Numerical Analysis of Nonlinear Dynamical Systems

with applications in Epidemiology and Disease Control

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1   Introduction

The long history of infectious diseases among humans causing the loss of countless lives has always kept their study and prevention at the forefront of Medicine. Several ingenious methods have been devised to cure and prevent most of the prevalent infections. However, the phenomena that have posed the biggest challenge to effective disease control are epidemics, as is underlined by the COVID-19 pandemic, which continues to wreak havoc across the globe.

Apart from the traditional approach to curbing an epidemic that involves developing cures and vaccinations against new pathogens, the 20th century saw the rise of mathematical models that could predict the future course of an epidemic and consequently allow the authorities to take necessary precautions. One of the earliest efforts in this direction was made by W.O. Kermack and A.G. McKendrick in 1927.

In their pioneering paper titled "A Contribution to the Mathematical Theory of Epidemics," Kermack and McKendrick outlined a simple mathematical model for epidemics. Their Model examines an infection that spreads due to direct contact between an infected and a healthy person. To account for the statistical interaction between the infected and healthy populations, the rate of spread of the infection is assumed to be the product of the total number of susceptible people and the number of sick people at any given instant.

Moreover, the Model assumes that the death rate is directly proportional to the total infected population, thus covering all the significant aspects of any disease.

In spite of its many successes, the Kermack-McKendrick Model remains an artifact of its time and has undergone many modifications to better suit new situations.

After establishing the basic features of the Model, this paper attempts two such revisions, which: i) account for the medical treatment provided to the infected persons and ii) mimic the "wave-like" behavior of the COVID-19 pandemic and test the effectiveness of mass vaccination.

2   The Kermack-McKendrick Model

2.1   Description and Analysis

Kermack and McKendrick formulated the following model describing the outbreak of an epidemic.

The total population is divided into three broad categories: number of healthy/susceptible people (represented by $x(t)$), number of sick people (represented by $y(t)$), and number of dead people (represented by $z(t)$). The equations governing the rates of change in these categories are

$$\dot{x} = -kxy$$
$$\dot{y} = kxy - ly$$
$$\dot{z} = ly$$

where k is the transmission rate (a measure of the disease's infectiousness and the probability of contact between people belonging to the healthy and infected populations) and l represents the mortality rate-number of deaths per infection. The coefficients k and l are both set to be constant. As can be understood from the equations, the model looks at a closed population.

As can be understood from the equations, the model looks at a closed population.

$$\dot{x} + \dot{y} + \dot{z} = 0$$

$$\Rightarrow \frac{d}{dt}(x + y + z) = 0$$

$$\Rightarrow (x + y + z) = constant$$

Thus the total number of people does not change over time, and variations due to birth rates, natural death rates, and migrations are negligible. At the start of the epidemic, a few infected people are assumed to be present in this closed population, which then go on to spread the disease.

The most important contribution of this paper to the existing literature in Epidemiology was deducing the reason for the termination of an epidemic. Prior to this work, it was believed that epidemics end because either the susceptible population runs out or the infectiousness of the pathogen decreases over time. In their paper, Kermack and McKendrick pointed out that-

" ...the course of an epidemic is not necessarily terminated by the exhaustion of the susceptible members of the community. It will appear that for each particular set of infectivity, recovery and death rates, there exists a critical or threshold density of population. If the actual population density be equal to (or below) this threshold value the introduction of one (or more) infected persons does not give rise to an epidemic, whereas if the population be only slightly more dense a small epidemic occurs. It will appear also that the size of the epidemic increases rapidly as the threshold density is exceeded, and in such a manner that the greater the population density (of susceptibles) at the beginning of the epidemic, the smaller will it be at the end of the epidemic. In such a case the epidemic continues to increase so long as the density of the unaffected population is greater than the threshold density, but when this critical point is approximately reached the epidemic begins to wane and ultimately die out. This point may be reached when only a small proportion of the susceptible members of the community have been affected."
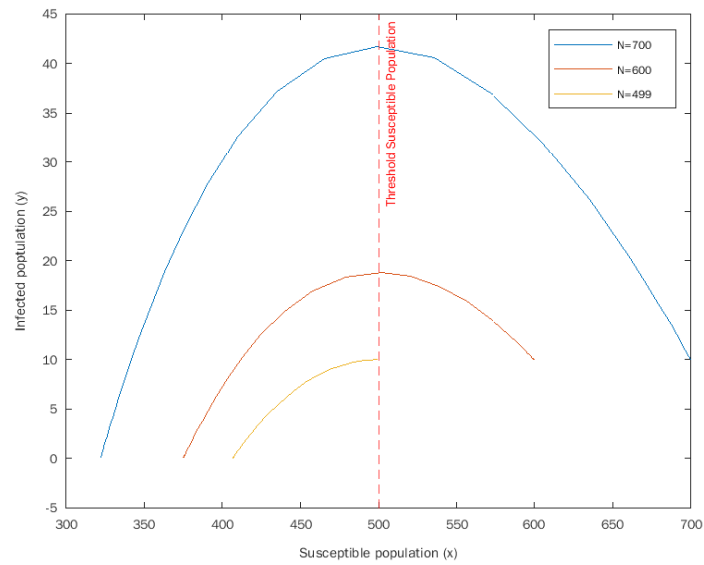
This threshold density is given by

$$N_T = \frac{l}{k}$$

In order to gain a more thorough understanding of the workings and implications of this model, MATLAB simulations involving different values of the coefficients l and k were performed and have been reported here.

1. k=**0.0004**, l=**0.2**
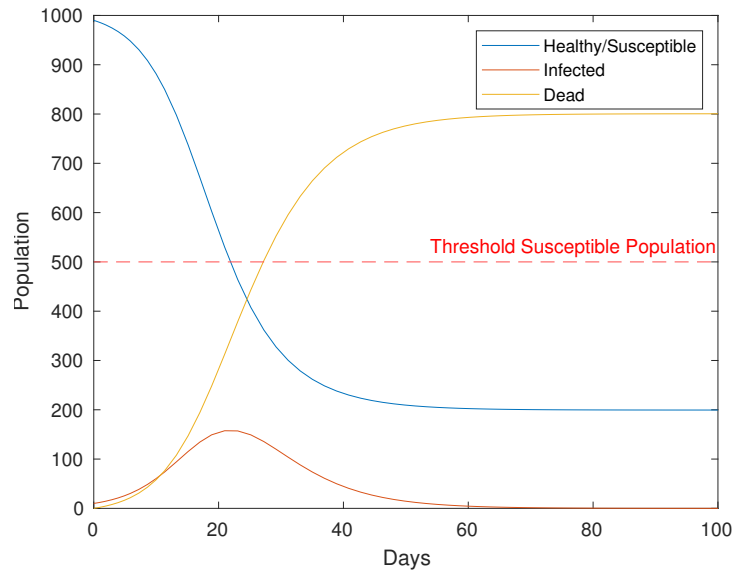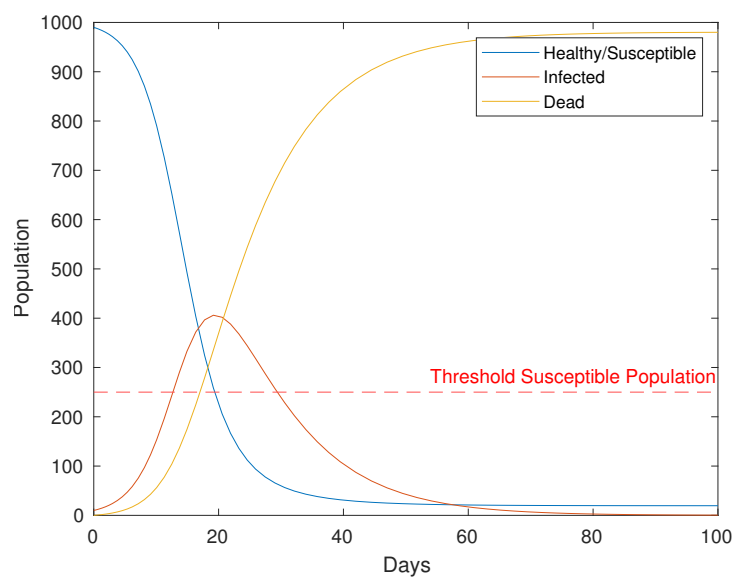

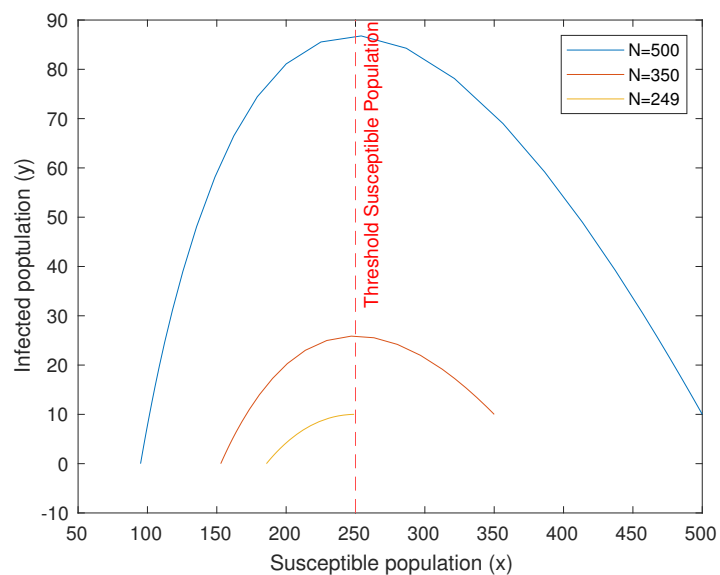Phase plots corresponding to different initial conditions:

Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)
0	990	10	0
21 (peak)	530	157	313
100 (end)	199	0	801

2. **$k=0.0004$, $l=0.1$**

Phase plots corresponding to different initial conditions:

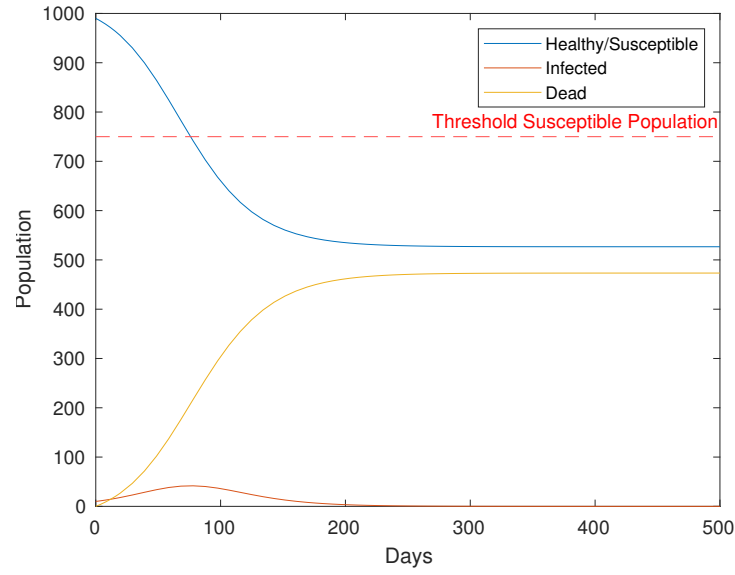| Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)
0	990	10	0
19 (peak)	259	406	335
100 (end)	20	0	980

3. $k=0.0001333$, $l=0.1$

Phase plots corresponding to different initial conditions:
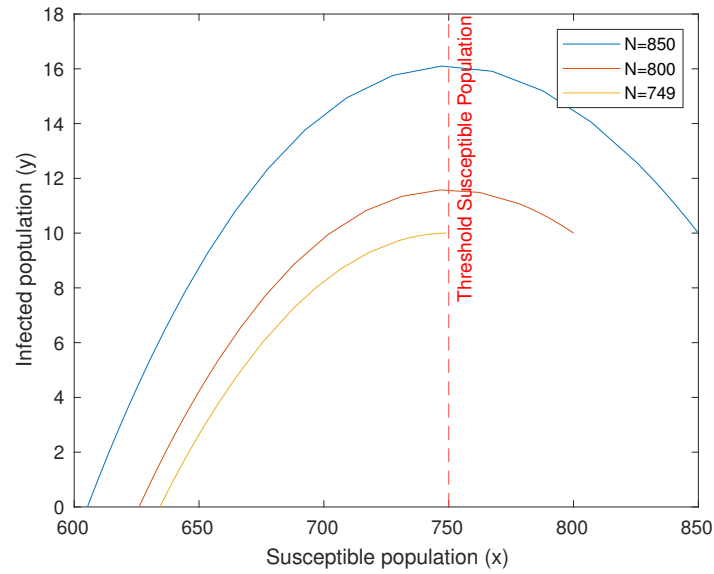
Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)
0	990	10	0
78 (peak)	741	42	217
325 (end)	527	0	473

2.2   Shortcomings and Potential Enhancements

As seen in the above simulations, the original Kermack-McKendrick Model, though a great triumph of its time, falls short of giving realistic predictions about the outcome of a pandemic. The two epidemiologists then published a series of papers between 1927 and 1939, improving upon their idea. Further work has been done by R. May and R. M. Anderson, expanding the study of epidemics to include several other factors like vaccination, varying potency of the infection for different age groups, etc.

In the context of qualitatively similar epidemics to the ongoing COVID-19 pandemic, the model is found wanting on the following points-

i) It is quite natural to assume that once someone gets infected, they will seek medical treatment. However, the model does not contain a population category for those who have recovered from the illness following treatment. Moreover, it does not take into account the fact that once a person has successfully recovered, they develop antibodies that protect them from getting infected again.

ii) The model fails to capture the "wave" nature of the ongoing epidemic. For example, India has already witnessed two distinct waves of the infection. However, no variation of the Kermack-McKendrick model predicts such waves for any values of k and l.

iii) An important aspect of disease control not accounted for by the model is vaccination. Vaccination is one of the most important means to curb the spread of an epidemic, as has been observed and repeatedly stressed upon during the ongoing COVID-19 pandemic. It is an integral part of the modern health care systems and must be incorporated in any model that aims to reliably predict the outcomes of an epidemic.

In an attempt to improve upon the shortcomings discussed above, the following sections examine each of them separately and suggest modifications that can be made to produce a more accurate mathematical model.

3   Treatment and Immunity after Recovery

Incorporation of medical treatment received by the sick population is found to be relatively straightforward. A new parameter h is introduced. This accounts for the recovery rate among the infected. It is defined as

$$h = 1 - l$$

i.e. (recovery rate)=1-(death rate)

The modified equations are as follows

$$\dot{x} = -kxy$$

$$\dot{y} = kxy - (l+h)y = kxy - y$$

$$\dot{z} = ly$$

$$\dot{r} = hy$$

where r is the number of people who have recovered from the illness.

Much like the original model, the total population is again considered closed with $\dot{x} + \dot{y} + \dot{z} = 0$.

The predictions of this modified model were assessed via the following MATLAB simulations involving different values of k and l.

Note: In the following plots, the Threshold Susceptible Population has not been represented due to it being of the order of 20 people (due to the different values of k and l assumed here), making the epidemic inevitable. The same reason has rendered the phase plots (n(Healthy/Susceptible) vs. n(Infected)) redundant and of little scientific interest. Hence, they, too, have been excluded.

1. k=**0.003**, l=**0.06**
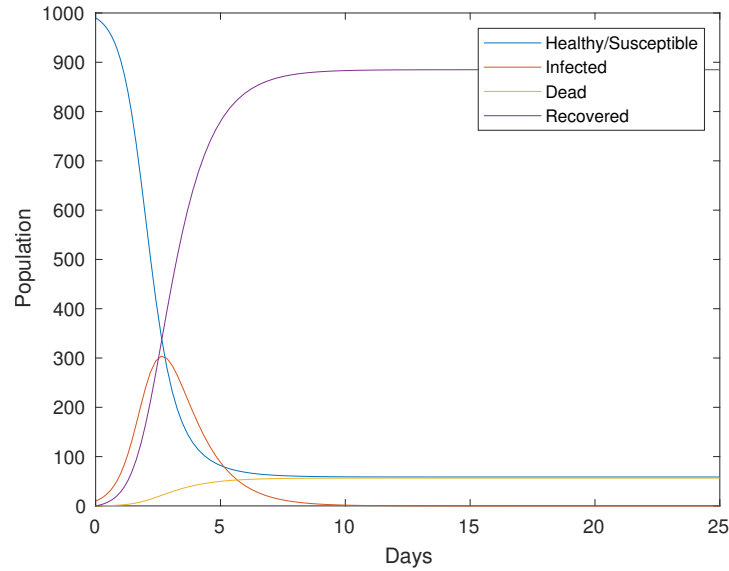
Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)	Recovered (r)
0	990	10	0	0
3 (peak)	343	304	21	331
20 (end)	59	0	56	885

2. k=**0.0018**, l=**0.1**
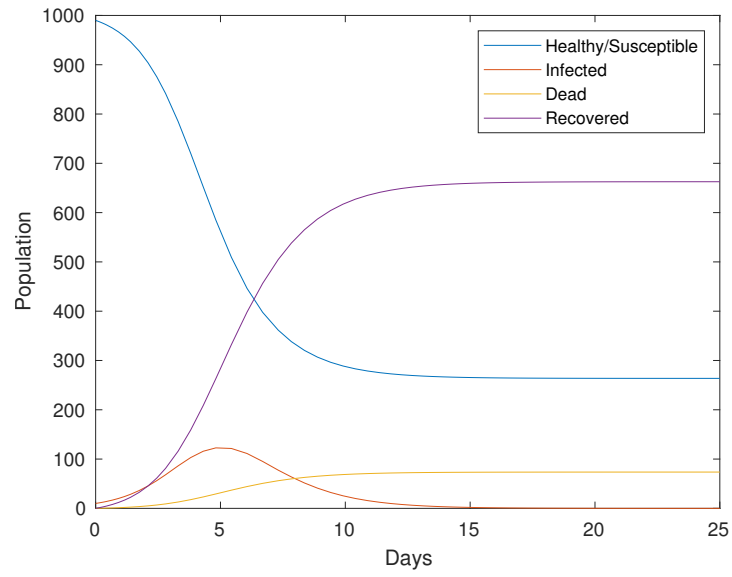
Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)	Recovered (r)
0	990	10	0	0
5 (peak)	585	123	29	263
20 (end)	264	0	74	662

3. $k=0.0025$, $l=0.15$
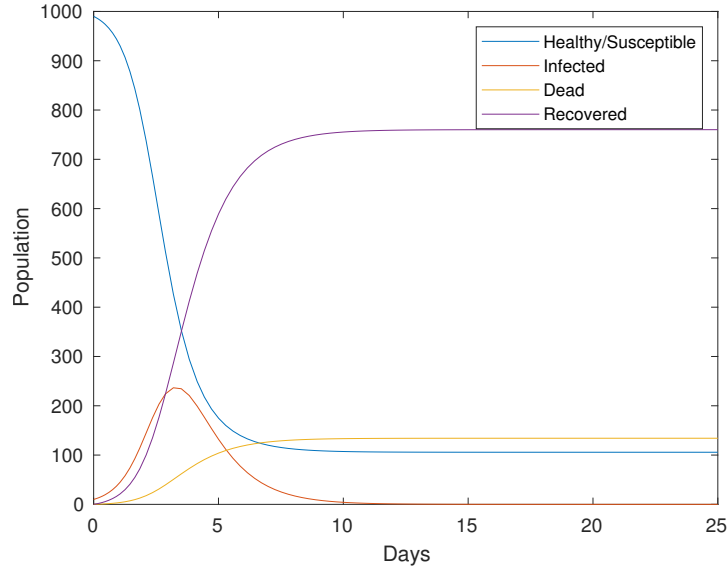
Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)	Recovered (r)
0	990	10	0	0
3 (peak)	427	236	51	286
20 (end)	106	0	134	760

In all of the above simulations, the initial conditions remained the same as those in Section 2 but the predictions of the post-epidemic state of the population were found to be much more realistic than those generated through the Kermack-McKendrick Model, with a maximum death toll of 134/1000 as compared to 980/1000 in the latter. It is worth noting that this was in spite of the fact that the infectivity coefficient, k, was increased by order of 10 in the modified models.

One major drawback of the modified model was that the infected population rose very steeply for the values of k considered above, reaching its peak in only three days and reduced just as quickly. For any lower values of k, the epidemic did not develop and quickly fizzled out. This behavior makes the modified model inaccurate while analyzing large population distributions like cities or countries, but it can prove to be useful when looking at small-scale variation of infected populations such as those in residential colonies and office complexes.

All in all, the introduction of the recovery coefficient h certainly gave much more reliable results than the 1927 model.

4   Testing the Effectiveness of Mass Vaccination

4.1   A Heuristic Model

A "wave-like" model for the epidemic requires a much more fundamental change to the Kermack-McKendrick Model. In the original equations, $\dot{x}$, $\dot{y}$, and $\dot{z}$ are independent of time. In this case, however, the infectivity coefficient k was considered to be a function of time.

$$k = k_0 + k_1 \sin^2\left(\frac{\pi t}{500}\right) \sin^2\left(\frac{\pi t}{60}\right)$$

which can be visualized trough the following plot
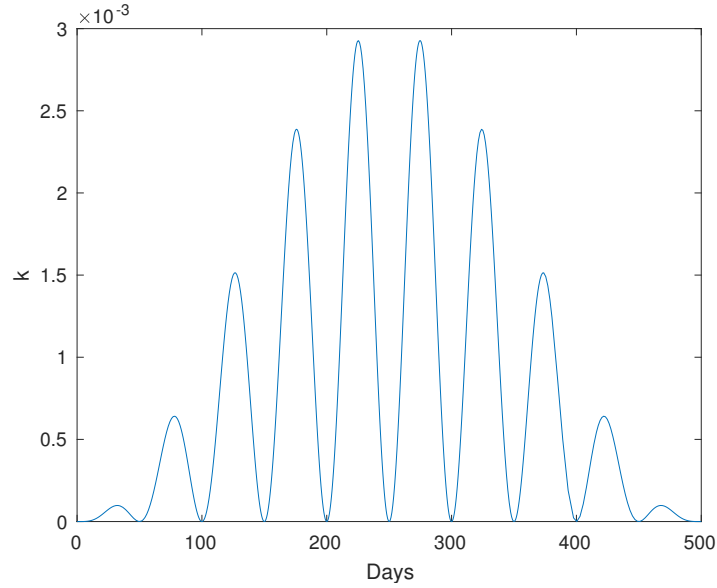
The epidemiological interpretation of this proposition is twofold:

i) Each crest represents a situation where there is no lockdown and people are moving about freely. The value of k decreases when lockdown is applied only to increase when it is lifted. This variation in activity causes changes in the rate of interaction between the susceptible and infected populations and, by extension, the infectivity coefficient k.

ii) Moreover, each peak represents a new variant of the pathogen, which is generated when it mutates. This mutation triggers the increase in k.
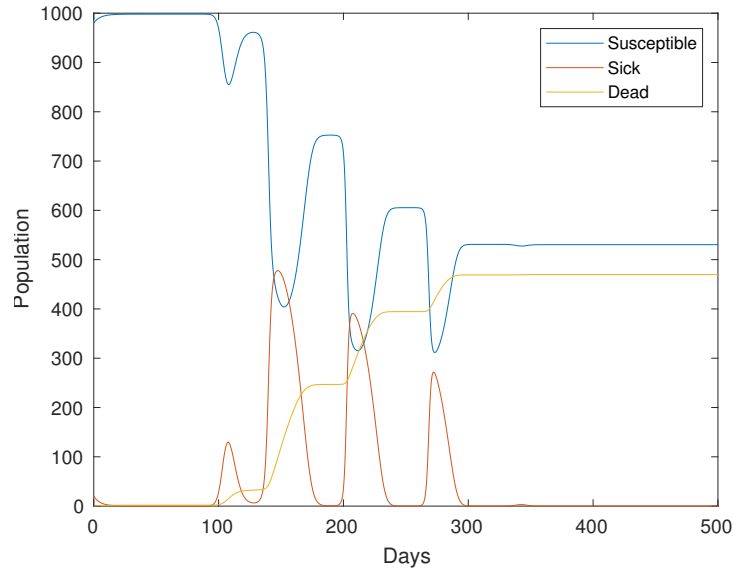
The resulting equations are as follows

$$\dot{x} = -kxy + hy$$

$$\dot{y} = kxy - y$$

$$\dot{z} = ly$$

It is important to note that here, the $+hy$ factor indicating recovery from the illness is being added back to x rather than an immune population r to account for the fact that someone recovering from one strain of the infection can catch another in a subsequent wave.

For $k = 0.00082 + 0.00245\sin^2\left(\frac{\pi t}{500}\right)\sin^2\left(\frac{\pi t}{60}\right)$ and $l = 0.0175$

Time (days)	Healthy/Susceptible (x)	Infected (y)	Dead (z)
0	980	20	0
108 (Peak: 1st wave)	855	130	15
147 (Peak: 2nd wave)	423	478	99
207 (Peak: 3rd wave)	327	391	282
272 (Peak: 4th wave)	314	272	414
500 (end)	530	0	470

The fact that the death toll rises to 470 by the end of the epidemic despite the meager death rate of 1.75% (much lower than any simulation above) highlights a fundamental consequence of recurring waves of infection. Even though each wave in itself has relatively low total deaths, their cumulative effects over 500 days cause widespread loss of life. Therefore, it becomes essential to suppress the magnitudes of these waves. One common means for achieving this is vaccination.

Taking this plot as a basis for a hypothetical epidemic, henceforth referred to as the Hypothesis, we can calculate the effectiveness of mass vaccination campaigns.

4.2   Mass Vaccination

A further modification needs to be made to the equations so that they can account for the subset of the population that has been vaccinated and is less likely to contract the infection.

This new set of equations is as follows

$$\dot{x} = -kxy + hy - c_1 x$$
$$\dot{y} = kxy - y + p_1(kv_1 y) + p_2(kv_2 y)$$
$$\dot{z} = ly$$
$$\dot{v_1} = c_1 x - c_2(c_1 x) - p_1(kv_1 y)$$
$$\dot{v_2} = c_2(c_1 x) - p_2(kv_2 y)$$

where two new subsets of the total population are introduced, v_1 and v_2. v_1 is the number of people who have received only the first dose of the vaccination, while v_2 is the number of double vaccinated people. x, y, and z retain their meanings from the Kermack-McKendrick Model.

As can be verified by $(\dot{x} + \dot{y} + \dot{z} + \dot{v_1} + \dot{v_2}) = 0$, the total population is again considered to be closed.

Here-

- $c_1 \equiv$ the rate at which healthy people receive the first dose of the vaccination

- $c_2 \equiv$ the rate at which singly vaccinated people receive the second dose of the vaccination

- $p_1 \equiv$ the probability that a singly vaccinated person catches the infection

- $p_2 \equiv$ the probability that a double vaccinated person catches the infection

Following are three simulations with different values of the parameters c_1, c_2, p_1, p_2 and a brief analysis of the aftermath of the epidemic in each case.
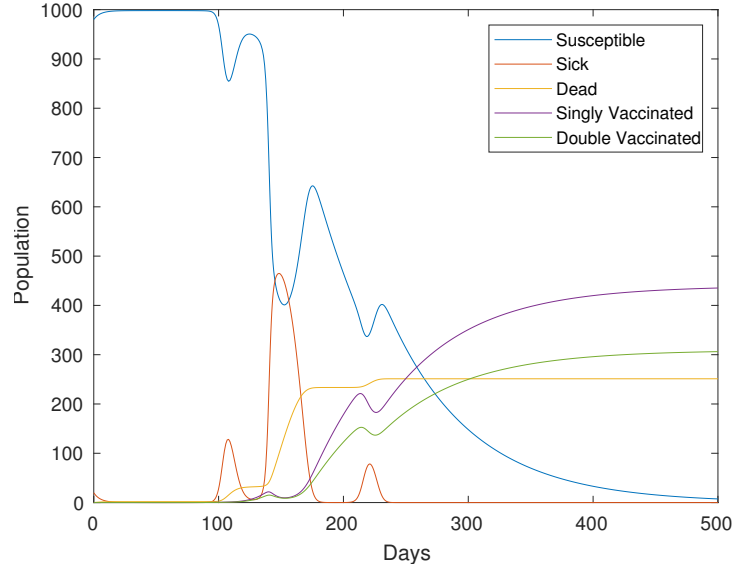
1. $c_1 = \frac{0.01}{1 + e^{15 - 0.1t}}$, $c_2 = 0.3$, $p_1 = 0.3$, $p_2 = 0.3333$
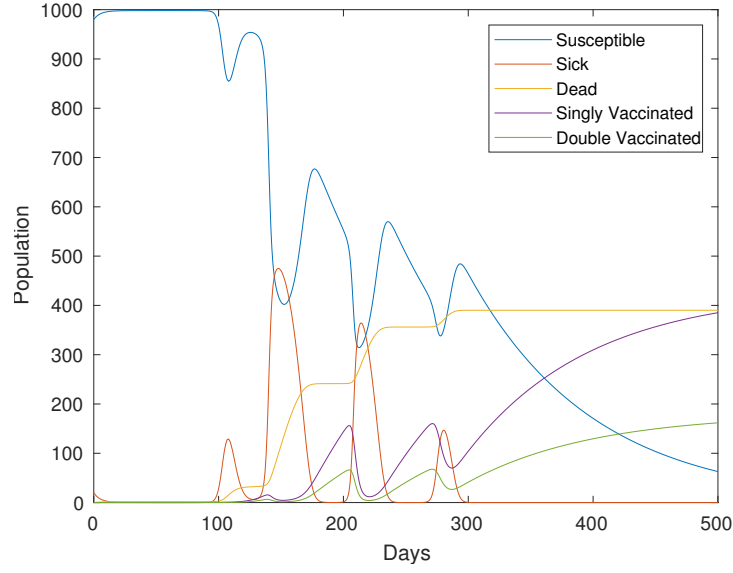
Time (days)	Susceptible (x)	Infected (y)	Dead (z)	Singly Vaccinated (v_1)	Double Vaccinated (v_2)
0	980	20	0	0	0
108 (Peak: 1st wave)	855	129	15	1	0
148 (Peak: 2nd wave)	417	475	101	5	2
214 (Peak: 3rd wave)	317	364	280	29	10
280 (Peak: 4th wave)	351	147	371	94	37
500 (end)	63	0	390	385	162

At the end of this simulation, the death toll is 390, which is 80 less than that in the Hypothesis, a reduction of 20%.

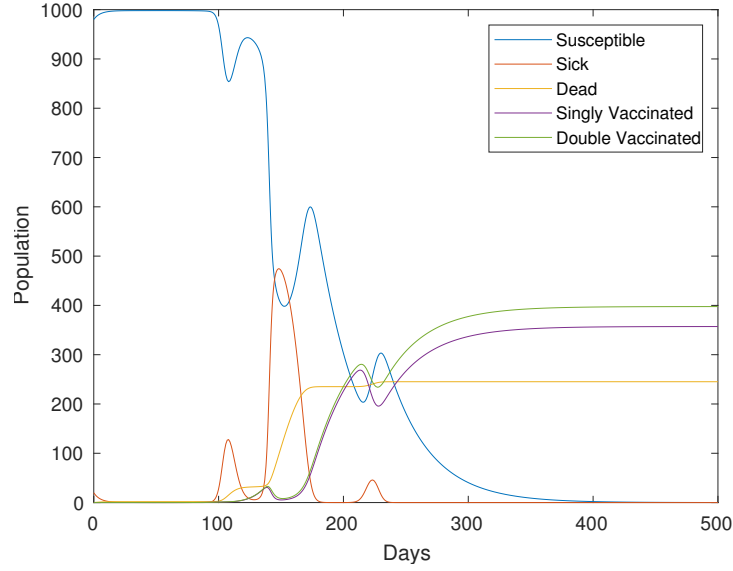2. $c_1 = \frac{0.015}{1+e^{15-0.1t}}$, $c_2 = 0.4$, $p_1 = 0.2$, $p_2 = 0.15$

Time (days)	Susceptible (x)	Infected (y)	Dead (z)	Singly Vaccinated (v_1)	Double Vaccinated (v_2)
0	980	20	0	0	0
108 (Peak: 1st wave)	855	128	15	1	1
149 (Peak: 2nd wave)	414	465	101	11	9
221 (Peak: 3rd wave)	342	78	242	196	142
500 (end)	8	0	251	435	306

At the end of this simulation, the death toll is 251, which is 219 less than that in the Hypothesis, a reduction of 46.6%.

3. $c_1 = \frac{0.03}{1+e^{15-0.1t}}$, $c_2 = 0.5$, $p_1 = 0.5$, $p_2 = 0.35$

Time (days)	Susceptible (x)	Infected (y)	Dead (z)	Singly Vaccinated (v_1)	Double Vaccinated (v_2)
0	980	20	0	0	0
108 (Peak: 1st wave)	854	128	15	2	1
148 (Peak: 2nd wave)	413	474	98	6	9
223 (Peak: 3rd wave)	258	46	241	211	244
500 (end)	0	0	245	357	398

At the end of this simulation, the death toll is 245, which is 225 less than that in the Hypothesis, a reduction of 47.8%.

It can be inferred from the above simulations that mass vaccination is indeed an effective strategy to combat epidemics. The decrease in death count was found to be proportional to the increase in the rate of vaccination and the effectiveness of the vaccines.

These simulations can also be used to illustrate *how* vaccines manage to stop the spread of infection. As the total number of vaccinated people increases, the susceptible population decreases and eventually goes below the threshold (see **Section 2**) required for the occurrence of an epidemic. Thus, the end of this epidemic is a direct consequence of the original work of Kermack and McKendrick.

5   Conclusions and Discussion

The effects of the several modifications introduced to the Kermack-McKendrick Model in this paper can be summarized as follows

1. Introduction of the recovery parameter h produced much more realistic death rates than the original model, an average death count of 88 out of 1000 people as opposed to 751 out of 1000 people for the original model. The average number of active cases at the peak of the epidemic were observed to increase mildly, from 202 to 221. This may be attributed to the increased values of the infectivity coefficient k.
The recovery parameter implements the phenomena that once a patient recovers from the illness, they develop immunity against it and neither spread nor catch the infection again. This is a common feature of many prevalent diseases and its inclusion enhances the reliability of the predictions of the Model.

2. In order to generate a model that could resemble the ongoing COVID-19 epidemic, the infectivity coefficient was considered to be a function of time. On generating a sample epidemic using these modified equations, the effectiveness of vaccination was tested. The simulations showed an average decrease of 175 people in the total death count, amounting to 17.5% of the initial population.
The two characteristic features of the ongoing pandemic captured by this model were the multiple waves of infection and two-dose vaccination scheme. The modifications also accounted for the fact that a single dose of vaccine only leads to partial immunity and double vaccination provides better protection against the infection.

Thus, modifications introduced here were found to enhance the accuracy of the model on several accounts.

It must be noted, however, that the modifications introduced above are not absolute, but leave room for further improvements. Some some such assumptions are

- From the outset the models consider a closed population. In reality, this is not found to be the case. Several parameters like migration, birth and death rates lead to small but considerable changes in the total population over time.

- The recovery coefficient h depends on many factors like GDP of the country, development of public health care system, etc. It may not even be constant over time.

- The modification of infectivity k in **Section 4** is only a convenient mathematical formulation which may not exactly represent the processes creating waves of infection. Further tests and analysis is necessary to put this assumption on a stronger footing.

- Lastly, the resemblance to the COVID-19 epidemic aimed at in **Section 4** is only heuristic. The model tries to illustrate the key features of the epidemic, but with several idealizations. A crucial and unique

factor of the Coronavirus not considered here is the 14-day incubation period. Another aspect neglected is that of quarantining the infected people to reduce the spread of infection. Inclusion of these is sure to provide more accurate results.

References

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Anderson, R. M. (1991), Discussion: The Kermack-McKendrick epidemic threshold theorem, *Bulletin of Mathematical Biology*,Volume 53(1), Pages 3-32, ISSN 0092-8240, https://doi.org/10.1016/S0092-8240(05)80039-4

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