STABILITY OF A MATHEMATICAL MODEL FOR COVID-19: A COMPUTATIONAL APPROACH

Đỗ Phương Anh, Nguyễn Thị Phương Anh, Lương Ngọc Như, Nguyễn Dương Toàn, Bùi Xuân-Quang

Khoa Toán và Khoa học tự nhiên

Email: phuonganh30600@gmail.com

Ngày nhận bài: 25/11/2021

Ngày PB đánh giá: 03/01/2022

Ngày duyệt đăng: 07/01/2022

DEDICATED TO THE VICTIMS OF THE COVID-19 PANDEMIC

ABSTRACT: In this paper, we consider a mathematical model describing the COVID-19 pandemic given by a system of ordinary differential equations. Using the Maple computer algebra system, we study the stability of the equilibrium points of the mathematical model. Finally, some numerical examples are given to illustrate the theoretical results.

Keywords: stability, disease-free-equilibrium point, endemic equilibrium point, reinfection, COVID-19 model

TÍNH ỔN ĐỊNH CỦA MỘT MÔ HÌNH TOÁN HỌC ĐỐI VỚI COVID-19: MỘT TIẾP CẬN TÍNH TOÁN

TÓM TẮT: Trong bài báo này, chúng tôi xét một mô hình toán học mô tả đại dịch COVID-19 được cho bởi một hệ phương trình vi phân thường. Sử dụng hệ thống đại số máy tính Maple, chúng tôi nghiên cứu tính ổn định của các điểm cân bằng của mô hình toán học. Cuối cùng, một số ví dụ số được đưa ra để minh họa cho các kết quả lý thuyết.

Từ khóa: ổn định, điểm cân bằng không dịch bệnh, điểm cân bằng đại dịch, tái nhiễm, mô hình COVID-19

1 Introduction

COVID-19 is the most recently discovered infectious disease affecting countries all around the world. SARS-CoV-2, which is a member of the coronavirus family, is the virus that spread the infection. In response to Covid, mathematics has been generally and efficiently used to model and predict the pandemic, … To describe the COVID-19 pandemic, one can use ordinary differential equations or partial differential equations. By using mathematical techniques such as statistics, stability analysis, combined with numerical methods, researchers obtain theoretical results. The results have yielded qualitative and quantitative insights into the COVID-19 pandemic.

Since its first appearance in the work by Kermack – McKendrick [3] dealing with the mathematical theory of epidemics, the SIR model plays a very important role in the study of the spread of an epidemic. A SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time. The name of this class of models derives from the fact that they involve coupled equations relating the number of susceptible people S, number of people infected I, and number of people who have recovered R.

In the theory of ordinary differential equations, Lyapunov stability theory was come out of Lyapunov, a Russian mathematician in

1892, and came from his doctoral dissertation [6]. Until now, the theory of Lyapunov stability is still the main theoretical basis of almost all phenomena in mechanics and ecology. Then, if the COVID-19 pandemic is described by an ordinary differential equation, the Lyapunov stability theory will be applied very successfully and profoundly to understand the asymptotic behavior of this model. We refer readers to the works [4, 5, 7, 8, 10] and references therein for more information on the matter. Along with such a mathematical approach, studies on mathematical modeling for COVID-19 using mathematical software have been carried out. For example, the very recent work Abreu [1] on this research direction can be mentioned. By using the free and open-source programming language Python and the mathematical software SageMath, Abreu [1] contributes a mathematical analysis of the stability of the equilibrium points of epidemic models and their fitting to real data.

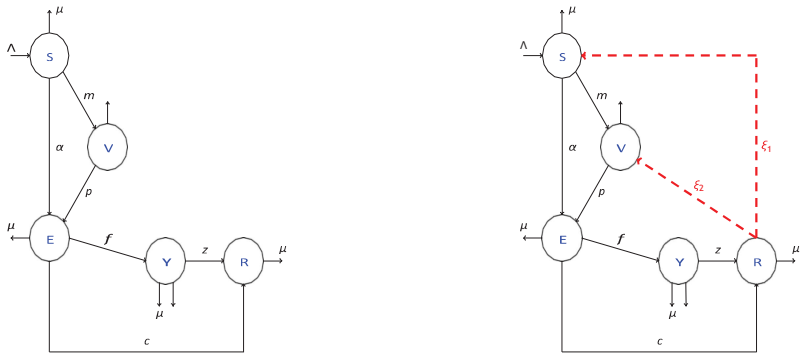
Equitable access to safe and effective vaccines is critical to ending the COVID-19 pandemic, so it is highly encouraging to see so many vaccines provided and developed. In this context, mathematical models for COVID-19 were developed to study the effects of vaccine treatment, see, e.g. [2, 5, 10]. It is important to emphasize that, Yavuz *et al.* [10] does not consider the reinfection of the recovered individuals and the vaccinated individuals. But unfortunately, COVID-19 is an epidemic with *reinfection* of the recovered and the vaccinated individuals [9]. Therefore, model (1) of Yavuz *et al*. [10] needs to be modified to describe this phenomenon.

We propose a new mathematical model based on model (1) in Yavuz *et al.* [10] by adding the quantities $\xi_1 R$ and $\xi_2 R$ (see disease transmission diagram in Figure 1b and model (2) below) describing reinfection of the recovered individuals and the vaccinated individuals. By using the Maple computer algebra system, we study the stability of the equilibrium points of the mathematical epidemic model and investigate some numerical examples. In the numerical simulations, the parameter values taken from the literature and estimated are used to perform the solutions of the proposed model. Our mathematical results are contained in Theorem 3.1 and Theorem 3.2 on the stability of the equilibrium points of the model (2). With the computational approach, the results of the paper show that Maple is a very powerful computer algebra system in the study of ordinary differential equations and stability theory. In particular, it is extremely convenient to verify the stability conditions of mathematical models.

This paper is organized as follows: In the next section, Section 2, we recall that the settings, biological assumptions, and mathematical model of Yavuz *et al.* [10] and present our mathematical model for COVID-19, model (2). Section 3 contains the main results of this paper. In Section 4, we discuss the importance of numerical results for the model we have constructed by considering the vaccination strategies.

2 Formulation of the Mathematical Models

We start with the work Yavuz *et al.* [10]. Consider the dynamic flow diagram of the COVID-19 given in Figure 1a and the biological assumptions of the model are as follows: (1) Vaccinated individuals are selected, either from those who have not been exposed, or who have not been immunized. (2) Vaccines may not completely protect vaccinated individuals. The model then uses the assumption that vaccinated individuals become infected by exposure to the virus.



(a) (b)

Figure 1: Dynamic flow diagram of the COVID-19 model

Parameter	Interpretation	Value
Λ	Recruitment rate of COVID-19 viruses	50
α	Rate of transition from susceptible (S) to exposed individuals (E)	0.002
m	Proportion of vaccinated susceptible individuals (V)	0.5
f	Rate at which exposed people (E) become infected (Y)	0.008
p	Disease exposure rate for vaccinated individuals (V)	0.08
z	The recovery rate of infected individuals (Y)	0.012
μ	Natural death rate	0.009
c	Recovery rate of exposed individuals (E)	0.05
σ	Disease-related mortality	0.25

Table 2: Parameters used for the COV 19 model

Yavuz *et al.* [10] have described the COVID-19 disease by a system of nonlinear ordinary differential equations with the parameters given in the Table 2

$$\begin{cases} \dot{S} = \Lambda - (\alpha E + m + \mu)S, \\ \dot{E} = \alpha SE + pVE - (fY + c + \mu)E, \\ \dot{Y} = fEY - (z + \mu + \sigma)Y, \\ \dot{V} = mS - (pE + \mu)V, \\ \dot{R} = zY + cE - \mu R. \end{cases} \quad (1)$$

In this context, the structure of the model (SEIVR) consists of the following compartments: As usual, $S(t), E(t), Y(t), V(t)$, and $R(t)$ represent for individuals susceptible, individuals exposed to the disease, infected individuals, vaccinated individuals, and recovered individuals, respectively. (There is a subtle reason we have to denote infected individuals by Y instead of I as is common in epidemiological models because the letter I is the imaginary unit in Maple.)

In model (1), parameters are given in Table 2. Detailed descriptions of these parameters can be found in Yavuz *et al.* [10, Section 2]. All these parameters are assumed to be positive real numbers.

It is worth discussing that the model (1), does not consider reinfection. With the diagram of the disease is shown in Figure 1b , this paper proposes a mathematical model that describes the reinfection as follows:

$$\begin{cases} \dot{S} = \Lambda - (\alpha E + m + \mu)S + \xi_1 R, \\ \dot{E} = \alpha SE + pVE - (fY + c + \mu)E, \\ \dot{Y} = fEY - (z + \mu + \sigma)Y, \\ \dot{V} = mS - (pE + \mu)V + \xi_2 R, \\ \dot{R} = zY + cE - \mu R - (\xi_1 + \xi_2)R. \end{cases} \quad (2)$$

In this model (1), the reinfection is described by terms $\xi_1 R$ and $\xi_2 R$ in the first and fourth equation, and $(\xi_1 + \xi_2)R$ in the fifth equation of the model (2).

3 Stability Analysis of the Mathematical Model

The purpose of this section is to provide a condition for the equilibrium points of the model (2) to be asymptotic stability.

First of all, positivity of the solutions, existence and uniqueness theorems for the model (2) can be done in a same way as in Masandawa *et al.* [7, Theorems 1 and 3].

The model (2) takes the form of ordinary differential equation $\dot{X}(t) = F(X)$ in Euclidean space $\mathbb{R}^5$ with the setting

$$X := \begin{bmatrix} S \\ E \\ Y \\ V \\ R \end{bmatrix}, F(X) := \begin{bmatrix} F_1(X) \\ F_2(X) \\ F_3(X) \\ F_4(X) \\ F_5(X) \end{bmatrix} := \begin{bmatrix} \Lambda - (\alpha E + m + \mu)S + \xi_1 \\ \alpha SE + pVE - (fY + c + \mu)E \\ fEY - (z + \mu + \sigma)Y \\ mS - (pE + \mu)V + \xi_2 R \\ zY + cE - \mu R - (\xi_1 + \xi_2)R \end{bmatrix}$$

To find all equilibrium points of the mathematical model (2) , we solve the system of nonlinear equations $F(X) = 0$. The Maple code as follows:

```
restart:
eq1 := 0 = Lambda - (E*alpha + m + mu)*S + xi[1]*R;
eq2 := 0 = alpha*S*E + p*V*E - (Y*f + c + mu)*E;
eq3 := 0 = f*E*Y - (z + mu + sigma)*Y;
eq4 := 0 = m*S - (E*p + mu)*V + xi[2]*R;
eq5 := 0 = z*Y + c*E - mu*R - (xi[1] + xi[2])*R;
solve({eq1, eq2, eq3, eq4, eq5}, {S, E, Y, V, R});
```

The output **solve** gives the two biological meaningful equilibrium points, disease-free-quilibrium point $\bar{X}^0 = (S_0, E_0, Y_0, V_0, R_0) = \left(\frac{\Lambda}{m+\mu}, 0, 0, \frac{\Lambda m}{\mu(m+\mu)}, 0\right)$ given by

```
S[0] := Lamda/(m+mu);          E[0] := 0;          Y[0] := 0;
V[0] := Lamda*m/(mu*(m+mu));          R[0] := 0;
```

and the endemic equilibrium $\bar{X}^1 = (S_1, E_1, Y_1, V_1, R_1)$, where

```
S[1] := simplify((Lambda*f^2*mu^2 + Lambda*f^2*mu*xi[1] + Lambda*f^2*mu*xi[2] +
  Lambda*f*mu^2*p + Lambda*f*mu*p*sigma + Lambda*f*mu*p*z +
  Lambda*f*mu*p*xi[1] + Lambda*f*mu*p*xi[2] + Lambda*f*p*sigma*xi[1] +
  Lambda*f*p*sigma*xi[2] + Lambda*f*p*z*xi[1] + c*f*mu^2*xi[1] +
  c*f*mu*sigma*xi[1] + c*mu^2*p*xi[1] + 2*c*mu*p*sigma*xi[1] +
```

```
c*mu*p*z*xi[1] + c*p*sigma^2*xi[1] + c*p*sigma*z*xi[1] -
f*mu^2*z*xi[1] - mu^2*p*z*xi[1] - mu*p*sigma*z*xi[1] - mu*p*z^2*xi[1])/
(alpha*f*mu^3 + alpha*f*mu^2*sigma + alpha*f*mu^2*z + alpha*f*mu^2*xi[1] +
alpha*f*mu^2*xi[2] + alpha*f*mu*sigma*xi[1] + alpha*f*mu*sigma*xi[2] +
alpha*f*mu*z*xi[2] + alpha*mu^3*p + 2*alpha*mu^2*p*sigma + 2*alpha*mu^2*p*z +
alpha*mu^2*p*xi[1] + alpha*mu^2*p*xi[2] + alpha*mu*p*sigma^2 + 2*alpha*mu*p*sigma*z +
2*alpha*mu*p*sigma*xi[1] +2*alpha*mu*p*sigma*xi[2] + alpha*mu*p*z^2 +
alpha*mu*p*z*xi[1] + alpha*mu*p*z*xi[2] + alpha*p*sigma^2*xi[1] + alpha*p*sigma^2*xi[2] +

 alpha*f*mu*z*xi[2] + alpha*mu^3*p + 2*alpha*mu^2*p*sigma + 2*alpha*mu^2*p*z +
 alpha*mu^2*p*xi[1] + alpha*mu^2*p*xi[2] + alpha*mu*p*sigma^2 +
 2*alpha*mu*p*sigma*z + 2*alpha*mu*p*sigma*xi[1] +2*alpha*mu*p*sigma*xi[2] +
 alpha*mu*p*z^2 + alpha*mu*p*z*xi[1] + alpha*mu*p*z*xi[2] + alpha*p*sigma^2*xi[1] +
 alpha*p*sigma^2*xi[2] +
  alpha*p*sigma*z*xi[1] + alpha*p*sigma*z*xi[2] + f^2*m*mu^2 + f^2*m*mu*xi[1] +
  f^2*m*mu*xi[2] + f^2*mu^3 + f^2*mu^2*xi[1] + f^2*mu^2*xi[2] + f*m*mu^2*p +
  f*m*mu*p*sigma + f*m*mu*p*z + f*m*mu*p*xi[1] + f*m*mu*p*xi[2] + f*m*p*sigma*xi[1] +
  f*m*p*sigma*xi[2] + f*mu^3*p + f*mu^2*p*sigma + f*mu^2*p*z + f*mu^2*p*xi[1] +
  f*mu^2*p*xi[2] +f*mu*p*sigma*xi[1] + f*mu*p*sigma*xi[2] + f*mu*p*z*xi[1]));

E[1] := (z + mu + sigma)/f;

Y[1] := simplify((Lambda*alpha*f^2*mu^2 + Lambda*alpha*f^2*mu*xi[1] +
  Lambda*alpha*f^2*mu*xi[2] + Lambda*alpha*f*mu^2*p + Lambda*alpha*f*mu*p*sigma +
  Lambda*alpha*f*mu*p*z + Lambda*alpha*f*mu*p*xi[1] + Lambda*alpha*f*mu*p*xi[2] +
  Lambda*alpha*f*p*sigma*xi[1] + Lambda*alpha*f*p*sigma*xi[2] + Lambda*alpha*f*p*z*xi[1] +
  Lambda*alpha*f*p*z*xi[2] + Lambda*f^2*m*mu*p + Lambda*f^2*m*p*xi[1] +
  Lambda*f^2*m*p*xi[2] - alpha*c*f*mu^3 - alpha*c*f*mu^2*sigma - alpha*c*f*mu^2*z -
  alpha*c*f*mu^2*xi[2] - alpha*c*f*mu*sigma*xi[2] - alpha*c*f*mu*z*xi[2] - alpha*c*mu^3*p -
  2*alpha*c*mu^2*p*sigma - 2*alpha*c*mu^2*p*z - alpha*c*mu*p*sigma^2 -
  2*alpha*c*mu*p*sigma*z - alpha*c*mu*p*z^2 - alpha*f*mu^4 - alpha*f*mu^3*sigma -
  alpha*f*mu^3*z - alpha*f*mu^3*xi[1] - alpha*f*mu^3*xi[2] - alpha*f*mu^2*sigma*xi[1] -
  alpha*f*mu^2*sigma*xi[2] - alpha*f*mu^2*z*xi[1] - alpha*f*mu^2*z*xi[2] -alpha*mu^4*p -
  2*alpha*mu^3*p*sigma - 2*alpha*mu^3*p*z - alpha*mu^3*p*xi[1] - alpha*mu^3*p*xi[2] -
  alpha*mu^2*p*sigma^2 - 2*alpha*mu^2*p*sigma*z - 2*alpha*mu^2*p*sigma*xi[1] -
  2*alpha*mu^2*p*sigma*xi[2] - alpha*mu^2*p*z^2 -
  2*alpha*mu^2*p*z*xi[1] - 2*alpha*mu^2*p*z*xi[2] -
  alpha*mu*p*sigma^2*xi[1] - alpha*mu*p*sigma^2*xi[2] - 2*alpha*mu*p*sigma*z*xi[1] -
  2*alpha*mu*p*sigma*z*xi[2] - alpha*mu*p*z^2*xi[1] - alpha*mu*p*z^2*xi[2] - c*f^2*m*mu^2 -
  c*f^2*m*mu*xi[1] - c*f^2*m*mu*xi[2] - c*f^2*mu^3 -
  c*f^2*mu^2*xi[1] -
  c*f^2*mu^2*xi[2] - c*f*m*mu^2*p - c*f*m*mu*p*sigma - c*f*m*mu*p*z -
  c*f*mu^3*p - c*f*mu^2*p*sigma - c*f*mu^2*p*z -c*f*mu^2*p*xi[1] -
  c*f*mu*p*sigma*xi[1] -
  c*f*mu*p*z*xi[1] - f^2*m*mu^3 - f^2*m*mu^2*xi[1] - f^2*m*mu^2*xi[2] -
  f^2*mu^4 -     f^2*mu^3*xi[1] - f^2*mu^3*xi[2] - f*m*mu^3*p -
  f*m*mu^2*p*sigma - f*m*mu^2*p*z -
  f*m*mu^2*p*xi[1] - f*m*mu^2*p*xi[2] - f*m*mu*p*sigma*xi[1] - f*m*mu*p*sigma*xi[2] -
  f*m*mu*p*z*xi[1] - f*m*mu*p*z*xi[2] - f*mu^4*p - f*mu^3*p*sigma - f*mu^3*p*z - f*mu^3*p*xi[1] -
  f*mu^3*p*xi[2] - f*mu^2*p*sigma*xi[1] -
  f*mu^2*p*sigma*xi[2] - f*mu^2*p*z*xi[1] - f*mu^2*p*z*xi[2])/(f*(alpha*f*mu^3 +
  alpha*f*mu^2*sigma + alpha*f*mu^2*z + alpha*f*mu^2*xi[1] +
  alpha*f*mu^2*xi[2] + alpha*f*mu*sigma*xi[1] + alpha*f*mu*sigma*xi[2] +
  alpha*f*mu*z*xi[2] + alpha*mu^3*p +
  2*alpha*mu^2*p*sigma + 2*alpha*mu^2*p*z +
  alpha*mu^2*p*xi[1] + alpha*mu^2*p*xi[2] + alpha*mu*p*sigma^2 +
  2*alpha*mu*p*sigma*z + 2*alpha*mu*p*sigma*xi[1] + 2*alpha*mu*p*sigma*xi[2] +
```

```
alpha*mu*p*z^2 +     alpha*mu*p*z*xi[1] +
alpha*mu*p*z*xi[2] + alpha*p*sigma^2*xi[1] + alpha*p*sigma^2*xi[2] +
alpha*p*sigma*z*xi[1] +
alpha*p*sigma*z*xi[2] + f^2*m*mu^2 + f^2*m*mu*xi[1] + f^2*m*mu*xi[2] + f^2*mu^3 +
f^2*mu^2*xi[1] + f^2*mu^2*xi[2] + f*m*mu^2*p + f*m*mu*p*sigma + f*m*mu*p*z + f*m*mu*p*xi[1] +
f*m*mu*p*xi[2] +
f*m*p*sigma*xi[1] + f*m*p*sigma*xi[2] + f*mu^3*p + f*mu^2*p*sigma + f*mu^2*p*z +
f*mu^2*p*xi[1] + f*mu^2*p*xi[2] + f*mu*p*sigma*xi[1] +
f*mu*p*sigma*xi[2]  +  f*mu*p*z*xi[1])));
```

```
V[1] := simplify((Lambda*alpha*f*z*xi[2] + Lambda*f^2*m*mu + Lambda*f^2*m*xi[1] +
Lambda*f^2*m*xi[2] + alpha*c*mu^2*xi[2] + 2*alpha*c*mu*sigma*xi[2] + alpha*c*mu*z*xi[2] +
alpha*c*sigma^2*xi[2] + alpha*c*sigma*z*xi[2] - alpha*mu^2*z*xi[2] - alpha*mu*sigma*z*xi[2]  -
alpha*mu*z^2*xi[2]  + c*f*m*mu*xi[1] + c*f*m*mu*xi[2] + c*f*m*sigma*xi[1] +
c*f*m*sigma*xi[2] + c*f*mu^2*xi[2] + c*f*mu*sigma*xi[2] - f*m*mu*z*xi[1] - f*m*mu*z*xi[2] -
f*mu^2*z*xi[2])/(alpha*f*mu^3 + alpha*f*mu^2*sigma + alpha*f*mu^2*z + alpha*f*mu^2*xi[1]
+ alpha*f*mu^2*xi[2] + alpha*f*mu*sigma*xi[1] + alpha*f*mu*sigma*xi[2] + alpha*f*mu*z*xi[2]
+ alpha*mu^3*p + 2*alpha*mu^2*p*sigma + 2*alpha*mu^2*p*z + alpha*mu^2*p*xi[1] +
alpha*mu^2*p*xi[2] + alpha*mu*p*sigma^2 + 2*alpha*mu*p*sigma*z +
2*alpha*mu*p*sigma*xi[1] + 2*alpha*mu*p*sigma*xi[2] + alpha*mu*p*z^2 +
alpha*mu*p*z*xi[1] + alpha*mu*p*z*xi[2] + alpha*p*sigma^2*xi[1] + alpha*p*sigma^2*xi[2] +
alpha*p*sigma*z*xi[1] + alpha*p*sigma*z*xi[2] + f^2*m*mu^2 + f^2*m*mu*xi[1] +
f^2*m*mu*xi[2] + f^2*mu^3 + f^2*mu^2*xi[1] + f^2*mu^2*xi[2] + f*m*mu^2*p +
f*m*mu*p*sigma + f*m*mu*p*z + f*m*mu*p*xi[1] + f*m*mu*p*xi[2] + f*m*p*sigma*xi[1] +
f*m*p*sigma*xi[2] + f*mu^3*p + f*mu^2*p*sigma + f*mu^2*p*z + f*mu^2*p*xi[1] +
f*mu^2*p*xi[2] + f*mu*p*sigma*xi[1]  + f*mu*p*sigma*xi[2] +  f*mu*p*z*xi[1]));

R[1] := simplify((Lambda*alpha*f^2*mu*z + Lambda*alpha*f*mu*p*z +
Lambda*alpha*f*p*sigma*z + Lambda*alpha*f*p*z^2 + Lambda*f^2*m*p*z + alpha*c*f*mu^3
+ 2*alpha*c*f*mu^2*sigma + alpha*c*f*mu^2*z  + alpha*c*f*mu*sigma^2 +
alpha*c*f*mu*sigma*z + alpha*c*mu^3*p + 3*alpha*c*mu^2*p*sigma + 2*alpha*c*mu^2*p*z
+ 3*alpha*c*mu*p*sigma^2 + 4*alpha*c*mu*p*sigma*z + alpha*c*mu*p*z^2 +
alpha*c*p*sigma^3 + 2*alpha*c*p*sigma^2*z + alpha*c*p*sigma*z^2 - alpha*f*mu^3*z -
alpha*f*mu^2*sigma*z - alpha*f*mu^2*z^2 - alpha*mu^3*p*z - 2*alpha*mu^2*p*sigma*z -
2*alpha*mu^2*p*z^2 - alpha*mu*p*sigma^2*z - 2*alpha*mu*p*sigma*z^2 - alpha*mu*p*z^3 +
c*f^2*m*mu^2 + c*f^2*m*mu*sigma + c*f^2*mu^3 + c*f^2*mu^2*sigma + c*f*m*mu^2*p +
2*c*f*m*mu*p*sigma + c*f*m*mu*p*z + c*f*m*p*sigma^2 + c*f*m*p*sigma*z + c*f*mu^3*p
+ 2*c*f*mu^2*p*sigma + c*f*mu^2*p*z + c*f*mu*p*sigma^2 + c*f*mu*p*sigma*z -
f^2*m*mu^2*z - f^2*mu^3*z - f*m*mu^2*p*z - f*m*mu*p*sigma*z - f*m*mu*p*z^2 -
f*mu^3*p*z - f*mu^2*p*sigma*z - f*mu^2*p*z^2)/(f*(alpha*f*mu^3 + alpha*f*mu^2*sigma +
alpha*f*mu^2*z + alpha*f*mu^2*xi[1] + alpha*f*mu^2*xi[2] + alpha*f*mu*sigma*xi[1] +
alpha*f*mu*sigma*xi[2]  +  alpha*f*mu*z*xi[2]  + alpha*mu^3*p + 2*alpha*mu^2*p*sigma +
2*alpha*mu^2*p*z + alpha*mu^2*p*xi[1] +alpha*mu^2*p*xi[2] + alpha*mu*p*sigma^2 +
2*alpha*mu*p*sigma*z + 2*alpha*mu*p*sigma*xi[1] + 2*alpha*mu*p*sigma*xi[2] +
alpha*mu*p*z^2 + alpha*mu*p*z*xi[1] + alpha*mu*p*z*xi[2] + alpha*p*sigma^2*xi[1] +
alpha*p*sigma^2*xi[2]  +  alpha*p*sigma*z*xi[1]  +  alpha*p*sigma*z*xi[2]  + f^2*m*mu^2 +
f^2*m*mu*xi[1] + f^2*m*mu*xi[2] + f^2*mu^3 + f^2*mu^2*xi[1] + f^2*mu^2*xi[2] +
f*m*mu^2*p + f*m*mu*p*sigma + f*m*mu*p*z + f*m*mu*p*xi[1] + f*m*mu*p*xi[2] +
f*m*p*sigma*xi[1] + f*m*p*sigma*xi[2] +  f*mu^3*p  + f*mu^2*p*sigma + f*mu^2*p*z +
f*mu^2*p*xi[1]  +  f*mu^2*p*xi[2]  + f*mu*p*sigma*xi[1]  +  f*mu*p*sigma*xi[2] +
f*mu*p*z*xi[1])));
```

3.1 Stability of the Disease-Free-Equilibrium Point

The main result of this subsection is to state the asymptotic stability of the disease-free-equilibrium point $\overline{X}^0 = (S_0, E_0, Y_0, V_0, R_0) = \left(\frac{\Lambda}{m+\mu}, 0, 0, \frac{\Lambda m}{\mu(m+\mu)}, 0\right)$ as

follows:

Theorem 3.1. *Consider the mathematical model (2). The disease-free-equilibrium point* $\overline{X}^0$ *is asymptotically stable if* $\kappa < 1$ *and is unstable if* $\kappa > 1$, *where*

$$\kappa := \frac{\Lambda(\alpha\mu + mp)}{\mu(m+\mu)(c+\mu)}. \qquad (4)$$

Proof. We need to compute the Jacobian determinant of the mapping F at the disease-free-equilibrium point $\overline{X}^0 = (S_0, E_0, Y_0, V_0, R_0)$. The Maple code to generate eigenvalues of the Jacobian matrix J_0 at $\overline{X}^0$ is given below

```
restart;
with(VectorCalculus);
with(LinearAlgebra):
F1 := Lambda - (E*alpha + m + mu)*S + xi[1]*R;
F2 := alpha*S*E + p*V*E - (Y*f + c + mu)*E;
F3 := f*E*Y - (z + mu + sigma)*Y;
F4 := m*S - (E*p + mu)*V +
xi[2]*R;
F5 := z*Y + c*E - mu*R - (xi[1] + xi[2])*R;
J[0] := Jacobian([F1, F2, F3, F4, F5], [S, E, Y, V, R]
    = [S[0], E[0], Y[0], V[0], R[0]]);
Eigenvalues(J[0]);
```

The Maple command **`Eigenvalues`** returns the eigenvalues $-\mu, -\mu-\xi_1-\xi_2, -\mu-\sigma-z, -m-\mu$ and $\frac{\Lambda\alpha\mu + \Lambda mp - cm\mu - c\mu^2 - m\mu^2 - \mu^3}{\mu(m+\mu)}$ of the Jacobian matrix J_0. We have

$$\frac{\Lambda\alpha\mu + \Lambda mp - cm\mu - c\mu^2 - m\mu^2 - \mu^3}{\mu(m+\mu)} = (\kappa - 1)(c+\mu).$$

Therefore, since the parameters c and μ are positive, stability of the disease-free-equilibrium point $\overline{X}^0 = \left(\frac{\Lambda}{m+\mu}, 0, 0, \frac{\Lambda m}{\mu(m+\mu)}, 0\right)$ depends on the sign of $\kappa - 1$. In other words, the proof is complete.

We can verify the condition of Theorem 3.1 with Maple command

```
Lambda := 50; alpha := 0.002; m := 0.5; f := 0.008; p := 0.08; z := 0.012;
mu := 0.009; c := 0.05; sigma := 0.25; xi[1] := 1/(6*30); xi[2] := 1/(12*30);
kappa := Lambda*(alpha*mu + m*p)/((m + mu)*(c + mu));
is(1 < kappa);
```

The **`is`** routine returns *true* or *false*. In this case, the result is *true*. This means, the disease-free-equilibrium point $\overline{X}^0$ is unstable.

3.2 Stability of the Endemic Equilibrium Point

For the stability of the endemic equilibrium point, we have characteristic polynomial of the Jacobian matrix J_1 at the endemic equilibrium point $\overline{X}^1 = (S_1, E_1, Y_1, V_1, R_1)$ has form

$$Q(\lambda) := a_0\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5 \qquad (5)$$

The Maple command **coeff** returns the coefficients of the characteristic polynomial:

```
J[1] := Jacobian([F1, F2, F3, F4, F5], [S, E, Y, V, R]
    = [S[1], E[1], Y[1], V[1], R[1]]);
P := CharacteristicPolynomial(J[1], lambda);
```

Theorem 3.2. *Consider the mathematical model (2). If the constants* $a_0, a_1, a_2, a_3, a_4, a_5$ *satisfythe following conditions*

$$a_1 > 0, \qquad a_5 > 0, \tag{6}$$

$$\kappa_1 := a_1 a_2 - a_3 > 0, \tag{7}$$

$$\kappa_2 := a_1^2 a_4 - (a_2 a_3 + a_5) a_1 + a_3^2 < 0, \tag{8}$$

$$\kappa_3 := a_1^2 a_4^2 + (-a_2 a_3 a_4 + a_5(a_2^2 - 2a_4)) a_1 - a_2 a_3 a_5 + a_3^2 a_4 + a_5^2 < 0, \tag{9}$$

then the endemic equilibrium point $\overline{X}^1$ *of the model (2) is asymptotically stable.*

Proof. We have characteristic polynomial of the Jacobi matrix J_1 at $\overline{X}^1 = (S_1, E_1, Y_1, V_1, R_1)$ is $Q(\lambda)$ as described in (5) with $a_0 = 1$. The Routh-Hurwitz stability criterion for $Q(\lambda)$ is the following system of inequalities

$$a_1 > 0, \quad a_5 > 0, \quad a_2 - \frac{a_3}{a_1} > 0, \quad \frac{-a_1^2 a_4 + (a_2 a_3 + a_5) a_1 - a_3^2}{a_1 a_2 - a_3} > 0, \tag{10}$$

$$\frac{a_1^2 a_4^2 + (-a_2 a_3 a_4 + a_5(a_2^2 - 2a_4)) a_1 - a_2 a_3 a_5 + a_3^2 a_4 + a_5^2}{a_1^2 a_4 + (-a_2 a_3 - a_5) a_1 + a_3^2} > 0. \tag{11}$$

Thus, if conditions (6)-(9) are satisfied then Routh-Hurwitz stability criterion is satisfied. Therefore, the endemic equilibrium point $\overline{X}^1 = (S_1, E_1, Y_1, V_1, R_1)$ is asymptotically stable, finishing the proof.

With the data in Table 2, the conditions (6)-(9) in Theorem 3.2 can be checked with the following Maple command

```
kappa[1] := a[1]*a[2] - a[3];
kappa[2] := a[1]^2*a[4] - (a[2]*a[3] + a[5])*a[1] + a[3]^2;
kappa[3] := a[1]^2*a[4]^2 + (-a[2]*a[3]*a[4] + a[5]*(a[2]^2 - 2*a[4]))*a[1]
    - a[2]*a[3]*a[5] + a[3]^2*a[4] + a[5]^2;

is(0 < a[1]); is(0 < a[5]);
is(0 < kappa[1]); is(kappa[2] < 0); is(kappa[3] < 0);
```

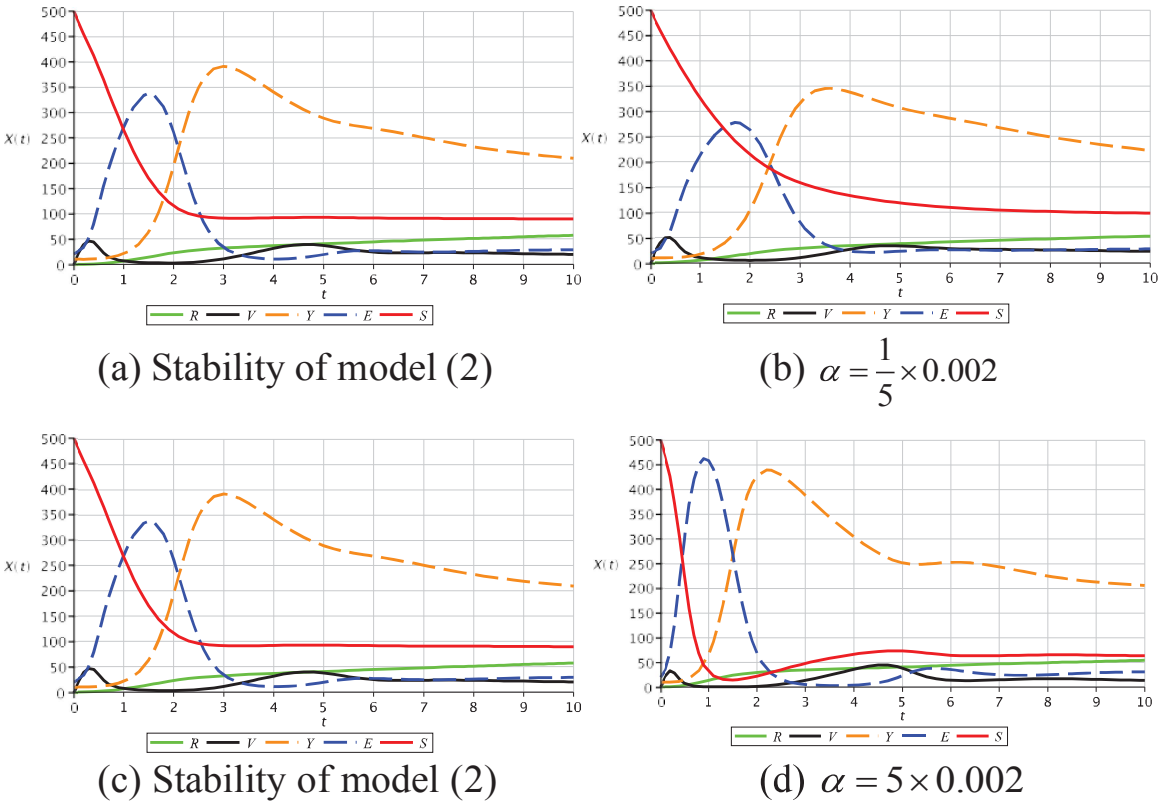
Maple returns all results as *true*. That is, point $\overline{X}^1$ is asymptotically stable.

4 Numerical Examples

We now discuss some numerical results for the model we have constructed by consideringthe vaccination strategies and the reinfection. For this simulation we have taken few parameter values from Yavuz *et al.* [10] (and the references therein) as given in Table 2.

Now, the initial values used are $S(0) = 500, E(0) = 20, Y(0) = 10, V(0) = 0$ and $R(0) = 0$. Figure 2a depicts the behaviors and densities of mathematical model (2) with the data given in Table 2.

The change of the parameter α. Parameter α is rate of transition from susceptible individ-uals to exposed individuals. We consider Figure 2b with $\alpha := \frac{1}{5} \times 0.002$. When α is reduced by 5 times we get the maximum point of the curve $E(t)$ (blue) describing the number of exposed individuals decreasing from about 340 (at $t \approx 1.5$) to 280 (at $t \approx 1.8$). At the same time, the maximum point of the curve $Y(t)$ (orange) representing the infected individual decreases from 400 (at $t \approx 3$) to about 350 (at $t \approx 3.5$).



(a) Stability of model (2) (b) $\alpha = \frac{1}{5} \times 0.002$

(c) Stability of model (2) (d) $\alpha = 5 \times 0.002$

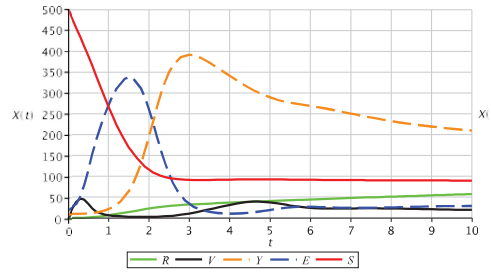
Figure 2: Dynamical behavior of the COVID-19 pandemic with the change of α

Figure 2d considers the value of α to be increased by 5 times, $\alpha = 5 \times 0.002$. For $\alpha = 5 \times 0.002$, we have a peak of the curve $E(t)$ (blue) describing the number of exposed individuals increasing from about 340 (at $t \approx 1.5$) to about 460 (at $t \approx 0.9$). At the same time, the peak of the curve $Y(t)$ (orange) representing the infected individual increases from 400 (at $t \approx 3$) to about 440 (at $t \approx 2.2$). Thus, the number of susceptible individuals and infected individuals will fluctuate proportionally to the transmission rate α.

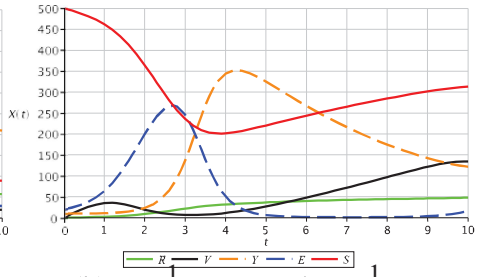
The change of the parameters p and m. Figure 3b consider the values of p and m to be decreased 5 times, $p=\frac{1}{5}\times 0.08$ and $m=\frac{1}{5}\times 0.5$. Figure 3b shows the peak of the curve $V(t)$ (black) describing the number of vaccinated individuals increasing from about 50 (at $t\approx 0.4$) to 140 (at $t\approx 9.8$). At the same time, the number of susceptible individuals is approximately doubled. In addition, the peak of the curve $E(t)$ (blue) representing the exposed individual decreased from about 340 (at $t\approx 1.5$) to about 270 (at $t\approx 2.7$). The curve $Y(t)$ in this case is similar to Figure 2b [and the peak of the curve $Y(t)$ (orange) depicts the number of infected individuals decreasing from 400 to about 350 (at $t\approx 3.5$)].

Figure 3d considers the values of p and m to be increased 5 times, $p=5\times 0.08$ and $m=5\times 0.5$. When the parameters p and m increase, observing the figure we see an unexpected phenomenon occurs. The graph of the number of susceptible people and the number of vaccinated people decreased by about 4 times. The number of people exposed and the number of infected people both increased. At the same time, the curves $S(t)$ (red) and $V(t)$ (black) both descend very close to the horizontal axis, which means that the number of susceptible individuals and the number of vaccinated individuals both die.

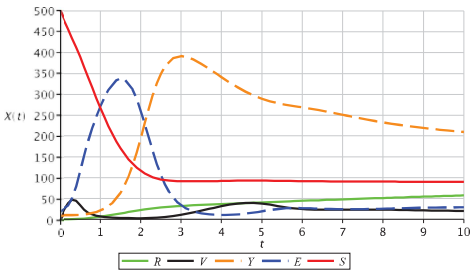
It is clearly seen that, when increasing the parameters p and m, it not only affects the number of individuals vaccinated against but also greatly affects other compartments.



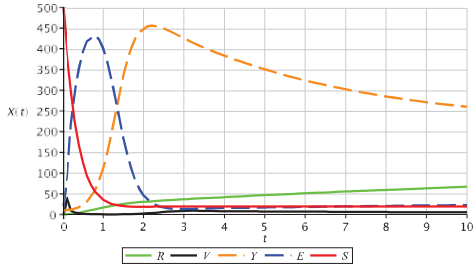
(a) Stability of model (2)



(b) $p=\frac{1}{5}\times 0.08$ and $m=\frac{1}{5}\times 0.5$



(c) Stability of model (2)



(d) $p=5\times 0.08$ and $m=5\times 0.5$

Figure 3: Dynamical behavior of the COVID-19 pandemic with the change of p and m

Acknowledgments. We would like to thank the reviewer for careful reading of our manuscript. His or her valuable comments, remarks, and corrections lead to improvement of our paper.

REFERENCES

1. Abreu Z., Cantin G., and Silva C.J. (2021). "Analysis of a COVID-19 compartmen- tal model: a mathematical and computa- tional approach". *Mathematical Biosciences and Engineering*, 18(6), 7979-7998. DOI: 10.3934/mbe.2021396.

2. Diagne M.L., Rwezaura H., Tchoumi S.Y., and Tchuenche J.M. (2021). "A mathematical model of COVID-19 with vaccination and treatment". *Computational and Mathematical Methods in Medicine*, Article ID 1250129, 16 pages.

3. Kermack W.O., McKendrick A.G. (1927). "A contribution to the mathematical theory of epi- demics". *Proceedings of The Royal Society A Mathematical Physical and Engineering Sciences*, 115, 700–711.

4. Kevrekidis P.G., Cuevas-Maraver J., Drossi- nos Y., Rapti Z., and Kevrekidis G.A. (2021). "Reaction-diffusion spatial modeling of COVID- 19: Greece and Andalusia as case exam- ples". arXiv:2005.04527v4 [q-bio.PE], July 01, 2021.

5. Kumar P., Erturk V.S., and Murillo-Arcila M. (2021). "A new fractional mathematical mod- elling of COVID-19 with the availability of vac- cine". *Results in Physics*, 24, 104213.

6. Lyapunov A.M. (1892). *The General Problem of the Stability of Motion* (In Russian), Doctoral dissertation, Univ. Kharkov. English translations: (1) *Stability of Motion*, Academ- ic Press, New-York & London, 1966; (2) *The General Problem of the Stability of Motion* (Fuller A.T. trans.) Taylor & Francis, London, 1992.

7. Masandawa L., Mirau S.S., and Mbalawata I.S. (2021). "Mathematical modeling of COVID-19 transmission dynamics between healthcare work- ers and community". *Results in Physics*, 29, 104731.

8. Nhu L.N., Huyen L.T.N., Giang V.T.H., and Hang P.T. (2021). "Stability of a mathematical model describing the Covid-19 pandemic in terms of the environment, social distancing and reinfection". *Hanoi National University of Education (HNUE) Journal of Science – Natural Science*, 66(3), 8– 19.

9. World Health Organization (WHO). *Episode #49 Can I get infected after vaccination?*. Link: https://www.who.int/emergencies/diseases/novel-coronavirus-2019/media-resources/science-in-5/episode-49-can-i-get-infected-after-vaccination (13 August 2021).

10. Yavuz M., Cos¸ar F.O¨ ., Gu¨nay F., and O¨ zdemir F.N. (2021). "A new mathematical modeling of the COVID-19 pandemic including the vaccina- tion campaign". *Open Journal of Modelling and Simulation*, 9, 299–321.