International Journal of Innovative Research and Scientific Studies, 8(3) 2025, pages: 1855-1864

IJIRSS International Journal of Innovative Research & Scientific Studies

ISSN: 2617-6548

URL: www.ijirss.com

Measuring susceptibility, infection, and recovery during the COVID-19 outbreak in Cambodia

Siphat Lim[1*], Matthew Richard Leigh[2]

[1,2]*CamEd Business School, Phnom Penh, Cambodia.*

Corresponding author: Siphat Lim (*Email:* lsiphat@cam-ed.com)

Abstract

The SIR model is considered one of the most popular mathematical models used to measure the development of the COVID-19 pandemic. Three pieces of basic information susceptibility, infection, and recovery rates were needed to incorporate into the model's estimation parameters. Daily data from February 20, 2021, to August 20, 2021, were applied to calculate two key parameters: the contraction rate and the recovery rate. The solution from the ordinary differential equations showed that the effective contact and recovery rates were 0.0461 and 0.0061, respectively. Using the two parameters for simulation, the infection of COVID-19 reached its peak on July 2, 2022. Among the four main strategies employed by the government curfew, lockdown, vaccination, and stringency index measured based on school and workplace closures; restrictions on public gatherings; transport restrictions; and stay-at-home requirements in controlling the spread of the COVID-19 disease, the lockdown strategy played the most important role in reducing the daily number of infections of the disease, followed by curfew, stringency index, and vaccination.

Keywords: COVID-19 Pandemic, ODE, SIR Model.

DOI: 10.53894/ijirss.v8i3.6894
Funding: This study received no specific financial support.
History: Received: 3 April 2025 / **Revised:** 7 May 2025 / **Accepted:** 8 May 2025 / **Published:** 9 May 2025
Copyright: © 2025 by the authors. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).
Competing Interests: The authors declare that they have no competing interests.
Authors' Contributions: Both authors contributed equally to the conception and design of the study. Both authors have read and agreed to the published version of the manuscript.
Transparency: The authors confirm that the manuscript is an honest, accurate, and transparent account of the study; that no vital features of the study have been omitted; and that any discrepancies from the study as planned have been explained. This study followed all ethical practices during writing.
Publisher: Innovative Research Publishing

1. Introduction

The spread of COVID-19 started at the end of 2019 in the province of Wuhan in China. The spread of the disease proved extremely difficult to control because the virus was airborne, there was no vaccine, not enough PPE, limited availability of testing facilities, and a lack of hospital beds available for COVID-19 patients. The lack of all of these factors combined caused the inefficient control of the pandemic. On average, the daily infection rate in Cambodia was about 482 cases. The authorities implemented some strategies to control the transmission of the virus better. Those strategies included social distancing, wearing masks, a centralized quarantine system, curfews, and lockdowns. During the height of the pandemic, lockdowns in the infected areas, even though they had substantial adverse economic impacts, were one of the most popular policies carried out by government authorities in many countries, such as China, Italy, Spain, France, and the United Kingdom. The level of infection was very high at the start of the pandemic in December 2019 and early 2020.

It was important that the government could predict the level of infection of the COVID-19 disease all over the country, especially when it is going to reach the peak or turning point. In order to define the turning point of the total infection rate, the SIR model is employed with the simulation of three observed variables: susceptible, infected, and recovery or decease. The simulation of the model can be carried out by estimating two parameters: contact rate and recovery rate. This research further investigated the effectiveness of potential strategies, including curfews, lockdowns, vaccinations, and social distancing, which the Royal Government of Cambodia could employ to cope with the COVID-19 pandemic a multiple regression between total infected cases and the four policies that have just been mentioned. The Ordinary Least Square (OLS) is applied to produce the sample parameters.

2. Literature Review

The outbreak of COVID-19 first occurred in Wuhan, Hubei province, China. The central government of China imposed a lockdown on Hubei on January 23, 2020, to control the outbreak. The Bass-SIR model was applied to investigate and analyze the spread of the COVID-19 disease following Wuhan's lockdown between January 24, 2020, and February 12, 2020. The model used three variables: cumulative infected cases, cured cases, and death cases in all provinces in China, excluding Hong Kong and Macau. The main objectives of this research were to determine the reproduction numbers and the adequate reproduction numbers to forecast the initial outbreak and the second wave, which would happen shortly. Using simulation analysis, the exogenous impacts of the lockdown policy were also evaluated. This study found that there were around two adequate reproduction numbers in Hubei, Heilongjiang, and Guizhou, but the numbers were close to one in other provinces by February 12, 2020. The exogenous force of infection, at 95% credible interval (CrI), was found to be 31% (CrI: 12%-55%) and 19% (CrI: 5%-44%) in Fujian and Shanghai, despite Wuhan's lockdown. In addition, the second wave of the epidemic was predicted to occur on February 24, 2020 [1].

The study of the outbreak of coronavirus in 2019 in China, Italy, and France was conducted using the susceptible (S), infected (I), recovered (R), dead (D) scheme (SIRD) model on the period cover from January 22, 2020 to March 15, 2020. Excluding the recovered and dead numbers, the maximum number of infected individuals was predicted to be 26,000 in Italy, which is expected to happen on March 21, 2020. The result of this study showed a definite universality in the evolution of COVID-19 in China, Italy, and France, as indicated by the time-lag plots of the confirmed infected populations [2].

Reproduction numbers, Rt, inferring the total population infected or attack rates of COVID-19, have been estimated in 11 European countries using a semi-mechanistic, joint Bayesian hierarchical model. This study further investigates the effectiveness of policies carried out by each country to reduce the mortality rate. The models that represent the number of infections, the number of deaths, and number of reproductions were created. Between March 2 and March 20, 2020, government policy interventions were implemented. Italy began to apply non-pharmaceutical interventions (social distancing encouraged, closing schools or universities, banning public events, case-based isolation, the onset of the first intervention, and lockdown). Effective policies aim to reduce the death rate to the lowest level. The death rate was observed until May 4, 2020. The initial average of Rt across all countries was estimated to be 3.8, with a credible interval between 2.4 and 5.6. This number has been found to be reduced owing to the combined non-pharmaceutical interventions. As of May 4, 2020, the highest attack rate was found in Belgium at a rate of 8% of the total population. The rates were 5.5% and 4.6% in Spain and Italy, respectively. The lowest attack rate was found in Germany, estimated to be 0.85% of the total population. Two models were developed, one with and one without intervention, to predict the total number of deaths in 11 European countries. If appropriate intervention policies had been carried out at the start of the pandemic, the cause of deaths would have been reduced by 3.1 million people across the 11 European countries. This research further revealed that the predicted infection rate was higher than reported. The deviation might have come from the tests to detect COVID-19 infection. The high level of uncertainty of infection that was estimated here may be due to the focus on hospital tests and settings that miss out on mild or asymptomatic cases in the community. Reproduction numbers were reduced by 81% at the credible interval between 75% and 87% if the lockdown was implemented [3].

One of the most famous mathematical models, the SIR model, was constructed to analyze the COVID-19 outbreak in the Kingdom of Saudi Arabia (KSA). The basis of the SIR model was created on the fundamentals of three subsets: Susceptible (S), Infected (I), and Recovered (R). Ordinary Differential Equation (ODE) was developed under these subsets. Two parameters, effective contact and recovery rates, were derived by solving the ODE. The main objective of the study was to predict the pandemic situation in the next 700 days. Three scenarios, no action, lockdown, and new medicine, were imposed. The implementation of the lockdown scenario was compared with the no-action and new medicine scenarios. This research found that lockdown intervention delays the peak point of the infection. The simulation prediction from the model showed that the highest rate of infection cases would occur between 15 and 30 November 2020. The outbreak had been predicted to be under complete control after June 2021. Lockdown and isolation of individuals are still not the best policy options to stop the spread of COVID-19, as indicated by the reproductive rate. The study recommended that authorities implement a strict long-term prevention strategy as soon as possible to reduce the size of the outbreak successfully [4].

A time-dependent SIR model was employed to investigate the number of infected persons in China. The infected persons were classified into detectable and undetectable individuals. Daily data was used between January 15, 2020, and March 2, 2020. The National Health Commission of the People's Republic of China (NHC) collected the dataset. The reproductive rate was greater than one, which indicated that there was an outbreak. The reproductive numbers were reduced by adopting effective social distancing based on the analysis of the independent cascade model, the so-called IC model, for disease propagation in a configuration random network. The effectiveness of social distancing was observed not just in China; this study found that it also worked in the cases of Japan, Singapore, South Korea, Italy, and Iran [5].

A discrete-time stochastic model using a binomial distribution was developed to study the COVID-19 epidemic in China. The study period was between January 11 and February 13, 2020, in China. Two main things were estimated to evaluate policies that the government had employed to control the transmission of the disease: the contact rate and adequate reproductive number. Based on the current control policy option, the peak was predicted to be the end of February 2020 under the simulation technique generated from the model [6].

Artificial Intelligence (AI) algorithms with time-dependent parameters and deep learning were incorporated into the SIR model, and deep learning was applied to study the COVID-19 pandemic in South Korea. Data were collected from the Korea Centers for Disease Control & Prevention (KCDC). The important parameters of the SIR model were estimated using Runge-Kutta (RK4) methods, which are traditional numerical algorithms [7].

To investigate the COVID-19 epidemic in China, the Susceptible-Exposed-Infectious-Removed (SEIR) model was applied with an AI approach. Migration populations before and after January 23 were taken into account to measure and evaluate the effectiveness of policies employed, such as large-scale quarantine, strict controls on travel, and extensive monitoring of suspected cases. The highest number of infections might be in February 2020, as predicted by the model. The total number of infections would increase threefold in mainland China if the government took inadequate policy and action [8].

A Markov Chain Monte Carlo technique and SEIR model were used to predict reproductive numbers caused by the COVID-19 pandemic in Italy and Hunan, China. Daily time-series data were applied and covered from January 22, 2020, to April 2, 2020. As indicated by the posterior mean with 95% CrI, the reproductive number of COVID-19 was estimated to be 4.34 at 95% CrI in the range between 3.04 and 6.00, and 3.16 at 95% CrI in the range between 1.73 and 5.25, for Italy and Hunan, respectively. The endpoint in Italy was predicted to be on August 5, 2020 [9].

The SIR model was one of the best models for predicting the transmission of COVID-19 disease [10]. A nonlinear SIR model was developed to study the COVID-19 epidemic in Germany, Spain, Italy, France, Algeria, and Morocco. The main objective of this research was to evaluate the social distancing policy introduced by the government in each respective country. This research showed that numerical simulation techniques create an effective tool for forecasting the transmission of COVID-19 disease [11].

SEIR model was extended to be susceptible (S), exposed (E), infectious (I), quarantined (Q), recovered (R), deaths (D), and vaccinated (V) (SEIQRDV) to investigate the spread of COVID-19 disease in KSA by taking into account vaccination compartment. The ensemble Kalman filter (EnKF) method was used to improve the efficiency of parameter estimation. In a short-term prediction, two weeks ahead, the level of recovered, deaths, and confirmed cases were simulated from the model, and the prediction error was a minor deviation compared to accurate data. The pandemic was being affected by vaccination, as revealed by this research [12]. The analysis of the COVID-19 pandemic was started with the basic epidemiological model developed by Kermack-McKendrick. The model was extended to observe the heterogeneity in the spread of the disease, especially to study the effectiveness of policy options that might have been used by any government to control the pandemic, such as non-pharmaceutical interventions, lockdown strategy, potential approaching of herd-immunity levels, and optimal deployment of COVID-19 vaccines. This research was theoretical [13].

The SEIR model was extended by including the asymptomatic isolated; for short, it was called SEIR-AQ, to conduct performance measurement, prevention, and control strategies for the COVID-19 pandemic in China, America, India, and Brazil. Instead of dividing the population into four categories: Susceptible people (S), Exposed (E), Infected (I), and Removed (R), the SEIR-AQ included four more in the model, such as isolation of susceptible people (Sq), isolation of contacts (Eq), isolation of infected people (Iq), asymptomatic patients (A), and hospitalized patients (H). The parameters of the model were calculated using the Euler method. The transmission of COVID-19 was significantly affected through the effective implementation of isolation and medical tracking, regarding the theoretical analysis. Studies have shown that in containing the spread of the COVID-19 pandemic, the local government's swift precautionary and control measures are vital to minimizing direct contact among people to reduce the exposure rate and ensure a proper isolation rate [14].

3. Methodology

This section is separated into two parts; the first part describes the Susceptible-Infected-Recovery model, known as the SIR model, which is developed aiming to determine the maximum number of infective of COVID-19 and when this number is going to happen, while the second part of this section represents a multiple regression between dependent variable, total infected COVID-19 cases, and the independent variables indicate policy options, which have been carried out by the government in order to fight with the infection of the deceased. The SIR model is an epidemiologic model used to understand the spread of an infectious disease; there are three observed variables: susceptible (S), infected (I), and recovery (R), which means the total population is classified into three components. The model specification is presented in the following three equations,

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Where β is the probability of infecting a contract in a specified time, and γ is the rate at which an infected individual recovers and moves into the resistance phase. This model had three key assumptions. The first assumption is that individuals are never infected and they can catch the disease. The second compartment is that infected individuals can spread the disease to susceptible individuals, and the third one is that individuals are assumed to be immune for life or have passed away.

Solving the three differential equations above, we get,

Susceptible	Infected	Recovered
$dS = (-\beta SI)dt$	$dI = (\beta SI - \gamma I)dt$	$dR = \gamma Idt$
$S_{i+1} - S_i = (-\beta S_i I_i)dt$	$I_{i+1} - I_i = (\beta S_i I_i - \gamma I_i)dt$	$R_{i+1} - R_i = \gamma I_i dt$
$S_{i+1} = S_i - (-\beta S_i I_i)dt$	$I_{i+1} = I_i + (\beta S_i I_i - \gamma I_i)dt$	$R_{i+1} = R_i - \gamma I_i dt$

This research also tried to evaluate the performance of government policies that are being implemented in coping with the level of infection of the disease in the country. The assessment is carried out through a multiple regression analysis between total infected cases, TC (dependent variables), and independent variables such as curfew (CF), lockdown (LD), vaccination (PVCIN), and stringency index (SINDEX) measured base on school an

d workplace closures; restrictions on public gatherings; transport restrictions; and stay-at-home requirements.

$$TC_t = \theta_1 CF_t + \theta_2 LD_t + \theta_3 PVCIN_t + \theta_4 SINDEX_t + \varepsilon_t$$

Where θ=θ1,θ2,θ3,θ4 is a vector of slope parameters to be estimated, ε is a residual or error term, and t represents the period. Curfew and lockdown are dummy variables, where one indicates the days of the curfew or lockdown and zero otherwise. The study period covers February 20, 2021, to August 20, 2021. All data are collected from the Ministry of Health.

This research employs time series data; hence, to avoid spurious results, Unit root tests are conducted on all data series except dummy variables. The estimated method is Ordinary Least Square (OLS). In order to fulfill the assumptions of OLS, diagnostic tests such as multicollinearity, autocorrelation, and heteroscedasticity will be carried out. The detection of multicollinearity is conducted through a correlation matrix. Any pair of variables with a correlation coefficient more significant than -0.9/+0.9 will be omitted from the regression analysis. The autocorrelation is detected using the Durbin-Watson statistic. As indicated by OLS techniques, the residual term variance is assumed to be constant, so-called homoscedasticity. One of the most popular heteroskedasticity tests is the Breusch-Pagan-Godfrey (BPG) test. The null hypothesis of the test is homoscedasticity.

4. Research Results

The interpretation of research findings is classified into three different parts. The first part is about descriptive statistics related to COVID-19 daily and total infected cases. The second part presents the forecasting of daily susceptible, infected, and recovered or deceased individuals. The empirical results, which explain the effectiveness of government policies, curfews, lockdowns, vaccinations, and social distancing measures on total COVID-19 infected cases, are shown in the last part of this section.

Table 1.
Daily New Infected Cases and Total Infected Cases.

	NC	TC
Mean	482.1868	31933.68
Median	549.0000	24401.00
Maximum	1130.000	88242.00
Minimum	0.000000	533.0000
Std. Dev.	310.1169	29019.29
Skewness	-0.204741	0.528999
Kurtosis	1.892583	1.882224
Jarque-Bera	10.57154	17.96325
Probability	0.005063	0.000126
Sum	87758.00	5811929.
Sum Sq. Dev.	17407216	1.52E+11
Observations	182	182

Over the period of the study, 182 days, the average daily and total infected were 482 and 31933 cases, respectively. The minimum daily infected case is zero, while the maximum infected cases are 1130. Daily new cases' standard deviation is 310, and the standard deviation of total cases is 29019. The maximum total number of infected cases is 88242. In addition, the two data series are not distributed as normal distributions regarding the estimated result of the Jarque-Bera (JB) tests. The probability of the tests for both NC and TC is lower than the level of significance of 1 percent, which claims that the null hypotheses are highly rejected. The movement of the two data series can be seen more precisely through Figure 1 and Figure 2.

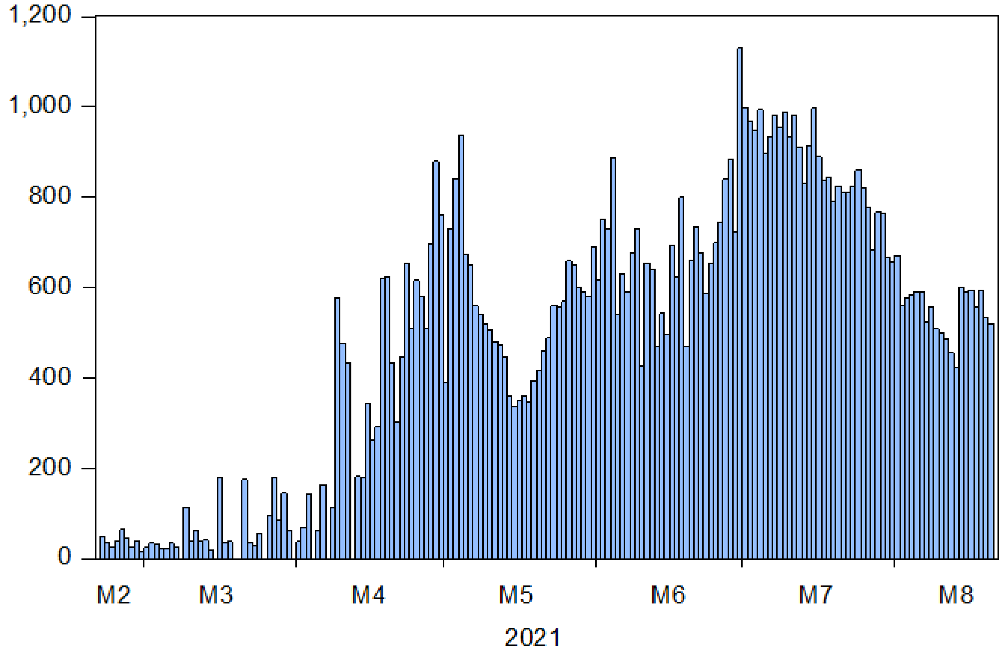

Figure 1.
Daily infected cases, February 20, 2021 to August 20,2021.

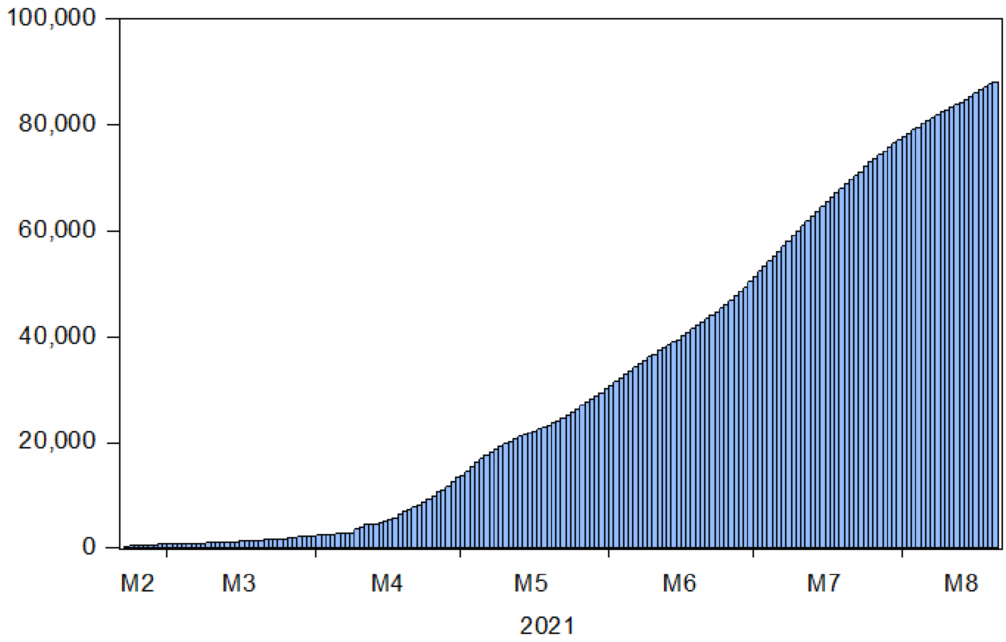

Figure 2.
Total infected cases, February 20, 2021 to August 20,2021.

The observed time series data combined with the estimated probability of an individual contracting an infection at a specific time and the rate at which an infected person recovers and moves into the resistance phase, along with the out-of-sample forecasting of susceptible, infected, and recovered individuals as a proportion of the total population in the country, which is derived from the Ordinary Differential Equation (ODE), are revealed. The simulation of the SIR model indicated that the infection of COVID-19 is expected to reach its peak point on July 2, 2022, which is regarded as a turning point.
β=0.0461 (Contact rate)
γ=0.0061 (Recovery rate)0.

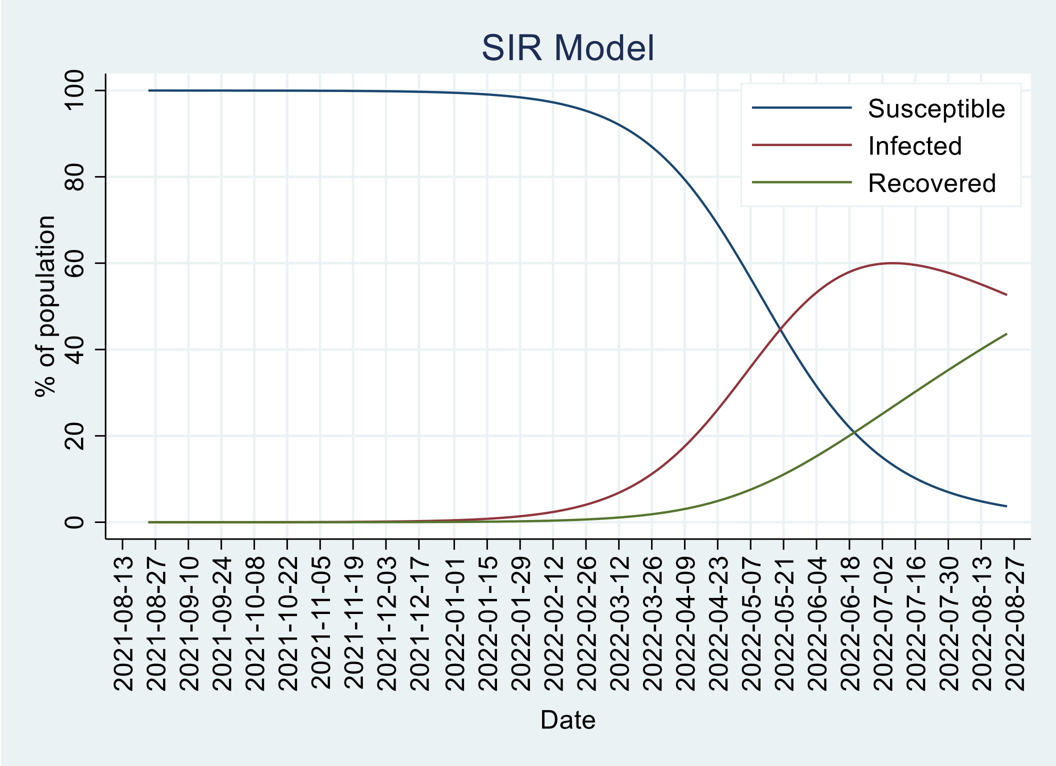

Figure 3.
SIR Model, Out-of-Sample Forecasting.

The data series used in this research are time series, and to avoid spurious results, unit root tests are applied. One of the most famous unit root tests, known as the Augmented-Dickey Fuller (ADF) test, is being selected to assess all the data series except the dummy variables, CF and LD. The null hypothesis of the test is that the series has a unit root. The result of the ADF tests presented in Table 2 indicated that TC, PVCIN, and SINDEX are all integrated of order one, I(1), which means that each series has a unit root at level but has no unit root at first difference. Therefore, a regression between dependent and independent variables can be performed at the level. However, a co-integration test must be conducted to check whether all data series are co-integrated or have a long-term relationship. Engle and Granger's two-step co-integration test is applied. In the first step, a multiple regression is carried out to get all estimated parameters, which will be used to predict the residual terms. The co-integration among variables under investigation does exist if the residual series is stationary or has no unit root. Instead of avoiding spurious regression results, the fulfillment of the assumptions of OLS, no multicollinearity among dependent variables, no first-order autocorrelation of the residual terms, and the variance of the error term must be constant or homoscedasticity are also needed to investigate.

Table 2.
ADF Tests.

	At Level			
		TC	**PVCIN**	**SINDEX**
With Constant	t-Statistic	4.1197	-0.5901	-1.1024
	Prob.	0.4619	0.8686	0.7147
		n0	n0	n0
With Constant & Trend	t-Statistic	-3.1581	-2.6122	-0.8219
	Prob.	0.7964	0.2755	0.9608
		n0	n0	n0
Without Constant & Trend	t-Statistic	7.6411	0.7694	-0.8095
	Prob.	0.6285	0.8789	0.3641
		n0	n0	n0
	At First Difference			
		d(TC)	d(PVCIN)	d(SINDEX)
With Constant	t-Statistic	-2.3383	-4.5358	-13.3725
	Prob.	0.1612	0.0002	0.0000
		n0	***	***
With Constant & Trend	t-Statistic	-3.4877	-4.5224	-13.6025
	Prob.	0.0437	0.0018	0.0000
		**	***	***
Without Constant & Trend	t-Statistic	-0.6388	-4.4568	-13.3791
	Prob.	0.4394	0.0000	0.0000
		n0	***	***

Note: ***, **, Significant at 1% and 5% level.

A multiple regression analysis is implemented after analyzing the correlation between all independent variables in the model, which are presented in the correlation matrix below. As indicated in Table 3, the correlation coefficient of all pairs of variables is no less than -0.9 or no more than +0.9, which claims that high or perfectly positive or negative correlations between variables in the model are not detected. On the other hand, the multicollinearity in the model is not detected, which means that none of the variables is omitted.

Table 3.
Correlation Matrix.

	CF	**LD**	**PVCIN**	**SINDEX**
CF	1			
LD	-0.1824	1		
PVCIN	-0.4766	0.1860	1	
SINDEX	-0.2347	0.1941	0.1322	1

As indicated by the ADF unit root test of the predicted residual series from the regression model, the null hypothesis, which stated that the residual series has a unit root, is highly rejected since the MacKinnon one-sided probability value or p-value is less than a 1 percent significant level. The series is stationary. All series in the model are co-integrated.

Table 4.
ADF Unit Root Test, Residual Series.

Null Hypothesis: RESID01 has a unit root			
Exogenous: Constant			
Lag Length: 2 (Automatic - based on SIC, maxlag=13)			
		t-Statistic	Prob.*
Augmented Dickey-Fuller test statistic		-5.861930	0.0000
Test critical values:	1% level	-3.466994	
	5% level	-2.877544	
	10% level	-2.575381	

Note: *MacKinnon [15] one-sided p-values.

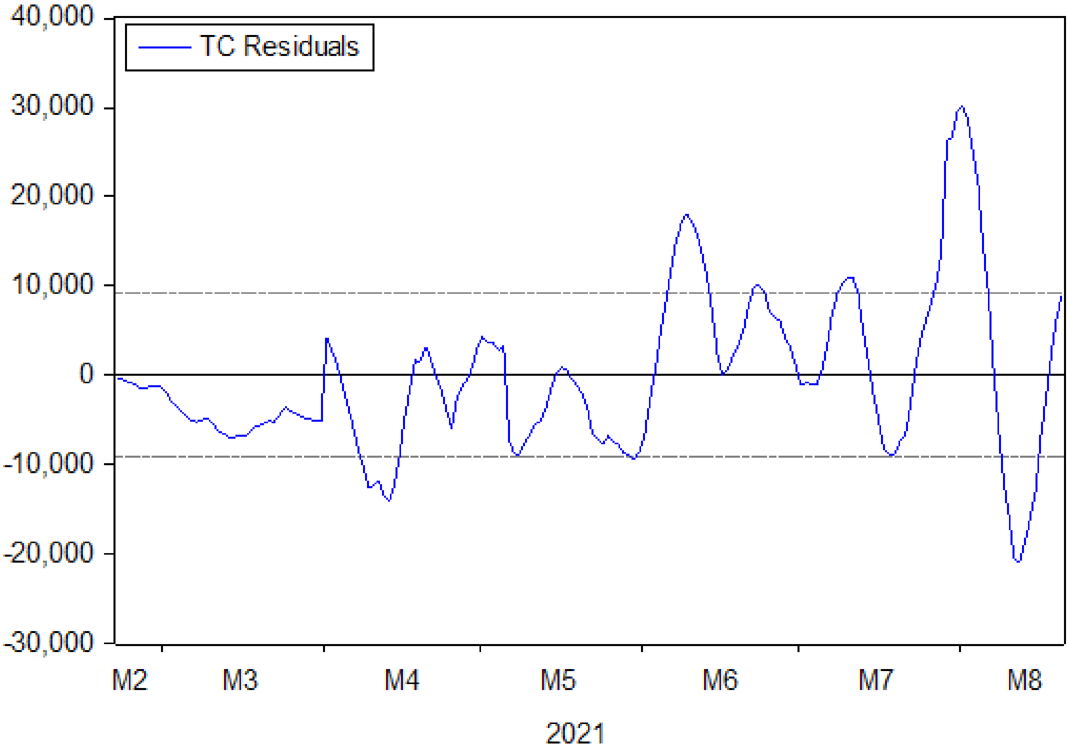

Figure 4.
Regression residual series.

The result of the ADF unit root test presented in Table 4 is consistent with the trend of the regression residual series in Figure 4, which shows that the series has a mean-reverting process, which is characteristic of a stationary process. The assessment of spurious regression results has been completed. The next issue is detecting the first-order autocorrelation of the residual series. Since the Durbin-Watson statistic, known as the d-statistic derived from the regression result, is 0.087, which is a difference from 2, indicates that the first-order autocorrelation of the residual terms is detected. The next step is to check whether the variance of the error terms is constant or not using the Breusch-Pagan-Godfrey heteroscedasticity test. The null hypothesis of the test is homoscedasticity, which means that the variance of the residual terms is constant.

Table 5.
Heteroskedasticity Test: Breusch-Pagan-Godfrey.

F-statistic	24.36488	Prob. F(4,177)	0.0000
Obs*R-squared	64.62750	Prob. Chi-Square(4)	0.0000
Scaled explained SS	108.0612	Prob. Chi-Square(4)	0.0000

The calculated F-statistic of the Breusch-Pagan-Godfrey test is 24.36 based on 4 degrees of freedom and 177 observations. Since the probability of the calculated F-statistic is 0.0000, which is far less than 1 percent significant, the null hypothesis of homoscedasticity is rejected, which claims that heteroscedasticity does exist.

Table 6.
Regression Results.

Dependent Variable: TC				
Method: Least Squares				
Sample: 2/20/2021 8/20/2021				
Included observations: 182				
HAC standard errors & covariance (Bartlett kernel, Newey-West fixed				
Bandwidth = 5.0000)				
Variable	**Coefficient**	**Std. Error**	**t-Statistic**	**Prob.**
CF	-9286.751	5260.985	-1.765211	0.0792
LD	-10362.02	1918.662	-5.400651	0.0000
PVCIN	-6.668291	0.350045	-19.04981	0.0000
SINDEX	-6.700497	29.69047	-0.225678	0.8217
R-squared	0.902006	Mean dependent var		31933.68
Adjusted R-squared	0.900354	S.D. dependent var		29019.29
S.E. of regression	9160.432	Akaike info criterion		21.10491
Sum squared resid	1.49E+10	Schwarz criterion		21.17533
Log likelihood	-1916.547	Hannan-Quinn criterion.		21.13345
Durbin-Watson stat	0.087266			

Two assumptions of OLS were violated: first-order autocorrelation and heteroscedasticity. Due to these violations, the test of statistics generated from the regression results is not reliable since each individual standard error of the t-statistic is significant, which means that the calculated t-test is small. In order to remedy first-order autocorrelation and heteroscedasticity problems, heteroscedasticity and autocorrelation consistent (HAC) standard error and covariance is employed to produce robust standard errors for hypothesis testing. The regression result is presented in Table 6. The adjusted R-squared is 0.90, which is considered high, meaning the model fits with the data well. The estimated slope parameter of CF is -9286, and the null hypothesis that the population parameter of CF is zero is weakly rejected since the p-value is 0.0792, which is less than a 10 percent significant level. A one-day curfew would be expected to reduce the infected cases by 9286. More interestingly, the estimated slope coefficient of LD is -10362 and highly statistically significant at a 1 percent level, which is greater than the p-value of 0.0000. The total infected cases would reduce by 10362, if the government announce a lockdown by one day. The number of vaccinated people has also helped reduce the spread of the disease. A one-vaccinated person would help prevent the infection of the disease by about seven people, and the estimated result is highly significant at a 1 percent level since the probability of the calculated t-test is low. Despite the estimated slope coefficient of SINDEX being -6.700497, which is negative, the null hypothesis failed to be rejected because the p-value of 0.8217 is more significant than the level of significance of 5 percent.

4. Conclusion Remarks

The objectives of this research are to study the interaction between susceptible, infected, and recovered COVID-19 individuals using Ordinary Differential Equations in order to conduct out-of-sample forecasts. Another objective is to assess government policies toward the fight against the spread of the disease throughout the country. Referring to the estimated contraction rate and the recovery rate, which were 0.0461 and 0.0061, respectively, the simulation of the SIR model indicated that the total infected COVID-19 cases were predicted to reach a peak point regarded as a turning point on July 2, 2022. From August 20, 2021, the present time, or end of the sample data point of this study, to July 2, 2022, which was predicted to be a peak point of the total infected cases as a proportion of the total population, there are about ten and a half months for the government to establish effective policies such as curfews, lockdowns, vaccinations, and social distancing measures in order to cope with the COVID-19 pandemic. Among the four policies employed, lockdowns were considered to be one of the most effective strategies to fight the pandemic since a one-day lockdown was expected to decrease the total infected cases by 10,362, followed by curfews, which helped reduce the spread of the disease by about 9,287 cases per day. In contrast, the last policy, vaccination, prevented infection by about seven cases per day. Of course, executing government policies, especially lockdowns and curfews, would help prevent the spread of the disease, but they have a negative impact on the economy. Therefore, they must be carefully and prudently implemented.

References

[1] C. Chang Ku, T. Chou Ng, and H. Ho Lin, *Epidemiological benchmarks of the COVID-19 outbreak control in China after Wuhan's lockdown: A modeling study with an empirical approach*. Sheffield: School of Health and Related Research, University of Sheffield, 2020.

[2] D. Fanelli and F. Piazza, "Analysis and forecast of COVID-19 spreading in China, Italy and France," *Chaos, Solitons & Fractals,* vol. 134, p. 109761, 2020. https://doi.org/10.1016/j.chaos.2020.109761

[3] S. Flaxman *et al.*, "Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe," *Nature,* vol. 584, no. 7820, pp. 257-261, 2020. https://doi.org/10.25561/77731

[4] S. A. Alanazi, M. Kamruzzaman, M. Alruwaili, N. Alshammari, S. A. Alqahtani, and A. Karime, "Measuring and preventing COVID-19 using the SIR model and machine learning in smart health care," *Journal of Healthcare Engineering*, vol. 2020, no. 1, p. 8857346, 2020. https://doi.org/10.1155/2020/8857346

[5] Y.-C. Chen, P.-E. Lu, C.-S. Chang, and T.-H. Liu, "A time-dependent SIR model for COVID-19 with undetectable infected persons," *Ieee Transactions on Network Science and Engineering*, vol. 7, no. 4, pp. 3279-3294, 2020. https://doi.org/10.1109/TNSE.2020.3024723

[6] S. He, S. Tang, and L. Rong, "A discrete stochastic model of the COVID-19 outbreak: Forecast and control," *Mathematical Biosciences and Engineering*, vol. 17, no. 4, pp. 2792-2804, 2020. https://doi.org/10.3934/mbe.2020153

[7] H. Jo, H. Son, H. J. Hwang, and S. Y. Jung, "Analysis of COVID-19 spread in South Korea using the SIR model with time-dependent parameters and deep learning," *medRxiv*, p. 2020.04. 13.20063412, 2020. https://doi.org/10.1101/2020.04.14.20060372

[8] Z. Yang *et al.*, "Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions," *Journal of Thoracic Disease*, vol. 12, no. 3, p. 165, 2020. https://doi.org/10.21037/jtd.2020.03.62

[9] J. Wangping *et al.*, "Extended SIR prediction of the epidemics trend of COVID-19 in Italy and compared with Hunan, China," *Frontiers in Medicine*, vol. 7, p. 169, 2020. https://doi.org/10.3389/fmed.2020.00169

[10] I. Cooper, A. Mondal, and C. G. Antonopoulos, "A SIR model assumption for the spread of COVID-19 in different communities," *Chaos, Solitons & Fractals*, vol. 139, p. 110057, 2020. https://doi.org/10.1016/j.chaos.2020.110057

[11] S. Gounane, Y. Barkouch, A. Atlas, M. Bendahmane, F. Karami, and D. Meskine, "An adaptive social distancing SIR model for COVID-19 disease spreading and forecasting," *Epidemiologic Methods*, vol. 10, no. s1, p. 20200044, 2021. https://doi.org/10.1515/math-2021-0142

[12] R. Ghostine, M. Gharamti, S. Hassrouny, and I. Hoteit, "An extended SEIR model with vaccination for forecasting the COVID-19 pandemic in Saudi Arabia using an ensemble Kalman filter," *Mathematics*, vol. 9, no. 6, p. 636, 2021. https://doi.org/10.3390/math9060636

[13] F. Saldaña and J. X. Velasco-Hernández, "Modeling the COVID-19 pandemic: A primer and overview of mathematical epidemiology," *SeMA Journal*, pp. 1-27, 2022. https://doi.org/10.14493/sema.00055

[14] Y. Yu *et al.*, "Evaluation and prediction of COVID-19 prevention and control strategy based on the SEIR-AQ infectious disease model," *Wireless Communications and Mobile Computing*, vol. 2021, no. 1, p. 1981388, 2021. https://doi.org/10.1155/2021/5589571

[15] J. G. MacKinnon, "Numerical methods for solving the one-sided p-value problem," *The Journal of Econometrics*, vol. 75, no. 1, pp. 51-73, 1996. https://doi.org/10.1016/0304-4076(95)01802-3