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MODEL ANALYSIS OF THE SPREAD OF COVID-19 WITH LOGISTIC GROWTH RECRUITMENT

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ABSTRACT

This paper analyzes the COVID-19 model with the growth of the logistics recruitment rate. Based on the model determined, the nonendemic stability points, threshold, and endemic stability points are obtained. The nonendemic stability point is asymptotically stable if the spread of COVID-19 decreases and vice versa. If the spread of COVID-19 increases, the endemic stability P_1 is globally asymptotically stable. Based on numerical simulations, the greater the recruitment rate, then the greater number of susceptible and vaccinated subpopulation individuals. The smaller value of the contact rate between infected individuals and those who are still healthy, the lower number of infected individuals and vice versa, while the number of recovered subpopulation individuals is increasing. The greater rate of treatment, the lower number of infected individuals.

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1. INTRODUCTION

The spread of COVID-19 until 2022 has decreased, but every country is still trying to overcome the disease. Mathematicians, in collaboration with experts in the health sector, continue to conduct research in modeling, analyzing, evaluating, and optimizing the handling of the spread of COVID-19. Din (2020) examines to system analysis of the overall spread of COVID-19 [1]. Mathematical modeling is also studied in the COVID-19 epidemic by taking into account the effects of awareness programs in Nigeria [2]. Analysis of the Suspect-Latent-Asymptomatic-Infectious-Healed COVID-19 pattern of disease spread was studied, determining the threshold and the stability point [3]. Tian (2020) analyzed COVID-19 modeling based on morbidity data in Anhui, China [4]. Epidemic Modeling of SARS-CoV-2 of the SEIR type was studied in Italy using insightful intelligence calculations [5]. COVID-19 dynamics models by taking hereditary diseases into account have also been studied [6]. Fang (2020) analyzes the dynamics of the transmission of COVID-19 with government intervention [7].

Ma (2020) examines the exponential model of a disease and determines the threshold [8]. The COVID-19 pandemic model with logistical growth has also been studied [9], [10]. Logistic transmission patterns in the COVID-19 pandemic have been researched in the Asian region [11], di China [12], [13]. Tene (2021) analyzed the COVID-19 outbreak in Ecuador using a logistical model [14]. Global dynamics research and epidemic control strategies, a model on logistical growth, taking into account the limitations of hospital facilities, have also been carried out [15].

A co-infection model of COVID-19 and tuberculosis with the effect of isolation treatment has been studied [16]. Control of preventing the COVID-19 pandemic in the SIR type has also been researched in Indonesia [17]. Optimal control and simulation on the model of the COVID-19 pandemic have been analyzed by Araz (2021) [18]. Based on the results of the COVID-19 research study above, there has not been any study on recruitment rates with logistical growth, which will be analyzed and simulated in this paper.

2. RESEARCH METHODS

Population growth is generally in a logistical model. For this reason, it is assumed that the growth in suspected COVID-19 will be in a logistical form. P. F. Verhulst (1838) examine the logistics model [10]:

$$\frac{dP}{dt} = wP\left(1 - \frac{P}{K}\right),$$

with P, w, and K respectively, are the number of residents, population growth level, and the carrying capacity of the number of residents. dP/dt is the change in the number of residents per unit of day, which is influenced by the rate of population growth and carrying capacity.

The number of residents studied in this study was grouped into five subsections. Individuals who do not yet have the characteristic symptoms of being infected with COVID-19 enter the susceptible subpopulation (S). Individuals who do not yet have symptoms of COVID-19 and have been vaccinated enter the vaccination subpopulation (V). Individuals who have experienced symptoms of COVID-19 enter the E subpopulation. Individuals who have confirmed COVID-19 enter the infected subpopulation (I). People who are healed from COVID-19 enter the R subpopulation.

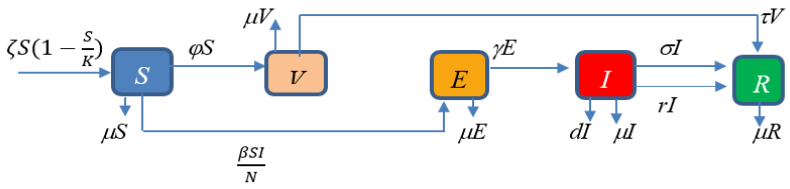

Figure 1. The Spread of SVEIR-type COVID-19 with Logistical Growth

The assumptions from the COVID-19 spread system studied are (1) Recruitment rate in the form of logistical growth. (2) Individuals of the S subpopulation who are in contact with the I subpopulation enter the E subpopulation. (3) Individuals from each subpopulation experience natural death, and I subpopulation individuals may die from COVID-19. (4) Individuals who are confirmed positive for COVID-19 can recover

due to increased body resistance through eating/drinking and multivitamins or due to treatment. Deployment dynamics of COVID-19 spread the distribution of the system is analyzed as shown in **Figure 1**.

Based on the assumptions and schematic diagrams above, a system of differential **Equation (1)** is obtained:

$$\begin{aligned}\frac{dS}{dt} &= \zeta S\left(1-\frac{S}{K}\right)-\frac{\beta SI}{N}-(\varphi+\mu)S\\ \frac{dV}{dt} &= \varphi S-(\tau+\mu)V\\ \frac{dE}{dt} &= \frac{\beta SI}{N}-(\gamma+\mu)E\\ \frac{dI}{dt} &= \gamma E-(\sigma+r+d+\mu)I\\ \frac{dR}{dt} &= \tau V+(\sigma+r)I-\mu R,\end{aligned} \tag{1}$$

with $N(t)=S(t)+V(t)+E(t)+I(t)+R(t)$.
Notation of parameters, description, and value of parameters as shown in **Table 1** below:

Table 1. Parameter Values for COVID-19 low transmission cases

Parameter	Description	Value	References
ζ	recruitment rate on logistics growth	0.1 – 0.99	[11]
β	infection rate	0.036	[6]
φ	vaccination rate	0.01 – 0.1	assumed
μ	natural death rate	1/(65 × 365)	[6]
τ	rate of vaccination immunity	0.01 – 0.1	assumed
g	rate from exposed to confirmed positive	0.06003	[1]
σ	natural healing rate	0.01	[1]
r	recovery rate due to treatment	0.01 – 0.1	assumed
d	the death rate due to COVID-19	0.0009	[1]

Based on the system model of **Equation (1)**, the number of each subpopulation is positive as stated in the following **Lemma 1**.

Lemma 1. *The solution system equation (1), $S(t),V(t),E(t),I(t)$, and $R(t)$ are non-negative $\forall t \geq 0$ with, $S(0)>0, V(0)\geq 0, E(0)\geq 0, I(0)\geq 0, R(0)\geq 0$.*

Proof. We assumed $\tilde{t}=\sup\{S(t)>0,V(t)>0,E(t)>0,I(t)>0,R(t)>0\}\in[0,t]$, from equation system (1) obtained that

$$\frac{dS}{dt}\geq \zeta S\left(1-\frac{S}{K}\right)-\frac{\beta SI}{N}-\mu S \tag{2}$$

Solving inequality (2), by using the integral factoring method,

$$\frac{d}{dt}\left\{S(t)exp\left[\mu t+\int_0^t\frac{\beta I(s)ds}{N}\right]\right\}\geq exp\left[\frac{S_0K}{S_0+(K-S_0)e^{-\zeta t}}+\mu t+\int_0^t\frac{\beta I(s)ds}{N}\right]$$

both sides are integrated

$$S(\tilde{t})exp\left(\frac{S_0K}{S_0+(K-S_0)e^{-\zeta\tilde{t}}}+\mu\tilde{t}+\int_0^{\tilde{t}}\frac{\beta I(s)ds}{N}\right)\geq exp\left(\frac{S_0K}{S_0+(K-S_0)e^{-\zeta\tilde{t}}}+\mu\tilde{t}+\int_0^{\tilde{t}}\frac{\beta I(v)dv}{N}\right)d\tilde{t}+C$$

with C is constant. So that $S(\tilde{t})\geq S(0)\exp\left(-[\frac{S_0K}{S_0+(K-S_0)e^{-\zeta\tilde{t}}}+\mu\tilde{t}+\int_0^{\tilde{t}}\frac{\beta I(s)ds}{N}]\right)$

$+exp\left(-[\frac{S_0K}{S_0+(K-S_0)e^{-\zeta\tilde{t}}}+\mu\tilde{t}+\int_0^{\tilde{t}}\frac{\beta I(s)ds}{N}]\right)\left(\int_0^{\tilde{t}}(\exp\left(\frac{S_0K}{S_0+(K-S_0)e^{-\zeta\tilde{t}}}+\mu\tilde{t}+\int_0^{\tilde{t}}\frac{\beta I(v)dv}{N}\right)d\tilde{t}\right)>0$. Hence,

$S(\tilde{t})>0,\forall\tilde{t}>0$. The same way to show $S(t)>0,V(t)\geq 0,E(t)\geq 0,I(t)\geq 0,R(t)\geq 0,\forall t>0$. □

Non-Endemic stability point

The non-endemic stability point obtained from the changes in each subpopulation per unit of the day is constant. A mount of non-infected individuals remain, and a mount of infected individuals is zero for $t\rightarrow\infty$. The non-endemic stability point of the equations system (1) is:

$$P_0=\left(\frac{K(\zeta-\varphi-\mu)}{\zeta},\frac{\varphi K(\zeta-\varphi-\mu)}{\zeta(\tau+\mu)},0,0,\frac{\tau\varphi K(\zeta-\varphi-\mu)}{\zeta\mu(\tau+\mu)}\right). \tag{3}$$

Threshold

The parameter of threshold, denoted by R_0, is a needed tool in an epidemic-spreading system to find out whether the size of the spread is increasing or has decreased. If $R_0 < 1$, then the spread of the illness

decreases, and vice versa. If $R_0 > 1$, then the illness increases. Based on the system (1) it can be obtained the Jacobian matrix of positively confirmed individuals who are in contact with healthy individuals at the stability point P_0,

$$U = \begin{bmatrix} 0 & 0 & 0 \\ 0 & \frac{\beta_1 K(\zeta-\varphi-\mu)}{\zeta N} + \frac{\beta_2 \varphi K(\zeta-\varphi-\mu)}{\zeta N(\tau+\mu)} & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Jacobian matrix of the model (1) confirmed positive individuals who were not in contact with healthy and dropped out of their subpopulation,

$$W = \begin{bmatrix} \gamma+\mu & 0 & 0 \\ -\gamma & (\sigma+r+d+\mu) & 0 \\ 0 & -(\sigma+r) & \mu \end{bmatrix}$$

apply threshold determination [19] is obtained

$$R_0 = \frac{(\zeta-\varphi-\mu)K(\beta_1(\tau+\mu)+\beta_2\varphi)}{\zeta N(\tau+\mu)(\sigma+r+d+\mu)}. \quad (4)$$

The non-endemic stability point for time $t \to \infty$, becomes constant at a certain number stated in **Theorem 1**.

Theorem 1. *The non-endemic stability point P_0 in the local asymptotically stable COVID-19 spread equation system if the spread of the disease decreases and vice versa.*

Proof. The Jacobian matrix of the system of **Equations (1)** at the non-endemic point P_0 is obtained

$$J(P_0) = \begin{bmatrix} \varphi+\mu-2\zeta & 0 & 0 & -\frac{\beta K(\zeta-\varphi-\mu)}{\zeta N} & 0 \\ \varphi & -(\tau+\mu) & 0 & 0 & 0 \\ 0 & 0 & -(\gamma+\mu) & \frac{\beta K(\zeta-\varphi-\mu)}{\zeta N} & 0 \\ 0 & 0 & \gamma & -(\sigma+r+d+\mu) & 0 \\ 0 & \tau & 0 & \sigma+r & -\mu \end{bmatrix}.$$

Matrix eigenvalues $J(P_0)$ are $\lambda_1 = -\mu,\ \lambda_2 = -\tau-\mu, \lambda_3 = \varphi+\mu-2\zeta$
$\lambda_4 = \frac{1}{2}(d_1-\gamma-\mu) + \frac{1}{2}\sqrt{\gamma^2+2\gamma(2\psi+d_1+\mu)+(d_1+\mu)^2}$, $\lambda_5 = \frac{1}{2}(d_1-\gamma-\mu) -$
$\frac{1}{2}\sqrt{\gamma^2+2\gamma(\psi+d_1+\mu)+(d_1+\mu)^2}$, with $\psi = \frac{\beta K(\zeta-\varphi-\mu)}{\zeta N}$. Characteristic roots of $J(P_0)$, $\lambda_i < 0$, i = 1, 2, 3, 4, 5 with the provision of $2\zeta > \varphi+\mu$ and $\gamma+\mu > d + \sqrt{\gamma^2+(4\psi+2d_1+2\mu)\gamma+(d_1+\mu)^2}$. If all the characteristic roots of $J(P_0)$, of equation system (1) at the nonendemic point P_0 are all negative equivalent to $R_0 < 1$ or the endemic stability point P_0 is locally asymptotically stable. □

Endemic stability point

The endemic stability point is obtained if the displacement of each subpopulation per day of t is constant, and infected people remain for $t \to \infty$. Based on **Equation (1)**, it is assumed that the logistic growth is constant Λ, obtained endemic point,

$$P_1 = (S_1^*, V_1^*, E_1^*, I_1^*, R_1^*), \quad (5)$$

with

$$S_1^* = \frac{d_1 N(\gamma+\mu)}{\beta\gamma},\ V_1^* = \frac{\varphi d_1 N(\gamma+\mu)}{\beta\gamma(\tau+\mu)},\ E_1^* = -\frac{d_1 N(\varphi+\mu)(\gamma+\mu)-\Lambda\beta\gamma}{\beta\gamma(\gamma+\mu)},\ I_1^* = -\frac{d_1 N(\varphi+\mu)(\gamma+\mu)-\Lambda\beta\gamma}{\beta d_1(\gamma+\mu)},$$
$$R_1^* = \frac{(\tau d_1^2\varphi N-(\tau+\mu)(\sigma+r)(d_1 N(\varphi+\mu)+\Lambda\beta)\gamma^2-\mu d_1\gamma N(-2\varphi\tau d_1+(\tau+\mu)(\sigma+r)(\varphi+\mu))+\tau\varphi d_1^2\mu^2 N}{\beta\mu(\tau+\mu)(\gamma+\mu)}, \text{ and}$$

$d_1 = \sigma+r+d+\mu$.

A mount of individuals who are confirmed positive for COVID-19 remains constant over time $t \to \infty$, which means the local asymptotically stable endemic point in the system of **Equation (1)**, stated in **Theorem 2**, and the global stable endemic point in the system of **Equation (1)** is stated in **Theorem 3**.

Theorem 2. *The endemic stability point P_1 in the local asymptotically stable COVID-19 transmission model, if the spread of the disease increases and vice versa.*

Proof. Look, the Jacobian matrix of the system of **Equation (1)** at the endemic point P_1,

$$J(P_1)=\begin{bmatrix} -\frac{\beta I_1^*}{N}-(\varphi+\mu) & 0 & 0 & -\frac{\beta K(\zeta-\varphi-\mu)}{\zeta N} & 0 \\ \varphi & -(\tau+\mu) & 0 & 0 & 0 \\ \frac{\beta I_1^*}{N} & 0 & -(\gamma+\mu) & \frac{\beta K(\zeta-\varphi-\mu)}{\zeta N} & 0 \\ 0 & 0 & \gamma & -(\sigma+r+d+\mu) & 0 \\ 0 & \tau & 0 & \sigma+r & -\mu \end{bmatrix}.$$

Based on the Jacobian matrix $J(P_1)$, it is obtained

$\frac{1}{N}(\lambda+\mu)(\lambda+\tau+\mu)[N\lambda^3+([d_1+2\mu+\gamma+\varphi]N+\beta I_1^*)\lambda^2+[(\mu^2+(2d_1+\gamma+\varphi)\mu$
$+(d_1+\varphi-\zeta_1)\gamma+\varphi d_1)N+\beta I_1^*(d_1+\gamma+\mu)]\lambda+(d_1\mu+\gamma(d_1-\zeta_1))(\varphi+\mu)N$
$+\beta_1 d_1 I_1^*(\gamma+\mu)]=0$, obtained $\lambda_1=-\mu$, $\lambda_2=-\tau-\mu$, and characteristic equation

$$\lambda^3+c_1\lambda^2+c_2\lambda+c_3=0, \quad (6)$$

with

$c_1=[d_1+2\mu+\gamma+\varphi]N+\beta I_1^*$,
$c_2=(\mu^2+(2d_1+\gamma+\varphi)\mu+(d_1+\varphi-\zeta_1)\gamma+\varphi d_1)N+\beta I_1^*(d_1+\gamma+\mu)$,
$c_3=\big(d_1\mu+\gamma(d_1-\zeta_1)\big)(\varphi+\mu)N+\beta_1 d_1 I_1^*(\gamma+\mu)$.

It can be seen that $c_1>0, c_2>0, c_3>0$, and

$c_1c_2=([d_1+2\mu+\gamma+\varphi]N+\beta I_1^*)[(\mu^2+(2d_1+\gamma+\varphi)\mu+(d_1+\varphi-\zeta_1)\gamma+\varphi d_1)N$
$+\beta I_1^*(d_1+\gamma+\mu)]$
$=([d_1+2\mu+\gamma+\varphi]N+\beta I_1^*)((\mu^2+(2d_1+\gamma+\varphi)\mu+([d_1+2\mu+\gamma+\varphi]N+\beta I_1^*)$
$\big((d_1+\varphi-\zeta_1)\gamma+\varphi d_1)N\big)+([d_1+2\mu+\gamma+\varphi]N+\beta I_1^*)(\beta I_1^*(d_1+\gamma+\mu))$
$>\big(d_1\mu+\gamma(d_1-\zeta_1)\big)(\varphi+\mu)N+\beta_1 d_1 I_1^*(\gamma+\mu)=c_3$. To be more real, you can enter the parameter values in **Table 1**. Based on the Routh-Hurwitz criteria, $c_1>0, c_2>0, c_3>0$, and $c_1c_2-c_3>0$, equivalently states that the characteristic roots of the polynomial system (6) all negative or $R_0>1$ equivalent to the local asymptotically stable P_1 endemic stability point. □

Theorem 3. *If the spread of COVID-19 increases, then the endemic stability P_1 is globally asymptotically stable.*

Proof. To prove **Theorem 3**, it is sufficient to prove that the differential of the Lyapunov function is negative **[20]**. Assume a Lyapunov function

$L=\int_{S_1^*}^{S}\left(1-\frac{S_1^*}{x}\right)dx+\int_{V_1^*}^{V_1}\left(1-\frac{V_1^*}{x}\right)dx+\int_{E_1^*}^{E_1}\left(1-\frac{E_1^*}{x}\right)dx+\int_{I_1^*}^{I_1}\left(1-\frac{I_1^*}{x}\right)dx+\int_{R_1^*}^{R_1}\left(1-\frac{R_1^*}{x}\right)dx$

The Lyapunov function differentiated is given by

$$L'=\left(1-\frac{S_1^*}{S_1}\right)S_1'+\left(1-\frac{V_1^*}{V_1}\right)V_1'+\left(1-\frac{E_1^*}{E_1}\right)E_1'+\left(1-\frac{I_1^*}{I_1}\right)I_1'+\left(1-\frac{R_1^*}{R_1}\right)R_1'$$

$\left(1-\frac{S_1^*}{S_1}\right)S_1'=\left(1-\frac{S_1^*}{S_1}\right)(pS\left(1-\frac{S}{K}\right)-\frac{\beta SI}{N}-(\varphi+\mu)S)$
$=(q_1u+\mu)S_2^*\left(2-\frac{S}{S_1^*}-\frac{S_1^*}{S}\right)+\left(1-\frac{S_1^*}{S}\right)(\frac{pS_1^*I_1^*}{N}-\left(1-\frac{S_1^*}{S}\right)\frac{\beta SI}{N}$

$\left(1-\frac{V_1^*}{V_1}\right)V_1'=\left(1-\frac{V_1^*}{V_1}\right)\left(\frac{q\beta SI}{N}-r_1V_1\right)$
$=\left(1-\frac{V_1^*}{V_1}\right)(\frac{q\beta S(S_1^*I_1^*+[r_1N-pqS_2^*])E_1}{r_2N^2-pqNS_1^*}-\frac{r_1S_1^*I_1^*}{r_3N-pqS_1^*})$

$\left(1-\frac{E_1^*}{E_1}\right)E_1'=\left(1-\frac{E_1^*}{E_1}\right)\left(\frac{(1-q)\beta SI}{N}-\vartheta E_1\right)$
$=\left(1-\frac{E_1^*}{E_1}\right)\left(\frac{(1-q)\beta S}{N}(I_1+I_1^*)\right)-\frac{(1-q)pr_1S_1^*I_1^*}{r_3N-(1-q)pS_1^*}\Big)$

$\left(1-\frac{I_1^*}{I_1}\right)I_1'=\left(1-\frac{I_1^*}{I_1}\right)(\vartheta E_1-(\sigma+r)I_1)$
$=\left(1-\frac{I_1^*}{I_1}\right)r_4\left(\frac{S_1^*I_1^*}{r_3N-pqS_1^*}-I_1^*\right)$

$\left(1-\frac{R_1^*}{R}\right)R_1'=\left(1-\frac{R_1^*}{R}\right)(\varrho(V_1-V_1^*)+\phi(I_1-I_1^*))$,

so that

$$L'=\mu S_1^*\left(2-\frac{S}{S_1^*}-\frac{S_1^*}{S}\right)+\frac{\beta}{N}\left(3-\frac{S_1^*}{S}-\frac{E_1^*I_1}{I_1^*E_1}-\frac{I_1}{I_1^*}\left(\frac{S_1I_1^*}{S_1^*I_1}-1\right)\right)+\frac{\beta}{N}\left(3-\frac{S_1^*}{S_1}-\frac{E_1^*I_1}{I_1^*E_1}-\frac{E_1}{E_1^*}\left(\frac{S_1I_1^*}{S_1^*I_1}-1\right)\right),$$

So, obtained

$$\mu S_2^* \left(2 - \frac{S_1}{S_1^*} - \frac{S_1^*}{S_1}\right) \leq 0,$$
$$\frac{\beta}{N}\left(3 - \frac{S_1^*}{S_1} - \frac{E_1^* I_1}{I_1^* E_1} - \frac{I_1}{I_1^*}\left(\frac{S_1 I_1^*}{S_2^* I_1} - 1\right)\right) \leq 0,$$
$$\frac{\beta}{N}\left(3 - \frac{S_1^*}{S_1} - \frac{E_1^* I_1}{I_1^* E_1} - \frac{E_1}{E_1^*}\left(\frac{S_1 I_1^*}{S_1^* I_1} - 1\right)\right) \leq 0.$$

Apply the invariance Principle by Lasalle [20], if the spread of the disease increases then P_1 is globally asymptotically stable.

3. RESULTS AND DISCUSSION

Writing Based on the system of equation (1), parameter values used in Table 1, by assuming the initial a mount of each, S_0 = 26780410, V_0 = 48440, E_0 = 19750, I_0 = 3840, R_0 = 280, N = 268000000, and K = 300000000. Solving the model (1) with the 4th order Runge-Kutta method approach. A sensitivity analysis of the recruitment rate in susceptible subpopulations, like in Figure 2, and the vaccination subpopulation, like in Figure 3 below.

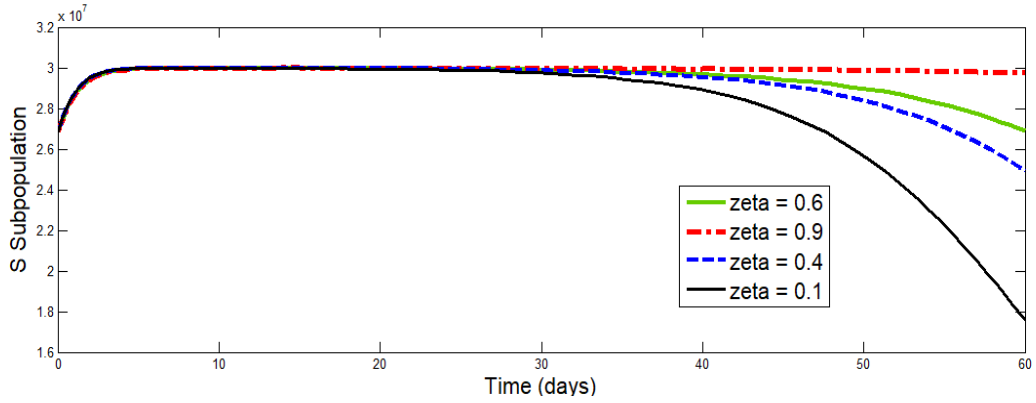

Figure 2. The dynamics of the distribution of susceptible subpopulations

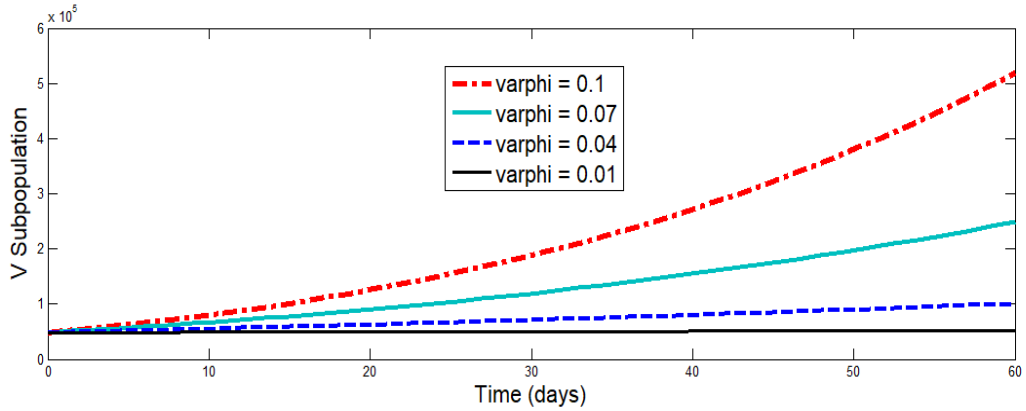

Figure 3. Dynamics of the spread of vaccination subpopulations

Based on Figure 2 and Figure 3, increasing the value of the rate of entry of individuals into the S subpopulation increases a mount of susceptible and vaccinated subpopulation people. Based on Figure 4, increasing the value of the contact rate with infected people and those who are still healthy increases the number of people exposed to COVID-19 from the initial time to t = 60 days.

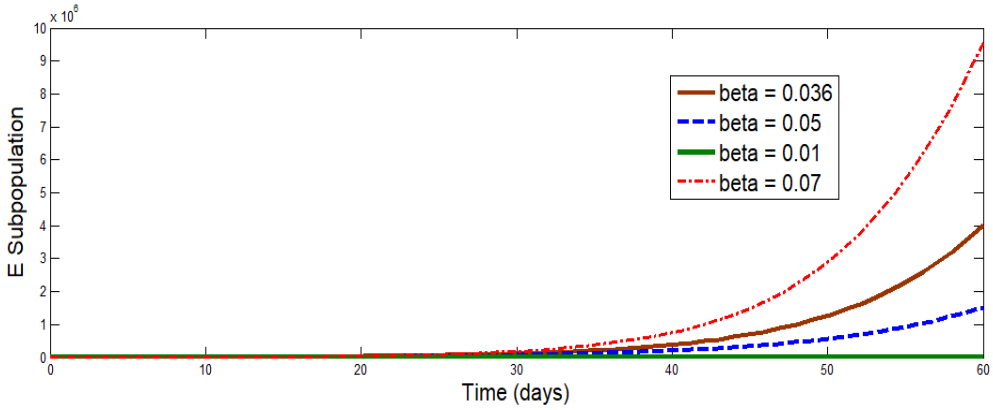

Figure 4. Dynamics of the spread of COVID-19 exposed subpopulations

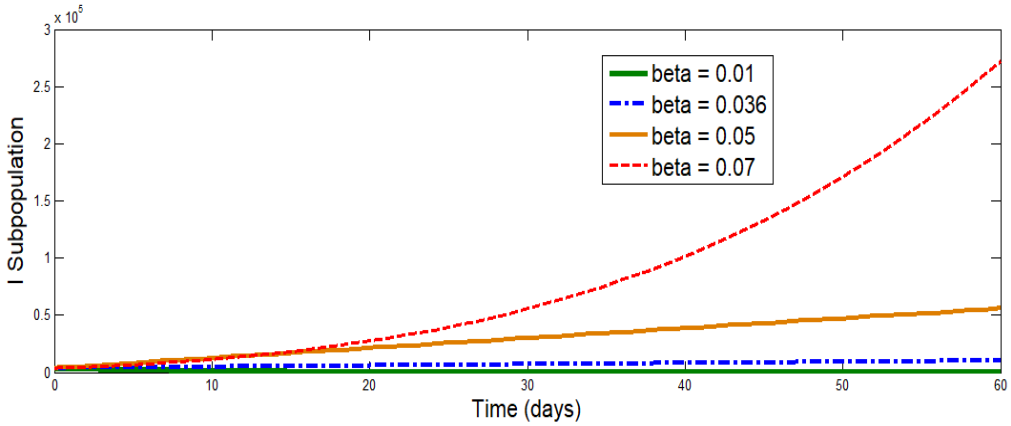

Figure 5. Dynamics of the spread confirmed positive for COVID-19

Based on **Figure 5**, increasing the value of the contact rate between infected people and those who are still healthy increases a mount of people who are confirmed positive for COVID-19 from the initial time to t = 60 days.

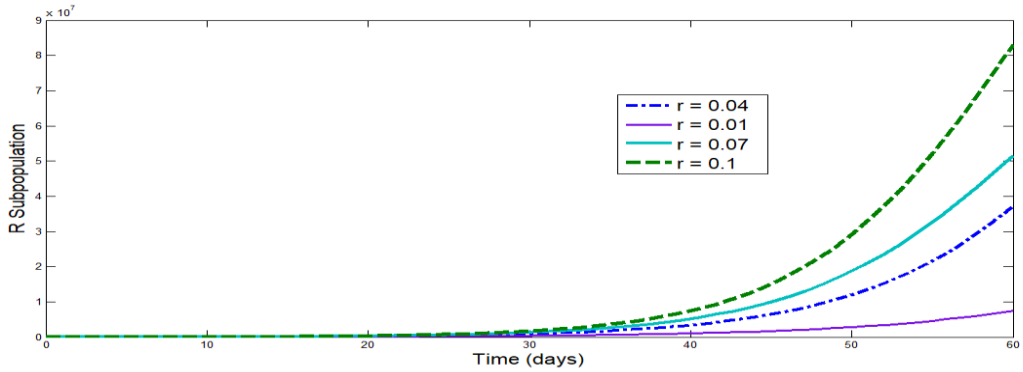

Figure 6. The dynamics of subpopulations recovered from COVID-19

Based on **Figure 6**, the greater the value of parameter *r*, the greater a mount of individuals recovered from COVID-19 from the initial time until t = 60 days.

4. CONCLUSIONS

The model studied in this paper analyzes the transmission of COVID-19 by taking into account the recruitment rate of logistical growth. Parameter values used in the model are from reference **[1]**, **[6]**, and **[11]**, partly assumed. Based on the analysis of the system of equations (1), it is obtained: (1) the existence of the positivity of each subpopulation at any time. (2) Endemic and non-endemic points of the system of **Equation**

(1). (3) The existence of local asymptotic stability of the non-endemic point P_0. (4) The existence of local asymptotic stability of the endemic point P_1. (5) The existence of global asymptotic stability of the endemic point P_1.

Based on numerical simulations, a mount of susceptible and vaccinated subpopulation individuals increases if the recruitment rate increases. If the coefficient of the vaccination subpopulation increases, then a mount of recovered subpopulation individuals increases. If the value of the contact rate of the parameter between infected individuals and those who are healthy increases, then a mount of infected individuals increases. If the value of the coefficient of the infected subpopulation increases, then a mount of infected subpopulation individuals decreases, while the number of recovered subpopulation individuals increases.

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