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STABILITY ANALYSIS OF SCPUR MATHEMATICAL MODEL FOR THE SPREAD OF COVID-19 (CORONA VIRUS DISEASE-19)

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Abstract. This article discusses SCPUR mathematical model for the spread of COVID-19 using data of people with COVID-19 in Makassar City. In this model, the population class is divided into five classes: susceptible, asymptomatic infectious, reported symptomatic infectious, unreported symptomatic infectious, and recovered classes. The proportion of body immunity to the increase of infected individuals, the proportion of large-scale social restrictions, and the proportion of quarantine as a healing process are also added. The research begins by determining the equilibrium point of the model, namely the disease-free equilibrium point and the endemic equilibrium point. Then, the stability test is carried out using linearization method and the eigenvalues are determined. The value of the basic reproduction number is obtained using next-generation matrix method, where the initial state of the basic reproduction number value $R_0 > 1$ mean COVID-19 will still exist in Makassar City. Treatment is carried out so that $R_0 < 1$ which means Makassar City will be free of COVID-19.

Keywords: equilibrium point; basic reproduction number; COVID-19.

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1. INTRODUCTION

There are various kinds of disease viruses in the world such as human immunodeficiency virus, ebola virus, dengue virus, etc. One of the viral diseases that is currently being discussed is the novel coronavirus. It is not a new virus in the health sector. The virus was first discovered in 2003 and caused severe acute respiratory (SARS). Then, a new type of the virus was found in 2012 and caused middle east respiratory syndrome-corona virus (MERS-CoV) [1,2]. Lately, this virus mutated to a new type of coronavirus (SARS-CoV-2) and caused the emergence of a disease called coronavirus disease-19 (COVID-19) [3,4]. From the first case of COVID-19 in Wuhan, China in late December 2019 [5,6] until July 10, 2020, the virus had infected 12.015.193 individuals, caused 549.247 death, and spread to 216 countries in the world. The highest cases were reported in the Americas with 6.264.626 cases. Asia was in the fourth place with 1.032.167 cases, 70.736 of which were from Indonesia with 32.651 recovered individuals and 3.417 deaths. It has been predicted that this number will increase given the absence of antiviral for this disease [7,8]. Based on these facts, as of March 11, 2020, the world health organization (WHO) decided that COVID-19 is a pandemic disease [9,10].

The field of mathematics is one of the fields of science that can provide solutions in a phenomena, by modeling and formulating the phenomena. The phenomena are transformed into either an equation or an equation system, for example in dynamical populations [11,12,13,14] and the field of epidemiology [15,16,17]. With an assumption that COVID-19 is an epidemiology, the dynamics of COVID-19 spread can also be considered in mathematical modeling [18,19].

Based on studies in [20] discusses the SIRU mathematical model (Susceptible, Asymptomatic Infected, Reported Infected Case, Unreported Symptomatic infected) to predict the cumulative number of COVID-19 cases in China. Furthermore, from [20] researchers will make modification by adding one class of individual namely recovery class, with the consideration that an increasing number of individuals who recovery from disease by quarantine. Furthermore, the assumption is added that individuals who are infected without symptoms and have good immunity will recovery

from the disease without quarantine. Then, another treatment is also added, namely Large-Scale Social Restrictions.

2. SCPUR MATHEMATICAL MODEL FOR THE SPREAD OF COVID-19

SCPUR model is a development of SIRU model, namely an epidemiological model with compartments consisting of susceptible (S) class which represents the number of individuals who are susceptible to COVID-19, asymptomatic infectious (I) class which represents the number of individuals infected with COVID-19 without clinical symptoms, reported symptomatic infectious (R) class which represents the number of individuals who show symptoms of being infected with COVID-19 and report it, and the unreported symptomatic infectious (U) class which represents the number of individuals who show symptoms of being infected with COVID-19 but do not report it [20].

In this model, one individual class is added, namely recovery (R) class which represents the number of individuals who have recovered from COVID-19, so that the individual class who shows symptoms of being infected with COVID-19 and reports it is symbolized as (P). Furthermore, the class of asymptomatic infectious (I) is termed a carrier (C) which represents the number of individuals who are infected with COVID-19 but do not show symptoms of infection. Then, the proportion of the effect of body immunity to the increase of infected individuals, the proportion of large-scale social restrictions, and the proportion of quarantine as a healing process are also added.

The assumptions used in constructing the mathematical model of COVID-19 are as follows:

1. The entire population is assumed to be susceptible to COVID-19 infection
2. The population is assumed constant
3. Population density and geographic location of the population are ignored.
4. Every individual has the same opportunity to make contact with individuals infected with COVID-19.

5. Individuals are infected by the virus if they make direct or indirect contact with infected individuals.
6. Asymptomatic infectious (C) and unreported symptomatic infectious (U) are the classes that could transmit the disease.
7. Reported symptomatic infectious are immediately quarantined so as not to spread the disease.
8. Carriers that have a good level of body immunity will recover without being given quarantine treatment.

Based on the above assumptions, a dynamic for the spread of COVID-19 is obtained as shown in Figure 1.

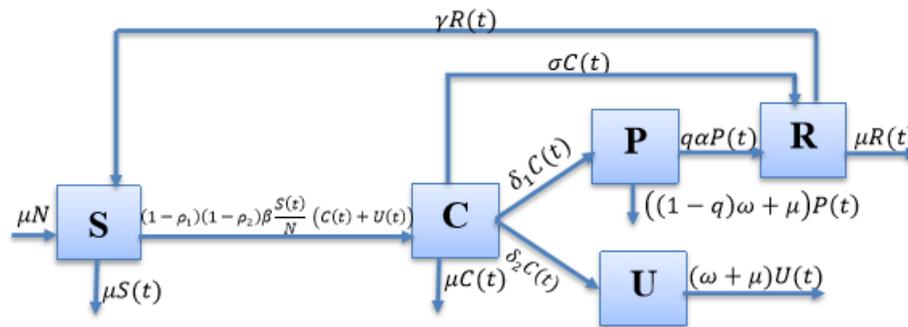


Figure 1. Transmission diagram of the mathematical model of the spread of COVID-19

Based on Figure 1., the nonlinear differential equation is obtained as follows

$$(1) \quad \frac{dS}{dt} = \mu N + \gamma R(t) - (1 - \rho_1)(1 - \rho_2)\beta \frac{S(t)}{N} (C(t) + U(t)) - \mu S(t)$$

$$(2) \quad \frac{dC}{dt} = (1 - \rho_1)(1 - \rho_2)\beta \frac{S(t)}{N} (C(t) + U(t)) - (\delta + \sigma + \mu)C(t)$$

$$(3) \quad \frac{dP}{dt} = \delta_1 C(t) - (q\alpha + (1 - q)\omega + \mu)P(t)$$

$$(4) \quad \frac{dU}{dt} = \delta_2 C(t) - (\omega + \mu)U(t)$$

$$(5) \quad \frac{dR}{dt} = \sigma C(t) + q\alpha P(t) - (\mu + \gamma)R(t)$$

with initial conditions $S(0) = S_0 > 0, C(0) = C_0 \geq 0, P(0) = P_0 \geq 0, U(0) = U_0 \geq 0, R(0) = R_0 \geq 0$. The variables and parameters used in the model are presented in Table 1.

Table 1. Variables and parameters of COVID-19 model

Symbols	Descriptions	Requirements	Unit
$N(t)$	The total population at time t	$N(t) > 0$	Population
$S(t)$	Size of sub-population who susceptible to COVID-19 infection at time t	$S(t) > 0$	Population
$C(t)$	Size of sub-population who asymptomatic infectious at time t	$C(t) \geq 0$	Population
$P(t)$	Size of sub-population who reported symptomatic infectious at time t	$P(t) \geq 0$	Population
$U(t)$	Size of sub-population who unreported symptomatic infectious at time t	$U(t) \geq 0$	Population
$R(t)$	Size of sub-population recovered individuals at time t	$R(t) \geq 0$	Population
μ	Natural death rate	$\mu > 0$	1/day
$1 - \rho_1$	Proportion of carrier individuals with bad immunity	$0 \leq \rho_1 \leq 1$	-
$1 - \rho_2$	Proportion with no large-scale social restrictions	$0 \leq \rho_2 \leq 1$	-
β	Transition rate from susceptible individuals to asymptomatic infected individuals due to interactions with infected individuals.	$\beta \geq 0$	1/(population · day)
δ	Transition rate due to symptoms	$\delta > 0$	population/day
σ	Transition rate from asymptomatic infectious to recovered from the disease	$\sigma > 0$	population/day
q	Proportion of infected to recovered individuals due to quarantine	$0 \leq q \leq 1$	-
$1 - q$	Proportion of failure of quarantine treatment in the healing process	$0 \leq q \leq 1$	-
α	Transition rate from reported symptomatic infectious to recovered	$\alpha > 0$	population/day
γ	Transition rate from recovered to susceptible reinfection	$\gamma > 0$	population/day
ω	Death rate due to COVID-19	$\omega > 0$	population/day

Furthermore, the equation (1) – (5) will be formed into a system of normalized equations by substituting non-dimension variables as follows:

$$s = \frac{S(t)}{N(t)}, c = \frac{C(t)}{N(t)}, p = \frac{P(t)}{N(t)}, u = \frac{U(t)}{N(t)}, r = \frac{R(t)}{N(t)}.$$

So that the following non-dimension nonlinear differential equation system is obtained:

$$(6) \quad \frac{ds}{dt} = \mu + \gamma r - (1 - \rho_1)(1 - \rho_2)\beta s(c + u) - \mu s$$

$$(7) \quad \frac{dc}{dt} = (1 - \rho_1)(1 - \rho_2)\beta s(c + u) - (\delta + \sigma + \mu)c$$

$$(8) \quad \frac{dp}{dt} = \delta_1 c - (q\alpha + (1 - q)\omega + \mu)p$$

$$(9) \quad \frac{du}{dt} = \delta_2 c - (\omega + \mu)u$$

$$(10) \quad \frac{dr}{dt} = \sigma c + q\alpha p - (\mu + \gamma)r$$

3. EQUILIBRIUM POINTS AND THEIR STABILITIES

The equilibrium point of SCPUR model is obtained when $\frac{ds}{dt} = 0, \frac{dc}{dt} = 0, \frac{dp}{dt} = 0, \frac{du}{dt} = 0, \frac{dr}{dt} = 0$. So

that the equation (11) – (15) becomes:

$$(11) \quad \mu + \gamma r - (1 - \rho_1)(1 - \rho_2)\beta s(c + u) - \mu s = 0$$

$$(12) \quad (1 - \rho_1)(1 - \rho_2)\beta s(c + u) - (\delta + \sigma + \mu)c = 0$$

$$(13) \quad \delta_1 c - (q\alpha + (1 - q)\omega + \mu)p = 0$$

$$(14) \quad \delta_2 c - (\omega + \mu)u = 0$$

$$(15) \quad \sigma c + q\alpha p - (\mu + \gamma)r = 0$$

Solutions, termed as disease-free equilibrium solution and endemic equilibrium solution, will be sought. The disease-free equilibrium solution is marked with $c = 0$ and $u = 0$ meaning that no infected individual can transmit the COVID-19 to other individuals. If it is assumed that $c = 0$ and $u = 0$ and the value is substituted into equation (11) - (15), then it is obtained that $s = 1, p = 0, r = 0$. Thus, the disease-free equilibrium point $E_0 = (s, c, p, u, r) = (1, 0, 0, 0, 0)$. Then,

we will look for the endemic equilibrium point. The condition in which $c \neq 0$ and $u \neq 0$ means that there are individuals who are infected and transmit the COVID-19 to other individuals so that if the value is substituted into equation (11) - (15) the endemic equilibrium point obtained is $E_1 =$

$$(s^*, c^*, p^*, u^*, r^*) \quad \text{where} \quad s^* = \frac{\mu + \gamma r^*}{(1 - \rho_1)(1 - \rho_2)(\beta(c^* + u^*) + \mu)}, \quad c^* = \frac{(1 - \rho_1)(1 - \rho_2)\beta s^* u^*}{\delta + \sigma + \mu - (1 - \rho_1)(1 - \rho_2)\beta s^*}, \quad p^* = \frac{\delta_1 c^*}{\alpha + (1 - q)\omega + \mu}, \quad u^* = \frac{\delta_2 c^*}{(\omega + \mu)}, \quad r^* = \frac{\sigma c^* + q\alpha p^*}{\mu + \gamma}.$$

After obtaining the equilibrium points, disease-free and endemic equilibrium stability analysis will be carried out. The first step is to linearize the equation system for the non-linear spread of COVID-19 using the Jacobi matrix [21]. The Jacobi matrix equation (6) – (10) is

$$(16) \quad J_E = \begin{bmatrix} (1 - \rho_1)(1 - \rho_2)\beta(c + u) - \mu & -(1 - \rho_1)(1 - \rho_2)\beta s & 0 & -(1 - \rho_1)(1 - \rho_2)\beta s & \gamma \\ 0 & (1 - \rho_1)(1 - \rho_2)\beta - \delta - \sigma - \mu & 0 & (1 - \rho_1)(1 - \rho_2)\beta s & 0 \\ 0 & \delta_1 & -q\alpha - (1 - q)\omega - \mu & 0 & 0 \\ 0 & \delta_2 & 0 & -\omega - \mu & 0 \\ 0 & \sigma & q\alpha & 0 & -\omega - \gamma \end{bmatrix}$$

If the disease-free equilibrium point $E_0 = (s, c, p, u, r) = (1, 0, 0, 0, 0)$ is substituted to the Jacobi matrix (16), we get

$$J_{E_0} = \begin{bmatrix} -\mu & -(1 - \rho_1)(1 - \rho_2)\beta & 0 & -(1 - \rho_1)(1 - \rho_2)\beta & \gamma \\ 0 & (1 - \rho_1)(1 - \rho_2)\beta - \delta - \sigma - \mu & 0 & (1 - \rho_1)(1 - \rho_2)\beta & 0 \\ 0 & \delta_1 & -(q\alpha + (1 - q)\omega + \mu) & 0 & 0 \\ 0 & \delta_2 & 0 & -(\omega + \mu) & 0 \\ 0 & \sigma & q\alpha & 0 & -(\omega + \gamma) \end{bmatrix}$$

Then, we will look for the eigenvalues of the matrix J_{E_0} . Characteristic equation of the matrix

J_{E_0} is

$$\det \begin{bmatrix} \lambda + \mu & -\beta & 0 & -\beta & \gamma \\ 0 & \lambda - (1 - \rho_1)(1 - \rho_2)\beta + \delta + \sigma + \mu & 0 & (1 - \rho_1)(1 - \rho_2)\beta & 0 \\ 0 & \delta_1 & \lambda + (q\alpha + (1 - q)\omega + \mu) & 0 & 0 \\ 0 & \delta_2 & 0 & \lambda + (\omega + \mu) & 0 \\ 0 & \sigma & q\alpha & 0 & \lambda + (\omega + \gamma) \end{bmatrix} = 0$$

or

$$\begin{aligned}
&(\lambda + \mu)(\lambda + \mu + \gamma)(\lambda^2 + (\beta\rho_1\rho_2 - \beta\rho_1 - \beta\rho_2 + \beta - \delta - 2\mu - \omega - \sigma)\lambda + \beta\delta_2\rho_1\rho_2 + \\
&\beta\mu\rho_1\rho_2 + \beta\omega\rho_1\rho_2 - \beta\delta_2\rho_1 - \beta\delta_2\rho_2 - \beta\mu\rho_1 - \beta\mu\rho_2 - \beta\omega\rho_1 - \beta\omega\rho_2 + \delta_2\beta + \beta\mu + \beta\omega - \\
&\delta\mu - \delta\omega - \mu^2 - \mu\omega - \mu\sigma - \omega\sigma)(\lambda + q\alpha + (1 - q)\omega + \mu) = 0.
\end{aligned}$$

From the characteristic equation, the eigenvalues are:

$\lambda_1 = -\mu$, $\lambda_2 = -\mu - \gamma$, $\lambda_3 = -q\alpha - (1 - q)\omega - \mu$, and other eigenvalues are the solution of polynomial equation

$$(17) \quad \lambda^2 + a_1\lambda + a_2 = 0$$

where

$$a_1 = \beta\rho_1\rho_2 + \beta - \beta\rho_1 - \beta\rho_2 - \delta - 2\mu - \omega - \sigma,$$

$$\begin{aligned}
a_2 = &\beta\delta_2\rho_1\rho_2 + \beta\mu\rho_1\rho_2 + \beta\omega\rho_1\rho_2 + \delta_2\beta + \beta\mu + \beta\omega - \beta\delta_2\rho_1 - \beta\delta_2\rho_2 - \beta\mu\rho_1 - \beta\mu\rho_2 - \\
&\beta\omega\rho_1 - \beta\omega\rho_2 - \delta\mu - \delta\omega - \mu^2 - \mu\omega - \mu\sigma - \omega\sigma.
\end{aligned}$$

Based on the routh-Hurwitz criteria [22], the roots of the equation (17) have a negative real part if and only if

$$H_1 = a_1 > 0, \quad H_2 = \begin{vmatrix} a_1 & 0 \\ 1 & a_2 \end{vmatrix} = a_1 a_2 > 0.$$

Because it is assumed that all parameters are positive, then $a_1 > 0$ if $\beta\rho_1\rho_2 + \beta > \beta\rho_1 + \beta\rho_2 + \delta + 2\mu + \omega + \sigma$ and $a_2 > 0$ if $\beta\delta_2\rho_1\rho_2 + \beta\mu\rho_1\rho_2 + \beta\omega\rho_1\rho_2 + \delta_2\beta + \beta\mu + \beta\omega > \beta\delta_2\rho_1 + \beta\delta_2\rho_2 + \beta\mu\rho_1 + \beta\mu\rho_2 + \beta\omega\rho_1 + \beta\omega\rho_2 + \delta\mu + \delta\omega + \mu^2 + \mu\omega + \mu\sigma + \omega\sigma$. As a result if $a_1 > 0$ and $a_2 > 0$ then $a_1 a_2 > 0$. If these conditions are met, $\lambda_4 < 0$ and $\lambda_5 < 0$ will be obtained. The values of $\lambda_i < 0, i = 1, 2, 3, 4, 5$. So that the disease-free equilibrium point $E_0 = (1, 0, 0, 0, 0)$ is locally asymptotically stable.

The endemic equilibrium point $E_1 = (s^*, c^*, p^*, u^*, r^*)$ is substituted to the Jacobi matrix (16), so that the result is

$$J_{E_1} = \begin{bmatrix} -a & -rh_1 & 0 & -rh_1 & rh_2 \\ rh_3 & -b & 0 & rh_4 & 0 \\ 0 & rh_5 & -c & 0 & 0 \\ 0 & rh_6 & 0 & -d & 0 \\ 0 & rh_7 & rh_8 & 0 & -e \end{bmatrix}$$

where $a = \beta(c^* + u^*) - \mu$, $b = \delta + \sigma + \mu + (1 - \rho_1)(1 - \rho_2)\beta s^*$, $c = (\alpha + (1 - q)\omega + \mu)$, $d = (\omega + \mu)$, $e = (\omega + \gamma)$, $rh_1 = \beta s^*$, $rh_2 = \gamma$, $rh_3 = (1 - \rho_1)(1 - \rho_2)\beta(c^* + u^*)$, $rh_4 = (1 - \rho_1)(1 - \rho_2)\beta s^*$, $rh_5 = \delta_1$, $rh_6 = \delta_2$, $rh_7 = \sigma$, $rh_8 = q\alpha$.

Based on the Jacobi matrix, we define the characteristic equation as $\det(\lambda I - J_{E_1}) = 0$ or

$$\lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 = 0,$$

where

$$A_1 = a + b + c + d + e$$

$$A_2 = ab + ac + ad + ae + bc + bd + be + cd + ce + de + rh_1rh_3 - rh_4rh_6$$

$$A_3 = abc + abd + abe + acd + ace + ade - arh_4rh_6 + bcd + bce + bde + cde + crh_1rh_3 - crh_4rh_6 + drh_1rh_3 - erh_1rh_3 - erh_4rh_6 - rh_2rh_3rh_7 + rh_1rh_3rh_6$$

$$A_4 = abcd + abce + acde + acrh_4rh_6 - aerh_4rh_6 + bcde + cdrh_1rh_3 + cerh_1rh_3 - cerh_4rh_6 - crh_2rh_3rh_7 - crh_2rh_3rh_6 + derh_1rh_3 - drh_2rh_3rh_7 + erh_1rh_3rh_6 - rh_2rh_3rh_5rh_8$$

$$A_5 = abcde - acerh_4rh_6 + cdrh_1rh_3 - cdrh_2rh_3rh_7 + cerh_1rh_3rh_6 - drh_2rh_3rh_5rh_8$$

Based on the routh-Hurwitz criteria, the endemic equilibrium point of the model is locally asymptotically stable if $A_1, A_2, A_3, A_4, A_5 > 0$ and $A_1A_2A_3A_4A_5 - A_1^2A_2^2A_5^2 - A_1^2A_4^2A_5 + 2A_1A_4A_5^2 - A_3^2A_4A_5 + A_3A_2A_5^2 - A_5^3 > 0$ [23].

4. BASIC REPRODUCTION NUMBER AND SENSITIVITY ANALYSIS

The basic reproductive number is the threshold for the transmission of a disease caused by infected individuals in a population who are susceptible to infection, which is usually denoted by R_0 [24].

$$\frac{dc}{dt} = (1 - \rho_1)(1 - \rho_2)\beta s(c + u) - (\delta + \sigma + \mu)c$$

$$\frac{dp}{dt} = \delta_1c - (q\alpha + (1 - q)\omega + \mu)p$$

$$\frac{du}{dt} = \delta_2 c - (\omega + \mu)u$$

Suppose $\mathcal{F}_i(x)$ is the addition rate of new infections in compartment c and $\mathcal{V}_i(x)$ is the rate of individual displacement in compartment c , so that $\mathcal{F}_i(x)$ and $\mathcal{V}_i(x)$ are as follows:

$$(18) \quad \mathcal{F}_i(x) = \begin{pmatrix} F_1 \\ F_2 \\ F_3 \end{pmatrix} = \begin{pmatrix} (1 - \rho_1)(1 - \rho_2)\beta s(c + u) \\ 0 \\ 0 \end{pmatrix},$$

$$(19) \quad \mathcal{V}_i(x) = \begin{pmatrix} V_1 \\ V_2 \\ V_3 \end{pmatrix} = \begin{pmatrix} (\delta + \sigma + \mu)c \\ -\delta_1 c + (q\alpha + (1 - q)\omega + \mu)p \\ -\delta_2 c + (\omega + \mu) \end{pmatrix}.$$

Furthermore, from equations (18) and (19) the matrix F and V are evaluated in point E_0 as follow:

$$F = \frac{\partial \mathcal{F}_i(E_1)}{\partial (c, p, u)} = \begin{pmatrix} \frac{\partial F_1}{\partial c} & \frac{\partial F_1}{\partial p} & \frac{\partial F_1}{\partial u} \\ \frac{\partial F_2}{\partial c} & \frac{\partial F_2}{\partial p} & \frac{\partial F_2}{\partial u} \\ \frac{\partial F_3}{\partial c} & \frac{\partial F_3}{\partial p} & \frac{\partial F_3}{\partial u} \end{pmatrix} = \begin{pmatrix} (1 - \rho_1)(1 - \rho_2)\beta & 0 & (1 - \rho_1)(1 - \rho_2)\beta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix},$$

$$V = \frac{\partial \mathcal{V}_i(E_1)}{\partial (c, p, u)} = \begin{pmatrix} \frac{\partial V_1}{\partial c} & \frac{\partial V_1}{\partial p} & \frac{\partial V_1}{\partial u} \\ \frac{\partial V_2}{\partial c} & \frac{\partial V_2}{\partial p} & \frac{\partial V_2}{\partial u} \\ \frac{\partial V_3}{\partial c} & \frac{\partial V_3}{\partial p} & \frac{\partial V_3}{\partial u} \end{pmatrix} = \begin{pmatrix} \delta + \sigma + \mu & 0 & 0 \\ -\delta_1 & (\alpha + (1 - q)\omega + \mu) & 0 \\ -\delta_2 & 0 & \omega + \mu \end{pmatrix}.$$

Then the generation matrix

$$,FV^{-1} = \begin{pmatrix} \frac{(1 - \rho_1)(1 - \rho_2)\beta}{A} + \frac{(1 - \rho_1)(1 - \rho_2)\beta\delta_2}{AC} & 0 & \frac{(1 - \rho_1)(1 - \rho_2)\beta}{C} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

where $A = \delta + \sigma + \mu$, $B = \alpha + (1 - q)\omega + \mu$, and $C = \omega + \mu$. Equation of characteristics

FV^{-1} is as follows:

$$\det(\lambda I - FV^{-1}) = 0$$

$$\begin{vmatrix} \lambda - \frac{(1 - \rho_1)(1 - \rho_2)\beta}{A} - \frac{(1 - \rho_1)(1 - \rho_2)\beta\delta_2}{AC} & 0 & -\frac{(1 - \rho_1)(1 - \rho_2)\beta}{C} \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{vmatrix} = 0$$

or

$$\left(\lambda - \frac{(1-\rho_1)(1-\rho_2)\beta}{A} - \frac{(1-\rho_1)(1-\rho_2)\beta\delta_2}{AC} \right) \lambda^2 = 0.$$

From the characteristic equation, we get the roots of the equation, namely $\lambda_{1,2} = 0$ and $\lambda_3 = \frac{(1-\rho_1)(1-\rho_2)\beta}{A} + \frac{(1-\rho_1)(1-\rho_2)\beta\delta_2}{AC}$, where $A = \delta + \sigma + \mu$ and $C = \omega + \mu$.

Because the value of the basic reproduction number is the radius spectral of FV^{-1} [21]. Then the value of the basic reproduction number is

$$R_0 = \frac{\beta(1-\rho_1)(1-\rho_2)(\delta_2 + \omega + \mu)}{(\sigma + \delta + \mu)(\omega + \mu)}.$$

Sensitivity of the basic reproduction number is analyzed to determine the effect of parameters on the basic reproduction number.

Definition 1. [25] *Normalization of the sensitivity index is obtained by normalization of the variable V which is differentiated in the parameter p , defined as follows:*

$$(20) \quad C_p^v = \frac{\partial V}{\partial p} \times \frac{p}{V}$$

where V is the variable to be analyzed and p is the parameter.

Definition 1 shows that the sensitivity index can be determined using the concept of the changing rate which is then measured. The greater the parameter index value, the greater the influence of these parameters on the measured variable value. Suppose the variable being measured is the basic reproduction number of the COVID-19 spread model, with respect to the influencing parameters. Then we assume $\mu = 3.22 \times 10^{-3}$, $\rho_1 = 0.3$, $\rho_2 = 0.08$, $\beta = 0.75$, $\delta = 0.2$, $\delta_2 = 0.04$, $\sigma = 0.17$, $\omega = 0.5$. Elasticity values obtained from the parameters affecting the value of the basic reproduction number are presented in Table 1.

Table 1. Parameter elasticity values that affect the R_0

Parameters	Values
β	$C_{\beta}^{R_0} = 1$
ρ_1	$C_{\rho_1}^{R_0} = -0.428571$
ρ_2	$C_{\rho_2}^{R_0} = -0.869565$
δ_2	$C_{\delta_2}^{R_0} = 0.06631$
ω	$C_{\omega}^{R_0} = 1.30347$
μ	$C_{\mu}^{R_0} = -1.421729$
σ	$C_{\sigma}^{R_0} = -0.455495$
δ	$C_{\delta}^{R_0} = -0.53587$

Based on Table 1, it can be concluded that some of the parameters have a negative relation to R_0 , which means, if the parameter value is increased then the value of R_0 will decrease. These parameters are displacement rate due to symptoms (δ), transition rate from asymptomatic infectious to natural recovering from disease (σ), natural death rate (μ), the proportion of body immunity (ρ_1) and the implementation of large-scale social restrictions (ρ_2). On the other hand, the parameters which have a positive relation to R_0 mean that if the parameter value is increased then the value of R_0 will also increase. These parameters are the interaction rate (β), transition rate from asymptomatic infectious to unreported symptom infected individuals (δ_2), and death rate due to COVID-19 (ω). As an example, the relation between the interaction parameter (β) and the implementation of large-scale social restrictions (ρ_2) when $R_0 = 1$ is shown in Figure 2.

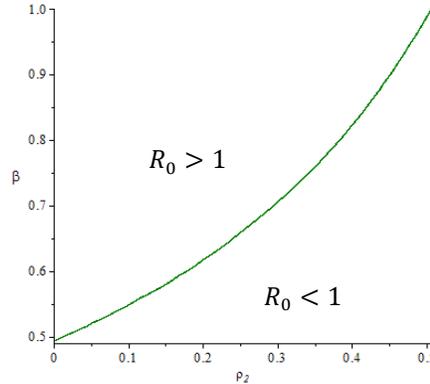


Figure 2. Relational function between β and ρ_2 when $R_0 = 1$

5. NUMERICAL SIMULATION

Suppose $\delta_1 = 0.16$, $q = 0.96$, $\alpha = 0.1$, $\gamma = 0.01$, and the previously assumed parameter values are substituted into the equation system (2). Then the disease-free equilibrium point obtained is $E_0 = (1, 0, 0, 0, 0)$ and the endemic equilibrium point is $E_1 = (0.734, 0.006, 0.0079, 0.00027, 0.134)$, the eigenvalues of the disease-free equilibrium point is $(-0.0032, -0.01322, -0.1216, -0.5907, 0.13735)$ and the eigenvalues of the endemic equilibrium point is $(-0.5880, -0.00769, -0.00769, -0.00509, -0.12189)$.

The value of the basic reproduction number is $R_0 = 1.386$. Based on the results obtained, it can be concluded that the disease-free equilibrium point is unstable due to a positive eigenvalue. Furthermore, for the stable endemic equilibrium point, it can be seen from the eigenvalues which are all negative and $R_0 > 1$. Then, we will observe four parameter values for the implementation of large-scale social restrictions and their effects on the basic reproduction number, namely $\rho_2 = 0.08, 0.2, 0.342, 0.6$. The results are presented in Table 2.

Table 2. The effect of the implementation of large-scale social restrictions (ρ_2) on the value of R_0

ρ_2	R_0	Eigenvalues of disease-free λ_4, λ_5 and their stabilities	Endemic equilibrium point and its stability
0.08	1.386	$\lambda_4 = -0.5907, \lambda_5 = 0.13735$ and E_0 unstable	E_1 exist and stable
0.2	1.2052	$\lambda_4 = -0.5896, \lambda_5 = 0.0731$ and E_0 unstable	E_1 exist and stable
0.3423	0.9908	$\lambda_4 = -0.5878, \lambda_5 = -0.0032$ and E_0 stable	E_1 does not exist
0.6	0.6026	$\lambda_4 = -0.5832, \lambda_5 = -0.1432$ and E_0 stable	E_1 does not exist

Based on Table 2, the results show that COVID-19 will still exist in Makassar City when parameter ρ_2 or the parameter for the implementation of large-scale social restrictions is given a value of 0.08, which means that only 8% section of Makassar City applying large-scale social restrictions. This can be seen from the value $R_0 = 1.386$ or $R_0 > 1$. In addition, the endemic equilibrium point exists and is stable. It is the same when the parameter value is increased to 0.2. However, when the parameter value is increased to 0.3423, which means 34.23% section of Makassar City apply the large-scale social restrictions, then Makassar City will be free of COVID-19. This can be seen from the value of $R_0 = 0.9908$ or $R_0 < 1$. In addition, all eigenvalues E_0 are negative, which means that the disease-free equilibrium point of the model is stable. And so on, greater parameter value of the implementation of large-scale social restrictions causes $R_0 \ll 1$, which means it causes a greater chance of freeing Makassar City from COVID-19. To evaluate the effect of the implementation of large-scale social restrictions (ρ_2), we plot the different parameter values which are presented in figure 3 and 4

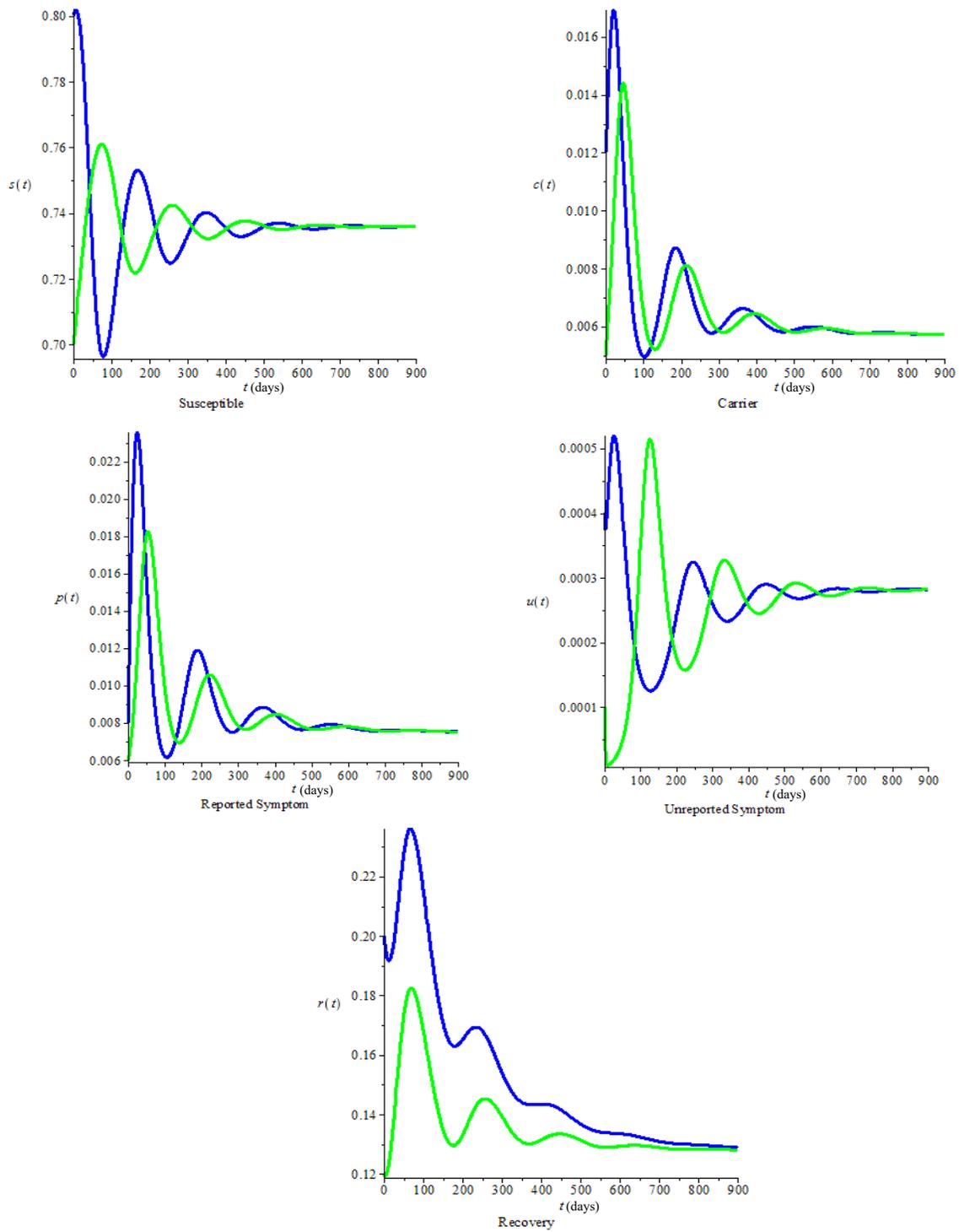


Figure 3. Graph of population when $\rho_2 = 0.08$

SCPUR MATHEMATICAL MODEL FOR THE SPREAD OF COVID-19

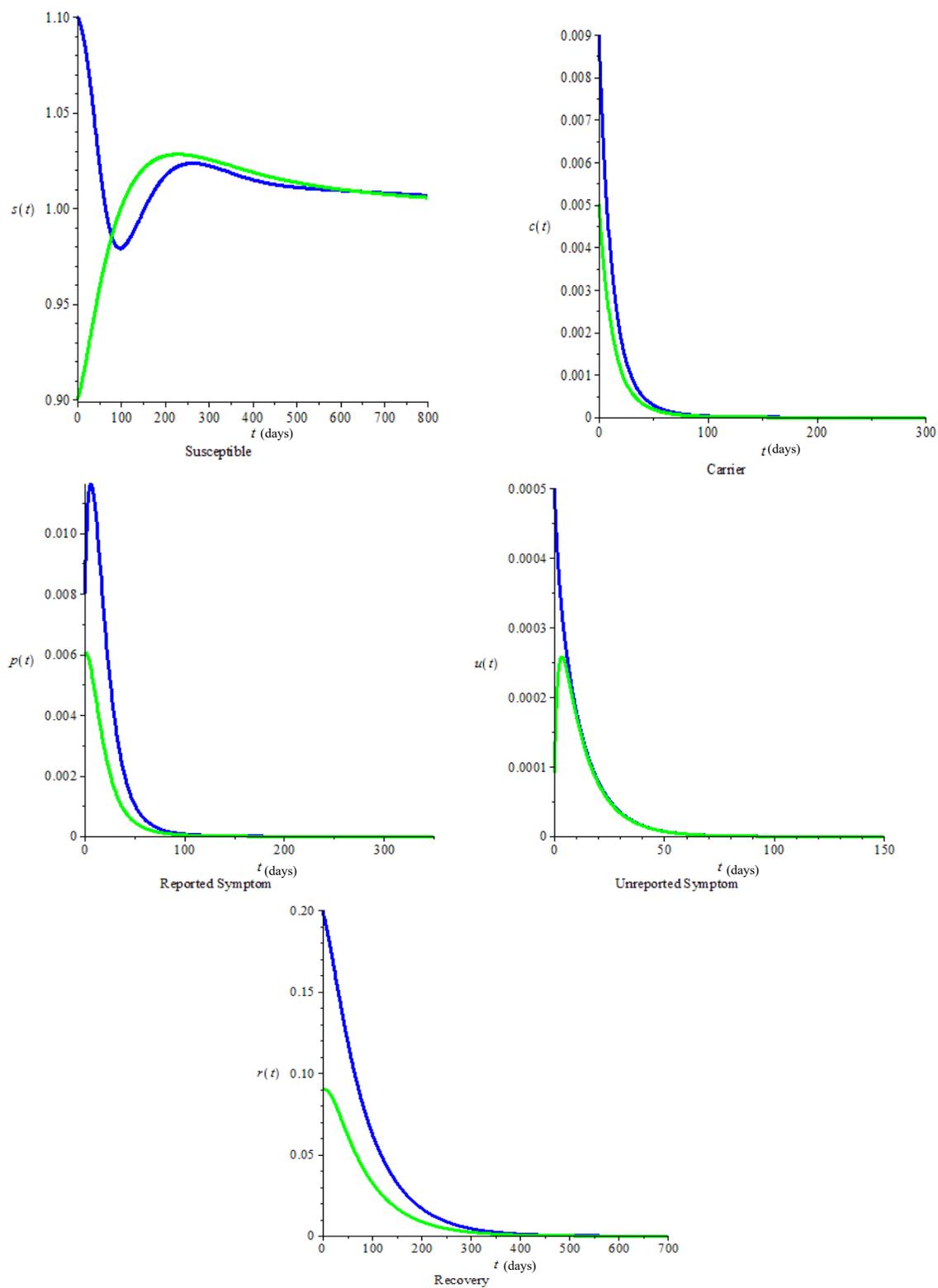


Figure 4. Graph of population when $\rho_2 = 0.3423$

Figure 3 shows that the population of Carrier, Reported Symptoms, and Unreported Symptoms with different initial values, the graph converge to the stabil equilibrium point (endemic equilibrium point). It means when we give parameter value of large-scale social restrictions is 0.08, COVID-19 does not disappear from Makassar City. Otherwise in Figure 4, when we give parameter value of large-scale social restrictions is 0.3423, the graph converge to the stabil equilibrium point (disease-free equilibrium point) or COVID-19 will disappear from Makassar City.

Furthermore, four parameter values for the interaction rate and their effects on the basic reproduction number, namely $\beta = 0.75, 0.65, 0.536, 0.3$, will be observed. The results are presented in Table 3.

Table 3. The effect of interaction rate (β) on the value of R_0

β	R_0	Eigenvalues of disease-free λ_4, λ_5 and their stabilities	Endemic equilibrium point and its stability
0.75	1.386	$\lambda_4 = -0.5907, \lambda_5 = 0.13735$ and E_0 unstable	E_1 exist dan stable
0.65	1.201	$\lambda_4 = -0.5895, \lambda_5 = 0.0717,$ and E_0 unstable	E_1 exist dan stable
0.536	0.9906	$\lambda_4 = -0.5879, \lambda_5 = -0.0037,$ and E_0 stable	E_1 does not exist
0.3	0.5544	$\lambda_4 = -0.5824, \lambda_5 = -0.1608,$ and E_0 stable	E_1 does not exist

Based on Table 3, the results show that COVID-19 will still exist in Makassar City when the interaction rate (β) is given the value of 0.75, which means that the people in Makassar City continue to interact intensely. It can be seen from the value of $R_0 = 1.386$. In addition, the endemic equilibrium point of the model exists and is stable. It is the same when the parameter value is lowered to a value of 0.65. However, when the parameter value is lowered to 0.536, which means the interaction between individuals in Makassar City is minimized, Makassar City will be free of COVID-19. This can be seen from the value of $R_0 = 0.9906$. In addition, all eigenvalues E_0 are negative, which means that the disease-free equilibrium point of the model is stable. And so on, smaller value of the interaction parameter causes $R_0 \ll 1$, which means the less contact the people of Makassar City has with each other, the greater the chance of freeing Makassar City from COVID-19. To evaluate the effect of interaction rate (β), we plot the different parameter values

which are presented in figure 5 and 6.

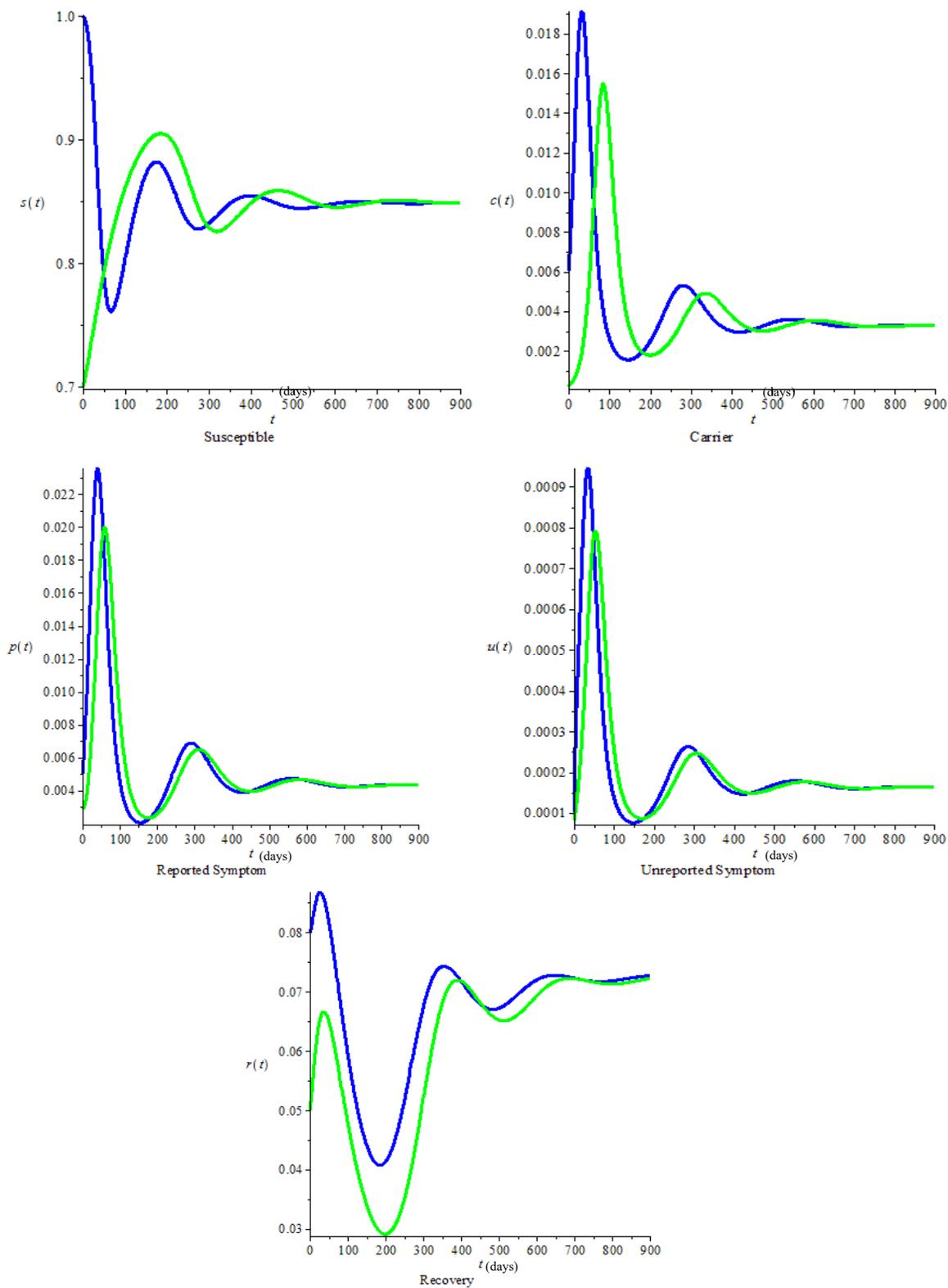


Figure 5. Graph of population when $\beta = 0.65$

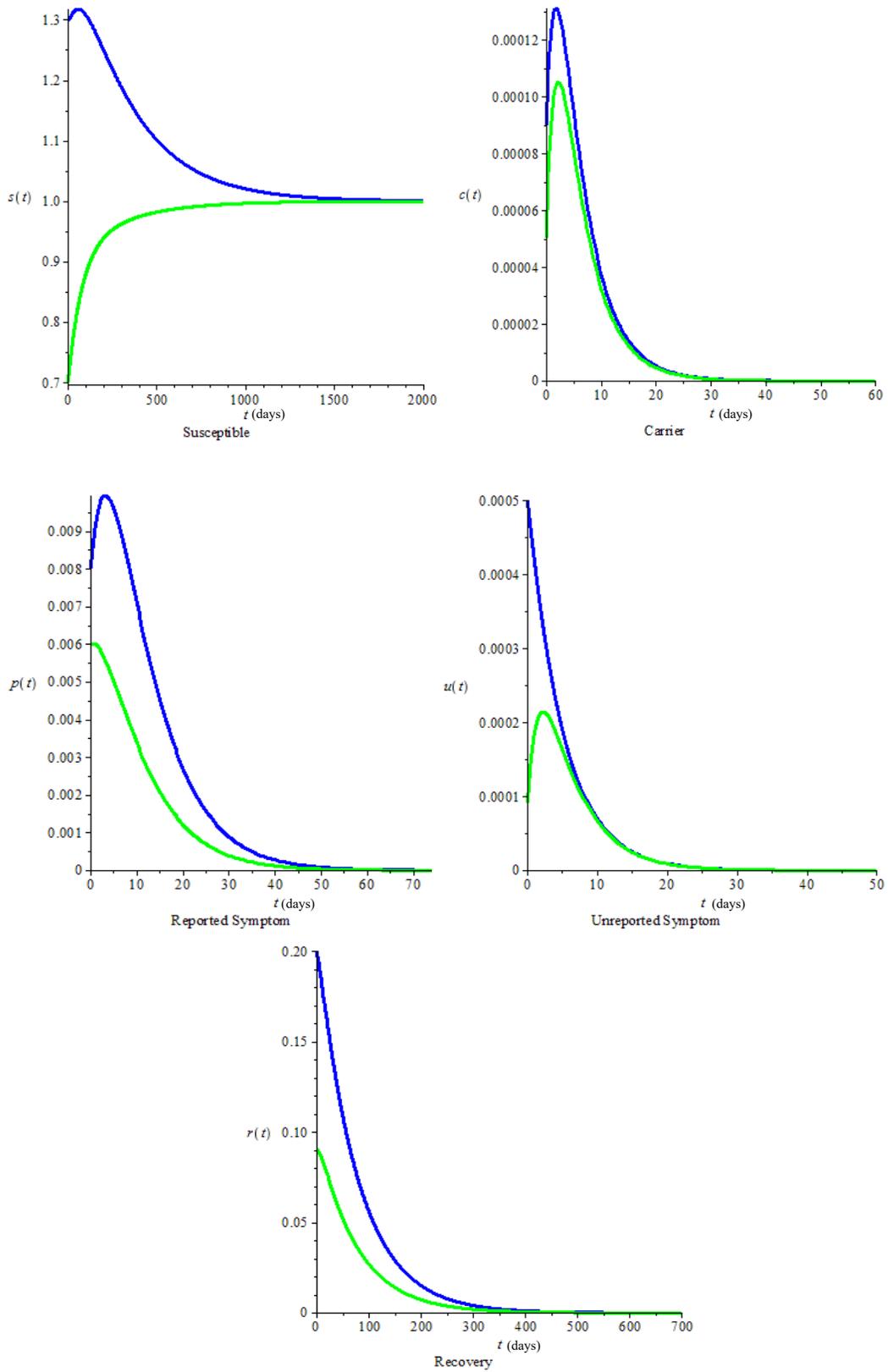


Figure 6. Graph of population when $\beta = 0.3$

Based on Figure 5 and 6, with different initial values, the graph will converge to the stable equilibrium point. In Figure 5 when we give parameter value of interaction rate is 0.65 or people in Makassar City continues interact intensely without social distancing, the stable equilibrium point is the endemic equilibrium point, meaning that COVID-19 still exist in Makassar City. Otherwise in Figure 6, when we give parameter value of interaction rate is 0.3 or people in Makassar City reduce intraction with other individual, the stable equilibrium point is the free-disease equilibrium point, meaning that COVID-19 will disappear from Makassar City.

6. CONCLUSIONS

SCPUR mathematical model for the spread of COVID-19 is an extension of the previous model. In this model, a new compartment is added, namely the compartment of individuals who have recovered from disease. Then, the proportion of body immunity to the increase of infected individuals, the proportion of the implementation of large-scale social restrictions to prevent the spread of the disease in Makassar City, and the proportion of quarantine as a healing process are also added. This SCPUR model has two equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point. The disease-free equilibrium point is stable, if the eigenvalues of the disease-free equilibrium point are all negative, so is the endemic equilibrium point. In the initial state, the basic reproduction number is 1.386. After we analysis the sensitivity, the value of the basic reproduction number can be lowered to 0.9908 and beyond. Then, based on the numerical simulations carried out, the results show that the best solution in reducing the spread of the COVID 19 in Makassar City is by increasing the implementation of large-scale social restrictions so that interaction or contact between individuals could be reduced. In this study, applying large-scale social restrictions on at least 34.23% of areas in Makassar City can free Makassar City from COVID-19.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests

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