An SEIR Model for Investigation on Covid-19 Pandemic of Indian Kerala Region with Vaccination and Quarantine

Yi Yang
Biomedical Engineering, Rutgers University, New Jersey, United States
Email: yy520@scarletmail.rutgers.edu

***Abstract*—The covid-19 pandemic has caused a considerable number of casualties around the whole world. Although the vaccine has been developed and spread to society, the new variants Delta (B1.617.2) are gradually overwhelming the efficiency of the vaccine. In India, where the B1.617.2 variant originated, the total confirmed cases of a specific region named Kerala had exceeded 4.5 million at the beginning of October 2021. To help simulate and predict the tendency of the new B1.617.2 variant in this region, we develop a new Susceptible-Exposed-Infected-Removed (SEIR) model that also contains the two vaccine shot variables and two quarantine variables to simulate the spread of this kind of new variant much closer to reality. The whole SEIR model has 9 ODE functions and 14 constant parameters. We used MATLAB to calculate the 14 constant parameters with the actual dataset for the Kerala region and to make the final prediction on five specific variables: Infection, Death, Recovery, Vaccine 1st shot, Vaccine 2nd Shot. The final result shows that this SEIR model can make a satisfactory prediction on those variables.**

***Index Terms*—SEIR, COVID-19, Kerala, prediction, model, vaccine shot, quarantine**

I. Introduction

A. Covid-19 Virus Introduction

Covid-19, caused by the SARS-CoV-2 virus, is a highly transmissible and fatal disease first discovered in Wuhan, the capital city of Hubei Province in China, in 2019 and then rapidly spread to the whole world after only a few months [1]. According to a 2020 study, the Covid-19 virus shows nearly 77% similarity in sequence with the SARS-CoV-1 virus, which causes more than 5000 cases and 700 cases in mainland China [2], [3]. However, instead of having a nearly 10% death rate, the Covid-19 shows a milder fatality rate but a much higher transmission rate [4]. In a previous study, the household secondary attack rate for SARS-CoV-2 was nearly 6% percent higher than that of SARS-CoV-1 [5]. This rate explains why the covid-19 virus can infect a considerable amount of people in a short period. According to the WHO report, by September 24, 2021, there were about 230 million confirmed cases and nearly 5 million death cases being reported. According to Fig. 1 A and B, the American continent contributed the most deaths and confirmed cases [6]. Although different types of vaccines have been widely used across the world, SARS-CoV-2 has mutated into several variants such as Delta and Beta, and a recent study has shown that the new type of variant Delta is more resistant to the vaccine [7]. It shows that, for any vaccine analysis, the vaccine efficiency only shows 79.6% efficiency against the Delta variant, which is 8% less than the efficiency of the Beta variant. This effect on the efficiency of the vaccine indicates that only using the vaccine would not be enough to combat this virus since it mutates quickly and gradually becomes more resistant to the immune system.

An epidemic model that can simulate and predict the tendency of this pandemic can be a necessary subsidized method to help a certain region or the whole world to prepare for a possible catastrophe in future. The first mathematical epidemic model was developed by Daniel Bernoulli to analyze the connection between the longevity and elimination of the smallpox virus in 1760 [8]. In 1906, W. H. Hamer proposed the relationship between the rate of susceptible population and rate of infectious population. This idea was then developed by Sir Ronald Ross to model malaria with unintermitted time intervals in1908, and, finally, the Kermack and McKendrick model, which is a type of SIR model, was developed in 1927 based on Ross and Hamer's ideas [9].

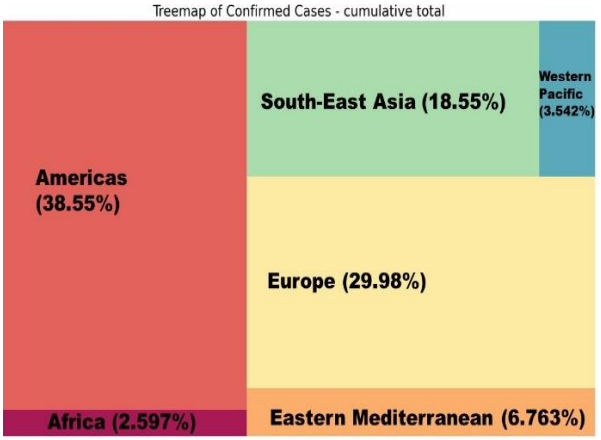
B. SEIR and SIR Model for Covid Prediction

The SEIR model is a type of time-dependent epidemic model that was improved from the original SIR model (Susceptible-Infected-Removed). (The standard SIR model was composed of three ODE equations: Susceptible, Infection, and Removed. Susceptible represents the population that is susceptible to the virus; Infection shows the population that has already been infected (from the susceptible population). The removed population arises from those in the infected group that have recovered or perished. The SEIR model contains one extra population, Exposed, which is the population that will be exposed to infection but still in the latent period [10]. The SEIR model has been proved with good accuracy in certain studies. In a study conducted by Leonardo Lopez and Xavier Rodo in

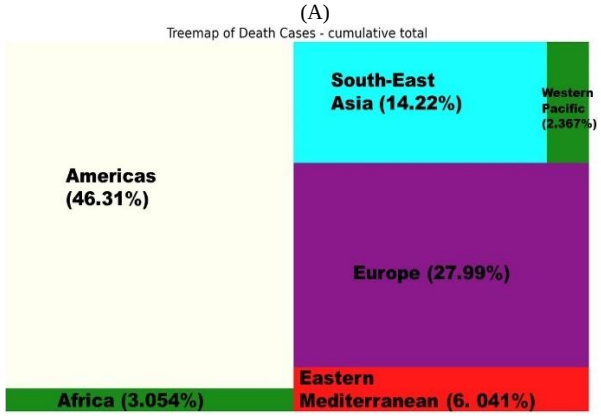
Manuscript received November 8, 2021; revised March 18, 2022.

doi: 10.18178/ijpmbs.11.4.76-83

2020, the SEIR model readily predicts Spain and Italy's infected, recovered, and dead population in 2020 [11]. Furthermore, the SIR model that has the time delay with the variable Infection, which has the nearly same theory as the Exposed variable of SEIR model, was also applied in a study in 2020 to simulate the tendency of the pandemic in certain regions of Chile, and the final result shows that this model has the ability to precisely simulate the infection variable of Antofagasta, Metropolitan, and Noble region of Chile [12].



(A)



(B)

Figure 1. The diagram shows that the American continent contributes the most confirmed (A) and deaths cases (B), Europe is the second one, and south-east Asia is the third one. The western-pacific and African region contributes the least death and confirmed cases.

However, the current normal SEIR model may not be not enough to correctly model real-world data since there exist more variables that can affect the tendency of this pandemic. For example, social distancing variable and hospital quarantine variable were shown more accurate ways to simulate the tendency of covid in two studies [13], [14]. The vaccination variable can be another important variable to affect the current situation of pandemic. In the recent study, vaccination has shown an important role in affecting other variables in the SEIR model, and the final result shows that the earlier the application of vaccination can control the spread of covid-19 pandemic much more efficiently [15].

In this study, we conducted comprehensive research on developing a more complex SEIR model and making the model much closer to reality. Compared to the model being conducted in previous studies, we add both Vaccine and Quarantine variables to predict the effect of the B1.617.2 variant of COVID-19 in the Indian Kerala Region with data from an official COVID-19 website [16], Kaggle [17], and Statista [18]. We picked this specific region from India for this study because this particular region has a much higher infected population than other regions and has a public database with several variables of interest. The Vaccine and Quarantine can play an essential role in controlling the Susceptible and Infected populations because they can affect the transmission between two related variants in the model. We used Python and MATLAB to perform data analysis and the SEIR model algorithm, and we used the results of the experiment to predict the next five months' tendency for COVID-19 in this region after the last day of the training dataset.

II. Method

A. Structure and Set up of SEIR Model

Before discussing the Structure of the model, there will be several rules that need to be clarified:

1) We postulate that the birth rate and death rate in the Kerala region is the same and as such the N0 will not change during the experiment and prediction time interval.
2) According to the database from Kaggle, we hypothesize that the fully vaccine shot efficiency will be 95% [17].
3) The Susceptible, Home quarantine, and the Hospital quarantine will be daily values (as opposed to cumulative) due to the restriction on source of the data.
4) The Vaccine 1st shot, Vaccine 2nd shot, Exposed, Infected, Recovered, and Death will be cumulative values.
5) We assume that the recovered population will not become susceptible again. According to previous studies, the acute immune response can last for about 6 months [19], and our prediction time period is shorter than that time interval.

The SEIR model was composed of 9 variables and 14 parameters, and their corresponding subjects and meaning were shown in Fig. 2 and Table I. The susceptible variable(S) was contributed by the population that were susceptible to being infected by the virus, and it was related to the exposed population with the rate "a*(I/N0)", which shows the percentage of infection in the exposed population at a later time, and that amount of population will be removed from the total N0 population daily. The vaccine 1 shot was connected to the susceptible population with the rate "1st shot". Considering the efficiency of the Indian vaccine with only one shot against B1.617.2 variant, it was being considered a part of the susceptible population, instead of removing from the Susceptible population directly. The vaccine 2nd shot was connected to the vaccine 1 shot with the rate "2nd shot". Furthermore, since the people who get the vaccine 2 shot must have the first shot, the vaccine 2nd shot number will not be removed from the vaccine 1 shot number also. However, they will

be removed from the susceptible population with 95% due the efficiency of the fully vaccinated people against B1.617.2 variant and they are immune to the infection of the virus. The Exposed population will receive the population being removed from the Susceptible population. Then, after the latent period, a certain amount of exposed population will become infective with the rate "θ" and be removed from the exposed population. The infected population will be connected to the Hospital quarantine and home quarantine population. Since we consider that people must be infected before they actually go to quarantine, the infective population will contain the population of home and hospital quarantine. The hospital quarantine population will be added with "β" rate from infective population, and home quarantine will receive population with rate "γ" from the infective population. Followed by that, the infective population, home quarantine population, and hospital quarantine population contribute the death population with the rate "IDE", "HSQD", and "HEQD" correspondingly. Finally, the total recovered population will be composed by Infection, Home quarantine, and Hospital quarantine with the rate "IRE", "HEQR", and "HSQR" separately.

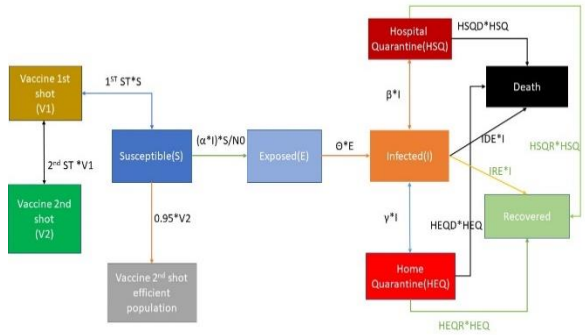


Figure 2. The structure of the SEIR model that contains vaccine 1st shot, vaccine 2nd, home quarantine, and hospital quarantine.

TABLE I. ALL PARAMETERS FOR THE SEIR MODEL AND THEIR CORRESPONDING MEANING

1st shot	First Vaccine shot rate	β	Rate of infection to hospital quarantine
2nd shot	Second vaccine shot rate	γ	Rate of infection to home quarantine
a	Rate of percentage of exposed population	HSQD	Rate of death in hospital quarantine
N0	Total population in Kerala region 34 million	HSQR	Rate of recover in hospital quarantine
θ	Rate of exposed population into infection	HEQD	Rate of death in home quarantine
IDE	Infection death rate	HEQR	Rate of recover in home quarantine
IRE	Infection recover rate	0.95	Indian covid vaccine efficiency

B. *Model Algorithm for Prediction and Parameter Calculation*

The whole system was composed of 9 ODE equations, and, due to the lack of previous studies focused on this region that we researched, we calculated all parameters with a real dataset of Indian Kerala region ranging from 01/01/2021 to 05/19/2021. The software MATLABMATLAB was used to do all the parameter calculations and the final prediction, and formula 10 and formula (11) show the linear regression and a noisy measurement method that we used to calculate parameters. The ODE equation is the rate of change and times with the change of time. Then the value was added to the specific value (x(t)) on that day and finally plus the constant error value (d) to predict the value on the next day. The next step is to calculate the Parameters on each ODE equation.

$$\frac{dV1}{dt} = 1st\ ST * S \tag{1}$$

$$\frac{dV2}{dt} = 2nd\ ST * V1 \tag{2}$$

$$\frac{dS}{dt} = -\frac{a*I}{N0} * S - 0.95 * V2 \tag{3}$$

$$\frac{dE}{dt} = \frac{a*I}{N0} * S - \theta * E \tag{4}$$

$$\frac{dI}{dt} = \theta * E - IDE * I - IRE * I \tag{5}$$

$$\frac{dHSQ}{dt} = \beta * I - HSQD * HSQ - HSQR * HSQ \tag{6}$$

$$\frac{dHEQ}{dt} = \gamma * I - HEQD * HEQ - HEQR * HEQ \tag{7}$$

$$\frac{dD}{dt} = HSQD * HSQ + HEQD * HEQ + IDE * I \tag{8}$$

$$\frac{dR}{dt} = HSQR * HSQ + HEQR * HEQ + IRE * I \tag{9}$$

System of Equation I. The ODE equations for Vaccine 1st shot, Vaccine 2nd shot, Susceptible, Exposed, Infect, Home Quarantine, Hospital Quarantine, Recovery, and Death.

As the Matrix 1 shows that difference between the day n and day n+1 is being considered as the change of population at certain time interval that the ODE equation will represent, and, to calculate all 4 parameters in the matrix, 4 equations at different times were used. A For loop in MATLAB was applied to do the calculation. The parameter n is a random value that was spread into all the equations. Value a, b, and c are three random values being assigned to three other equations separately and must follow the rule: a is smaller than b and b is smaller than c. Furthermore, to deal with the parameter shared with several equations, those parameters will be collected and finally pick the most fitting one with the P-value test between the simulation data and actual data. After all the parameters were calculated and collected, a for loop was coded in the MATLAB script and calculated the prediction

value for the next 4 months from 05/17/2021. Table II shows part of the actual data table for training parameters of the SEIR model.

$$x(t+1) = \frac{\Delta x}{\Delta t} * \Delta t + x(t) + d \quad (10)$$

$$\mathrm{I(t+1)} = \frac{\mathrm{dI}}{\mathrm{dt}} * \Delta \mathrm{t} + \mathrm{I(t)} + \mathrm{dI} \quad (11)$$

Formula (10) and (11): Linear regression prediction model and the example of the infection formula for prediction. dI is the error range of the Infection prediction formula. For example, the error for vaccine 1 shot will be dV1.

$$\begin{matrix} D(n+1)-D(n) \\ D(n+a+1)-D(n+a) \\ D(n+b+1)-D(n+b) \\ D(n+c+1)-D(n+c) \end{matrix} = \begin{matrix} HSQ(n) & HEQ(n) & I(n) & 1 \\ HSQ(n+a) & HEQ(n+a) & I(n+a) & 1 \\ HSQ(n+b) & HEQ(n+b) & I(n+b) & 1 \\ HSQ(n+c) & HEQ(n+c) & I(n+c) & 1 \end{matrix}$$

The matrix shows how the parameter of the Recover equation was calculated.

TABLE II. PARTIAL ACTUAL DATA FOR TRAINING PARAMETERS OF THE SEIR MODEL. THE SUSCEPTIBLE VALUE WAS ESTIMATED FROM ALL THE OTHER VARIABLES AND THE EXPOSED VALUE WAS ESTIMATED FROM THE INFECTION VARIABLE

Date	Recover	Death	Infected	Susceptible	Exposed	Vaccine1	Vaccine2	HospitalQ	HomeQ
1-May-21	1261801	5308	1571183	23671094	2050888	6069726	1355690	25687	632316
2-May-21	1277294	5356	1606819	23585189	2085582	6069760	1356416	26526	663559
3-May-21	1293590	5405	1638778	23481616	2118262	6092349	1419105	27365	694801
4-May-21	1313109	5450	1664789	23388267	2147966	6110419	1466885	28204	726044
5-May-21	1339257	5507	1701979	23295531	2169368	6118358	1482126	29043	757286
6-May-21	1362363	5565	1743932	23179450	2200705	6137985	1567300	29882	788529

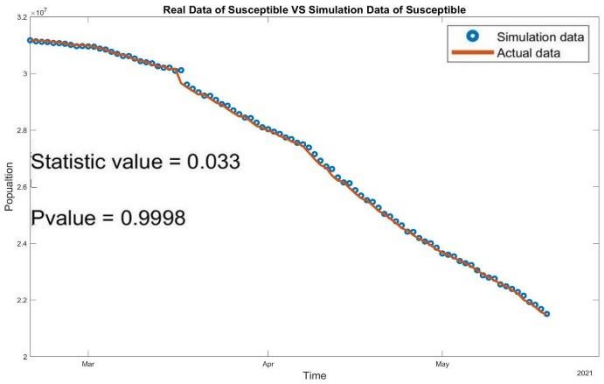
C. Analysis on the Prediction and Actual Data

To test the goodness of fitness between the prediction data and the actual data, we used Kolmogorov-Smirnov test (K-S test) of Python SciPy package to test the null hypothesis that the two dataset has the same distribution with P-value and the statistical value of the prediction and actual dataset. The Statistical Value represents the difference between the distribution of two datasets, and the P-value shows if the null hypothesis was rejected. Furthermore, the MATLAB Corr2 and GoodnessOfFit functions were deployed to test the corresponding fitness between the prediction data and the real data with the correlation coefficient value and Normalized Root Mean Square Error (NRMSE) that two functions returned. If the R square value and the Normalized RMSE value are close to 1and 0 separately, we will consider this as the model shows a good fitness with the corresponding actual dataset. Finally, the MATLAB Plot tool was also used to graph all the diagrams to show the visual difference between the model data and the actual data.

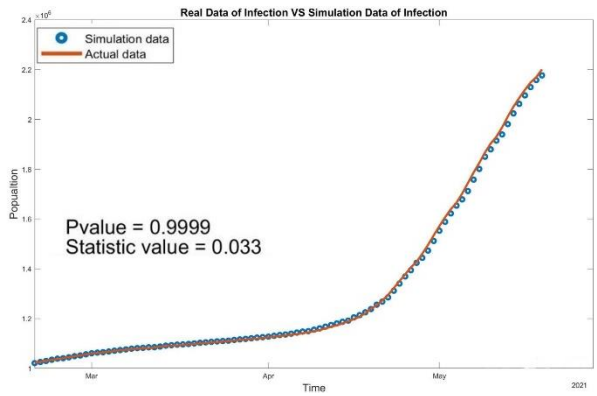
III. RESULT

A. Training Data and Parameter Result

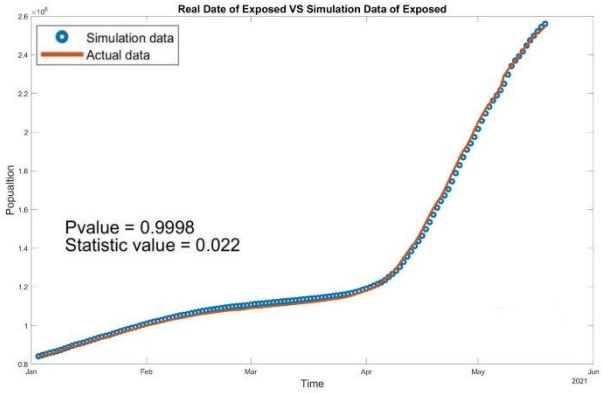
Fig. 3 shows the result of the training dataset of the SEIR model, and all the diagrams show a good visual fitness with the original data. The K-S test of nearly all variables fails to reject the null hypothesis that the distribution is same between the train and test dataset. The Susceptible, Exposed, and Infected variables show the best results. The P-value are considerably close to 1, and Statistic value is also smaller than 0.1, which shows a strong support on the null hypothesis. Compared to the others, hospital quarantine shows the greatest K-S statistic value, which shows there exists a difference between the distribution of training and testing data, and P-value is very close to 0.5. However, since it was not absolutely smaller than 0.05, we still decided to accept it and use parameters of this variable. Table III shows all the constant parameters of each equation and the corresponding error value of each variable equation. This result shows that the model has certain abilities to simulate the tendency in the training data and time interval. We use it to predict the next four months' data for vaccine, infection, recovery, and death variables and we collect the actual data that we can collect for the recent time for comparison.



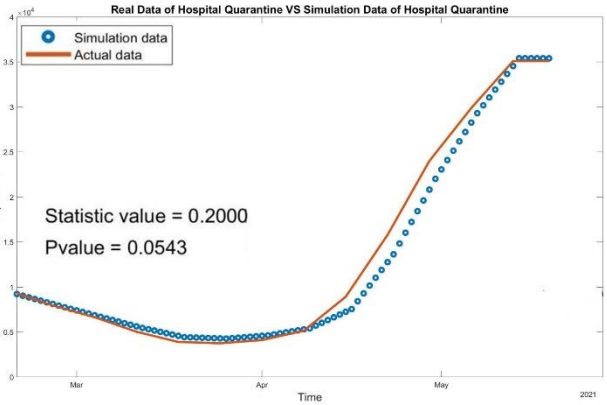
A. Susceptible diagram.



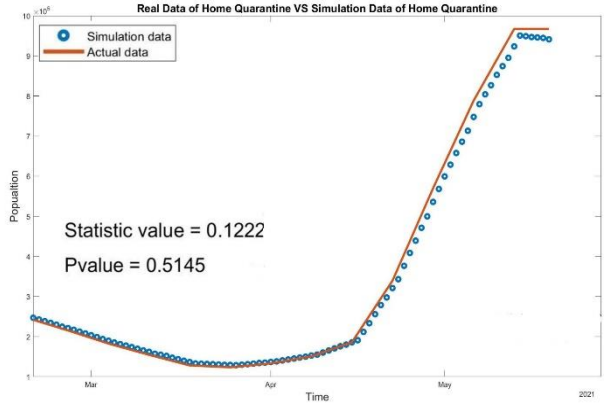
B. Infection diagram.



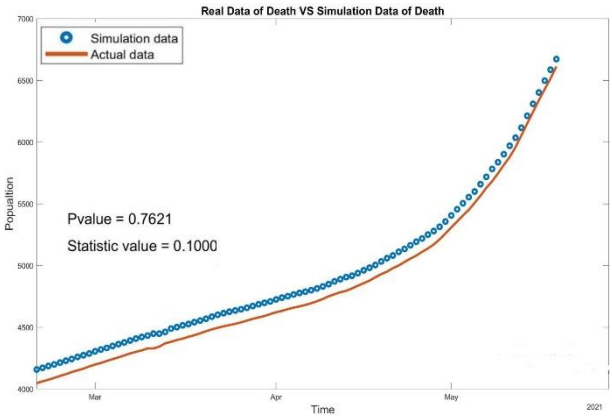
C. Exposed diagram.



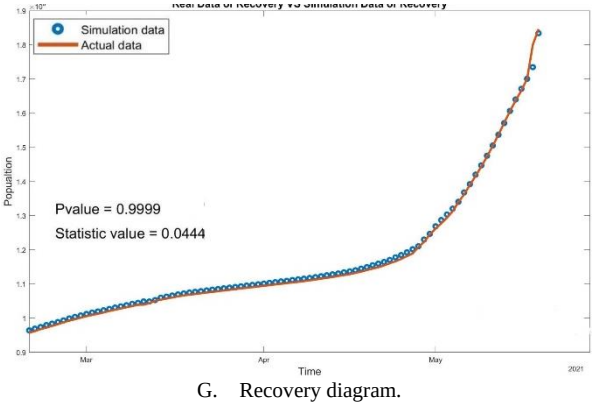
D. Hospital quarantine diagram.



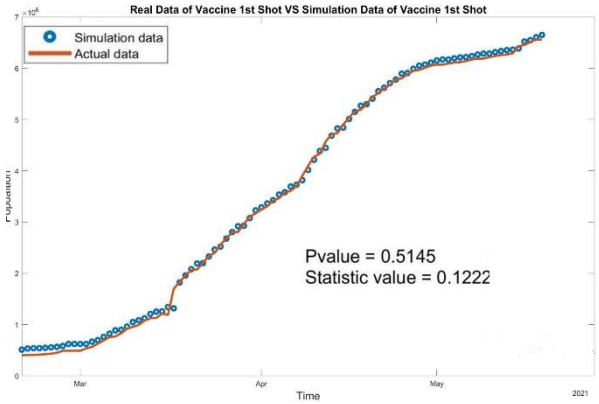
E. Home quarantine.



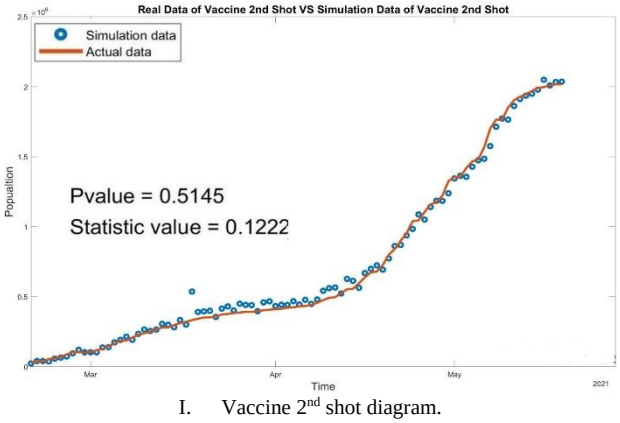
F. Death diagram.



G. Recovery diagram.



H. Vaccine 1st shot diagram.



I. Vaccine 2nd shot diagram.

Figure 3. (A, B, C, D, E, F, G, H, I): The collection of all the comparison diagrams——Susceptible(A), Infection(B), Exposed(C), Hospital Quarantine(D), Home Quarantine(E), Death(F), Recovery(G), Vaccine 1st Shot(H), and Vaccine 2nd Shot(I)——between the training data of the model and the actual data of the Kerala region from 02/19/2021 to 05/19/2021.

The corresponding values for rate for vaccine first shot (1st shot) and second shot (2nd shot) were 0.00726 and 0.42605, and the error for those variable prediction formulas were both 2,000. The rate of percentage of exposed parameter (a) for susceptible and exposed equations were 0.04332, and the rate of turning into infection (Θ) for exposed and infected equation was 0.38737. The errors for exposed and susceptible formulas are 2,000 and 1,000 according to the calculation. For the infection equation, the death rate of the infection (IDE) and recovery rate (IRE) of the infection were 1.10735e-04 and 0.03614, and the error value for infection prediction

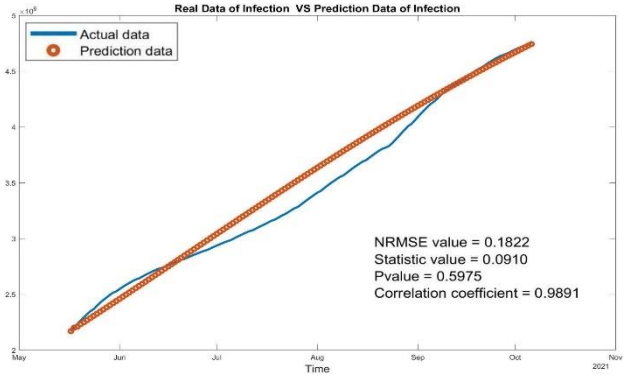
formula was about 2000. The rate of the infection to hospital quarantine (β) and to home quarantine (ϒ) were 0.00495 and 0.42521, and the death rate hospital (HSQD) and home quarantine (HEQD) were 0.00101 and 5.4743e-6. The reason that the death rate in the hospital was higher than that at home is that, depending on the local policy, patients who are already more severely infected are the ones who require hospitalization quarantine. The recovery rate for the hospital (HSQR) and home quarantine (HEQR) population were 0.18600 and 0.02247, and the error values for each equation were 0 and 1000, respectively. The hospital shows a place with the higher recovery rate and also the death rate. Finally, the death and recovery equations were composed by the death and recovery rate that has been introduced, and the extra two error values for them were 0 and 4900. The Recovery formula shows the highest error value among the calculations.

TABLE III. ALL THE PARAMETERS FOR EACH EQUATION AND THE CORRESPONDING ERROR OF EACH EQUATION

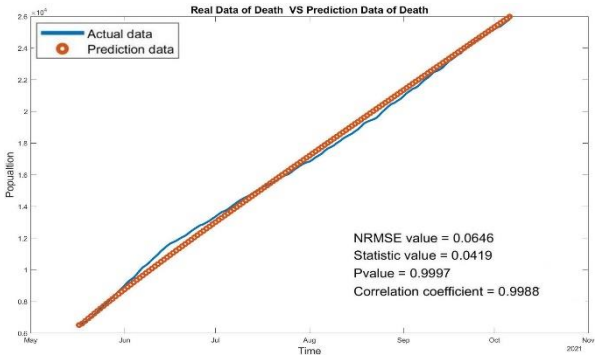
1st shot: 0.00726	Θ: 0.38737	HSQD: 0.00101	dV2: 2000	dHEQ: 1000
2nd shot: 0.42605	IDE: 1.10735e-04	HSQR: 0.18600	dS: 1000	dR: 4900
α: 0.04332	IRE: 0.03614	HEQD: 5.4743e-6	dE: 2000	dD: 0
N0: 34,000,000	β: 0.00495	HEQR: 0.02247	dI: 2000	
Vaccine efficiency: 0.95	ϒ: 0.42521	dV1: 2000	dHSQ: 0	

B. *Prediction Data and Actual Data Result*

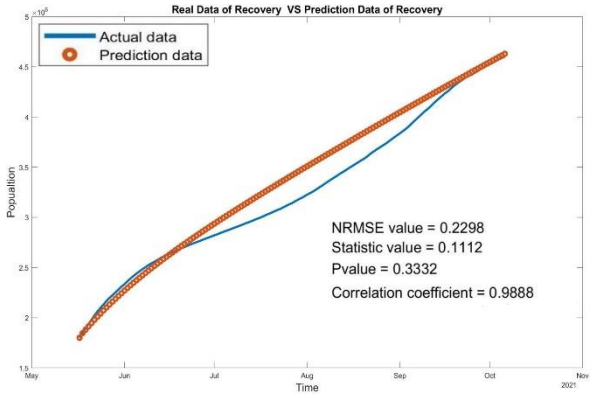
Fig. 4 shows the result of the diagram of the comparison between the prediction data and the actual data of five variables. The K-S Test result shows that the Statistic values for infection and recovery is about 0.0909 and 0.1112, and the P-value for them are 0.5975 and 0.3332. The p-value for each two variables was higher than 0.05, which fails to reject the null hypothesis that there exists a significant difference. Furthermore, the Statistic value is also very small that shows the difference in distribution of prediction and actual dataset is small. The death prediction is the most accurate in the prediction. The P-value is about 0.99, and the Statistics value is only 0.04, which shows that distribution between two values is negligible and fails to suggest a difference between two datasets. The vaccine 1st shot and vaccine 2nd shot two diagrams show the less accurate performance on the prediction. The Statistic value for vaccine 1st shot and 2nd shot were nearly 0.24 and 0.2 for each, and this shows a small but no significant difference on distribution on two datasets. However, the P-value for vaccine 1st shot and 2nd shot were nearly 0.006 and 0.008, which suggests the comparison between model data and the prediction rejected the null hypothesis, which shows the model has less ability to show certain tendency for vaccine prediction with current training parameter and SEIR model.



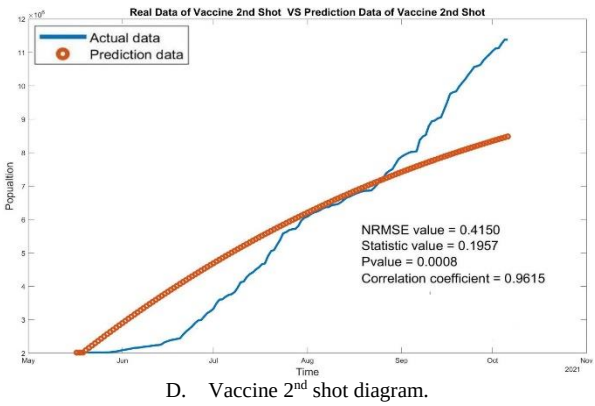
A. Infecction diagram.



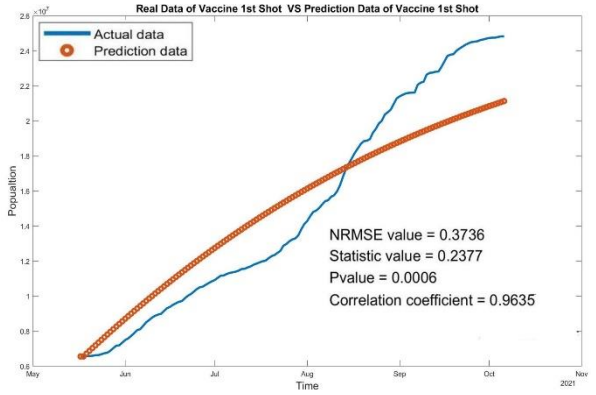
B. Death diagram.



C. Recovery diagram.



D. Vaccine 2nd shot diagram.



E. Vaccine 1st shot diagram.

Figure 4. (A, B, C, D, E): Infection(A), Recovery(B), Death(C), Vaccine 2nd Shot(D), and Vaccine 1st Shot(E) comparison diagrams for prediction data of model and actual data of Kerala Region ranged from 05/17/2021 to 10/06/2021, which is 5 months after our dataset. Since there is a lack of dataset for the quarantine values, we only show the diagram for the dataset that has the Actual dataset at the end of the experiment.

The Corr2 and GoodnessOfFit test show the different results, the coefficient correlation value for all 5 variables is all close to 1, which shows a good relationship between the prediction and actual value for all variables. The Normalized RMSE values from the GoodnessOfFit function show similar results to the K-S Test. The NRMSE value commonly shows a goodness of fit when the values are small enough and close to 0, and poor performance on the fitness when the value is bigger than 0.5. According to the test result, the NRMSE values for death, recovery, and infection were 0.0646, 0.2298, and 0.1822. The death model shows the best fitness between the predicted value of model and actual value, and predicted value for recovery and for infection also shows tendency with the fine performance due the small NRMSE value. The NRMSE values of vaccine 1st shot and vaccine 2nd shot, compared to the others, shows a relatively unsatisfactory performance. Both values of two variables are not small and also very close to 0.5, which shows an unsatisfactory fitness between the predicted value and the actual value.

IV. Discussion

The COVID-19 pandemic has already been around for about two years, and it still shows a possibility of not slowing down in the near future. Until October 2021, about 200 million cases have already been diagnosed in the whole world, and, according to WHO report, the total cases in countries like India have entered the scope of 34 million. In this study, we designed a new SEIR model that contains the quarantine and the vaccine variable to check the tendency of COVID-19 in the Indian Kerala region since May 2021. Comparing the currently available dataset and the prediction dataset from the model shows the ability to precisely predict the tendency of the death, confirmation, and recovery variable in the studies. The K-S Test shows that result of these three significant variables fail to reject the null hypothesis that two datasets have the same distribution, and the GoodnessOfFit test shows the Normalized Root Mean Square Error (NRMSE) value of three value are also small and close to 0, which also shows a proper fitness between the Actual dataset and the prediction dataset. The prediction diagram shows the tendency of the continuously blooming on three variables. We predict the total infection and recovery cases will go beyond 5 million by the end of October, and the death case will also reach 2,800 at the end of October.

The vaccine 1st shot and vaccine 2nd shot variable did not show a satisfactory result on the prediction. The K-S Test shows the result of the P-value of both variables rejecting the null hypothesis that the distribution is identical of two datasets. The GoodnessOfFit of both variables also shows relatively significant NRMSE values compared to the other three variables. However, this result is partially acceptable for us since certain varieties happen in the real world, which our model cannot adapt to. For example, the available vaccine resources can be booming when the government realizes the vaccine shortage and begins to push the manufacture of vaccines and import vaccines from other countries. Comparing the actual data of the training and prediction dataset, we find that the vaccine shot numbers show an unpredictable boom after May 19, which can cause problems that our model gradually loses the ability to predict vaccine shot tendency later. Therefore, a later improvement of the model on the vaccine shot prediction is still necessary, and we will publish the result in the latter study.

V. Conclusion

In conclusion, the Covid-19 pandemic is still causing distress and uncertainty around the world. A model that helps predict the tendency of disease related variables in the whole world and can be a critical factor that helps governments or medical systems to control this pandemic. And we hope the later study will create a better model and help stop this pandemic in certain countries.

Conflict of Interest

The author declares no conflict of interest.

Author Contributions

Yi Yang contribute all content in this paper, including data analysis, model creation, and writing the whole report.

References

[1] K. G. Andersen, A. Rambaut, W. I. Lipkin, E. C. Holmes, and R. F. Garry, "The proximal origin of SARS-CoV-2," *Nature Medicine*, vol. 26, no. 4, pp. 450-452, 2020.

[2] P. Zhou, *et al.*, "A pneumonia outbreak associated with a new coronavirus of probable bat origin," *Nature*, vol. 579, pp. 270-273, 2020.

[3] L. S. Hung, "The SARS epidemic in Hong Kong: What lessons have we learned?" *Journal of the Royal Society of Medicine*, vol. 96, no. 8, pp. 374-378, 2003.

[4] Y. Shi, *et al.*, "An overview of COVID-19," *Journal of Zhejiang University Science B*, vol. 21, no. 5, pp. 343-360, 2020.

[5] Z. J. Madewell, Y. Yang, I. M. Longini, M. E. Jr, Halloran, and N. E. Dean, "Household transmission of SARS-CoV-2: A systematic review and meta-analysis,"*JAMA Network Open*, vol. 3, no. 12, article e2031756, 2020.

[6] World Health Organization. World Health Organization. Retrieved November 4, 2021.

[7] J. L. Bernal, *et al.*, "Effectiveness of Covid-19 vaccines against the B.1.617.2 (Delta) variant," *The New England Journal of Medicine*, vol. 385, pp. 585-594, 2021.
[8] F. Brauer, "Mathematical epidemiology: Past, present, and future," *Infectious Disease Modelling*, vol. 2, no. 2, pp. 113-127, 2017.
[9] R. M. Anderson, "Discussion: The Kermack-McKendrick epidemic threshold theorem," *Bulletin of Mathematical Biology*, vol. 53, no. 1-2, pp. 3-32, 1997.
[10] P. Widyaningsih, D. R. Saputro, and A. W. Nugroho, "Susceptible Exposed Infected Recovery (SEIR) model with immigration: Equilibria points and its application," *AIP Conference Proceedings*, vol. 2014, article 020165, 2018.
[11] L. López and X. Rodó, "A modified *SEIR* model to predict the COVID-19 outbreak in Spain and Italy: Simulating control scenarios and multi-scale epidemics," *Results in Physics*, vol. 21, article 103746, 2021.
[12] P. Cumsille, Ó. Rojas-Díaz, P. M. de Espanés, and P. Verdugo-Hernández, "Forecasting COVID-19 Chile' second outbreak by a generalized SIR model with constant time delays and a fitted positivity rate," *Mathematics and Computers in Simulation*, vol. 193, pp. 1-18, 2022.
[13] S. Mwalili, M. Kimathi, V. Ojiambo, D. Gathungu, and R. Mbogo, "SEIR model for COVID-19 dynamics incorporating the environment and social distancing," *BMC Research Notes*, vol. 13, no. 1, p. 352, 2020.
[14] G. Rohith, "An augmented SEIR model with protective and hospital quarantine dynamics for the control of covid-19 spread," medRxiv preprint, 2021.
[15] Z. Xu, B. Wu, and U. Topcu, "Control strategies for COVID-19 epidemic with vaccination, shield immunity and quarantine: A metric temporal logic approach," *Plos One*, vol. 16, no. 3, article e0247660, 2021.
[16] Coronavirus in India: Latest Map and Case Count. (November 4, 2021). Coronavirus Outbreak in India. [Online]. Available: https://www.covid19india.org/
[17] Srk. (August 11, 2021). Covid-19 in India. Kaggle. [Online]. Available: https://wwwnc.cdc.gov/travel/notices/covid-2/coronavirus-india
[18] Statista Research Department, & 1, N. (November 1, 2021). *I*ndia: Number of suspected COVID-19 patients in Kerala by type 2021. Statista. [Online]. Available: https://www.pharmaceutical-technology.com/news/india-covid-19-coronavirus-updates-status-by-state/
[19] A. Radbruch and H. D. Chang, "A long-term perspective on immunity to COVID. *Nature*, vol. 595, pp. 359-360, 2021.

Yi Yang was born on June 22, 1999. He is a Senior undergraduate student in Biomedical engineering of Rutgers University (Bachelor 2022).