

# Modeling the Infection Disease (Covid-19) and the Effect of Vaccination

Hanadi Alzubadi

Department of Mathematic, Umm alQura University, Makkah, KSA

Email: hhzubadi@uqu.edu.sa

**How to cite this paper:** Alzubadi, H. (2023) Modeling the Infection Disease (Covid-19) and the Effect of Vaccination. *Applied Mathematics*, 14, 437-449.  
<https://doi.org/10.4236/am.2023.147027>

**Received:** May 26, 2023

**Accepted:** July 10, 2023

**Published:** July 13, 2023

Copyright © 2023 by author(s) and Scientific Research Publishing Inc.

This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).

<http://creativecommons.org/licenses/by/4.0/>



Open Access

---

## Abstract

In this paper we provide different types of approach in mathematical biology about infection disease and understanding the dynamic of epidemic mathematical models specially in COVID-19 disease which first outbreaked in China and fast spread around the world. We work in the connection between the mathematical models and the solution analytically and numerically. At first, we emphasize the Susceptible-Infectious-Recovered (SIR) models' extension for policy significance. Then, we found the improved SIER model done by research. In third section, we examine the improved model when an appropriate vaccine has been found, we introduce the model of SIR with vaccine term which ends up with discussion and conclusion about the effect of vaccine. The comprehension of COVID-19 transmission methods, structures, and characteristics is greatly aided by these mathematical models analytically and numerically.

## Keywords

SIR Model, SEIR Model, COVID-19, Travelling Wave, Vaccine Effect, Numerical Solution

---

## 1. Introduction

When the World Health Organization (WHO) first reported a cluster of pneumonia cases in Wuhan in January 2020, no one anticipated that COVID-19, also known as coronavirus disease 2019, would become a pandemic in March 2020 [1].

In the following sections, we will study the dynamic of COVID-19, which outbreaked in Wuhan, China, and quickly spread around the world, causing many deaths. Scientists worldwide searched for the secret of this disease, and finally, they found a vaccine that helps reduce its risk. Researchers and the general pub-

lic actively worked to find ways to reduce infection rates until a cure or vaccination procedure was developed to reduce the harm of this disease. The analysis governs most of the global spread and the significant solutions covered by scientific research [2].

In this paper, we write an epidemic model using the SIR model, which is the Susceptible-Infectious-Recovered extension for policy significance.

Then, in the next section, we examine the improved model when an appropriate or perfect vaccine has been found against the disease, *i.e.*, we introduce the SIR model with a vaccine term. Then, we finish with the discussion and conclusion. The comprehension of COVID-19 transmission methods, structures, and characteristics is aided by these mathematical models analytically and numerically.

In the last section, we discussed three types of equations; moreover, we analyzed some situations. Although our approaches to their solutions were different, we recognized how the models were built and how they support the research questions, which answer about what is the rate of disease spread? What kind of epidemic will it be? What happens if the model disease SIR had vaccine term?

The answers to these questions are discussed in the context of the current COVID-19 outbreak. The model tells us that to reduce the impact of the disease, we need to lower the contact ratio as much as possible, which is exactly what current social distancing measures are designed to do, and to have several vaccines. Also, the following paper answers whether a vaccine is the condition for an epidemic to stop.

## 2. Literature Review

Despite the harm of diseases in human communities, little work was done on mathematical models of them until the last century. Since its inception, infectious diseases have been a part of human history. They have had a significant impact on the fate of all nations when they have developed local epidemics or large pandemics. An interesting early example is a paper by Daniel Bernoulli, which was published in 1766 and was the first study of the deaths from smallpox [3].

In this century, the world has addressed different types of epidemics, such as the severe acute respiratory syndrome coronavirus (SARS-CoV) in 2002-2003; the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012; Ebola in 1976 and 2013; H1N1 in 2009; and finally, SARS-Cov-2, or COVID-19, in December 2019.

### 2.1. History of Using Epidemics Model of Infection Disease

Since the beginning of time, infectious diseases have been a part of human history. They have had a significant impact on the fate of entire nations when they have developed into local epidemics or large pandemics. An interesting early example is a paper by Daniel Bernoulli, which was published in 1766 and was the first study of the deaths from smallpox [4]. Another important work in infec-

tious disease was done in the early 20<sup>th</sup> century by Hamer, who studied the regular recurrence of measles epidemics. Then, Kermack and McKendrick 1927 discovered the conditions for the spread of the disease and investigated the effect of mechanisms and control theory [5].

In 2014-2015 in West Africa, the Ebola virus posed an unprecedented health threat to humans, considered by far the largest spread of the virus in history. The virus spreads through human-to-human transmission, and the epidemic increased rapidly due to socioeconomic deprivation and inadequate health systems in the affected countries. Regional transmission is the origin of the spread of Ebola [6].

The spread occurs via the air when sick people congregate with healthy people and cough or sneeze droplets into the air. Scientists and politicians are working to prevent the transmission and spread of infection, as the reason for the transmission of this type of pandemic is the movement of infected individuals from one place to another, which results in the spread of the disease. It is also spread by placing hands or fingers on the surface of objects that infected people touch. According to its emergence and spread, health organizations have informed the world about the symptoms of viral pneumonia, including fever, cough, and chest discomfort. Most studies have found that the international spread of COVID-19 accelerated from late February 2020 [7].

According to their genetic characteristics, the coronavirus family consists of four genera: beta coronavirus, gamma coronavirus, and delta coronavirus. The coronavirus RNA genome, which is 26 - 32 kb, is the largest of all known viral genomes. Coronaviruses can infect humans and other mammals, reptiles, and birds. Most coronavirus infections are subclinical. The Middle East respiratory syndrome coronavirus (MERS-CoV) and the severe acute respiratory syndrome coronavirus (SARS-CoV) belong to the family of beta coronaviruses, which can cause serious respiratory illnesses in humans. COVID-19 can quickly adapt to new hosts and ecological niches, attain a propensity for genetic recombination, and increase the rate at which normal RNA viruses naturally mutate. The E-protein, S-protein, M-protein, and HE-protein segments are highlighted in **Figure 1** along with other protein segments, which form the typical structural representation of COVID-19. A total of 81,009 confirmed pneumonia/COVID-19 cases were reported in the Mainland of China as of March 16, 2020. At the same time, new cases were also reported in Thailand, South Korea, Japan, the United Kingdom, the USA, India, and other countries. In contrast to SARS-CoV, COVID-19 appears to induce moderate viral pneumonia, with the potential for person-to-person transmission [8].

## 2.2. The Important of Mathematical Model of Covid-19

Mathematical analysis of the spread and control of the novel coronavirus (COVID-19) in China informed the WHO (World Health Organization) of the outbreak. Later, on January 20, 2020, scientists from China's National Health

Commission expressed its potential to spread from one human to another upon the confirmation of two cases in Guangdong upon visiting Wuhan. Later, the Wuhan authorities announced new measures for the control and prevention of this epidemic, canceling Chinese New Year celebrations and starting to examine body temperature upon traveling via public transport on January 14, 2020. In addition, the general public were safeguarded during the quarantine period introduced on January 23, 2020, and the lockdown of Wuhan was initiated [8].

The importance of mathematical models of COVID-19 is obvious when we compare the estimation results of the transmission for different periods. The strict travel restrictions occurred in Wuhan in the period of January 2-6, 2020, which reduced transmission by half in 2 weeks. Comparing different case studies in early February 2020, finding the effect of control on the measure of biological parameters in the models, the estimation provided some evidence of multiple data sets. Comprehensive analysis was used in the study of COVID-19's dynamic of transmission. These estimates are better in exploring the effect of transmission, including later in vaccinated persons [9].

Our study focuses on COVID-19, a virus that outbreaked in the Chinese city of Wuhan and spread quickly around the globe. After the virus struck at the end of 2019, it was provided the moniker COVID-19. It is a contagious disease that affects millions of people. COVID-19, brought about by SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), is, in any case, the principal pandemic to arrive in each country on the planet in this time of worldwide data. In addition, this occurred despite what may have been the largest lockdown in history. Compared to our proposed model, the main shortcoming of other models in the literature found in [10] is that they do not consider societal feedback or delays in their computations. The countries examined in the present study have adopted different policies throughout the pandemic, and considering such a factor seems quite valuable [11].

### 3. SIR Model

An individual in the SIR model removes their infection by either having a high immune response or death. Most childhood diseases are already at R. In recent years, when the recent effect of COVID-19 arose, the research area of this disease has become more common. In modeling an epidemic, we need to assume the population that is affected, the way the disease spreads, and the mechanism of recovery from the disease and removal from the population that we start with. The SIR model is one of the simplest ways to understand the spread of a disease such as COVID-19 through a population. Allowing the movement of populations makes the model slightly more realistic and results in "traveling wave" solutions [4].

The SIR model is based on mass-action kinetics, which means, in this case, the elements are individual hosts, and the kinetics quantify host transitions between states. The infection rate ( $\beta SI$ ) and recovery rate ( $\gamma I$ ) are assumed to follow kinetics

where the recovered rate is proportional to the concentrations of its reagents. This means that susceptible individuals become infected at a rate proportional to the number of infected individuals and that infected individuals recover at a constant rate. The mass-action assumption holds for reactions in reagent molecules at random because the rate of increases proportionally to the concentrations of the reagents [12]. The population remains constant, as does the rate of infection constant (transition).

The basic model includes  $S(t)$ , which is the group of susceptible people that are not yet affected, and  $I(t)$  refers to ineffective people who can spread the disease. The last important factor is  $R(t)$ , which includes the removed people who have died or recovered after they had the disease [3].

#### The basic model

$$\begin{aligned}\frac{ds}{dt} &= -\mu IS, \\ \frac{dI}{dt} &= \mu IS - \alpha I, \\ \frac{dR}{dt} &= \alpha I.\end{aligned}\tag{1}$$

where  $\mu, \alpha$  are constant rate, Equation (1) gives three of differential equations which we can solve Initial number effective. The dynamical system (1) has two equilibrium points the first one gives

$$\begin{aligned}s &= s_0, \quad I = I_0, \quad R = 0 \\ \frac{\mu}{dt}(S + I + R) &= 0 \\ S + R + I &= S_0 + I_0\end{aligned}$$

The second equilibrium corresponds to the case in which there is a significant group of infectious individuals, and which will be referred to as the epidemic equilibrium

$$S_1^* = \frac{r + \delta\rho}{\gamma}, \quad I_1^* = \frac{\delta(R_0 - 1)}{\delta R_0(1 - \rho) + \gamma}, \quad R_1^* = \frac{r(R_0 - 1)}{\delta R_0(1 - \rho) + \gamma},$$

If we figure out if the disease spread

$$\begin{aligned}S &\leq S_0 \\ \frac{dI}{dt} &< I(rS_0 - \mu)\end{aligned}$$

If  $S_0 > \frac{\mu}{r} = \frac{1}{q}$  the disease spread, where  $q$  is a constant of the population. If

$S_0 > 1$ , then on average, each infected individual infects more than one other member of the population [13].

### 3.1. Analytic Solution

Assume we have following assumptions for one person

Lte:  $N = 1$

$$\begin{aligned} \frac{dS}{dt} &= -\beta S(t)I(t), \\ \frac{dI}{dt} &= \beta S(t)I(t) - \alpha I(t), \\ \frac{dR}{dt} &= \alpha I(t). \end{aligned}$$

where  $\beta \rightarrow$  infection force and  $\alpha \rightarrow$  removal rate.

Assume that all equations are constant

$$\begin{aligned} I^* &= 0, \quad S^* = \frac{a}{b} \\ R^* &= N - S^* - I^* = \frac{bN - a}{b} \\ (S^*, I^*, R^*) &= \left[ \frac{a}{b}, 0, \frac{bN - a}{b} \right] \end{aligned}$$

if it was  $S(t) > \frac{a}{b}$  the number of infections is growing. We assume that there is a CPT convalescent plasma translation in the SIR model  $\delta \rightarrow$  CPT, 1 the rate is proportional to  $I(t)$  [14].

**The rate is proportional** to  $I(t), R(t)$ :

$$\begin{aligned} \frac{dS}{dt} &= -bS(t)I(t); \\ \frac{dI}{dt} &= bS(t)I(t) - (a + \delta R(t))I(t); \\ \frac{dR}{dt} &= (a + \delta R(t))I(t) = (a + \delta)I(t) \\ (S_\delta^*, I_\delta^*, R_\delta^*) &= \left( \frac{a + \delta R_\delta^*}{b}, 0, \frac{bN - a}{b + \delta} \right) = \left( \frac{a + \delta N}{b + \delta}, 0, \frac{bN - a}{b + \delta} \right) \end{aligned}$$

The critical size of the susceptible at which the infective reaches maximum in the presence of CPT is higher than the size in the absence of CPT.

$$\frac{S^*}{S_\epsilon^*} = \left( \frac{a}{b} \right) \div \left( \frac{a + \delta R_\delta^*}{b} \right) = \frac{a}{a + \delta R_\delta^*} < 1.$$

which gives the restriction in the solution.

### 3.2. Travelling Wave Solution

From the basic model (1), we introduce a travelling wave solution by assuming

$$y = x - ct$$

Then the model becomes

$$0 = c \frac{dS}{dt} - IS \tag{3}$$

$$0 = \frac{d^2 I}{dy^2} + c \frac{dI}{dy} + I \left( S - \frac{1}{R_0} \right) \quad (4)$$

Let the time tend to  $-\infty$  as  $y$  tend  $\infty$ . We need to find the value of wave speed solution  $c$

If we have

$$\begin{aligned} S &= 1 - P \\ -c \frac{dP}{dy} - I &= 0 \end{aligned}$$

This yield  $\frac{d^2 I}{dy^2} + c \frac{dI}{dy} + I \left( 1 - \frac{1}{R_0} \right) = 0$

The face plane solution  $c \geq 2 \sqrt{1 - \frac{1}{R_0}}$

The speed is better to be small, we can set  $R_0 = S_0 q$ , where  $q$  is the constant rate. That can occur if susceptible stay home and have social distancing which effect the speed spread of  $c$ .

#### 4. SEIR Model

SEIR is a model development of relative SIR model that analyze the epidemiological case of Covid-19 in countries from information is allowed at period of time (Efimov, etc.). The model applied the predict of spread the virus and design the predictor by time interval [9]. The susceptible individual  $S$  capable of controlling the disease, the asymptotic exposed  $E$  and the infections population  $I$  capable of giving the disease to susceptible.  $R$  is per mentally immune after healing or dying  $D$ . The model gives generic behavior of epidemics ( $\alpha$ ,  $\beta$ ,  $a$ ) which are transition rates. This gives a novel of SEIR model which predicts the outbreak of Covid-19 in different restriction discussed in (Yang *et al.*, 2020).

The model of SEIR

$$\begin{aligned} \frac{dS}{dt} &= -\eta IS - dSE, \\ \frac{dE}{dt} &= \mu SI - cE + dSE, \\ \frac{dI}{dt} &= cE - \alpha I, \\ \frac{dR}{dt} &= \alpha I. \end{aligned} \quad (5)$$

where  $\mu$ ,  $\alpha$ ,  $c$  and  $d$  are constant rate.

##### 4.1. Stability Analysis of SEIR Model

The improvement of the model can be found by searching of the impact of natural birth considering period. The dynamic process of SEIR describes as following:

$$\begin{aligned}
 \frac{ds}{dt} &= -r\eta_1 \left( \frac{S}{N} \right) I, \\
 \frac{dE}{dt} &= r\eta_2 \left( \frac{S}{N} \right) I - \eta_1 E, \\
 \frac{dI}{dt} &= \eta_1 E - \eta_2 I, \\
 \frac{dR}{dt} &= (I - \beta)\eta_2 I, \\
 \frac{dD}{dt} &= \beta\eta_2 I.
 \end{aligned}
 \tag{4}$$

$E(t), I(t), S(t), D(t)$  are the number of individual in susceptible, Exposed infection, recovered and death model.  $C = I + E + R + D$ , in spread the disease  $E(t), I(t), R(t) \leq C$  where  $C$  represent the total of population.

The linear expansion of SEIR model is

$$\begin{aligned}
 \frac{dE}{dt} &= r\eta_2 I - \eta_1 E, \\
 \frac{dI}{dt} &= \eta_1 E - \eta_2 I.
 \end{aligned}$$

The general solution gives

$$\begin{aligned}
 E(\gamma) &= \int_0^\infty E(t) e^{-\gamma t} dt, \\
 I(\gamma) &= \int_0^\infty I(t) e^{-\gamma t} dt
 \end{aligned}$$

where  $\gamma = -\frac{\eta_1 + \eta_2}{2} \pm \frac{1}{2} \sqrt{\Delta}$ , and  $\Delta = (\eta_1 - \eta_2)^2 + 4\eta_1\eta_2$ .

For more analysis see ref [15].

#### 4.2. The Effect of the Vaccine in Corona Model SIRV

Covid-19 is a threat of infection being spread around the world. Scientists work hard to introduce a perfect vaccine against the disease. The questions arise in this situation of the population. The questions arise after scientist found vaccine which reduces the risk of Coronavirus.

What's the condition for an epidemic to stop, how many people do we need to vaccinate?

What would happen if the vaccine were 100% effective in people. If the population remain constant over time,  $N$  is equal to  $S(t) + I(t) + R(t)$ . In this case there is a homogeneous mixture of the population, and everyone gets sick in the same period. The population susceptible to contracting the disease decreases monotonically over time. Moreover, is no distinction between asymptotically and symptomatically infected persons. Considering the mortality rate is the same for all people, that yield the average age in the population is 60 years and there is no age distinction between people infected by Covid-19.

This model is based on the following



$$\begin{aligned}
 \frac{ds}{dt} &= -\eta IS - dv \\
 \frac{dI}{dt} &= \eta IS - \alpha I \\
 \frac{dR}{dt} &= \alpha I + dv
 \end{aligned}
 \tag{6}$$

where  $dv$  is a vaccine term add to the basic model of SIR (1), and  $\mu$ ,  $\alpha$  are constant rate.

## 5. Vaccination Effect

$\rho$  is the proportion of those vaccinated successfully (with  $0 < \rho < 1$ ). In fact, constant vaccination reduces the birth rate  $\mu$  of susceptible, so that

$$\begin{aligned}
 \frac{dS}{dt} &= \mu(S + R) - \beta SI - \mu S + \mu\rho I - pS, \\
 \frac{dI}{dt} &= \beta SI - \mu I + (1 - \rho)\mu I - rI, \\
 \frac{dR}{dt} &= rI - \mu R + pS, \\
 S(t) + I(t) + R(t) &= 1.
 \end{aligned}$$

The basic reproductive rate of the epidemic  $R_1$  is as the following:

$$\begin{aligned}
 R_1 &= \frac{\beta}{r + \mu\rho} \cdot \frac{\mu}{\mu + \rho} < \frac{\beta}{r + \mu\rho} = R_0. \\
 R_+^3 &= \{(S, I, R) \in R^3 \mid S > 0, I > 0, R > 0\}
 \end{aligned}$$

The purpose of this section is to find the effect of the vaccine for reduce the number of people that are affected  $I(t)$  to do this

$$\frac{dI}{dt} = I(aS - \infty) < 0$$

That means  $R = \frac{aS}{\infty} < 1$ , where  $S$  is number of people susceptible from

$$S^* < \frac{\infty}{a}$$

which gives us the number of people that vaccinate about  $\frac{1}{R_0}$ , disease free equilibrium of COVID-19 will be locally asymptotically stable otherwise the number of infected people will arise. If  $S^* + V = 1$ , The vaccine term must be  $V > 1 - \frac{1}{R_0}$ . Vaccination program will be helpful only if a large portion of people have it under some conditions [16].

## Numerical Results

In the numerical solution, we used MATLAB to plot the system of Equation (1) using the ode45 code. The plot gives us an idea of how the different groups of people,

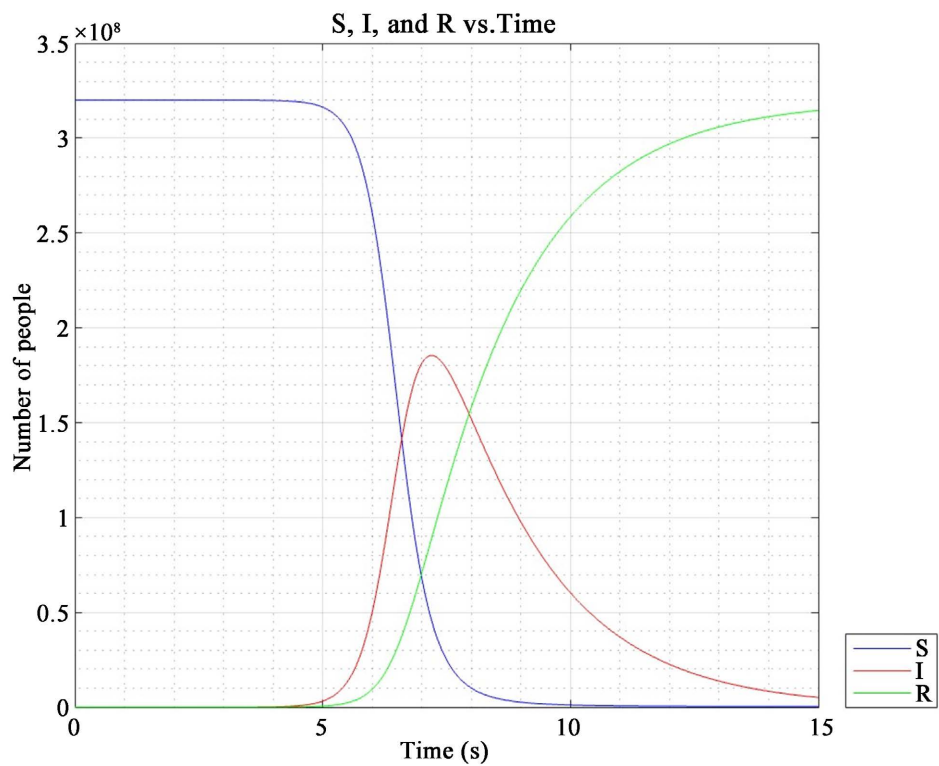
susceptible, infected, or recovered, rise or fall during a period of weeks. **Figure 1** illustrates the blue line, representing susceptibility to high state, which then decreases. The red line represents when the patient’s infection rose, peaked, and gradually decreased, while the green line represents the recovered growth and is a stable approach 1. First, everyone is susceptible to the blue line. The number decreases, and some of the infected change to the red line; after a series of weeks, everyone becomes sick, as shown by the green line, but they recover from the disease or die.

From the SEIR Equation (2) we can learn how counts change over time. Using the aforementioned ideas, we can consider a discrete-time version of these equations that describe the daily changes. We can increase the precision of the graph in **Figure 2** by decreasing the specified step values.

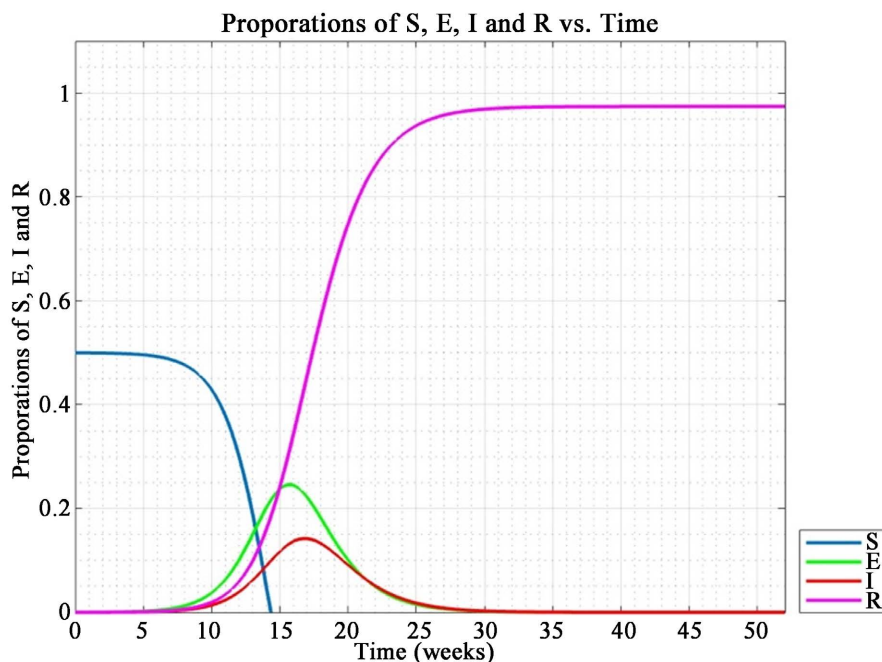
If we change the number of people to be vaccinated, graph **Figure 3** explains

**Table 1.** Parameters value used in the code of numerical solution.

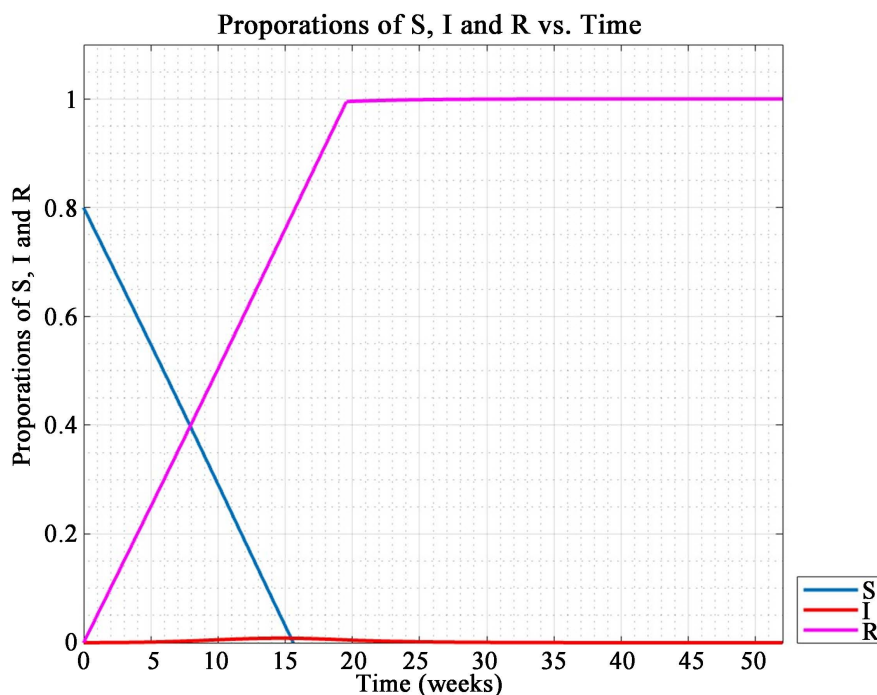
Parameters values of SIR and SEIR model		
Parameter	value	Used for
a	0.8	Initial coefficient
b	0.2	Removable coefficient
t-max	52	Number of weeks
dt	0.01	Size of time steps in week
I max	1.1	Max number of infected



**Figure 1.** The plot of SIR model, the graph shows number of people verses time.



**Figure 2.** The plot of SEIR model, the graph shows number of people verses time.



**Figure 3.** The plot of the SIR model with the vaccine when increasing the population of people vaccinate.

how the term of affected people falls over time. People who have taken the full dose acquire a high immune response, so the disease does not spread.

Moreover, **Figure 3** shows the solution to this disease when we increase the number of vaccinated people; for example,  $dV = 0.005$  means that half of the population is vaccinated. These results reduced the number of infected people

and increased the number of susceptible individuals.

**Table 1** represents all the parameters values used in numerical analysis in **Figures 1-3** which gives us a numerical solution and its behaviour.

## 6. Conclusions

In this paper, we have approached some works we have previously done in modeling infectious diseases, such as SARS. We provide a brief description of the history and improvement of the models. The mathematical model explains, analyzes, and numerically plays an essential role in developing solutions, such as social distancing and vaccination. In this study, we discussed different types of pandemics related to infectious diseases, especially in the case of the COVID-19 model using SIR. We have seen that susceptible people become infected and then recover or are removed from the disease. The solution is generalized in Section 2 of the SIR model.

Subsequently, in Section 3, we added the vaccine term, which provided the full model of recent COVID-19. As described in the previous section, the vaccination program succeeded for many people. The model would also be more accurate if the transmission and recovery rate parameters were closer to the actual data. Finally, the SIR model demonstrates the importance of technology and mathematics in solving real-world problems. As described in the previous section, a solution to COVID-19 was found when we increased the number of vaccinated people to half or more of the population. These results reduced the number of infected people and increased the number of susceptible individuals.

In the future, we expect to work with more diseases that appear and discuss how these conditions are transmitted and affect others. All these studies must be related to mathematical models of epidemics.

## Acknowledgements

My acknowledgments go to my family and friends. I would like to thank my family and especially my parents who help me to success in my study, career and life; my daughters and son who understand when I am busy and give me a support. Also, my thanks go to my organization Umm Al-Qura University and all my colleagues.

## Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

## References

- [1] Beira, M.J. and Sebastiao, P.J. (2021) A Differential Equations Model-Fitting Analysis of Covid-19 Epidemiological Data to Explain Multi-Wave Dynamics. *Scientific Reports*, **11**, Article No. 16312. <https://doi.org/10.1038/s41598-021-95494-6>
- [2] Adekola, H.A., Adekunle, I.A., Egberongbe, H.O., Onitilo, S.A. and Abdullahi, I.N. (2020) Mathematical Modelling for Infectious Viral Disease: The Covid-19 Perspec-

- tive. *Journal of Public Affairs*, **20**, e2306. <https://doi.org/10.1002/pa.2306>
- [3] Britton, N.F. and Britton, N. (2003) Essential Mathematical Biology. Vol. 453, Springer, Berlin. <https://doi.org/10.1007/978-1-4471-0049-2>
- [4] Bernoulli, D. and Blower, S. (2004) An Attempt at a New Analysis of the Mortality Caused by Smallpox and of the Advantages of Inoculation to Prevent It. *Reviews in Medical Virology*, **14**, 275-288. <https://doi.org/10.1002/rmv.443>
- [5] Fine, P.E. (1979) John Brownlee and the Measurement of Infectiousness: An Historical Study in Epidemic Theory. *Journal of the Royal Statistical Society: Series A (General)*, **142**, 347-362. <https://doi.org/10.2307/2982487>
- [6] Jiang, S., Wang, K., Li, C., Hong, G., Zhang, X., Shan, M., Li, H. and Wang, J. (2017) Mathematical Models for Devising the Optimal Ebola Virus Disease Eradication. *Journal of Translational Medicine*, **15**, Article No. 124. <https://doi.org/10.1186/s12967-017-1224-6>
- [7] Hu, B., Guo, H., Zhou, P. and Shi, Z.-L. (2021) Characteristics of Sars-Cov-2 and Covid-19. *Nature Reviews Microbiology*, **19**, 141-154. <https://doi.org/10.1038/s41579-020-00459-7>
- [8] Din, A., Li, Y., Khan, T. and Zaman, G. (2020) Mathematical Analysis of Spread and Control of the Novel Corona Virus (Covid-19) in China. *Chaos, Solitons & Fractals*, **141**, Article ID: 110286. <https://doi.org/10.1016/j.chaos.2020.110286>
- [9] Colizza, V., Barrat, A., Barthélemy, M. and Vespignani, A. (2007) Predictability and Epidemic Pathways in Global Outbreaks of Infectious Diseases: The SARS Case Study. *BMC Medicine*, **5**, Article No. 34. <https://doi.org/10.1186/1741-7015-5-34>
- [10] Efimov, D. and Ushirobira, R. (2021) On an Interval Prediction of Covid-19 Development Based on a SEIR Epidemic Model. *Annual Reviews in Control*, **51**, 477-487. <https://doi.org/10.1016/j.arcontrol.2021.01.006>
- [11] Xavier, J.B., Monk, J.M., Poudel, S., Norsigian, C.J., Sastry, A.V., Liao, C., Bento, J., Suchard, M.A., Arrieta-Ortiz, M.L., Peterson, E.J., *et al.* (2022) Mathematical Models to Study the Biology of Pathogens and the Infectious Diseases They Cause. *Is-science*, **25**, Article ID: 104079. <https://doi.org/10.1016/j.isci.2022.104079>
- [12] Kucharski, A.J., Russell, T.W., Diamond, C., Liu, Y., Edmunds, J., Funk, S., Eggo, R.M., Sun, F., Jit, M., Munday, J.D., *et al.* (2020) Early Dynamics of Transmission and Control of Covid-19: A Mathematical Modelling Study. *The Lancet Infectious Diseases*, **20**, 553-558.
- [13] Kroger, M. and Schlickeiser, R. (2020) Analytical Solution of the Sir-Model for the Temporal Evolution of Epidemics. Part A: Time-Independent Reproduction Factor. *Journal of Physics A: Mathematical and Theoretical*, **53**, Article ID: 505601. <https://doi.org/10.1088/1751-8121/abc65d>
- [14] Husniah, H., Supriatna, A.K., *et al.* (2021) Sir Mathematical Model of Convalescent Plasma Transfusion Applied to the Covid-19 Pandemic Data in Indonesia to Control the Spread of the Disease. *Journal of Physics: Conference Series*, **2084**, Article ID: 012022. <https://doi.org/10.1088/1742-6596/2084/1/012022>
- [15] Piovella, N. (2020) Analytical Solution of SEIR Model Describing the Free Spread of the Covid-19 Pandemic. *Chaos, Solitons & Fractals*, **140**, Article ID: 110243. <https://doi.org/10.1016/j.chaos.2020.110243>
- [16] Mohajan, H. (2022) Mathematical Analysis of Sir Model for Covid-19 Transmission.