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Modeling the Impact of COVID-19 Variants and Vaccination Rate in Malaysia using SEIR Model

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Abstract
Malaysia has been hit with the novel coronavirus disease (COVID-19) since March 2020 until it is declared as an endemic in April 2022. There are a few COVID-19 variants that have emerged since there is evolution of the disease. This study aims to analyses the transmission dynamics of the COVID-19 variants, which are focusing on two different variants namely Delta and Omicron using the SEIR (Susceptible-Exposed-Infected- Removed) model, based on the compartmental models of infectious diseases. By using structure of SEIR model, a predictive model is developed based on ordinary differential equations (ODEs) system with the consideration of the rate of vaccinated population. The generation matrix method and Descartes's Rule of Sign has been used to check the stability of the model. The basic reproduction number, $R0$ also has been obtained. The equilibrium points of the system consist of two cases, which are disease-free equilibrium point (DFEP) and endemic equilibrium point (EEP) where both equilibrium points are stable. The simulation of the SEIR model was carried out using MATLAB. The finding shows that the symptoms and graphic for each variant is different and the number of vaccinated populations plays a huge role in the outcome. The results can be utilized to take pre-emptive actions against COVID-19 disease.

Keywords: COVID-19; Delta; Omicron; SEIR model; Generation matrix method; basic reproduction number; Descartes's Rule; DFEP; EEP

1. Introduction

The novel coronavirus disease or is known as COVID-19 is an infectious disease that is caused by SARS-CoV-2 virus and was announced as a pandemic on 12 March 2020 because of the global spread and has caused thousands of deaths since it first started in Wuhan, China in December 2019. According to WHO [1], it takes 5-6 days on average for the symptoms to be visible for the infected where it affects the lungs, kidneys, heart, liver, intestines, and brain [2]. However, the symptoms can vary according to the severity of the infection where the common symptoms are cough and dry fever while patients with severe symptoms will be having chest pain, shortness of breath and the inability to stay awake. Therefore, people with the conditions of high blood pressure, diabetes and cardiovascular diseases are more at risk of COVID-19 as it can lead to organ injury and multisystem organ failures.

In controlling the spread of the virus among the citizen, most countries have implemented the Movement Control Order or known as lockdown whilst waiting for the COVID-19 vaccines to be developed. Unfortunately, there are no specific cure for the COVID-19 disease. One of the ways to control the disease is by limiting the spread of virus with social distancing and vaccination. However, the cases were rising very quickly after several sporadic cases. Hence, the people need to get vaccinated as soon as they can to get the herd immunity and lower the number of cases in the country and could retain the economy back to normal. The first vaccine that has been administered in Malaysia was administered since the early of 2021 with the frontliners being among the earliest that were injected.

Mathematical models are widely used in epidemiology where it aids in forecasting the progression of infectious diseases and predict the likely result of an epidemic. This study will be using SEIR compartmental model to model the trend of cases in COVID-19 for Delta Variant and Omicron variant to understand the model. This model is typically extended by defining multiple compartments to introduce subpopulations hence that is why it is selected to solve the problem as it can be extended to include more parameters such as the number of vaccinated suspected population, v. The number of vaccinated suspected population is an important parameter in the compartmental models to see if the vaccines are working. Mathematical models may aid in exploring vaccine's protection at the individual level where it could help in assessing and building effective vaccination strategies. In 2022, the COVID-19 in Malaysia had become an endemic even though the number of cases is still high. Therefore, it is important to have the knowledge in trend of the cases with the symptoms that each variant carry to minimize the consequences for everyone.

This research aims to (1) obtain parameters in SEIR model by considering different variant of COVID-19 in Malaysia, (2) apply SEIR model in investigating the effectiveness of vaccines based on the different variant of COVID-19, (3) present the dynamic of the model graphically by using MATLAB.

2. Literature Review

Infectious diseases are the leading cause of death worldwide, especially in low- income countries. Several methods were being used in forecasting and predicting the trend of infectious disease to efficiently control and prevent breakouts on a wide scale. COVID-19 has been detected in Malaysia since January 2020 where the first three cases of COVID-19 were imported cases involving three Chinese tourists from Mainland China that had entered Malaysia and had been confirmed on January 25, 2020 [3].There are a few variants that has emerged from the COVID-10 disease such as Alpha variant, Beta variant and others. Each variant that emerged has their own symptoms to different individuals. A study by Menni et al. [4] shows that the prevalence of symptoms associated with an omicron infection varies from that of the delta SARS-CoV-2 variant, seemingly with less involvement of the lower respiratory tract and a lower likelihood of hospitalization.

Focusing on the importance and uses of compartmental models in epidemiology, a compartmental model is a framework in which a system is viewed as a series of compartments. There are many compartmental models with extension depending on the assumptions and parameters being studied. The Susceptible-Infected-Recovered (SIR) model is a basic statistical tool to analyses infectious disease outbreaks that were established by Ronald Ross, William Hamer and others in the twentieth century [5]. There was also another study done by Kar & Batabyal [6] where they had investigated the optimal control strategies in vaccination form to control the number of susceptible individuals and increase the number of recovered individuals where they used the SIR epidemic model in which the focus is in controlling and eradicating the diseases. Poonia et al. [7] had investigated the effect of vaccination and the implementation of social distancing in reducing the infection of COVID-19. Eventually, from the result of the simulation study, it can be deduced that social distance intervention and vaccination play a key role in combating COVID-19. Wang & Jia had investigated the stationary distribution of the SIRD epidemic model of Ebola disease with the consideration of double saturated incident rates and vaccination [8]. In the study, in order to obtain the stationary distribution, Lyapunov functions and Khasminkii’s theory had been used. From the result of the study, the calculations of the basic reproduction number shows that the disease dies out with the probability one. Different mathematical model with different parameters and assumptions could be used in modelling the spread of infectious disease according to the suitability.

3. Methodology

3.1. Model Formulation

SEIR model is a commonly used forecast method in forecasting the trend of infectious disease. The assumed progression in this model is for a susceptible individual to become infected through exposure with another infected individual. Following a period as an infected person, during which the individual is presumed to be contagious, the individual progresses to a noncontagious state, referred to as removed, which may entail death or had recovered. This model could be presented schematically as Figure shown below as proposed by Annas et al. [9].

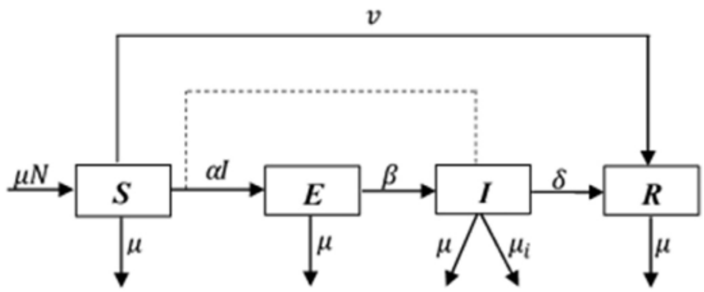

Figure 3.1 Schematic Diagram of SEIR Model

The model starts with some basic notations where the total population, N(t) is divided into four classes that is S(t),E(t),I(t) and R(t) where S(t) is the number of susceptible individuals at time t, E(t) is the number of exposed individuals at time t, I(t) is the number of infected individuals at time t, and R(t) is the number of recovered individuals at time t.

The governing equations describing the SEIR model can be described by a set of ordinary differential equations as below:

$$\frac{dS}{dt} = \mu N - (\alpha I + \mu + v)S \tag{1}$$

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E \tag{2}$$

$$\frac{dI}{dt} = \beta E - (\mu_i + \delta + \mu)I \tag{3}$$

$$\frac{dR}{dt} = \delta I + vS - \mu R \tag{4}$$

where the parameters are

α : the transmission of disease between S(t) and E(t) in a time period
β : the transmission of disease between E(t) and I(t) in a time period
μ : is the death and birth rate which are assumed to be equal
μ_i: the disease induced death rate
δ : the recovery rates
v : the vaccinated susceptible population

3.2. Stability Analysis of SEIR model

3.2.1 Equilibrium Points

Based on the equation (1) – (4), stability analysis is carried out to determine the disease-free equilibrium point and endemic equilibrium point. In order to determine the equilibrium points, the equations in (1) – (4) must be equal to zero.

Thus,

$$\mu - (\alpha I + \mu + v)S = 0 \quad (5)$$
$$\alpha IS - (\beta + \mu)E = 0 \quad (6)$$
$$\beta E - (\mu_i + \delta + \mu)I = 0 \quad (7)$$
$$\delta I + vS - \mu R = 0 \quad (8)$$

3.2.1.1 Disease Free Equilibrium Point (DFEP)

The equilibrium points for disease-free are conditions where there is no spread of COVID-19, hence $E = I = 0$.

From Equation (5),

$$\mu - (\alpha I + \mu + v)S = 0$$
$$\mu - (\mu + v)S = 0$$
$$(\mu + v)S = \mu$$
$$S = \frac{\mu}{(\mu + v)}$$

From Equation (8),

$$\delta I + vS - \mu R = 0$$
$$vS - \mu R = 0$$
$$vS = \mu R$$
$$R = \frac{v}{(\mu + v)}$$

Hence, the DFEP obtained are

$$(S, E, I, R) = \left(\frac{\mu}{(\mu + v)}, 0, 0, \frac{v}{(\mu + v)}\right) \quad (9)$$

3.2.1.2 Endemic Equilibrium Point (EEP)

The endemic equilibrium points are used in indicating the possibility of the spread of the disease. The conditions for endemic disease spread is $S \neq 0, E \neq 0, I \neq 0, R \neq 0$.

From Equation (5) – (8), the EEP obtained are

$$(S,E,I,R) = (\frac{(\mu_I+\delta+\mu)(\beta+\mu)}{\alpha\beta}, \frac{\alpha\beta\mu-(\mu_I+\delta+\mu)(\mu+v)}{\alpha\beta}, \frac{\alpha\beta\mu-(\mu_I+\delta+\mu)(\mu+v)(\beta+\mu)}{\alpha(\mu_I+\delta+\mu)(\beta+\mu)}, \frac{\delta\alpha\beta\text{^}2\,\mu-\beta(\mu\_I+\delta+\mu)(\mu+v)(\beta+\mu)-v\big((\mu_I+\delta+\mu)(\beta+\mu)\big)^2}{\beta\alpha^2((\mu_I+\delta+\mu)(\beta+\mu))}) \quad (10)$$

3.2.1.3 Stability Analysis of the Equilibrium Points

To study the stability analysis of the equilibrium points, Jacobian Matrix is used to linearize the model. Based on the equation (4) – (7), the Jacobian matrices are

$$\boldsymbol{J} = \begin{bmatrix} -(\alpha I+\mu+v) & 0 & \alpha S & 0 \\ \alpha I & -(\mu+\beta) & \alpha S & 0 \\ 0 & \beta & -(\mu_i+\delta+\mu) & 0 \\ v & 0 & \delta & -\mu \end{bmatrix} \quad (11)$$

Then, find the eigenvalue of the Jacobian matrix by using determinant,

$$\det(\lambda I - J) = \begin{vmatrix} \lambda+(\alpha I+\mu+v) & 0 & -\alpha S & 0 \\ -\alpha I & \lambda+(\mu+\beta) & -\alpha S & 0 \\ 0 & -\beta & \lambda+(\mu_i+\delta+\mu) & 0 \\ -v & 0 & \delta & -\mu \end{vmatrix} = 0$$

Substitute $S = \frac{\mu}{(\mu+v)}$ and $I = 0$,

$$\begin{vmatrix} \lambda+(\mu+v) & 0 & -\alpha\mu(\mu+v)^{-1} & 0 \\ 0 & \lambda+(\mu+\beta) & -\alpha\mu(\mu+v)^{-1} & 0 \\ 0 & -\beta & \lambda+(\mu_i+\delta+\mu) & 0 \\ -v & 0 & -\delta & \lambda+\mu \end{vmatrix} = 0$$

The eigenvalues are

$$(\lambda+\mu)\big(\lambda+(\mu+v)\big)\left(\big((\lambda+(\mu+\beta)\big)(\lambda+(\mu_i+\delta+\mu)\big) - \frac{\alpha\beta\mu}{(\mu+v)}\right) = 0 \quad (12)$$
$$(\lambda+A)(\lambda+B)\big((\lambda+C)(\lambda+D)-E\big) = 0$$

With $A = \mu, B = (\mu+v), C = (\mu+\beta), D = (\mu_i+\delta+\mu), E = \frac{\alpha\beta\mu}{(\mu+v)}$

Thus, the characteristic equations are:

$$\lambda^4 + (A+B+C+D)\lambda^3 + (AB+(A+B)(C+D)+CDE)\lambda^2 + \big((A+B)(CD-E)+AB(C+D)\big)\lambda + ABCD - ABE = 0 \quad (13)$$

Based on the Descartes' rule, the number of possible negative roots of the characteristic equations rely on the coefficient sign, hence it has four negative values if it is in the form as below:

$$P(\lambda) = L_1\lambda^4 - L_2\lambda^3 + L_3\lambda^2 - L_4\lambda + L_5 \quad (14)$$

where

$$L_1 = 1$$
$$L_2 = A + B + C + D$$
$$L_3 = AB + (A + B)(C + D) + CD - E$$
$$L_4 = (A + B)(CD - E) + AB(C + D)$$
$$L_5 = ABCD - ABE$$

From Equation (14), the number of variations $P(-\lambda) = 4$.
Hence, the equilibrium point is asymptotically stable as the characteristic value of the equation system in the COVID-19 model are negative.

3.2.2 Basic Reproduction Number (R_0) for COVID-19

R_0 or is known as basic reproduction number, is an epidemiological metric that is used to determine the contagiousness of an infectious disease. R_0 values are estimated using the ordinary differential equations. In this case, the R_0 of the SEIR model is determined using the matrices generation method. Matrix F represents the rate of appearance of new infections in different compartments while matrix V represents the transmission rate of individuals from one compartment to another.

From Equation (3.1) – (3.4),

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E$$

$$\frac{dI}{dt} = \beta E - (\mu_i + \delta + \mu)I$$

Let F = $\begin{pmatrix} \alpha IS \\ 0 \end{pmatrix}$ and V = $\begin{pmatrix} -(\beta + \mu)E \\ \beta E - (\mu_i + \delta + \mu)I \end{pmatrix}$

Then, let $F_1 = \alpha IS$ and $F_2 = 0$

$$F = \begin{pmatrix} \frac{\partial}{\partial E}(\alpha IS) & \frac{\partial}{\partial I}(\alpha IS) \\ \frac{\partial}{\partial E}(0) & \frac{\partial}{\partial I}(0) \end{pmatrix}$$

$$= \begin{pmatrix} 0 & \alpha S \\ 0 & 0 \end{pmatrix}$$

$$= \begin{pmatrix} 0 & \frac{\alpha\mu}{\mu+v} \\ 0 & 0 \end{pmatrix}$$

Next, let $V_1 = -(\beta + \mu)E$ and $V_1 = \beta E - (\mu_i + \delta + \mu)I$

$$V = \begin{pmatrix} \frac{\partial}{\partial E}(-(\beta+\mu)E) & \frac{\partial}{\partial I}(-(\beta+\mu)E) \\ \frac{\partial}{\partial E}(\beta E-(\mu_i+\delta+\mu)I) & \frac{\partial}{\partial I}(\beta E-(\mu_i+\delta+\mu)I) \end{pmatrix}$$

$$= \begin{pmatrix} -\beta-\mu & 0 \\ \beta & -\mu_i-\delta-\mu \end{pmatrix}$$

Finding the inverse of V,

$$V^{-1} = \frac{1}{|V|}\begin{pmatrix} \mu_i-\delta-\mu & 0 \\ -\beta & -\beta-\mu \end{pmatrix}$$

$$= \frac{1}{(\beta+\mu)(\mu_i+\delta+\mu)}\begin{pmatrix} \mu_i-\delta-\mu & 0 \\ -\beta & -\beta-\mu \end{pmatrix}$$

$$= \begin{pmatrix} \frac{-\mu_i-\delta-\mu}{(\beta+\mu)(\mu_i+\delta+\mu)} & 0 \\ \frac{-\beta}{(\beta+\mu)(\mu_i+\delta+\mu)} & \frac{-1}{(\mu_i+\delta+\mu)} \end{pmatrix}$$

Then, finding FV^{-1},

$$FV^{-1} = \begin{pmatrix} 0 & \frac{\alpha\mu}{\mu+v} \\ 0 & 0 \end{pmatrix}\begin{pmatrix} \frac{-\mu_i-\delta-\mu}{(\beta+\mu)(\mu_i+\delta+\mu)} & 0 \\ \frac{-\beta}{(\beta+\mu)(\mu_i+\delta+\mu)} & \frac{-1}{(\mu_i+\delta+\mu)} \end{pmatrix}$$

$$= \begin{pmatrix} \frac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)} & \frac{-\alpha\mu}{(\mu+v)(\mu_i+\delta+\mu)} \\ 0 & 0 \end{pmatrix}$$

Find the eigenvalues of FV^(-1) using determinant,

$$det(FV^{-1}-\lambda I) = \begin{vmatrix} \frac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)}-\lambda & \frac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)} \\ 0 & -\lambda \end{vmatrix} = 0$$

$$= \left(\frac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)}\right)(-\lambda) = 0$$

$$|\lambda_1| = \lambda_1 = \frac{\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)}, \lambda_2 = 0$$

Hence, the R_0 is as follows as λ_1 is the dominant eigenvalue

$$R_0 = \left(\frac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)}\right)$$

4. Results and Discussion

The numerical simulation for SEIR Model for two of the COVID-19 variants namely Delta variant and Omicron variant is carried out using the ODE45 solver in MATLAB R2021b software. The dynamics of the graphical simulation is then analysed.

4.1 SEIR model of COVID-19

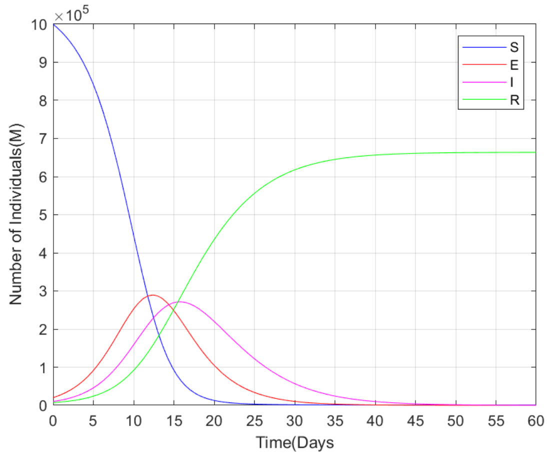

Figure 4.1 Graph of SEIR model

The graph above shows the classes of SEIR model where during this time, the number of vaccinated populations are zero. It shows a huge difference where the susceptible population decreases slowly until the twentieth day approximately while the exposed and infected population are quite high. The number of recovered populations goes up slowly until all who is infected are removed either they recovered or die.

4.1 Delta Variant

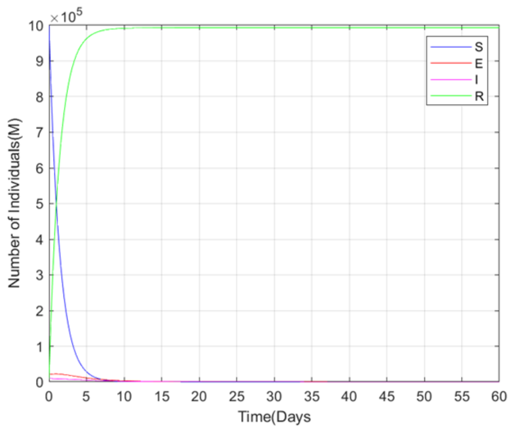

Figure 4.2 Graph of Delta Variant in Malaysia

Based on the graph above, it shows the graph of the classes of SEIR model where the parameters are set for the data taken during August 2021 to September 2021. It is suspected that during this range of time, the Delta variant is dominant among other COVID-19 variants that exist in Malaysia up to September 2021. The susceptible population decreases after 5 days while the exposed population and the infected population increases for 5 days before rapidly decreases and going flat after 10 days. The recovered population increases to the peak on day 5. Up until August 2021, at least 70% of the human populations in Malaysia had taken the COVID-19 vaccine whether it is Pfizer, Sinovac, or AstraZeneca.

4.2 SEIR Model for Omicron Variant

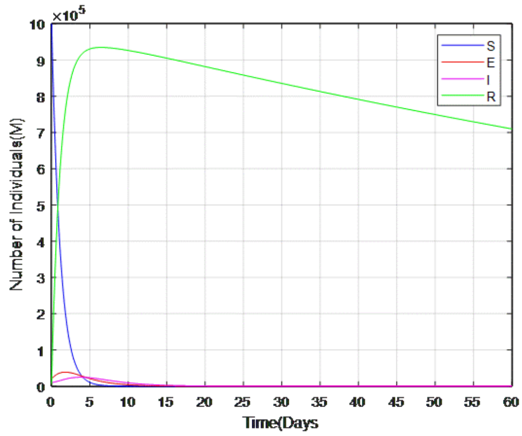

Figure 4.3 Graph of Omicron variant in Malaysia

The graph in Figure 4.3 shows the classes of SEIR model for Omicron variant. From the graph, it shows that the susceptible population decreases by day 5 while the exposed population increases rapidly only for the first 3 days approximately before decreasing and going flat before day 15. The same goes to infected population where the infected population starts declining and the line is flat by day 15. The recovered population increases rapidly before day 5 as the number of vaccinated people has reached at least 80.4%. The Omicron variant is different compared to Delta variant as it is highly contagious. However, the symptoms are mild compared to Delta variant as the hospitalization rates and death rates decreases even though the number of infected cases is rising rapidly during this range of time where the suspected range of time for Omicron variant to be dominant would be around early of the year 2022.

5. Conclusion

In this research, we studied the trend of COVID-19 variants namely Delta and Omicron and the relationship of vaccination rate of COVID-19 in Malaysia. We employed a SEIR compartmental model which is an extended model from the basic SIR model as an appropriate model to model the COVID-19 disease. Since April 1, 2022, COVID-19 disease has been declared as endemic as the possibility for the disease to dies out is impossible for the time being. As new variant emerged, the symptoms are becoming less severe and the hospitality rates and death rates are very low, where vaccination rate could be one of the biggest factors to cause the reduction of these rates. The findings from this study could be used to keep track on the variants that had emerged and might emerge from the mutation of the virus. The analysis of this model provides information on the severity of the variants of concern. The results showed that vaccination is the most effective way to combat the COVID-19 disease and reduce the hospitalisation rates and death rates.

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References

[1] World Health Organization: WHO. (2020, March 29). Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations. Retrieved December 1, 2021, from Who.int website: https://www.who.int/news- room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19- implications-for-ipc-precaution-recommendations

[2] Kumar, V., Doshi, K. U., Khan, W. H., & Rathore, A. S. (2020). COVID-19 pandemic: mechanism, diagnosis, and treatment. Journal of Chemical Technology & Biotechnology, 96(2), 299–308. https://doi.org/10.1002/jctb.6641

[3] Hashim, J. H., Adman, M. A., Hashim, Z., Mohd Radi, M. F., & Kwan, S. C. (2021). COVID-19 Epidemic in Malaysia: Epidemic Progression, Challenges, and Response. Frontiers in Public Health, 9. https://doi.org/10.3389/fpubh.2021.560592

[4] Menni, C., Valdes, A. M., Polidori, L., Antonelli, M., Penamakuri, S., Nogal, A., … Chan, A. T. (2022). Symptom prevalence, duration, and risk of hospital admission in individuals infected with SARS-CoV-2 during periods of omicron and delta variant dominance: a prospective observational study from the ZOE COVID Study. The Lancet. https://doi.org/10.1016/S0140-6736(22)00327-0

[5] Sir, W., & Ross, R. (2013). The SIR model and the Foundations of Public Health. 17(3), pp. Retrieved from https://mat.uab.cat/matmat_antiga/PDFv2013/v2013n03.pdf

[6] Kar, T. K., & Batabyal, A. (2011). Stability analysis and optimal control of an SIR epidemic model with vaccination. Biosystems, 104(2-3), 127–135. https://doi.org/10.1016/j.biosystems.2011.02.001

[7] Poonia, R. C., Saudagar, A. K. J., Altameem, A., Alkhathami, M., Khan, M. B., & Hasanat, M. H. A. (2022). An Enhanced SEIR Model for Prediction of COVID-19 with Vaccination Effect. Life, 12(5), 647. https://doi.org/10.3390/life12050647

[8] Wang, P., & Jia, J. (2019). Stationary distribution of a stochastic SIRD epidemic model of Ebola with double saturated incidence rates and vaccination. Advances in Difference Equations, 2019(1). https://doi.org/10.1186/s13662-019-2352-5

[9] Annas, S., Isbar Pratama, Muh., Rifandi, Muh., Sanusi, W., & Side, S. (2020). Stability analysis and numerical simulation of SEIR model for pandemic COVID-19 spread in Indonesia. *Chaos, Solitons & Fractals*, *139*, 110072. https://doi.org/10.1016/j.chaos.2020.110072