A MATHEMATICAL MODEL IN THE TIME OF COVID-19

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ABSTRACT

A novel coronavirus, called COVID-19, was found in Wuhan, China, in December 2019 and has spread to various urban areas in China as well as to 24 different nations. The number of confirmed cases is proliferating on a daily basis and has been declared a pandemic lately. In this brief current study, we present a new mathematical model where we show how protection, exposure, immigration, death and cure rates affect the healthy and infected population with time.

1 Introduction

On 31 December 2019, the World Health Organization (WHO) reported the presence of a novel coronavirus (2019-nCoV) in Wuhan City, Hubei Province of China. It was named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by International Committee on Taxonomy of Viruses on 11 February, 2020. The outbreak was first identified in Wuhan with most early cases being reported in the city and later spread to the other countries in an alarming rate. There are several theories behind the origin of the virus - it might be bat origin [3], or might related to a seafood market exposure [4]. International travel of any form has been declared a potential reason for the fast spread of the virus [5]. So, immigration has a severe impact on the severity of spreading of this virus. There are a lot of ongoing research where mathematical models have been fabricated to predict confirmed cases in future, to study transmission dynamics and so on. But, as of yet, no such study has been done to show how protection, exposure, immigration, death and cure rates affect the healthy and infected population with time. This study has not been tested on any real data. The model is just an indication to show what might happen if we do not control the immigration of individuals in the community.

2 Model

The mathematical model that we used in this paper is inspired from the classic Lotka-Volterra model [1, 2] for simulating predator-prey dynamics. The classic model has been suitably modified to build the healthy-infected individual population dynamics model.

The healthy individual population is given by $h(t)$ at time t . The infected individual population is given by $i(t)$ at time t . The infection rate is given by b which is $(1 - \text{protection rate})$. The immigration rate of healthy individuals is given by a . The immigration rate of infected individuals is given by c . The death rate is given by d and the cure rate is given by e .

The population dynamics are dictated by the following state-space differential equations:

$$\frac{dh(t)}{dt} = ah(t) - bh(t)i(t) + ei(t) \quad (1)$$

$$\frac{di(t)}{dt} = bh(t)i(t) + ci(t) - di(t) - ei(t) \quad (2)$$

3 Simulations and Results

We simulated some results using different values of the model parameters and plotted the outcomes. For simulation purposes, in each of the cases we will start with equal number of healthy and infected population, that is, each will be

Figure 1: Dynamics with $a = 0.0$, $b = 0.3$, $c = 0.5$, $d = 0.5$, $e = 0.5$

Figure 2: Dynamics with $a = 0.0$, $b = 0.1$, $c = 0.5$, $d = 0.5$, $e = 0.5$

50 percent (or 0.5) of the total population. The x-axis of the plot refers to the time in days and the y axis refers to the percentage of population.

3.1 Case 1

In this case, we consider the values of $a = 0.0$, $b = 0.3$, $c = 0.5$, $d = 0.5$, $e = 0.5$ and we see the dynamics of healthy and infected population in fig 1. We see that it takes almost 200 days for the infected population to reach a value of 0.

3.2 Case 2

In this case, we consider the values of $a = 0.0$, $b = 0.1$, $c = 0.5$, $d = 0.5$, $e = 0.5$ and we see the dynamics of healthy and infected population in fig 2. Here, we see that increasing the protection rate, thus decreasing the rate of infection only the infected population reaches 0 in almost 130 days.

Figure 3: Dynamics with $a = 0.0$, $b = 0.1$, $c = 0.5$, $d = 0.5$, $e = 0.7$

Figure 4: Dynamics with $a = 0.0$, $b = 0.1$, $c = 0.0$, $d = 0.5$, $e = 0.7$

3.3 Case 3

In this case, we consider the values of $a = 0.0$, $b = 0.1$, $c = 0.5$, $d = 0.5$, $e = 0.7$ and we see the dynamics of healthy and infected population in fig 3. Here, increasing the protection rate and the recovery or the cure rate together gives better results - in almost 80 days the infected population reaches 0.

3.4 Case 4

In this case, we consider the values of $a = 0.0$, $b = 0.1$, $c = 0.0$, $d = 0.5$, $e = 0.7$ and we see the dynamics of healthy and infected population in fig 4. Here, we see that increasing the protection rate and the recovery or the cure rate and decreasing the immigration rate to 0, gives even better results - in almost 60 days the infected population reaches 0.

Figure 5: Dynamics with $a = 0.05$, $b = 0.3$, $c = 0.6$, $d = 0.5$, $e = 0.5$ Figure 6: Dynamics with $a = 0.05$, $b = 0.3$, $c = 0.2$, $d = 0.5$, $e = 0.5$

3.5 Case 5

In this case, we consider the values of $a = 0.05$, $b = 0.3$, $c = 0.6$, $d = 0.5$, $e = 0.5$ and we see the dynamics of healthy and infected population in fig 5. Here the number of days has been increased to 300. In this particular case we see that an increase in the immigration rate leads to instability in the system. The eigen values of the system are 0.2280 and 0.0 respectively. Positive eigen value make the system unstable. It can be easily seen that although initially there is a decrease in the population of infected individuals, the value rises exponentially with time afterwards and the population after approximately 270 days.

3.6 Case 6

In this case, we consider the values of $a = 0.05$, $b = 0.3$, $c = 0.2$, $d = 0.5$, $e = 0.5$ and we see the dynamics of healthy and infected population in fig 6. Here the number of days has been increased to 3000. We see there are some fluctuations in the dynamics before the steady states are reached. The eigen values of the system are 0.0 and -0.1128 respectively.

Figure 7: Phase portrait with $a = 0.05$, $b = 0.3$, $c = 0.2$, $d = 0.5$, $e = 0.5$

The phase space plot in fig. 7 shows the convergence of the system to steady state. So, decreasing the immigration rate of infected individuals, the system becomes stable and reaches steady state.

4 Conclusions

The simulations and model used in this particular research are not properly estimated and compared with respect to the real data. Even though the numbers can be misleading, the sole idea of this research was to give an idea about how varying some factors we can control the population of healthy and infected individuals. In this particular research the trend of the population dynamics is important. It can be easily seen that by increasing protection and cure rates and decreasing the immigration rate we can successfully decrease the number of infected individuals to 0 eventually. This particular model can be applied to any social gathering as well in a country-wide or province-wide setting.

References

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