Investigating and Predicting the Future Trajectory of COVID-19 in the Region of Waterloo

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Abstract

The COVID-19 pandemic has caused drastic chaos in the society and burdens on the global health systems in the past three years. Now with cases settling down and economy reopening, it is worth the effort to ask how the future trajectory of the disease looks like so preparations can be made beforehand. In this study, we developed an ODE based compartmental model as an attempt to investigate the future dynamic of COVID-19 in the Region of Waterloo. It was found that increasing vaccination rate can significantly help to delay and lower the major peaks of cases initially, while increasing vaccine effectiveness has no significant effect. As a result, it is hoped that public health agencies can focus on increasing vaccination coverage even with older vaccines that are less effective against the new variants so that future big resurgence of cases can be prevented.

Keywords: COVID-19; Mathematical model; Epidemiology; Vaccination

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Introduction

The SARS-CoV-2 virus, a member of the subgenus *Sarbecovirus*, genus *Betacoronavirus*, and family *Coronaviridae* [1], was first emerged in late 2019 and is responsible for the COVID-19 global scale pandemic that places significant burdens on the health systems of almost every single nation for the past three years [2, 3]. As of March 2023, over 760 million people have been infected with COVID-19 and over 6 million people have died from it, making it the annual leading cause of death for some nations [4].

Now with the implementation of vaccinations and gaining of natural immunity around the world, the SARS-CoV-2 virus poses a much smaller threat than it did in early 2020 [5]. However, the arrival of novel variants remains a challenge for the globe as they are still capable of causing spikes in infection numbers by overcoming established immunities and resulting in re-infections [6]. There have been several major variants of concern, including Alpha (first appeared in 2020), Delta (first appeared in 2021), and Omicron (first appeared in early 2022), of the SARS-CoV-2 virus since the emergence of the original strain [7-9]. Those variants appear as a result of their spread in the population as each replication of the virus introduces potential novel mutations to be selected to improve their overall fitness [10]. Studies have shown that this increase in fitness of the novel variant is evident in the form of increasing infectivity due to the evolutionary arm-race between the virus and host, resulting in each variant to be more infectious and spreads faster than its previous ancestors [11, 12]. Because of this, many studies have predicted that as the world reopens, more variants of SARS-CoV-2 with higher infectivity will emerge in the future, resulting in the viruses keep circulating within the population [13, 14]. Therefore, since symptoms of COVID-19 can be still discomforting for most people and even severe for the elderly, infection peaks caused by the novel variants in the future can result in a lot of undesirable consequences such as a loss of productivity due to people taking sick leaves and an influx of patients to the hospital.

As a result, it is critical for the public to understand how often the world will see the infection number to rise so that appropriate actions can be taken by the public health authorities to minimize the effect. Thanks to the advancement of computational and numerical simulations, such predictions can be done by employing mathematical epidemiology models and analyzing their behaviours given various conditions. By having a good model, epidemiologist can simply tweak the parameters to evaluate the effects of various public health actions, which can be informative and provide a solution for the government agencies on how they should make the most appropriate decisions [15, 16]. As a result, this study aims to create a mathematical ordinary differential equation (ODE) based model to predict the future trajectory of COVID-19 cases in the Region of Waterloo by using parameter values estimated from literature and data available from the Region of Waterloo Public Health. It is hoped that this model can provide some insights into how the pandemic will evolve in the future so that the public can be prepared before the infection resurges.

Methods

Model Descriptions

In mathematical epidemiology, a common model to describe the population dynamics of a disease that can reinfect people who have had it before is known as a Susceptible-Infected-Recovered-Susceptible (SIRS) model [17]. In particular, this compartmental model employs three different species: susceptible individuals, infected individuals, and recovered individuals. Susceptible individuals, whose population proportion is denoted with *S*, can be infected by the infected individuals, whose population proportion is denoted with *I*. After a period of infection, those infected individuals will become recovered individuals, whose population proportion is denoted with *R*, and are immune from the disease. Finally, after a period of immunity, those recovered individuals will become susceptible again. Assuming that the population size is constant (i.e.: there is no birth, death, or migration in the population), the above mentioned model can be formulated through **equation set (1)**, where τ is the rate at which an infected person transmits the disease to a susceptible person, δ is the rate at which an infectious person recovers, and ω is the rate at which a recovered person loses immunity and becomes susceptible [18].

$$\begin{aligned} \frac{d}{dt}S(t) &= -\tau I(t)S(t) + \omega R(t) \\ \frac{d}{dt}I(t) &= \tau I(t)S(t) - \delta I(t) \\ \frac{d}{dt}R(t) &= \delta I(t) - \omega R(t) \end{aligned} \tag{1}$$

However, this model is not suitable for describing COVID-19 dynamics for various reasons. Firstly, vaccination has been largely implemented as an effort to control the pandemic [19], and new vaccines are constantly being developed to fight the new variants [20]. Therefore, we introduced a new variable, the vaccinated individuals (represented by *V*). We assumed that vaccines are introduced to the population at a constant rate (α) and is proportional to the population of suspectable individuals, and the vaccine has an effectiveness (ϵ) that is the same for all vaccinated individuals. Lastly, the vaccinated

individuals lose their immunity at the same rate as an individual who acquires their immunity through infection (ω). The modified model then becomes **equation set (2)**.

$$\begin{aligned}
\frac{d}{dt}S(t) &= -\tau I(t)S(t) + \omega R(t) + \omega V(t) - \alpha S(t) \\
\frac{d}{dt}I(t) &= \tau I(t)S(t) + \tau(1-\epsilon)I(t)V(t) - \delta I(t) \\
\frac{d}{dt}R(t) &= \delta I(t) - \omega R(t) \\
\frac{d}{dt}V(t) &= \alpha S(t) - \tau(1-\epsilon)I(t)V(t) - \omega V(t)
\end{aligned} \tag{2}$$

In addition, τ is a constant in this model, meaning that the rate of infectivity never changes. To account for the increasing in infectivity, τ was modified to be a function of time (i.e.: $\tau(t)$). **Equation set (3)** outlines the final SIRVS (Susceptible-Infected-Recovered-Vaccinated-Susceptible) model (**Figure 1**) used in this study.

$$\begin{aligned}
\frac{d}{dt}S(t) &= -\tau(t) I(t)S(t) + \omega R(t) + \omega V(t) - \alpha S(t) \\
\frac{d}{dt}I(t) &= \tau(t) I(t)S(t) + \tau(t)(1-\epsilon)I(t)V(t) - \delta I(t) \\
\frac{d}{dt}R(t) &= \delta I(t) - \omega R(t) \\
\frac{d}{dt}V(t) &= \alpha S(t) - \tau(t)(1-\epsilon)I(t)V(t) - \omega V(t)
\end{aligned} \tag{3}$$

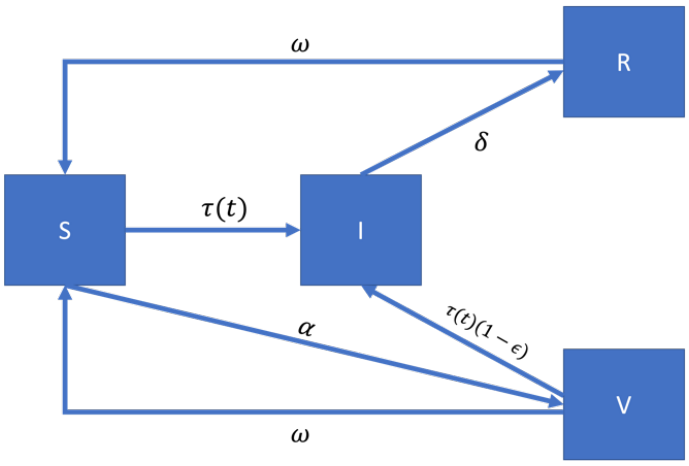

Figure 1: Schematic diagram for the SIRVS model. This diagram shows the interactions between Susceptible (S), Infected (I), Recovered (R), and Vaccinated (V).

Parameter Estimations

Most of the parameters in this model are well documented in the literatures and outlined in **Table 1**.

Table 1: Estimation of parameter values based on existing literatures.

Parameter	Literature Reported Value	Parameter Value	Reference
α	4356 vaccines were given in the Region of Waterloo in the month of February 2023. The population in the region is 630,978.	$\frac{4356}{630978} \approx 0.007 \left(\frac{people}{months}\right)$	[21]
ω	Strong immunity lasts for about 6 months.	$\frac{1}{6} \approx 0.17 \left(\frac{people}{months}\right)$	[22]
ϵ	Long term effectiveness is about 62% against infections for COVID-19 vaccine.	0.62	[23]
δ	Most people recover within 10 days.	$\frac{1}{10/30} = 3 \left(\frac{people}{months}\right)$	[24]

In addition, we assumed that there would be one new SARS-CoV-2 variant that has a higher rate of infectivity emerging after a certain period of time. To capture this dynamic, the rate of infectivity ($\tau(t)$) is defined in **equation (4)**:

$$\tau(t) = \tau^o + \lfloor t/\sigma \rfloor \times \zeta \quad (4)$$

where ζ is the rate at which the rate of infectivity increases each year, σ is the mean duration time of a virus remain dominant before a variant takes over, and τ^o is the original infectivity.

We assumed that one new variant emerges once a year ($\sigma = 12$) and the rate of infectivity increases by the same amount each year, and the rate (ζ) is related to the base reproductive (R_0) value of each variant [18]. This relationship is outlined in **equation (5)**,

$$\zeta n + \tau^o \approx \delta R_0 \quad (5)$$

where n is the number of times that the rate of emergence jumps (n = 0, 1, 2, or 3) and can be calculated by $\left\lfloor \frac{t}{\sigma} \right\rfloor$. Therefore, to estimate ζ, we used the R_0 values (**Table 2**) for various SARS-CoV-2 variants and performed a linear regression on those values time the rate of recovery versus time in years.

Table 2: R_0 and δR_0 values for various SARS-CoV-2 variants.

Variant	Average R_0	δR_0	Reference
Original variant (n=0)	2.00	6.00	[25]
Alpha (n=1)	3.50	10.50	[26]
Delta (n=2)	5.08	15.24	[27]
Omicron (n=3)	9.50	28.50	[28]

The slope for the linear regression (ζ) is 7.224, and the y-intercept (τ^o) is 4.224.

Initial Conditions

Several initial conditions were used in the simulation, and their situations are corresponding to:

- Shortly after an infection peak, where some individuals are infectious, yet most of them have just recovered (i.e.: *S(0) = 0, I(0) = 0.20, R(0) =0.80, V(0) = 0*)
- At the beginning of an infection peak but with high vaccination rate (i.e.: *S(0) = 0.30, I(0) = 0.20, R(0) =0, V(0) = 0.50*)
- At the end of an infection peak but with high vaccination rate (i.e.: *S(0) = 0.05, I(0) = 0.25, R(0) =0.40, V(0) = 0.30*)
- Long after an infection peak, where most all individuals are susceptible and not infected or vaccinated and some of all individuals are still infectious (i.e.: *S(0) = 0.90, I(0) = 0.10, R(0) = V(0) = 0*)

Analysis for the Model

We used Python to generate a time series plot for this model, with various initial conditions to investigate the prediction of different conditions by the model. In addition, we also generated power spectra of the infected individuals by using fast Fourier transform (FFT) to obtain the frequency of resurgence with various mean duration time of virus (σ). Last but not the least, different vaccination rates (α) and different vaccination effectiveness (ϵ), which are the two parameters that humans could influence, were used to determine their effect on the population of the infectious individuals and investigate the effect of different levels of public health responses. All the Python codes used to generate those simulation results are available in **Supplementary Material**.

Results

Several time series plots with different initial conditions corresponding to the ones listed in **Methods** are shown in **Figure 2**. Those simulations were all run with the default set of parameters outlined in **Table 1** and estimated from **Table 2**. Those simulations provide an intuitive understanding of the dynamics of the model given the current estimated parameters.

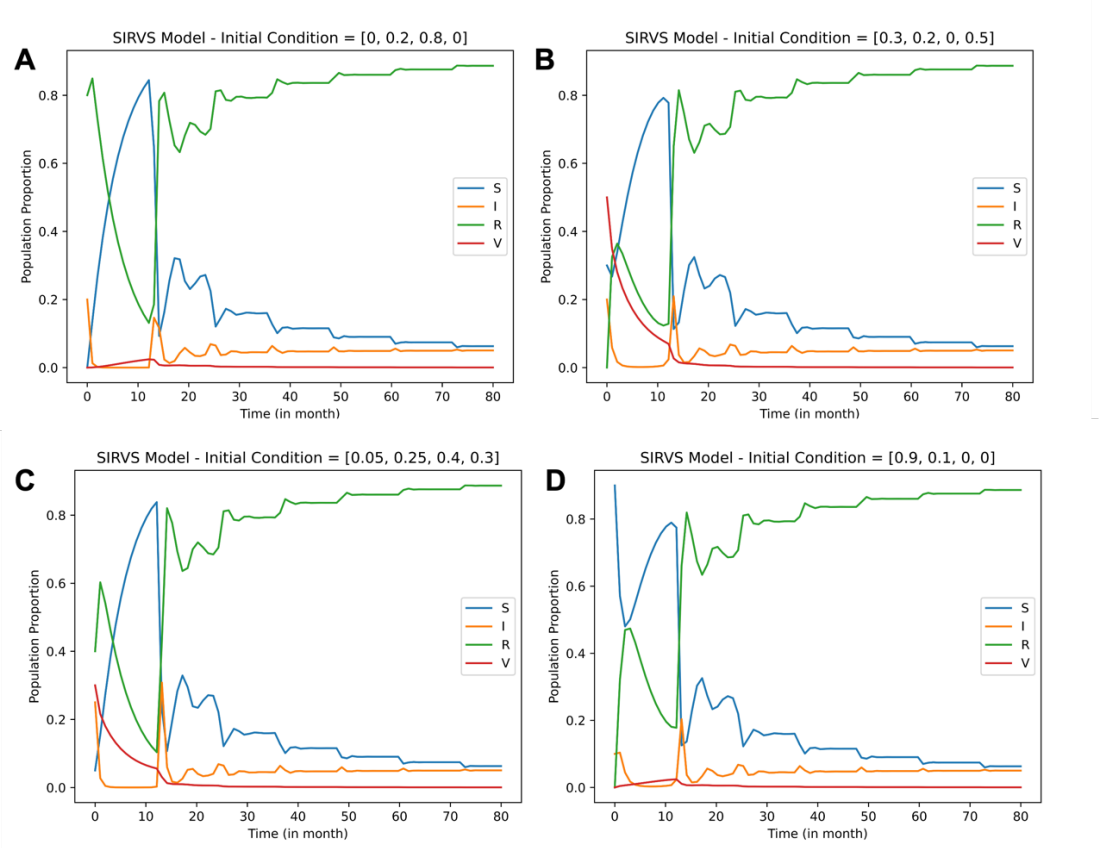

Figure 2: Time series plot by simulating the model with different initial conditions. The initial conditions correspond to the situations that happen A) shortly after an infection peak, B) at the beginning of an infection peak with high vaccinated population, C) at the end of an infection peak with high vaccination rate, and D) long after an infection peak.

In order to investigate the period of resurgence of disease as well as whether the mean duration time of virus would have an effect, a representative initial condition *([S(0), I(0), R(0), V(0)] = [0.9, 0.1, 0, 0]*) was chosen and several power spectra were generated with different mean duration time of virus (σ, **Figure 3**). Finally, two parameters, vaccinated rate (α) and effectiveness (ϵ), were varied to investigate the effect of different public health responses. The time series plots and the steady state proportion plots of the infected individuals for various α and ϵ are show in in **Figure 4** and **Figure 5**, respectively, with the same initial condition as the power spectra.

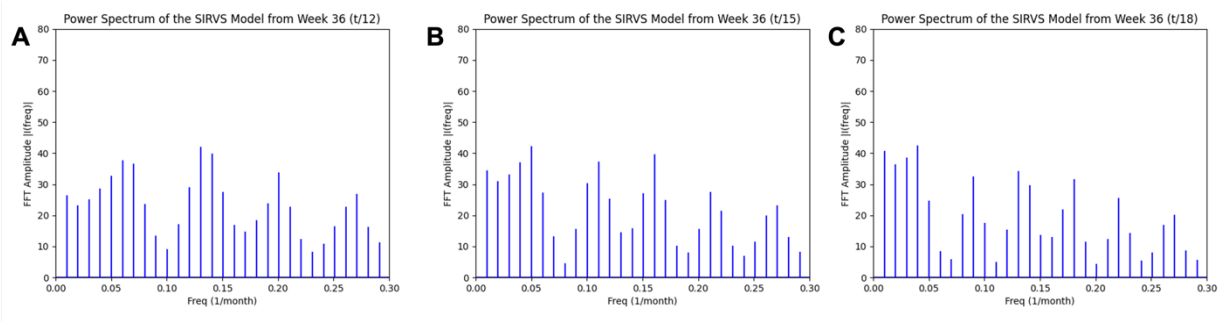

Figure 3: Power spectra of the SIRVS model with various mean duration time of a virus (σ). The power spectrum of $\sigma = 12$ is shown in A), the power spectrum of $\sigma = 15$ is shown in B), and the power spectrum of $\sigma = 18$ is shown in C). The plots were constructed by taking the fast Fourier transform (FFT) of the infected data points.

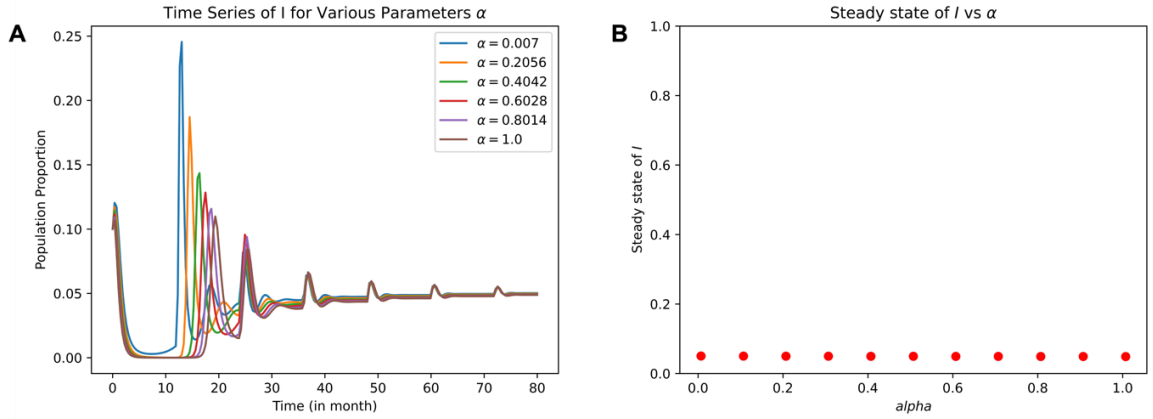

Figure 4: Simulation results of varying vaccinated rate (α) of the model. A) Time series plots of the proportion of the infected individual (*I*) of various α value, ranging from 0.007 (current value) to 1.0. B) The steady state values of *I* when simulated with various α values.

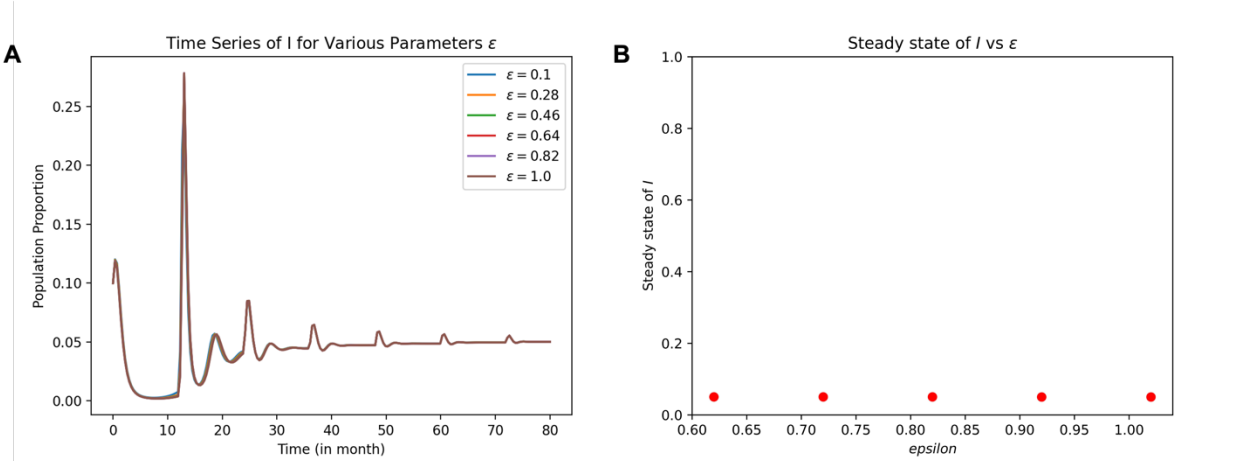

Figure 5: Simulation results of varying vaccine effectiveness (ϵ) of the model. A) Time series plots of the proportion of the infected individual (*I*) of various ϵ value, ranging from 0.1 (current value) to 1.0. B) The steady state values of *I* when simulated with various ϵ values.

Discussion

SIRVS Model is Not Sensitive to Initial Conditions

Some models are mathematically known to be chaotic as they are sensitive to initial conditions, making predictions about the future dynamics difficult [29]. Therefore, it is important to identify if this SIRVS model is chaotic before we can trust the prediction it makes. From the time series plot in **Figure 2**, it is evident that regardless of the initial condition, the long-term behaviours of the model are identical as they share similar dynamics and have the same steady states. In particular, all those simulations predict that there would be a relatively large peak of the infected individuals in about a year since the initial condition, followed by various small peaks that occur after the initial big peak. In addition, the sizes of the peak are decreasing as time progresses and the disease stabilizes, making the first big peak the major concern when it comes to pandemic control and prevention. This simulation result indicates that based on the present nature of the virus and public health response, the dynamics in the future will be very similar regardless of which initial situation that the Region of Waterloo is current in with respect to each category of the population. This means that the system described in the study is not chaotic in nature, and therefore predictions can be made without known the exact real-life initial condition.

Period of Resurgence Depends on the Mean Duration Time of Virus (σ)

It is important to understand how often the society will see a resurgence of cases. To do this, we performed FFT on the simulation data points for the infected individuals to see which frequencies have the highest contribution. The sampling period was set to be beyond week 36 to sample the long-term dynamics once the infection settles. In addition, the highest frequency that can be detected was set to be 0.3 (about 3 months period) to reduce noise, and frequencies starting from 0.08 (period shorter than 12 months) were noted to investigate the yearly dynamic. Based on the power spectrum for our initial assumption ($\sigma = 12$) (**Figure 2A**), it is evident that the two largest peak frequencies (in month^{-1}) are found to be around 0.2 and 0.13. This means that the periods of resurgence for the disease are $\frac{1}{0.2} \approx 5$ months and $\frac{1}{0.12} \approx 8$ months. This suggests that a surge in case

will be observed twice a year, like some studies have found over the course of the pandemic [30]. In fact, despite the different σ values used (**Figure 2B** and **Figure 2C**), all power spectra indicate that there are at least two peaks, indicating a surge in case at least twice with two different frequencies in a year. However, it is worth noting that changing σ would have an effect on the frequencies of resurgence of cases, as the peaks in **Figure 2B** with $\sigma = 15$ are found to be at 0.16 month^{-1} (corresponding to 6 months) and 0.11 month^{-1} (corresponding to 9 months), while the peaks in **Figure 2C** with $\sigma = 18$ are found to be at 0.13 month^{-1} (corresponding to 8 months) and 0.09 month^{-1} (corresponding to 11 months). This indicates that the period of resurgence is longer with a longer virus mean duration time. As a result, if the society keeps the rate of emergence of new variants lower, which can be accomplished through measures such as vaccinations [31], resurgence of cases would be delayed to allow the society to have more time to respond to the threat of the new variant.

Varying Vaccination Rate Has an Effect on the Peak of the First Outbreak

As an effort to investigate more on the effect of vaccination, different vaccination rates (α) were tested to see the effect on the proportion of the infected individual. It is evident from **Figure 4A** that as we increase the vaccinate rate, the first major peak is delayed and lower in magnitude. Although **Figure 4B** indicates that the overall steady states of the infected individual given various vaccination rates are not significantly different, increasing vaccination rate can still help the society to better handle the first and the biggest surge of infection by having more time to respond. This finding is consistent with the finding outlined in **Period of Resurgence Depends on the Mean Duration Time of Emergence of New Variants (σ)**, suggesting that vaccination rates play a critical role in controlling the spread of the disease as new variants emerge in the future.

Varying Vaccine Effectiveness Has No Significant Effect on the Dynamics

Last but not the least, the effectiveness of the vaccine (ϵ) was varied to evaluate the situation where science cannot keep up with emergence of new variants by always having the most up-to-date vaccine against the newest variant. It is evident that unlike varying vaccination rate, varying vaccine effectiveness has very little effect on not only the steady

states of the infected individual (**Figure 5B**), but also the progression and spread of the disease (**Figure 5A**). This means that as long as the vaccine provides some level of protection against the disease, flattening the first major curve can be done with increasing vaccination coverage. Therefore, it is concluded that in order to prevent the society from the chaos caused by future resurgence of cases, it is more important to get people vaccinated to increase overall vaccination coverage, even if the vaccine used is not the most up-to-date vaccine for the primary variant currently circulating.

Conclusion and Future Perspectives

In this study, a compartmental based SIRVS model was developed by modifying the SIRS model with a new vaccination component and a variable rate of infection. Based on the simulations run with different initial conditions, it was found that this model is insensitive to the initial conditions as the overall behaviour remains constant regardless which initial conditions were used. This demonstrates that this COVID-19 model is not chaotic, making the predictions reliable despite knowing the exact real-life initial condition. In addition, according to the power spectra, it was also found that the frequency of peaks of the infected individuals depends on the mean duration time of a virus and can be delayed with increased vaccination coverage. Furthermore, with greater vaccination rate, humans could delay the first major peak and allow society to better handle the surge in cases. Last but not the least, varying vaccination efficiencies was found to not have a strong effect on the progression of the disease, and therefore humans should focus on getting more people vaccinated even if the vaccine is not designed specifically for the present variants. All of those findings demonstrate the importance of vaccination coverage as a weapon against COVID-19 in the foreseeable future.

Despite the promising finding, this study is not without limitations. The biggest limitation lies in the methods of obtaining the infectivity function, as it largely depends on the assumptions that there is only one major variant circulating at a given time, and the rate of increase of infectivity is a constant. Therefore, in the future, a better model for the rate of infectivity could be developed to improve the overall predicting power of the model. This could be done by fitting a better model for the step function, for example, the transmission rate can also be computed from the previous data through mathematical inverse problem [32], or using a supervised learning algorithm that is trained with past coronavirus data to better estimate the rate of emergence in order to better predict the period of emergence. It is hoped that the finding of this study can provide public health agencies with some insights into the future trajectory of the disease so that appropriate actions can be taken before each peak to protect the health care system and keep the society functioning.

Supplementary Material

All codes used in this project can be found at the following GitHub repository:

https://github.com/YinniKun/covid-trajectory

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