdot e^{-R_0\,\overline{r}(\tau)}. \tag{38}$$

Now that the equations describing the ratios of resistant and susceptible individuals have been determined, the behaviour of the post-epidemic equilibrium can be examined. Utilizing the earlier defined long-term values of all three variables and equation (38), the long term relation between the two variables is found to be

$$S_\infty = \overline{s}_0 \cdot e^{-R_0 R_\infty}. \tag{39}$$

Additionally recall from subsection 2.6 that in the long-term, $I_\infty = 0$ and $S_\infty + R_\infty = 1$. By substituting in the S_∞ value from equation (39), it is found that

$$S_\infty + R_\infty = \overline{s}_0 \cdot e^{-R_0 R_\infty} + R_\infty = 1. \tag{40}$$

Therefore, it can be concluded that the limit $R_\infty \in \mathbb{R}$ exists such that the equation holds. As a result, the limit $S_\infty \in \mathbb{R}$ exists. Considering equation (37) in the long term,

$$R_\infty = \frac{1}{R_0} \ln \frac{\overline{s}_0}{S_\infty}. \tag{41}$$

Note that this equation represents the total proportion of the population that was infected during the epidemic. Since $R_\infty \in \mathbb{R}$ exists, $S_\infty \neq 0$ as there can not be a zero in the denominator of any fraction. Due to this, since a fraction of the population must be susceptible in the long-term, $R_\infty \neq 1$ by the restriction of ratios. For these reasons, $S_\infty \in (0, 1]$ and $R_\infty \in [0, 1)$.

Next, to further simplify the model, considering the initial condition where the full population is susceptible, $\overline{s}_0 = 1$, equation (40) becomes

$$e^{-R_0 R_\infty} = 1 - R_\infty. \tag{42}$$

Furthermore, the eventual long-term ratio of resistant individuals will be varied to investigate the relation between infected and thus resistant and susceptible individuals. Note that a possible solution to equation (42) is when there have been no infection so $R_\infty = 0$. Other solutions will be examined where $R_\infty \in (0, 1)$. To do this, define a new variable, $x \coloneqq R_\infty$, and the new functions

$$\begin{aligned} f : [0, 1) \to (0, 1] \quad &\text{where} \quad f(x) = e^{-R_0 x} \quad \text{and} \\ g : [0, 1) \to (0, 1] \quad &\text{where} \quad g(x) = 1 - x. \end{aligned}$$

Observe that the function $f(x)$ is equivalent to the ratio of susceptible individuals. Additionally, due to the restriction of the post-epidemic equilibrium where $S_\infty + R_\infty = 1$, function $g(x)$ is also equivalent to this ratio.

Note that trivially $f(x) = g(x)$ at $x = 0$. This coincides with the idea that if there is no infection at all, the long term result of resistant individuals will be zero. Thus the full population is still susceptible in the long term. Due to this, the sum of the long-term ratio of resistant and susceptible individuals will add up to 1, signifying a solution for equation (42).

If the derivative of the exponential function $\dfrac{df(x)}{dx}$ is smaller than $\dfrac{dg(x)}{dx} = -1$ at $x = 0$, then the equation $f(x) = g(x)$ has a nontrivial solution where $x \in (0, 1)$. This is due to the fact that since the slope of $f(x)$ is steeper than that of $g(x)$, it results in an additional intersection of the two functions, indicating that another solution can be found where $R_\infty + S_\infty = 1$ for $R_\infty \neq 0$. The derivative of f is found to be

$$f\,'(x) = -R_0\, e^{-R_0 x}. \tag{43}$$

To observe this derivative at the initial point where $x = 0$, varying the R_0 parameter effects whether or not a non-trivial solution can be found. Note that initially, $f\,'(0) = -R_0$. Therefore, the solution where $x \in (0, 1)$ exists if $R_0 > 1$. Additionally, if $R_0 < 1$, there is only the trivial solution. This is pictured in Fig. (5) and Fig. (6) with arbitrary R_0 values in their respective ranges, below.

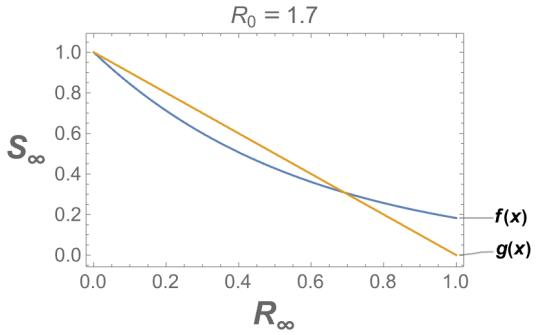

Figure 5: $R_0 > 1$

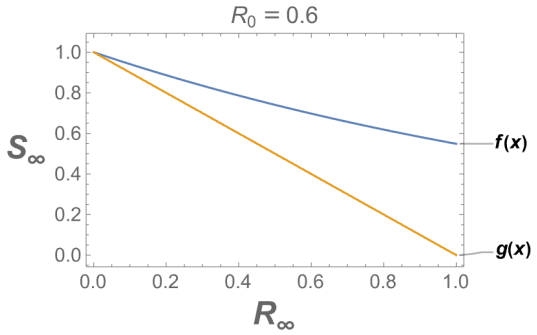

Figure 6: $R_0 < 1$

As can be clearly seen, in Fig. (5) there is an additional intersection between the two functions, indicating that a non-zero solution to equation (42) exists when $R_0 > 1$. Recalling from subsection 2.4, for this R_0 value, an epidemic is created. Thus for a post-epidemic equilibrium, in the long-term there exists a non-trivial balanced ratio between susceptible and recovered individuals.

On the other hand, Fig. (6) illustrates the case where an epidemic does not even occur. Recall that for $0 \leq R_0 < 1$, the disease goes extinct when a small number of infected individuals are introduced while the entire population started as susceptible. Biologically this means that the select few infected people may recover from the disease before they could even transmit it. Thus the ratio of recovered individuals is very small and due to this, only the trivial solution of the post-epidemic equilibrium can be found. The only significant R_∞ and S_∞ values are that coincide with the initial conditions.

2.9 Long Term Behaviour of the Resistant Population

In this section, the long term behaviour of the resistant population will be investigated. Therefore, to begin a new and closed differential equation for the proportion of the resistant as a function of τ is created. In previous sections, it was determined that

$$\frac{d\overline{r}(\tau)}{d\tau} = \overline{i}(\tau) = 1 - \overline{s}(t) - \overline{r}(t)$$

and

$$\overline{s}(\tau) = \overline{s}_0 \cdot e^{-R_0\,\overline{r}(\tau)}.$$

Hence, by substitution, a singular ODE can be generated where

$$\frac{d\overline{r}(\tau)}{d\tau} = \overline{i}(\tau) = 1 - \overline{s}_0 \cdot e^{-R_0\,\overline{r}(\tau)} - \overline{r}(t).$$

The further investigation the behaviour of the resistant proportion of the population, the differential equation will be solved. To do this, the ODE is approximated using the exponential Maclaurin Series where

$$e^{-R_0\,\overline{r}(\tau)} = \sum_{i=0}^{\infty} \frac{(-1)^n\big(-R_0\,\overline{r}(\tau)\big)^n}{n!}. \tag{44}$$

When looking at the first three terms of this series, the ODE can be approximated using a quadratic function in the case where R_0 is slightly greater than 1. Thus the differential equation becomes

$$\frac{d\overline{r}(\tau)}{d\tau} = (1 - \overline{s}_0) + (\overline{s}_0 R_0 - 1)\overline{r}(\tau) - \frac{\overline{s}_0 {R_0}^2}{2}\,\overline{r}^2(\tau). \tag{45}$$

To simplify this ODE, the quadratic portion of the equation will be factorized by using

$$(1 - \overline{s}_0) + (\overline{s}_0 R_0 - 1)\overline{r}(\tau) - \frac{\overline{s}_0 {R_0}^2}{2}\,\overline{r}^2(\tau) = 0.$$

After applying the quadratic formula, the solutions to the equation are found to be

$$\frac{(1 - \overline{s}_0 R_0) \pm \sqrt{(1 - \overline{s}_0 R_0)^2 - 4(\frac{-\overline{s}_0 {R_0}^2}{2})(1 - \overline{s}_0)}}{-\overline{s}_0 {R_0}^2}$$
$$= \frac{(1 - \overline{s}_0 R_0) \pm \sqrt{1 - 2\overline{s}_0 R_0 + 2\overline{s}_0 {R_0}^2 - {\overline{s}_0}^2 {R_0}^2}}{-\overline{s}_0 {R_0}^2}.$$

To simplify these solutions, they are defined as

$$\alpha_1 = \frac{(1 - \overline{s}_0 {R_0}^2) + \sqrt{1 - 2\overline{s}_0 R_0 + 2\overline{s}_0 {R_0}^2 - {\overline{s}_0}^2 {R_0}^2}}{-\overline{s}_0 {R_0}^2} \tag{46}$$

and

$$\alpha_2 = \frac{(1 - \overline{s}_0 R_0) - \sqrt{1 - 2\overline{s}_0 R_0 + 2\overline{s}_0 {R_0}^2 - {\overline{s}_0}^2 {R_0}^2}}{-\overline{s}_0 {R_0}^2} \tag{47}$$

Using this new factorization, equation (45) becomes

$$\frac{d\overline{r}(\tau)}{d\tau} = -\big(\frac{\overline{s}_0 {R_0}^2}{2}\big)\big(\overline{r}(\tau) - \alpha_1\big) \cdot \big(\overline{r}(\tau) - \alpha_2\big)$$

$$\Leftrightarrow$$

$$\frac{d\overline{r}(\tau)}{\big(\overline{r}(\tau) - \alpha_1\big)\big(\overline{r}(\tau) - \alpha_2\big)} = \frac{-\overline{s}_0 {R_0}^2}{2} d\tau$$

and by solving separable differential equations,

$$\int \frac{d\overline{r}(\tau)}{\big(\overline{r}(\tau) - \alpha_1\big)\big(\overline{r}(\tau) - \alpha_2\big)} = \frac{-sr^2}{2} \int d\tau. \tag{48}$$

It is assumed that $\alpha_1 \neq \alpha_2$. In other words, $1 - 2sr + 2sr^2 - s^2r^2 \neq 0$. To further simplify the solution of the differential equation, let

$$\frac{1}{\big(\overline{r}(\tau) - \alpha_1\big)\big(\overline{r}(\tau) - \alpha_2\big)} = \frac{A}{\overline{r}(\tau) - \alpha_1} + \frac{B}{\overline{r}(\tau) - \alpha_2} \tag{49}$$

for some $A, B \in \mathbb{R}$. For this to hold,

$$\begin{aligned} \frac{A}{\overline{r}(\tau) - \alpha_1} + \frac{B}{\overline{r}(\tau) - \alpha_2} &= \frac{A\big(\overline{r}(\tau) - \alpha_2\big) + B\big(\overline{r}(\tau) - \alpha_1\big)}{\big(\overline{r}(\tau) - \alpha_1\big) \cdot \big(\overline{r}(\tau) - \alpha_2\big)} \\ &= \frac{(A + B) \cdot \overline{r}(\tau) - (A \cdot \alpha_2 + B \cdot \alpha_1)}{\big(\overline{r}(\tau) - \alpha_1\big) \cdot \big(\overline{r}(\tau) - \alpha_2\big)} \\ &= \frac{1}{\big(\overline{r}(\tau) - \alpha_1\big) \cdot \big(\overline{r}(\tau) - \alpha_2\big)} \end{aligned} \tag{50}$$

By equating the numerators it is found that $(A + B) \cdot \overline{r}(\tau) - (A \cdot \alpha_2 + B \cdot \alpha_1) = 1$. By this logic, it can be concluded that

$$A + B = 0 \Rightarrow B = -A$$

and

$$-(A \cdot \alpha_2 + B \cdot \alpha_1) = 1 \Rightarrow A(\alpha_1 - \alpha_2) = 1$$

Therefore, the two parameters are found to be $A = \dfrac{1}{\alpha_1 - \alpha_2}$ and $B = \dfrac{1}{\alpha_2 - \alpha_1}$.

Using this partial fraction decomposition, equation (48) becomes,

$$\int \left(\frac{A}{\overline{r}(\tau) - \alpha_1} + \frac{B}{\overline{r}(\tau) - \alpha_2}\right) dr = \frac{-\overline{s}_0 {R_0}^2}{2} \int d\tau \tag{51}$$

$$\Rightarrow$$

$$A\ln|\overline{r}(\tau)-\alpha_1|-A\ln|(\overline{r}(\tau)-\alpha_2|=\frac{-\overline{s}_0{R_0}^2}{2}\tau+c_1 \tag{52}$$

for some constant of integration c_1. Through the use of the laws of logarithms this can further be simplified where

$$A\ln\left|\frac{\overline{r}(\tau)-\alpha_1}{\overline{r}(\tau)-\alpha_2}\right|=\frac{-\overline{s}_0{R_0}^2}{2}\tau+c_1. \tag{53}$$

The goal is to generate a single equation for $\overline{r}(\tau)$. To do this, the equation is divided by the parameter A, and then to remove the logarithmic function, e is raised to its power. To simplify, define $\frac{c_1}{A}=c$. This generates the equation

$$\begin{aligned} e^{\frac{-\overline{s}_0{R_0}^2}{2A}\tau+c} &= \frac{\overline{r}(\tau)-\alpha_1}{\overline{r}(\tau)-\alpha_2} \\ &= \frac{\overline{r}(\tau)+(\alpha_1-\alpha_1)-\alpha_1}{\overline{r}(\tau)-\alpha_2} \\ &= 1+\frac{\alpha_2-\alpha_1}{\overline{r}(\tau)-\alpha_2}. \end{aligned} \tag{54}$$

Recall that $\alpha_2-\alpha_1=\frac{-1}{A}$. Thus equation (54) can be further simplified to

$$\begin{aligned} &\frac{1}{\overline{r}(\tau)-\alpha_2}=-A\big(e^{-\frac{\overline{s}_0{R_0}^2}{2A}\tau+c}-1\big) \\ &\Rightarrow\quad \overline{r}(\tau)=\frac{1}{A}\big(1-e^{-\frac{\overline{s}_0{R_0}^2}{2A}\tau+c}\big)^{-1}+\alpha_2. \end{aligned} \tag{55}$$

This is the equation that models the behavior of the proportion of resistant individuals within the system.

Next, the long-term behaviour of this equation will be investigated. To do this, τ will tend to ∞. This creates the limit,

$$\begin{aligned} \lim_{\tau\to\infty}\overline{r}(\tau) &= \lim_{\tau\to\infty}\left(\frac{1}{A}\big(1-e^{\frac{-\overline{s}_0{R_0}^2}{2A}\tau+c}\big)^{-1}+\alpha_2\right) \\ &= \frac{1}{A}\lim_{\tau\to\infty}\big(1-e^{\frac{-\overline{s}_0{R_0}^2}{2A}\tau+c}\big)^{-1}+\alpha_2. \end{aligned} \tag{56}$$

To further investigate this long-term behaviour, 2 cases will be considered. First, if $A>0$, then $\alpha_1>\alpha_2$. The limit is then simplified to,

$$\lim_{\tau\to\infty}\big(1-e^{\frac{-sr^2}{2A}\tau+C}\big)^{-1}=\left(1-\left(\frac{1}{e}\right)^{\infty}\right)^{-1}=(1-0)^{-1}=1.$$

By applying this simplified limit to equation (56),

$$\lim_{\tau\to\infty}\overline{r}(\tau)=\frac{1}{A}\cdot 1+\alpha_2=\alpha_1-\alpha_2+\alpha_2=\alpha_1. \tag{57}$$

Therefore it can be concluded that in the long term where $\alpha_1>\alpha_2$, the ratio of resistant individuals converges to the solution α_1.

Next, in the case that $A < 0$, where $\alpha_1 < \alpha_2$. The limit is then simplified to,

$$\lim_{\tau\to\infty}\left(1 - e^{\frac{-sr^2}{2A}\tau + C}\right)^{-1} = \frac{1}{1 - e^{\infty}} = 0.$$

By applying this simplified limit to equation (56), it is found that

$$\lim_{\tau\to\infty} \overline{r}(\tau) = \frac{1}{A} \cdot 0 + \alpha_2 = \alpha_2. \tag{58}$$

Therefore it can be concluded that in the long term where $\alpha_1 < \alpha_2$, the ratio of resistant individuals converges to zero.

Assume that $\overline{s}_0 = \overline{s}(\tau_0) \approx 1$ the solutions of the quadratic equation simplify to

$$\begin{aligned}
\alpha_1, \alpha_2 &= \frac{(1 - \overline{s}_0 R_0) \pm \sqrt{1 - 2\overline{s}_0 R_0 + 2\overline{s}_0 {R_0}^2 - {\overline{s}_0}^2 {R_0}^2}}{-\overline{s}_0 {R_0}^2} \\
&\approx \frac{(1 - R_0) \pm \sqrt{1 - 2R_0 + 2{R_0}^2}}{-{R_0}^2} \\
&= \frac{(1 - R_0) \pm \sqrt{(1 - R_0)^2}}{-{R_0}^2} \\
&= \frac{(1 - R_0) \pm (1 - R_0)}{-{R_0}^2}
\end{aligned} \tag{59}$$

for an R_0 value slightly greater than 1, $(1 - R_0) < 0$. With this information, equation (59) can be further simplified for each of the two solutions. Note that α_1 approximately simplifies to

$$\begin{aligned}
\alpha_1 &\approx \frac{(1 - R_0) + (1 - R_0)}{-{R_0}^2} \\
&= \frac{2(R_0 - 1)}{{R_0}^2}.
\end{aligned} \tag{60}$$

Additionally, α_2 approximately simplifies to

$$\alpha_2 \approx \frac{(1 - R_0) - (1 - R_0)}{-{R_0}^2} = 0. \tag{61}$$

This only holds when $R_0 > 1$, so $\alpha_1 \approx \dfrac{2(R_0 - 1)}{{R_0}^2} > 0 \approx \alpha_2$. Therefore, the first case where $\alpha_1 > \alpha_2$ is relevant in this scenario. Due to this, it can be concluded from equation (57) that,

$$\lim_{\tau\to\infty} \overline{r}(\tau) = \alpha_1 \approx \frac{2(R_0 - 1)}{{R_0}^2}. \tag{62}$$

This is the approximation of the long-term behavior of the proportion of resistant individuals.

Note that with these defined solutions, $\alpha_1 \approx \dfrac{2(R_0 - 1)}{{R_0}^2}$ and $\alpha_2 \approx 0$, and with the approximated $\overline{s}_0 = 1$, the factorized version of the differential equation portraying the rate of change proportion of resistant individuals,

$$\frac{d\overline{r}(\tau)}{d\tau} = -\left(\frac{\overline{s}_0 {R_0}^2}{2}\right)\left(\overline{r}(\tau) - \alpha_1\right)\left(\overline{r}(\tau) - \alpha_2\right)$$

approximately simplifies to

$$\begin{aligned}
\frac{d\overline{r}(\tau)}{d\tau} &= -\left(\frac{{R_0}^2}{2}\right)\left(\overline{r}(\tau) - \frac{2(R_0-1)}{{R_0}^2}\right)\overline{r}(\tau) \\
&= -\left(\frac{{R_0}^2}{2}\right)\left(\overline{r}^2(\tau) - \frac{2(R_0-1)}{{R_0}^2}\,\overline{r}(\tau)\right) \\
&= -\left(\frac{{R_0}^2}{2}\right)\overline{r}^2(\tau) - (R_0-1)\,\overline{r}(\tau) \qquad (63) \\
&\approx (1-\overline{s}_0) + (\overline{s}_0 R_0 - 1)\overline{r}(\tau) - \frac{\overline{s}_0 {R_0}^2}{2}\,\overline{r}^2(\tau). \qquad \text{(equation (45))}
\end{aligned}$$

Therefore, it can be found that with these solutions, limits, and parameters, the right hand side of equation (45) can be approximated where $R_0 > 1$ and when $\overline{s}_0 = 1$. The equation (45) is equal to equation (63).

2.10 Modelling the Bombay Bubonic Plague Epidemic

In this section, the Bubonic plague is modeled. In this case, it is assumed that all the infected individuals end up dead. Therefore within the model, the proportion of dead individuals is equal to the resistant individuals, as once someone recovers, they are assumed to be dead. Considering the case in which the majority of population is susceptible, $\overline{s}_0$ is approximated to 1. From equation (45),

$$\begin{aligned}
\frac{d\overline{r}(\tau)}{d\tau} &= (1-\overline{s}_0) + (\overline{s}_0 R_0 - 1)\overline{r}(\tau) - \frac{\overline{s}_0 {R_0}^2}{2}\big(\overline{r}(\tau)\big)^2 \\
&\approx (R_0-1)\overline{r}(\tau) - \frac{{R_0}^2}{2}\big(\overline{r}(\tau)\big)^2. \qquad (64)
\end{aligned}$$

Solving this ODE gives

$$\overline{r}(\tau) = \frac{2(R_0-1)}{R_0^2\left(1+e^{(1-R_0)\tau+c}\right)} \qquad \text{(for some constant } c \in \mathbb{R}\text{).} \qquad (65)$$

Furthermore, the long-term behavior of $\overline{r}(\tau)$ is

$$\begin{aligned}
R_\infty = \lim_{\tau\to\infty}\overline{r}(\tau) &= \lim_{\tau\to\infty}\frac{2(R_0-1)}{R_0^2\left(1+e^{(1-R_0)\tau+c}\right)} \\
&= \frac{2(R_0-1)}{{R_0}^2\left(1+e^{-\infty}\right)} = \frac{2(R_0-1)}{{R_0}^2}. \qquad (66)
\end{aligned}$$

Note that this is equivalent to the limit found in subsection 2.9. From this information, equation (65) is rephrased as

$$\overline{r}(\tau) = \frac{R_\infty}{1+e^{(1-R_0)\tau+c}} \qquad (67)$$

Week Number		Week Number		Week Number		Week Number		Week Number	
1	8	7	51	13	442	19	925	25	106
2	10	8	92	14	644	20	802	26	64
3	12	9	124	15	779	21	578	27	46
4	16	10	178	16	702	22	404	28	35
5	24	11	280	17	695	23	296	29	27
6	48	12	387	18	870	24	162	30	28

Figure 7: Table of number of deaths per week during the plague epidemic in Bombay in 1906, from The Journal of Hygiene (London), Vol. 7, No. 6, Reports on Plague Investigations in India (Dec. 1907), p. 753

To be able to use this model to approximate the mortality rate of the Bombay Bubonic Plague in 1906 with data from [5], the model must be transformed to counting the number of resistant (dead) individuals at a time, t. In this case, this time will be specified in weeks. This data is shown in table below.

The proportion of dead individuals, $\overline{r}(\tau)$ is scaled into the number of dead individuals by multiplying it the total number of the population. In other words, $R(t) = N \cdot \overline{r}(\tau)$. Likewise, the long-term number of dead individuals is $N \cdot R_\infty$. The long-term number of dead individuals is approximated to the sum of the dead individuals from Week 1 to Week 30 in figure (7). Therefore the equation to model the number of recovered (dead) individuals is,

$$\begin{aligned} R(t) = N \cdot \overline{r}(\tau) &= \frac{N \cdot R_\infty}{1 + e^{(1-R_0)\tau + c}} \\ &= \frac{8835}{1 + e^{(1-R_0)\tau + c}} \end{aligned} \tag{68}$$

To model the mortality rate, the derivative of this equation is found to be,

$$\frac{dR(t)}{dt} = \gamma \cdot \frac{dR(t)}{d\tau} = \frac{8835\,\gamma\,(R_0 - 1)e^{(1-R_0)\tau + c}}{1 + e^{(1-R_0)\tau + c}} \tag{69}$$

where $\tau = \gamma t$ and γ represents the reciprocal of the average recovery (death) time.

Parameters γ, c, and R_0 of equation (69) are varied to match up with the data from Figure (7) [5]. It is still assumed that R_0 is slightly bigger than 1. The accuracy of these parameters to the real world situation will be investigated. The most accurate curve with the data points are plotted in Figure (8) below.

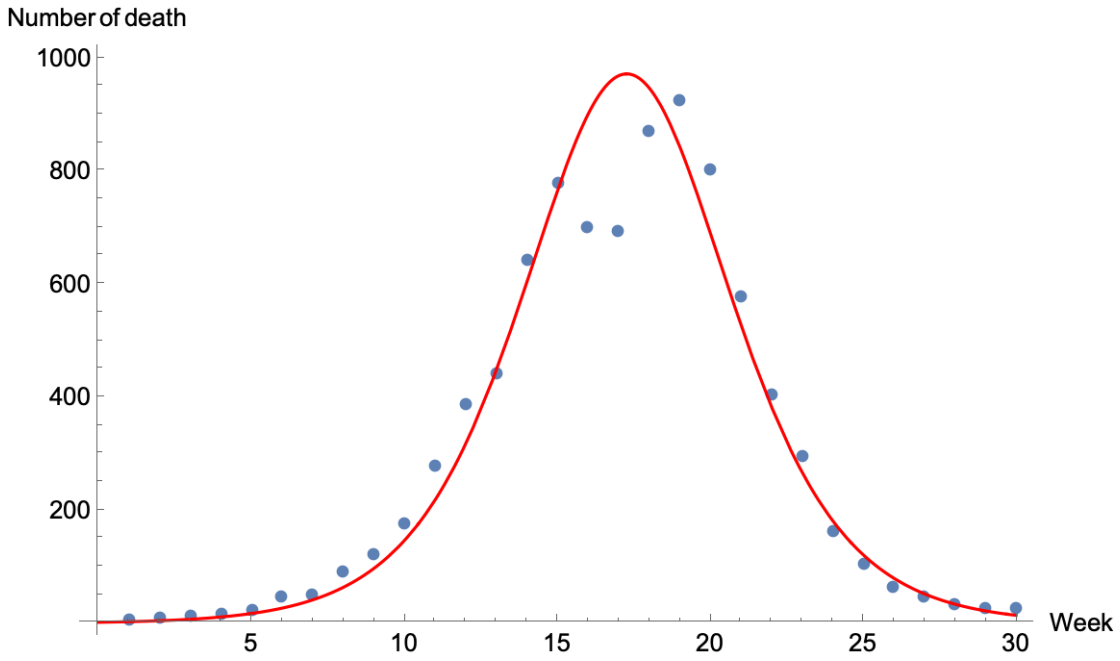

Figure 8: Death information from [5] in blue, and equation (69) in red where $R_0 = 1.44$, $\gamma = 1$, and $c = 7.6$

To have equation (69) match up as closely as possible to the bell-curve formed by the data, the parameters specified in the caption of Figure (8) are used. Next, to analyse the realistic accuracy of these parameters, they are compared to the realistic data at that time. Note that the $R_0 = 1.44$ value is slightly larger than 1, which was specified for the disease to spread. The Bubonic Plague was highly infective and thus the R_0 value must realistically be above 1; it was an epidemic. Additionally, the recovery rate γ is found to approximately be equal to 1. With regards to the average recovery time where $t_A = \frac{1}{\gamma}$, the average recovery (death) time is 1 week. This corresponds with the data from [2] where it is estimated that once an individual is infected with the Bubonic Plague, they die between 6-10 days later. Thus an estimate of a recovery (death) time of 7 days accurately fits within this range. Lastly the parameter $c = 7.6$. This is an arbitrary integration constant thus it is indifferent within the model and its realistic expectation.

Note that the width of the bell curve corresponds to the standard deviation. Note that since the total population N, must be constant, the area underneath the curve, no matter the width of the peak, will be constant. For a low standard deviation, the majority of the deaths occur around the mean time, at the peak of the curve. Therefore the curve will be more narrow yet the peak reaches higher. For a higher standard deviation, the number of deaths per week is more spread out, with a wider but flatter curve. The width of the curve in Figure (8) is dependent on the R_0 parameter. Its relation will be explored by varying its value. Below are three figures describing how the curve changes when varying the R_0 value. For all three, the fact that R_0 is slightly greater than 1 is still used.
From these figures, it can be seen that for an R_0 value closer to 1, the width of the peak is slightly wider as the curve flattens out. However, for an R_0 value slightly further from 1, the width of the peak decreases as the curve stretches upwards. Thus as the R_0 parameter strays further from the base-line of $R_0 = 1$, the standard deviation of the curve decreases, meaning the majority of the deaths cluster around the mean value. In biological terms, individuals are dying more often around the actual peak of the deaths per week.

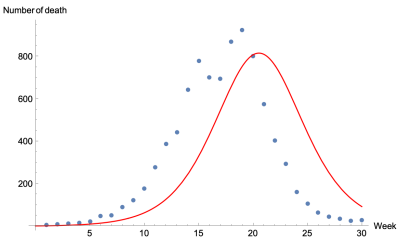

Figure 9: $R_0 = 1.37$

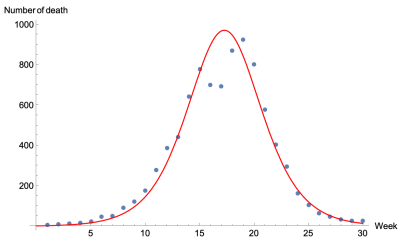

Figure 10: $R_0 = 1.44$

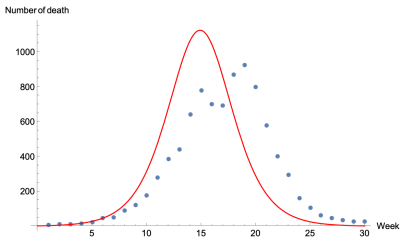

Figure 11: $R_0 = 1.51$

This analysis was made with the assumption that all resistant individuals have died. In the case that this is not true, the resistant individuals are made up of those who have recovered and are immune, and those who have died. Realistically, the curve from figure (8) would be stationed above the data, as the data from [5] only counts those that are dead. Therefore, in the case that individuals also recover and become resistant, the change in resistant individuals per week, $\frac{dR(t)}{dt}$ will be the sum of the number of deaths, and the number of recovered and immune individuals per week. The peak of the normal curve will therefore be higher.

2.11 Analysis of the Vaccination Factor for the Spread of the Disease

In real world scenarios, vaccines play a large part in the control of the spread of disease. With regards to our model, vaccinations correspond to the resistant individuals. In this section, it is assumed that a proportion of the susceptible individuals are vaccinated initially, and are thus resistant. The proportion of these resistant individuals at the initial time, τ_0 is denoted as $\overline{r}(\tau_0) = \overline{r}_0 = 1 - \overline{s}_0$ under the assumption that the proportion of infected individuals at this time, $\overline{i}_0$ is 0. The overall model changes by varying the initial vaccinated proportion of the population.

Due to this, there will be a smaller change in the proportions of susceptible and infected individuals than the prior model: As once someone is resistant, they can no longer be effected by the disease. Therefore there is a smaller proportion of the population whose states will actually change, going from susceptible to infected and eventually to resistant.

With this newly introduced initially vaccinated proportion of the population, the spread of disease will now be studied. To do this, the equation for the rate of change of the proportion of infected individuals, $\frac{d\overline{i}(\tau)}{d\tau}$ from system (31) will be utilized. Recall that this equation states that

$$\frac{d\overline{i}(\tau)}{d\tau} = (R_0\ \overline{s}(\tau) - 1)\overline{i}(\tau). \tag{70}$$

This equation will be analysed with these new initial conditions, specifically to investigate for which value of $\overline{r}_0$, the disease will not spread. If, initially, the disease does not spread, it will also not spread in later time periods. That is because it has reached a stable equilibrium at its initial point. Due to this, the initial conditions will be the influential variables as predicted above. There at two possible cases that can be found where $\frac{d\overline{i}(\tau)}{d\tau} = 0$ when using equation (70).

1. If $\overline{i}(\tau) = 0$, there is no disease spread.

2. If $\left(R_0\ \overline{s}(\tau) - 1\right) = 0$, there is no disease spread.

Note that only this second case is dependent on a parameter that can be adjusted since $\overline{i}_0 = 0$. Using the initial τ_0, substitute in the ratios $\overline{s}_0 = 1 - \overline{r}_0$ to generate $R_0\ (1 - \overline{r}(\tau)) - 1 = 0$. After rearranging the formula, it is found that the disease does not spread if

$$\overline{r}_0 = 1 - \frac{1}{R_0}. \tag{71}$$

Thus, the proportion of the public that must initially be vaccinated to stop the spread of disease is dependent on the R_0 parameter.

2.12 Model for the Endemic Disease

Within this section, an endemic disease such as the flu will be modelled. An endemic disease is one that is constantly present within a population, and its infection and recovery rates can therefore easily be predicted [1]. Contrasting the previous sections, within an endemic disease, the population is no longer considered to be constant. To do this there are two additional variables added, the births (the generation of new vulnerable individuals) and natural death (death not induced by the disease).

Define the rate of new births as $\dfrac{dB}{dt}$ and $\dfrac{dD}{dt}$ as the rate of disease induced deaths. Moreover, assume that all new births will be directly considered as susceptible. Observe that the model will be constructed in terms of population size and not in terms of proportion to the whole population since births and deaths cause the population size may vary.

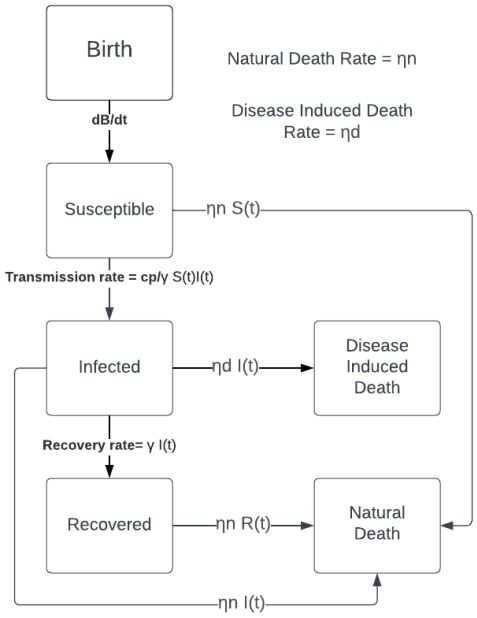

Figure 12: Flow diagram in which the arrows between classes of individuals represent transitions from one class to the other including their respective transition rates

Considering the rates in Figure (12), the system of ODE's with regards to the number of susceptible, infected, resistant, and dead individuals is

$$\begin{cases} \dfrac{dS}{dt} &= \dfrac{dB}{dt} - cp \cdot S(t)I(t) - \eta n \cdot S(t) \\ \dfrac{dI}{dt} &= cp \cdot S(t)I(t) - \eta d \cdot I(t) - \gamma \cdot I(t) - \eta n \cdot I(t) \\ \dfrac{dR}{dt} &= \gamma \cdot I(t) - \eta n \cdot R(t) \\ \dfrac{dD}{dt} &= \eta d \cdot I(t) \end{cases} \tag{72}$$

An assumption is made that the rate of birth is proportional to the population. Namely, $\dfrac{dB}{dt} = \xi\big(S(t) + R(t) + I(t)\big)$ and to avoid confusion within the derivatives, the diseased proportion of the population $\dfrac{D}{N} = \tilde{D}$. Since the rate of birth is proportional to the population, re-scale the equations using the fact that $s(t) + i(t) + r(t) = 1$. Then, $\dfrac{dB}{dt} = \xi$. With this substitution, the system above becomes

$$\begin{cases} \dfrac{ds}{dt} &= \xi - cp \cdot s(t)i(t) - \eta n \cdot s(t) \\ \dfrac{di}{dt} &= cp \cdot s(t)i(t) - \eta d \cdot i(t) - \gamma \cdot i(t) - \eta n \cdot i(t) \\ \dfrac{dr}{dt} &= \gamma \cdot i(t) - \eta n \cdot r(t) \\ \dfrac{d\tilde{D}}{dt} &= \eta d \cdot i(t) \end{cases} \tag{73}$$

Moreover, an assumption is made that the rate of birth is equal to the rate of natural death, $\xi = \eta n$. The equation is re-scaled to produce,

$$\begin{cases} \dfrac{ds}{dt} &= \xi - cp \cdot s(t)i(t) - \xi \cdot s(t) \\ \dfrac{di}{dt} &= cp \cdot s(t)i(t) - \eta d \cdot i(t) - \gamma \cdot i(t) - \xi \cdot i(t) \\ \dfrac{dr}{dt} &= \gamma \cdot i(t) - \xi \cdot r(t) \\ \dfrac{d\tilde{D}}{dt} &= \eta d \cdot i(t) \end{cases} \tag{74}$$

For the infection to be breaking out again, it is required to have $\frac{di}{dt} > 0$. Now, calculate new R_0 as the only combination of the parameters. First, assume that the disease does not cause any additional deaths. Then $\eta d = 0$ and the rate of infection simplifies to,

$$\begin{aligned}\frac{di}{dt} &= cp \cdot s(t) \cdot i(t) - \xi \cdot i(t) - \gamma \cdot i(t) \\ &= i(t)\big(cp \cdot s(t) - \xi - \gamma\big) > 0. \end{aligned} \tag{75}$$

In order for the disease to be spreading, the rate of transmission of the disease needs to be bigger than the rate of recovery and the rate of natural death. Thus, $cp \cdot s(t) > \xi + \gamma \Rightarrow cp > \xi + \gamma$. Define the new R_0 as $\frac{cp}{\xi + \gamma}$. This new parameter is additionally dependent on the birth rate/natural death rate $\xi = \eta n$. For the disease to spread, this parameter R_0 must be greater than 1.

Lastly, consider the case where the disease does cause additional deaths. Thus $\eta d \neq 0$ and the rate of infection simplifies to,

$$\begin{aligned}\frac{di}{dt} &= cp \cdot s(t) \cdot i(t) - \eta d \cdot i(t) - \xi \cdot i(t) - \gamma \cdot i(t) \\ &= i(t)\big(cp \cdot s(t) - \eta d - \gamma - \xi\big) > 0. \end{aligned} \tag{76}$$

Then, $cp \cdot s(t) > \eta d + \gamma + \xi \Rightarrow cp > \eta d + \gamma + \xi$. Define the new R_0 as $\frac{cp}{\eta d + \gamma + \xi}$. Hence, R_0 will additionally be dependent on ηd, not only on ξ as in the case prior. By comparing it to the previously defined $R_0 = \frac{cp}{\gamma}$, it can be seen that in the case of both natural births and two types of deaths, the parameter is now dependent on the natural birth rate/natural death rate and the disease induced death rate.

3 Conclusion

In this report, different simplified scenarios for infectious disease were explained via employing differential equations. Simplified infection and recovery models were combined together to investigate the parameters that impact the spread of infectious diseases. In addition, the cause of an epidemic was considered. Furthermore, the idea of immunity was introduced and long-term results were analysed with regards to multiple equilibria.

Infectious diseases are often worth monitoring using mathematical models. With this, the greatest effects of the spread of disease can be concluded, and possible fatal results can be avoided. This could be seen with the global pandemic of COVID-19 [3]. The overall combined model concluded that the change in the ratio of the infected individuals and cause for an epidemic was solely based on a few simple parameters. It was dependent on the average recovery time of the disease, the probability of the disease spreading, and finally, the total expected amount of contact the entire population has. Though most of these factors are out of human control and are based on the nature of the disease itself, there is one factor that can be regulated to prevent an epidemic. This is the amount of interpersonal contact. Encouraging individuals to have social distance and stay at home has now been proven to aid in the control of the spread of infection.

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