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# Analyzing The Spread of The COVID-19 Pandemic Using The SIR Model

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#### Abstract

It is difficult to control the SARS-CoV-2 virus with many complicated strains with a fastspreading speed. In Vietnam, the number of new infections gradually shows signs of increasing, potentially posing many future diseases outbreak risks. The SIR model is a model that provides a practical approach to current and future epidemics; the SIR model is a classical, simple model of community infection. The model can add or change relevant components in the community, such as mortality, immigration or birth rates, resilience, and immunity. In this paper, we focus on COVID-19 data from Vietnam and model it is using the SIR epidemiological model to analyze the spread of the disease and forecast the future disease situation. The results include an assessment of the fit or not of the model through the prediction over the periods.

# 1 Introduction

The COVID-19 pandemic remains an acute global emergency. At the present time, there continue to be millions of people infected each week and in the first eight months of 2022, more than one million people were reported to have died from COVID-19 with access and appropriate use of lifesaving tools that exist, COVID-19 can become a manageable disease with significantly reduced morbidity and mortality and lives can be saved. However more work remains to achieve this globally. The World Health Organization (WHO) recognizes the challenges countries face for maintaining their COVID-19 response while addressing competing public health challenges, conflicts, climate change and economic crises, and will continue to support countries in adjusting COVID-19 strategies to reflect

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the successes and leverage learnings of national responses [1]. Though fever with coughing and respiratory problems are the main symptoms of COVID-19 which resemble the primary indications of simple flu, but later complexity arises resulting very low oxygen saturation in body. Primarily it was apprehended that Corona viruses are transmitted in two modes: droplets during coughing or sneezing and contact transmission (contaminated hands). Disinfectants like hydrogen peroxide and sodium hypochlorite, etc. can destroy this virus. It is difficult to find out the spreading mechanism of COVID-19 because it can be silently carried by and transmitted from people without showing any symptoms, but this is critical to prevent the pandemic outbreak. The spread of the disease is frightening and a threat to human civilization [2].

In the rapid spread of epidemics, it is necessary to build mathematical models to estimate disease transmission, recovery rate, mortality, and other important parameters for different countries and different specific areas. From there, different countries can take precise and differentiated measures to control the spread of the disease. However, so far, important factors such as population density, policies, transmission mechanisms, and the lack of suitable vaccines, make it difficult to deal with a potentially contagious diseases such as high and fatal infections, especially in densely populated countries like India. In the past, various models have been proposed to understand the spread of disease. These models can be classified into two categories, namely agent-based models (Bonabeau 2002; Schelling 1971; Sun 2006) and compartmentalized models (Kermack and McKendrick 1927; Hethcote 2000; Goel et al. 2019)... Agent-based models are used to simulate the entire actions and interactions of autonomous agents (Epstein 2009). These actors can be both individual or collective entities such as organizations or groups. In contrast, differential equations are used in compartment models, in which the population is divided into different compartments such as suspected (S), infected (I) and recovered (R) (Kermack et al. McKendrick 1927). Several other variants of these models have also been proposed such as SI (Hurley et al. 2006), SIS (Nåsell 1996), SIR (Kermack and McKendrick 1927) and SIRS (Jin et al. 2007) [3].

Due to the rapid spread and danger of respiratory infections, the application of disease prediction models is really necessary. Therefore, this topic proposes to build a dashboard and predictive model of the COVID-19 epidemic by SIR model to contribute a small part in limiting the spread of the disease.

# 2 Methodology

### 2.1 Formula of SIR model



Figure 1 Scheme of the SIR model

The SIR model is used to describe disease transmission through the interaction of three different variables:

S = Number of individual but not yet infected with the disease.

I = Number of individual infected with COVID-19

R = Number of individual who have recovered from the disease and now have immunity to it.

Assume that a fixed population of N individual, whereby there are no births and deaths by natural cause i.e.

N=S+I+R

The variables change overtime, so we will define the variable  $t = time in days and the model haves two parameters <math>\beta$  and  $\gamma$  with  $\beta$ ,  $\gamma > 0$ . With these parameters, the model uses three differential equations.

The rate of change of the number of the individual susceptible to the disease over time

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

The rate of change of the number of the individual infected

$$\frac{dS}{dt} = \beta IS - \gamma I$$

The rate of change of the number of the individual recovered over time

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

The basic reproduction number  $(R_0)$  is defined as the average number of people infected by a single individual. It represents the ratio of transmission and recovery rates

$$R_0 = \frac{\beta}{\gamma}$$

### 2.2 Fourth-order Runge-Kutta method

This method was discovered by German mathematician Carl Runge (1856-1927) and Wilhelm Kutta (1867-1944). The rationale behind this method is to defend almost Taylor, but in the settlement of GDP by Taylor method is not practical because the method requires derivative calculations [4]. In comparison to the Runge-Kutta method of previous orders, the fourth-order Runge-Kutta method is the most exacting. In order to solve a differential equation, the fourth-order Runge-Kutta method is frequently employed.

$$\frac{dy}{dt} = f(t, y)$$
$$y(t_0) = y_0$$

Where y(t) is the unknown function (scalar or vector). The form as follows equation of the fourthorder Runge-Kutta method:

$$y_{n+1} = y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

With

$$k_{1} = hf(t_{n}, y_{n})$$

$$k_{2} = hf(t_{n} + \frac{1}{2}h, y_{n} + \frac{1}{2}k_{1})$$

$$k_{3} = hf(t_{n} + \frac{1}{2}h, y_{n} + \frac{1}{2}k_{2})$$

$$k_{4} = hf(t_{n} + k_{3}, y_{n} + k_{3})$$

In addition to being easier to program, stable, and with smaller cut and rounding mistakes than the previous order Runge-Kutta method, this method also has a superior accuracy of the answer.

#### 2.3 Datasets

Via Microsoft Power Bi software, this dataset was collected from Novel Coronavirus (COVID 19) Cases by the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) supported by ESRI Living Atlas Team and the Johns Hopkins University Applied Physics Lab (JHU APL) [5].

Country/Region	Date	Confirmed Cases	Deaths	Recovered
Vietnam	Wednesday, January 22, 2020	0	0	0
Vietnam	Thursday, January 23, 2020	2	0	0
Vietnam	Friday, January 24, 2020	2	0	0
Vietnam	Saturday, January 25, 2020	2	0	0
Vietnam	Sunday, January 26, 2020	2	0	0
Vietnam	Monday, January 27, 2020	2	0	0
Vietnam	Tuesday, January 28, 2020	2	0	0
Vietnam	Wednesday, January 29, 2020	2	0	0
Vietnam	Thursday, January 30, 2020	2	0	0
Vietnam	Friday, January 31, 2020	2	0	0
Vietnam	Saturday, February 01, 2020	6	0	1
Total		10779632	43093	54332
Figure 2 Datasets				

The Dataset including Confirmed Cases, Deaths Case, Recovered Cases collected up to June 2022 as shown by Figure 2.

# 3 Result and discussion

# 3.1 COVID-19 Dashboard

In this paper, Dashboard created using Microsoft Power BI data visualization blocks combines with datasets to build dynamic data tables and combine them to form dashboard, with open source data from the internet is collected and processed using Microsoft Power BI software along with data visualization through the COVID-19 Dashboard. The results shown in figure 3 include information such as Confirmed Cases, Deaths Cases, Recovered Cases, Active Cases, New Cases, New Deaths, Fatality Rate, Recovery Rate. There are two tables used for data retrieval, the same data filtering table and some basic statistical charts about the epidemic.



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The use of Microsoft Power Bi comprehensively supports and improves processing and querying, retrieving data quickly and easily. Through the dashboard for an overview of the epidemic in Vietnam with the amount of data updated synchronously with the COVID-19 data warehouse of the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) on 24 hours a day.

#### 3.2 SIR model

Figure 4 shows the simulation results of the SIR model through the three factors Susceptible, Infected and Recovered according to simulation date.



The results of the SIR model show that in the first 150 days or so the value of infected begins to show signs of increasing, infected values accelerated between 170 days of the epidemic, to between 200 and 250 days the spread of the disease peaked, the epidemic began to show signs of decreasing and declining from the 250th day onwards.

To survey the applicability of the SIR model to reality, in this article the SIR model has been fit with the actual data represented in Figure 5.



Figure 5 Fit SIR Model for Vietnam

Figure 4 shows that the suitability of the SIR model is feasible in the first 400-500 days of the COVID-19 pandemic in Vietnam, this is the time when the epidemic has just appeared, so there are not many variable factors affecting the community. However, by the 550th day onwards the model began to have many errors resulting in diminished suitability. Typically, on the 800th day is the peak of the epidemic in Vietnam with the number of cases >400 000 cases, but the model only predicts a strong outbreak with a scale of <100000 cases.

With the simulation of the SIR model, the three basic parameters of the forecast model are the infection rate, recovery rate, the basic reproduction number is  $\beta = 0.4484$ ,  $\gamma = 0.4333$ ,  $R_0 = 1.035$ . The basic reproduction number  $R_0 = 1.035$  near the epidemic equilibrium  $R_0 = 1$  means that the epidemic is entering the "clean" period, which means that the infection rate is decreasing, recovery will increase rapidly, the epidemic becomes safe.

There are several reasons why the SIR model error has ignored factors that have a great influence on the course of the epidemic such as vaccines, overcrowded hospitals, social distancing.... the model lacks objectivity when based on unrealistic assumptions such as the population being considered closed in the SIR model. but in fact, that the population moves, changes constantly lead to the composition of susceptible (S) constantly changing distorting the model. In addition, the SIR model follows the assumption that individuals are infected with COVID-19 or vaccinated against the disease is not at risk of disease i.e., completely immune, this assumption is unrealistic as these individuals are still capable of reinfection. [6]

# 4 Conclusion

The amount of data collected from the COVID-19 Dashboard through Power BI makes sense for future researches. Dashboard brings a clearer view of the COVID-19 pandemic in the current situation to give directions to handle and control the pandemic. SIR model is a simple and accessible model that

helps give an overview of the COVID-19 pandemic on Susceptible, Infected, Recovered and the progress of infection as well as forecasting some temporary peaks in the future.

Overall, the results show that the applicability of the SIR model to the epidemic is feasible in the early stages of the epidemic and in a situation where there is not much variation and is constrained by certain factors in terms of individual size and external factors, so it is necessary to make some adjustments to the situation of each research subject to achieve more accurate results.

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