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COVID-19 OVERVIEW IN SAUDI ARABIA USING THE *SIRV* MODEL

Sadiqah Al Marzooq [1]

[1] Al Yamamah University, Department of Mathematics and Natural Sciences, College of Engineering and Architecture, Riyadh, Saudi Arabia

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Corresponding Author

Sadiqah Al Marzooq,
S_Almarzooq@yu.edu.sa

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ABSTRACT

In this paper, we propose a modified SIR model with the consideration of vaccinated individuals called SIRV. We provide a proof that the model's solution is non-negative and derive the model reproduction number and steady state. Finally, we apply the model to analyze COVID -19 pandemic in Saudi Arabia over the last three years.

Keywords: *SIRV*, COVID-19, Model, Vaccine, Outbreak, Pandemic

1. INTRODUCTION

The COVID-19 pandemic is considered the most signifcant pandemic in this century, Alboaneen et al. (2020). To date, according to WHO dashboard, there are all most 652, millions confirmed cases including about 6.5 million deaths with almost thirteen billion vaccinated individuals. The virus was recognized on December 8, 2019, in Wuhan, China and then it spread worldwide. It's been considered as a pandemic on March 11, 2020, by the World Health Organization and called COVID-19. Saudi Arabia was one of the suffered by the pandemic Barry et al. (2020). The first COVID- 19 case in the kingdom was reported on March 2nd, 2020, and then the number has been increased rapidly to reach 4919 cases by the mid of

June 2020. On December 17, 2020, the ministry of health in Saudi Arabia has offered the first dose of the vaccine without fees to all citizens and residents in the kingdom, and the second dose in February 2021 which led to decrease the cases by the end of 2021.

One of the most significant methods that's been used to analyze the COVID-19 outbreak is mathematical modeling. Researchers have developed the susceptible - infected SI model by considering other compartments such as exposed, recovered, quarantined, and vaccinated individuals to predict the outbreak long term behavior applied them to their studies based on real data in different countries.

In Alboaneen et al. (2020), they apply the logistic growth model and the susceptible-infected-recovered SIR on real- time data of COVID-19 in Saudi Arabia during the first three months of the pandemic. The result of this paper predicts that the outbreak's end point is the end of June 2020.

In Riyapan et al. (2021), a new mathematical model called "SEI_sI_aQRD" formulated based on the seven compartments; the authors considered exposed, quarantined and death individuals beside (symptomatically and asymptomatically) infected, and recovered ones to study and analyze the long term behaviour of the COVID-19 in Thailand by calculating the equilibrium of the nonlinear system and the related reproduction number, the result provides the threshold at which the pandemic steady state is stable; that is if the reproduction number is greater than 1 which indicates that the outbreak won't die -out.

In Kozioł et al. (2020). a generalization of SIR model is presented based on the Grunwald- Letnikov derivative and discretization. The new model predicts the effects of fractional orders of the model derivatives on the dynamics of COVID-19. the simulations of the model have applied for two countries, namely Italy and Spain. The result of Italy indicates the effectiveness of this proposed model while it is limited in Spain.

In this paper, we introduce a model to study the dynamics of the COVID-19 outbreak with consideration of four compartments, set the model assumptions and prove that the proposed model has nonnegative solutions in Section 2. The model's steady state and the reproduction number along with the steady state stability analysis are presented in Section 3. Results and simulations are given for two different scenarios in Saudi Arabia in Section 4 and we discuss conclusions in Section 5.

2. THE CONTINUOUS SIRV MODEL

In this section, we introduce a classic model denoted by $SIRV$ analyze the dynamic of the COVID-19 virus based on four sub-populations which are susceptible, infected, recovered, and vaccinated individuals denoted by S, I, R and V, respectively. The model is governed by the system of non- linear ODEs (1) and subject to non- negative initial values

$$S(0) = S_o, \qquad I(0) = I_o, \qquad R(0) = R_o, \qquad V(0) = V_o$$

$$\frac{dS}{dt} = \omega - \alpha IS - \gamma S - \sigma S + \mu R$$

$$\frac{dI}{dt} = \alpha IS - \beta I - \sigma I$$

$$\frac{dR}{dt} = \beta I - \mu R - \sigma R \quad (1)$$

$$\frac{dV}{dt} = \gamma S - \sigma V$$

with consideration of the following assumption:

- All compartments are functions in time t with $N(t) = S(t) + I(t) + R(t) + V(t)$
- The four sub- populations are mixing around and they are equally at risk of getting infected by the virus.
- At time t, new births and residents are denoted by ω.
- The virus is transmitted from susceptible individuals to infected ones with a constant rate α.
- The recovery rate is also constant denoted by β.
- Due to loss of immunity, recovered individuals might have the virus again which means they return to the susceptible statue with a constant rate μ.
- The rate of natural death is represented by σ.
- The parameter 0 ≤ γ ≤ 1 represents the vaccination rate.

Figure 1 represents the model of the four compartments.

Figure 1

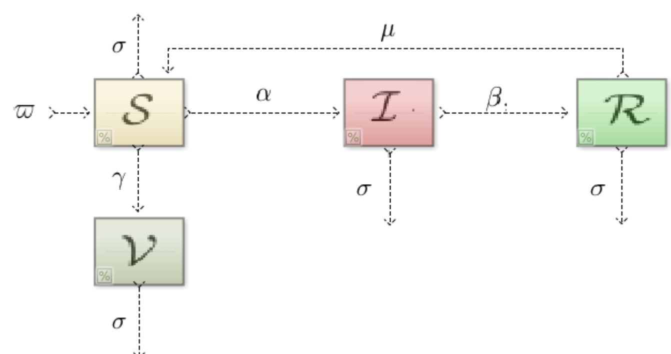

Figure 1 SIRV Model Flowchart

2.1. THEOREM

Under non-negative initial conditions, the system (1) has non- negative and bounded solutions.

Proof:

Let's prove that system (1) has non-negative solutions for all $t > 0$.

Starting with the first equation, let $\vartheta = \alpha + \gamma + \sigma$ since π and μ are positive, we get

$$\frac{dS}{dt} = \omega - \alpha IS - \vartheta S + \mu R \geq -\vartheta S$$

By integrating both sides and applying the IC, we get $S(0) = S_0$, we have $S \geq S_0 e^{-\vartheta t} \geq 0$ Similarly, we can prove that other solutions are non-negative for all t > 0.

Now, let's prove that the solutions are bounded.

By the assumption

$$N = S + I + R + V$$

we get

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} \tag{2}$$

and hence

$$dN + \sigma N = \omega\, dt$$

Therefore, the solution of the linear equation is

$$N = \frac{1}{\sigma}[\omega + ce^{-\sigma t}]$$

Apply the initial condition $N(0) = N_o$ we get $c = \sigma N_o - \omega$ and then

$$N = \frac{1}{\sigma}[\omega + (\sigma N_o - \omega)e^{-\sigma t}]$$

As $t \to \infty$ we deduce that which proves that the solutions are bounded.

$$N \leq \omega\sigma$$

3. STABILITY ANALYSIS OF THE MODEL'S STEADY STATE

3.1. THE MODEL'S STEADY STATE

The goal in section is to obtain the steady state of the proposed $SIRV$ of the system (1) by solving the homogeneous system governed by setting

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = \frac{dV}{dt} = 0$$

as a result, we get then non- trivial steady state given by

$$(S^*, I^*, R^*, V^*) = \left(\frac{\omega}{\gamma + \sigma}, 0, 0, \frac{\gamma\omega}{\sigma(\gamma + \sigma)}\right)$$

3.2. THE MODEL'S STEADY STATE

The dynamic of the infectious disease depends on $\mathcal{R}_0$, the reproduction number, which is denoted by the number of secondary cases can be caused by a single case. To calculate $\mathcal{R}_0$, consider the inequality $S \leq S_o$ at $t = t_0$ which leads to

$$\frac{dI}{dT} \leq (\alpha S_o - \beta - \sigma)I \tag{3}$$

and hence,

$$I \leq e^{(\alpha S_o - \beta - \sigma)t} \tag{4}$$

Inequality (4) indicates that if $\alpha S_o - \beta - \sigma < 0$ then $I \to 0$. Here, the ratio $\mathcal{R}_0 = \frac{\alpha S_o}{\beta + \sigma}$

represents the reproduction number which controls the pandemic if $\mathcal{R}_0 < 1$, otherwise the number of infected individuals will grow.

3.3. STABILITY OF THE STEADY STATE

To obtain the condition at which the steady state is stable, we calculate the linearized Jacobian matrix of system (1) about the fixed point (S^*, I^*, R^*, V^*) which given by the matrix

$$\mathfrak{J} = \begin{pmatrix} -(\gamma + \sigma) & 0 & \mu & 0 \\ 0 & \frac{\alpha\omega}{\gamma + \sigma} - (\beta + \sigma) & 0 & 0 \\ 0 & \beta & -(\mu + \sigma) & 0 \\ \gamma & 0 & 0 & -\sigma \end{pmatrix}$$

The eigenvalues of $\mathfrak{J}$ are

$$\begin{pmatrix} \lambda_1 \\ \lambda_2 \\ \lambda_3 \\ \lambda_4 \end{pmatrix} = \begin{pmatrix} -(\mu + \sigma) \\ -\beta + \frac{\alpha\omega}{\gamma + \sigma} - \sigma \\ -\sigma \\ -(\gamma + \sigma) \end{pmatrix}$$

Since we assumed that the parameters σ, μ and γ are non-negative, it is clear that $\lambda_1 = -(\sigma + \mu) < 0$, $\lambda_3 = -\sigma < 0$ and $\lambda_4 = -(\gamma + \sigma) < 0$. Now, we Notice that $\lambda_2 = -\beta + \frac{\alpha\omega}{\gamma+\sigma} - \sigma < 0 \leftrightarrow S^* < \frac{S_o}{R_0} \leftrightarrow \mathcal{R}_0 < \frac{S_o}{S^*}$ So, we can conclude that the steady state is stable if $\mathcal{R}_0 < 1 \leftrightarrow S_o < S^*$.

4. SIMULATION AND RESULTS

In this section we provide approximated solutions of system (1) by solving the associated discrete system numerically

$$
\begin{aligned}
S_n &= S_{n-1} + \Delta(\omega - \alpha I_{n-1} S_{n-1} - \gamma S_{n-1} - \sigma S_{n-1} + \mu R_{n-1}) \\
I_n &= I_{n-1} + \Delta(\alpha I_{n-1} S_{n-1} - \beta I_{n-1} - \sigma I_{n-1}) \qquad (5) \\
R_n &= R_{n-1} + \Delta(\beta I_{n-1} - \mu R_{n-1} - \sigma R_{n-1}) \\
V_n &= V_{n-1} + \Delta(\gamma S_{n-1} - \sigma V_{n-1})
\end{aligned}
$$

We apply the model to data sets in Saudi Arabia on three periods of time; year 1, year 2 and year 3 which represent the years 2020, 2021 and 2022, respectively, with a total number of populations $N = 35013 \times 10^{-3}$ and a constant new birth $\omega = 42200$. The parameters used in this study are as follow: $\beta = 0.007$, $\sigma = 3 \times 10^{-5}$ and $\mu = 3.5 \times 10^{-3}$ based on Ghostine et al. (2021). Figure 1 shows the result of the year 1 when $\alpha = 8.43 \times 10^{-9}$ and $\gamma = 0$ which provides a high value of the reproduction $\mathcal{R}_0 = 4.3$ due to the large number of infected individuals with non-vaccinated ones. In Figure 2, we study the case of the year 2 when $\alpha = 3.43 \times 10^{-9}$ and $\gamma = 1.2 \times 10^{-3}$, the result shows a significant decrease in $\mathcal{R}_0 = 1.7$ as the number of vaccinated people exceeds the number of infected individuals. Figure 3 shows the result of the year 3 when $\alpha = 1.43 \times 10^{-9}$and $\gamma = 2.4 \times 10^{-3}$and this provides $\mathcal{R}_0 = 0.7 < 1$ which provides that the number of infected people vanished and the virus die-out.

Figure 2

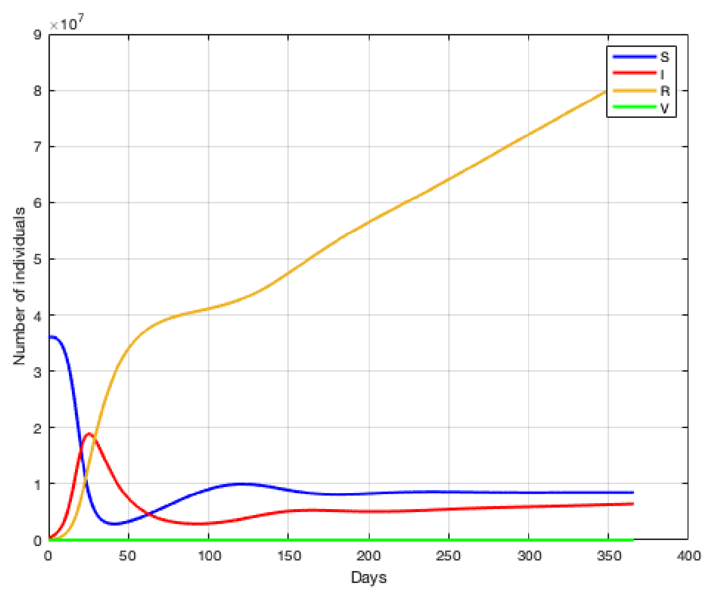

Figure 2 The Dynamic of COVID-19 in Year 1

Figure 3

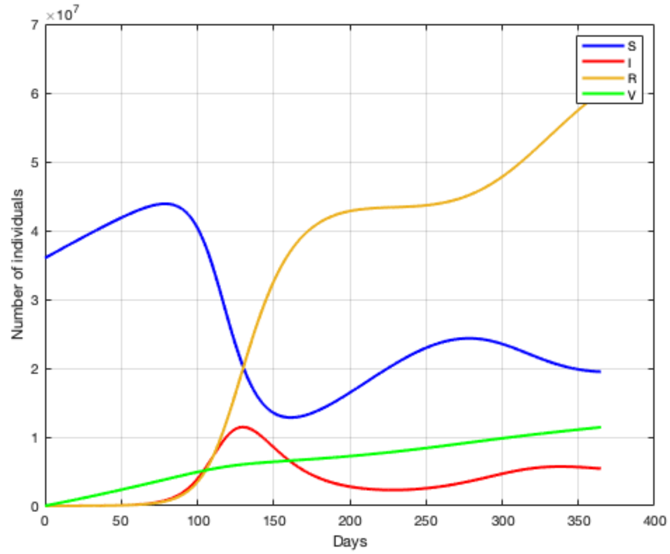

Figure 3 The Dynamic of COVID-19 in Year 2

Figure 4

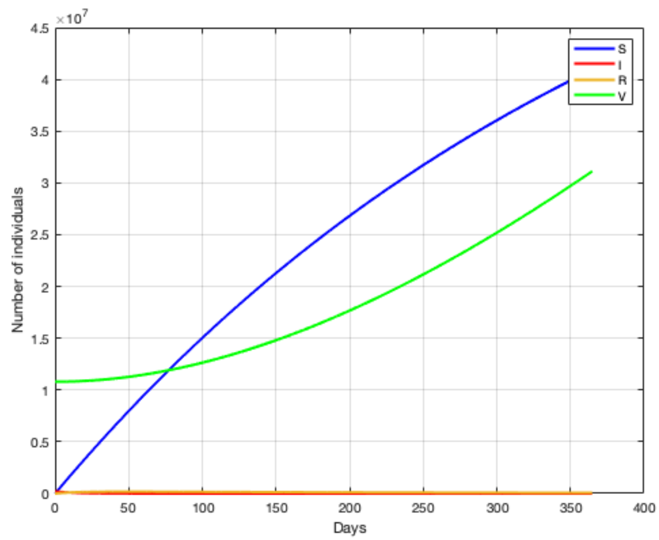

Figure 4 The Dynamic of COVID-19 in Year 3

5. CONCLUSION

In this paper, we present a classical model called the $SIRV$ in which we study four compartments to analyze the dynamic of the COVID-19 disease. The model is an extended model of the SIR with consideration of vaccinated individuals to study the impact of the vaccine on the virus's dynamic. We derived the model reproduction number along with the non-zero steady state theoretically. Simulations have been applied by solving the system numerically using three sets of real-time data in Saudi Arabia which provide a general overview of the pandemic in KSA.

CONFLICT OF INTERESTS

None.

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