# A mathematical model for the dynamics of COVID-19 pandemic involving the infective immigrants

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**Abstract**

Since the first outbreak in Wuhan, China, in December 31, 2019, COVID-19 pandemic has been spreading to many countries in the world. The ongoing COVID-19 pandemic has caused a major global crisis, with 554,767 total confirmed cases, 484,570 total recovered cases, and 12,306 deaths in Iraq as of February 2, 2020. In the absence of any effective therapeutics or drugs and with an unknown epidemiological life cycle, predictive mathematical models can aid in the understanding of both control and management of coronavirus disease. Among the important factors that helped the rapid spread of the epidemic are immigration, travelers, foreign workers, and foreign students. In this work, we develop a mathematical model to study the dynamical behavior of COVID-19 pandemic, involving immigrants' effects with the possibility of re-infection. Firstly, we studied the positivity and roundedness of the solution of the proposed model. The stability results of the model at the disease-free equilibrium point were presented when $\mathcal{R}_0 < 1$. Further, it *was* proven that the pandemic equilibrium point will persist uniformly when $\mathcal{R}_0 > 1$. Moreover, we confirmed the occurrence of the local bifurcation (saddle-node, pitchfork, and transcritical). Finally, theoretical analysis and numerical results were shown to be consistent.

**Keywords:** COVID-19, Coronavirus, Immigrants, Mathematical model, Stability, Local bifurcation.

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## النمذجة الرياضية لديناميات جائحة كورونا المتضمن المهاجرين المصابين

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الخلاصة:

منذ 31 ديسمبر 2019 تفشى جائحة COVID–19 في مدينة ووهان في الصين ، وبعد ذلك انتشر إلى العديد من دول العالم. تسبب جائحة COVID–19 المستمر في حدوث أزمة عالمية كبيرة ، حيث بلغ إجمالي الحالات المؤكدة 554,767 حالة، وتعافي إجمالي 484,570 حالة، و 12,306 حالة وفاة في العراق اعتبارًا من 2 فبراير 2020. في غياب أي علاجات أو عقاقير فعالة. مع وجود دورة حياة وبائية غير معروفة، يمكن للنماذج الرياضية التنبؤية أن تساعد في فهم كل من السيطرة على وباء فيروس كورونا وإدارته. لذا، فإن احد العوامل المهمة التي ساعدت على الانتشار السريع للوباء هي الهجرة والمسافرين والعمال والطلاب الأجانب. في هذا العمل، قمنا بتطوير إنموذج رياضي لدراسة السلوك الدينامي لوباء COVID–19 الذي يتضمن تأثير المهاجرين مع إمكانية الإصابة مرة أخرى. أولاً ، قمنا بدراسة الإيجابية والقيود لحل الإنموذج المقترح. ناقشنا نتائج الاستقرار للإنموذج عند نقطة التوازن الخالية من المرض عندما $R_0 < 1$ ، وعلاوة على ذلك ثبت أن نقطة توازن الجائحة ستستمر بشكل موحد عندما $R_0 > 1$ . علاوة على ذلك، ناقشنا حدوث التفرعات المحلية ايضاً. وأخيرًا، يظهر التحليل النظري والنتائج العددية متسقة.

## 1. Introduction

In December 2019, the spread of nCoV-19 disease commenced in Wuhan, China. The World Health Organization (WHO) has classified the new disease as pandemic on March 11, 2020. Recently, COVID-19 has spread fast to many countries in all continents, such as United States, Brazil, India, Russia and South Africa. The outbreak of COVID-19 has become a globally public health concern the in medical community, as the virus is spreading around the world [1, 2]. Initially, the Iraqi government adopted a social distancing strategy and lockdown in all provinces after the discovery of the first infection to a traveling student on February 2, 2020 [3].

The migration factor is one of the reasons that help the spread of the epidemic, especially if the immigrant is infected but without symptoms. This case is considered a dangerous source of spreading the epidemic. For example, Naji and Mohsen performed a stability analysis on an *SVIR* epidemic model, involving immigrants [4]. Kiran *et al*. suggested the modeling of SARS-CoV2 with effects of population migration and punctuated lockdown [5].

A COVID‑19 is a new disease; it spreads between people more easily than influenza. People are most infectious when they show symptoms (even mild or non-specific symptoms), but may be infectious for up to two days before symptoms appear (pre-symptomatic transmission). They remain infectious for an estimated 7 to 12 days in moderate cases and an average of two weeks in severe cases. People can also transmit the virus without showing any symptom (asymptomatic transmission); some studies found that 40–45% of infected people are asymptomatic [6-8].

Also, sputum and saliva carry large amounts of virus. Thus, the direct contact routes such as kissing, intimate contact, and speaking are sources to transmit the virus (Figure-1). The virus may occur in breast milk, but whether it is transmittable to the baby is unknown [9].
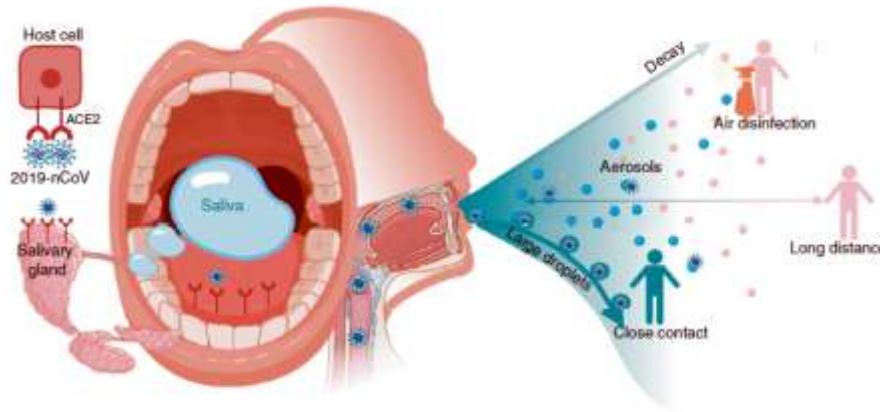
**Figure 1-**Spread of coronavirus by saliva due to speaking and coughing

Obviously, COVID-19 has become a global disease. Thus, several researchers suggested epidemiological mathematical models to understand the dynamics of the spread of the epidemic, as in the study of Mohsen *at el*. [10]. They proposed and analyzed a modeling of COVID-19 with media coverage effects and quarantine strategy to control the spread of the disease. Mamo [11] developed a mathematical model for transmission dynamics of COVID-19 propagation with public health intervention. Yang and Wang [12] suggested a mathematical model for the novel coronavirus epidemic in Wuhan, China. Samui *et al*. [13] proposed a mathematical model for COVID-19 in India. Garba *et al*. [14] studied a model of COVID-19 pandemic outbreak in South Africa.

In this paper, a mathematical model that describes the dynamics of COVID-19 pandemic, involving immigrants' effects with the possibility of re-infection, is proposed and studied. The order of this paper is as follows; the mathematical modeling of the novel coronavirus is shown in Section 2. Some basic properties of the model (positivity, boundedness of solution, calculated basic reproduction number, and existence equilibrium points) are discussed in Section 3. The local stability analysis is studied by using Gersgorin's theorem in Section 4. By using Castillo-Chavez method and Lyapunov function, the global stability of the proposed model at all equilibrium points was analyzed in Section 5. The occurrence of local bifurcation near the disease-free equilibrium point is discussed in Section 6. Finally, in Section 7, the effects of varying all the system parameters are investigated using numerical simulation.

## 2. The Model Formulation

At the beginning of Coronavirus outbreak, there were many countries that did not record any infection with the epidemic. However, as their citizens, travelers, or immigrants returned, the infections began to increase. Accordingly, one of the main reasons for the spread of the epidemic is the migration factor. For example, in Iraq, the first infection case appeared was that of a foreign student who was carrying the virus, but without symptoms. On the other hand, most of the mathematical models that have studied the spread of Coronavirus depended on the basic model of SIR- type of disease, which implies that the patient acquires permanent immunity against the virus after recovery. Meanwhile, there are many reports that prove the opposite, meaning that a person infected with the virus acquires temporary immunity against the virus. Therefore, in this paper, a mathematical model that simulates the dynamics of coronavirus pandemic is proposed. It is assumed that the model taking into account the effect of immigrants. In addition, loss of immunity to coronavirus after recovery is also included. In this work, we create a mathematical model that describes COVID-19 transmission. The model considers a total population of $N$ on time $t$ such that $S(t) + E(t) + C(t) + I(t) + R(t) = N$. We assume that the total population is divided into to five compartments, which are: $S(t)$ individuals are susceptible for being exposed, $E(t)$ susceptibility due to direct contact with asymptomatic individuals (Carriers) and symptomatic individuals (Infected), denoted by $C(t)$ and $I(t)$, respectively. The number of individuals $R(t)$ represents those carriers and infected people, respectively, who have recovered , and can be reinfected. Thus, the assumption can be written by the following set of differential equations,

$$\dot{S} = \Lambda + (1-p)A - \beta SC - \frac{\beta_1 SI}{1+mI} + \epsilon R - \mu S,$$

$$\dot{E} = \beta SC + \frac{\beta_1 SI}{1+mI} - (\alpha + \mu + \sigma_1)E,$$

$$\dot{C} = pA + q\alpha E - (\mu + \gamma_1 + \theta)C, \tag{1}$$

$$\dot{I} = (1-q)\alpha E - (\mu + \gamma_2 + \theta + \sigma_2)I,$$

$$\dot{R} = \gamma_1 C + \gamma_2 I - (\epsilon + \mu)R.$$

under the initial point condition $S(0) > 0, E(0) \geq 0, C(0) \geq 0, I(0) \geq 0, R(0) \geq 0$. The recruitment rate of the population in model (1) is represented by $\Lambda$, while $A$ is the number of immigrants with fraction rate $p \in [0,1]$, and $\beta$ is the infection rate. $\frac{\beta_1 SI}{1+mI}$ (with $\beta_1 > 0$ and $m > 0$) denotes the saturated contact rate. $\mu$ is the natural death rate of the population, and $\theta$ is the death rate from carrier and infected individuals due to disease. $\alpha$ is the transmission rate between the number of exposed people and the number of all carriers and infected people, with a fraction rate of $q \in [0,1]$. $\sigma_i, i = 1,2$ are quarantine rates of exposed and infected subjects, respectively. $\gamma_i, i = 1,2$ are recovery rates of carrier and infected subjects, respectively. $\epsilon \geq 0$ is the rate of immunity loss and return to susceptibility.

## 3. Basic analysis of the model (1)

### 3.1 Positivity and boundedness

In this section, we discuss the case when the solution of model (1) is non-negative, as in the following theorem.

***Theorem 1:*** All solutions $S(t), E(t), C(t), I(t), R(t)$ of model (1), starting from positive initial conditions, remain positive for all $t \geq 0$.

***Proof:*** We have

$$\dot{S}\big|_{S=0} = \Lambda + (1-p)A + \epsilon R > 0 \,, for\ all\ R \geq 0 \,,$$

$$\dot{E}\big|_{E=0} = \beta SC + \frac{\beta_1 SI}{1+mI} \geq 0 \,, for\ all\ S, C, I \geq 0,$$

$$\dot{C}\big|_{C=0} = pA + q\alpha E > 0 \,, for\ all\ E \geq 0,$$

$$\dot{I}\big|_{I=0} = (1-q)\alpha E \geq 0, for\ all\ E \geq 0,$$

$$\dot{R}\big|_{R=0} = \gamma_1 C + \gamma_2 I \geq 0, for\ all\ C, I \geq 0.$$

Since all the above rates are non-negative, then, clearly, it is easy to show that the region is positive.                                                                                    □

For the boundedness of solutions, we consider the following function
$N(t) = S(t) + E(t) + C(t) + I(t) + R(t)$.
Then, taking the time derivative of $N(t)$ along the solution of model (1) gives

$$\frac{dN}{dt} \leq \Lambda + A - LN \quad \Rightarrow \quad \frac{dN}{dt} + LN \leq \Lambda + A,$$

where
$L = \min\{\mu, \mu + \sigma_1, \mu + \theta, \mu + \theta + \sigma_2\}$.
Now, it is easy to verify that the solution of the above linear differential inequalities can be written as
$$N(t) \leq \frac{\Lambda + A}{L} + \left(N_0 - \frac{\Lambda + A}{L}\right)e^{-Lt},$$
where $N_0 = (S(0), E(0), C(0), I(0), R(0))$, so that
$$\lim_{t \to \infty} supN(t) \leq \frac{\Lambda + A}{L} \quad \Rightarrow \quad N(t) \leq \frac{\Lambda + A}{L} \,; \quad \forall t > 0,$$
Thus, all solutions are uniformly bounded and the proof is complete.                          □

### 3.2 Basic reproduction number

The infection components in this model are $E$ and $I$. The new infection matrix $\mathcal{F}$ and the transition matrix $v$ are given by

$$\mathcal{F} = \begin{vmatrix} 0 & \beta S_0 & \beta_1 S_0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{vmatrix}, v = \begin{vmatrix} \alpha + \mu + \sigma_1 & 0 & 0 & 0 \\ -q\alpha & \mu + \gamma_1 + \theta & 0 & 0 \\ -(1-q)\alpha & 0 & \mu + \gamma_2 + \theta + \sigma_2 & 0 \\ 0 & -\gamma_1 & -\gamma_2 & \epsilon + \mu \end{vmatrix}.$$

The basic reproduction number of model (1) is then defined as the spectral radius of the next generation matrix $FV^{-1}$ [15], as follows

$$\mathcal{R}_0 = \frac{q\alpha\beta S_0}{(\alpha+\mu+\sigma_1)(\mu+\gamma_1+\theta)} + \frac{(1-q)\alpha\beta_1 S_0}{(\alpha+\mu+\sigma_1)(\mu+\gamma_2+\theta+\sigma_2)}, \qquad (2)$$

Clearly, by results in theorem 2 [15], we have that the model (1) always exhibits a disease-free equilibrium $e_0 = (S_0, 0,0,0,0)$ where $S_0 = \frac{\Lambda+A}{\mu}$, if $\mathcal{R}_0 < 1$. Hence, we get the following summaries.

***Theorem (2)***: The disease-free equilibrium point $e_0$ of model (1) is locally asymptotically stable when $\mathcal{R}_0 < 1$, and vice versa.                                                                        □

Otherwise, the existence of the pandemic equilibrium point of the model (1) is investigated by equating the right hand of model (1) to zero and by solving the following set of algebraic equations simultaneously

$$\begin{aligned} &\Lambda + (1-p)A - \beta SC - \frac{\beta_1 SI}{1+mI} + \epsilon R - \mu S = 0, \\ &\beta SC + \frac{\beta_1 SI}{1+mI} - (\alpha + \mu + \sigma_1)E = 0, \\ &pA + q\alpha E - (\mu + \gamma_1 + \theta)C = 0, \\ &(1-q)\alpha E - (\mu + \gamma_2 + \theta + \sigma_2)I = 0, \\ &\gamma_1 C + \gamma_2 I - (\epsilon + \mu)R = 0. \end{aligned} \qquad (3)$$

The simultaneous solution of equation (3) gives the pandemic equilibrium point, denoted by $e_1 = (S_1, E_1, C_1, I_1, R_1)$, where

$$C_1 = \frac{pA + q\alpha E_1}{D_1}, \qquad I_1 = \frac{(1-q)\alpha E_1}{D_2}, \qquad R_1 = \frac{D_3}{(\epsilon + \mu)D_1 D_2},$$

here
$D_1 = \mu + \gamma_1 + \theta,$
$D_2 = \mu + \gamma_2 + \theta + \sigma_2,$
$D_3 = \gamma_1(pA + q\alpha E_1)D_2 + \gamma_2(1-q)\alpha E_1 D_1.$

while $(S_1, E_1)$ represents a positive intersection point of the following two isoclines:
$$f(S, E) = r_1 E^2 + r_2 SE^2 + r_3 E + r_4 SE + r_5 S = 0, \qquad (4a)$$
$$g(S, E) = n_1 SE^2 + n_2 E + n_3 SE + n_4 S + n_5 = 0, \qquad (4b)$$
here
$\quad r_1 = -\alpha m(\alpha + \mu + \sigma_1)(1-q)D_1,$
$\quad r_2 = m(1-q)\alpha^2 q\beta,$
$\quad r_3 = -(\alpha + \mu + \sigma_1)D_1 D_2,$
$\quad r_4 = \beta\alpha q D_2 + \alpha(1-q)(pA\beta m + \beta_1 D_1),$
$\quad r_5 = \beta pA D_2,$
$\quad n_1 = -\beta\alpha^2 qm(1-q)(\epsilon + \mu)D_2,$
$\quad n_2 = \alpha m\big((\Lambda + (1-p)A)(1-q)(\epsilon + \mu)D_1 D_2 + \epsilon(1-q)D_3\big),$
$\quad n_3 = -\alpha(\epsilon + \mu)D_1\{\beta pmA(1-q) + \beta q D_2^2 + (\beta_1 + \mu m)(1-q)D_1 D_2\},$

$$n_4 = -(\beta p A + \mu D_1)(\epsilon + \mu)D_2^2,$$
$$n_5 = (\Lambda + (1-p)A)(\epsilon + \mu)D_1 D_2^2 + \epsilon D_2 D_3.$$

Clearly, as $E \to 0$, the first isocline (4a) intersects the $S-$ axis at zero.
However, when $E \to 0$, the second isocline (4b) will intersect the $S-$ axis at a unique positive point, say $S_1$.

Consequently, these two isoclines (4a) and (4b) have an intersection point in the interior of the positive quadrant of $SE$ – plane, namely $(S_1, E_1)$, provided that the following conditions are satisfied

$$\frac{\partial S}{\partial E} = -\frac{\partial f/\partial E}{\partial f/\partial S} > 0 \quad and \quad \frac{\partial S}{\partial E} = -\frac{\partial g/\partial E}{\partial g/\partial S} < 0, \tag{4c}$$

Therefore, the pandemic equilibrium point $e_1 = (S_1, E_1, C_1, I_1, R_1)$ exists uniquely in the interior of $R_+^5$ if $\mathcal{R}_0 > 1$ and condition (4c) holds.

## 4. Local stability analysis

In this section, the local stability conditions of the pandemic equilibrium point $e_1$ of model (1) are established in the following theorem.

***Theorem (3):*** The pandemic equilibrium point $e_1$ of the model (1) is locally asymptotically stable when $\mathcal{R}_0 > 1$, with the following condition holds:

$$\mu + \theta \; > max \left\{ 2\beta S_1 \; , \frac{2\beta_1 S_1}{(1+mI_1)^2} - \sigma_2 \right\}, \tag{5}$$

***Proof:*** The Jacobian matrix of model (1) at $e_1$ can be written as

$$J(e_1) = \begin{pmatrix} b_{11} & 0 & b_{13} & b_{14} & b_{15} \\ b_{21} & b_{22} & b_{23} & b_{24} & 0 \\ 0 & b_{32} & b_{33} & 0 & 0 \\ 0 & b_{42} & 0 & b_{44} & 0 \\ 0 & 0 & b_{53} & b_{54} & b_{55} \end{pmatrix},$$

here

$$b_{11} = -\beta C_1 - \frac{\beta_1 I_1}{1+mI_1} - \mu \; ; \; b_{13} = -\beta S_1 \; ; \; b_{14} = -\frac{\beta_1 S_1}{(1+mI_1)^2} \; ; \; b_{15} = \epsilon;$$

$$b_{21} = \beta C_1 + \frac{\beta_1 I_1}{1+mI_1} \; ; \; b_{22} = -(\alpha + \mu + \sigma_1); \; b_{23} = \beta S_1 \; ;$$

$$b_{24} = \frac{\beta_1 S_1}{(1+mI_1)^2} \; ; \; b_{32} = q\alpha \; ; \; b_{33} = -(\mu + \gamma_1 + \theta); \; b_{42} = (1-q)\alpha \; ;$$

$$b_{44} = -(\mu + \gamma_2 + \theta + \sigma_2); \quad b_{53} = \gamma_1; \quad b_{54} = \gamma_2; \quad b_{55} = -(\epsilon + \mu);$$

Now, according to Gersgorin's theorem [16], if the following condition holds:

$$|b_{ii}| \; > \; \sum_{\substack{i=1 \\ i \neq j}}^{5} |b_{ij}| = P_i \tag{6}$$

then all the eigenvalues of $J(e_1)$ exist in the region:

$$\Omega = \cup \left\{ U^* \epsilon \, H : \; |U^* - b_{ii}| < \sum_{\substack{i=1 \\ i \neq j}}^{5} |b_{ij}| \right\}$$

Then, all the eigenvalues of $J(e_1)$ exists in the disc centered at $b_{ii}$ with radius $P_i$. Thus, if the diagonal elements are negative and the condition (5) holds, all the eigenvalues will exist in the left half plane and the $e_1$ of model (1) is locally asymptotically stable with $\mathcal{R}_0 > 1$.

## 5. Global stability analysis

In this section, the region of global stability (basin of attraction) of all equilibrium points of model (1) is presented as shown in the following theorems.

***Theorem (4):*** The disease-free equilibrium point $e_0$ is globally asymptotically stable in the sub region of $R_+^5$ that satisfies $\mathcal{R}_0 < 1$.

***Proof:*** Let $Y = S$, $Z = (E, C, I, R)$ and $e_0 = (Y_0, 0) = (S_0 , 0)$. Then,

$$\frac{dX}{dt} = K(Y,Z) = \Lambda + A - \mu S - \beta SC - \frac{\beta_1 SI}{1+mI} + \epsilon R \qquad (7)$$

If $S = S_0$ and $K(Y,0) = 0$, it becomes

$$\frac{dX}{dt} = K(Y,0) = \Lambda + A - \mu S_0 \qquad (8)$$

as $t \to \infty$ and $Y \to Y_0$. Therefore, $Y = Y_0 = S_0$, is globally asymptotically stable.

Now,

$$BZ - \bar{M}(Y,Z) = \begin{bmatrix} -(\alpha + \mu + \sigma_1) & \beta_1 S_0 & \beta S_0 & 0 \\ q\alpha & -(\mu + \gamma_1 + \theta) & 0 & 0 \\ (1-q)\alpha & 0 & -(\mu + \gamma_2 + \theta + \sigma_2) & 0 \\ 0 & \gamma_1 & \gamma_2 & -(\epsilon + \mu) \end{bmatrix}.$$

$$\begin{bmatrix} E \\ C \\ I \\ R \end{bmatrix} - \begin{bmatrix} \left[\beta C + \frac{\beta_1 I}{1+mI}\right][S_0 - S] \\ 0 \\ 0 \\ 0 \end{bmatrix}, \qquad (9)$$

where

$$B = \begin{bmatrix} -(\alpha + \mu + \sigma_1) & \beta_1 S_0 & \beta S_0 & 0 \\ q\alpha & -(\mu + \gamma_1 + \theta) & 0 & 0 \\ (1-q)\alpha & 0 & -(\mu + \gamma_2 + \theta + \sigma_2) & 0 \\ 0 & \gamma_1 & \gamma_2 & -(\epsilon + \mu) \end{bmatrix}, \quad Z = \begin{bmatrix} E \\ C \\ I \\ R \end{bmatrix}$$

$$\bar{M}(Y,Z) = \begin{bmatrix} \left[\beta C + \frac{\beta_1 I}{1+mI}\right][S_0 - S] \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

In model (1), $S_0 = \frac{\Lambda + A}{\mu}$ is the bound of the total population. We summarize $S, E, C, I, R \le S_0$. Therefore, $\bar{M}(Y,Z) \ge 0$. Thus, the conditions $Q_1$ and $Q_2$ hold, by Lemma (1), see [17]. Then, the disease-free equilibrium point is globally asymptotically stable.

**Theorem (5):** The pandemic equilibrium point $e_1$ is globally asymptotically stable, provided that $\mathcal{R}_0 > 1$.

**Proof:** Let $S_1, E_1, C_1, I_1$ and $R_1$ satisfy equations

$$\begin{aligned} \Lambda + (1-p)A - \beta SC - \frac{\beta_1 SI}{1+mI} + \epsilon R - \mu S &= 0 \\ \beta SC + \frac{\beta_1 SI}{1+mI} - (\alpha + \mu + \sigma_1)E &= 0 \\ pA + q\alpha E - (\mu + \gamma_1 + \theta)C &= 0 \\ (1-q)\alpha E - (\mu + \gamma_2 + \theta + \sigma_2)I &= 0 \\ \gamma_1 C + \gamma_2 I - (\epsilon + \mu)R &= 0 \end{aligned} \qquad (10)$$

By applying (7) and denoting

$$\frac{S}{S_1} = x \ , \quad \frac{E}{E_1} = y \ , \quad \frac{C}{C_1} = z \ , \quad \frac{I}{I_1} = u \ , \quad \frac{R}{R_1} = v \qquad (11)$$

we have

$$x' = x\left[\frac{(\Lambda + (1-p)A)}{S_1}\left(\frac{1}{x} - 1\right) - \beta C_1(z - 1) - I_1\left(\frac{\beta_1}{1+mI_1}\right)\left(\frac{1+mI_1}{1+mI}u - 1\right) + \frac{\epsilon R_1}{S_1}\left(\frac{v}{x} - 1\right)\right]$$

$$y' = y\left[\frac{\beta S_1 C_1}{E_1}\left(\frac{xz}{y} - 1\right) + \frac{\beta_1 S_1 I_1}{(1+mI_1)E_1}\left(\frac{1+mI_1}{1+mI}\cdot\frac{xu}{y} - 1\right)\right]$$

$$z' = z\left[\frac{pA}{C_1}\left(\frac{1}{z} - 1\right) + \frac{q\alpha E_1}{C_1}\left(\frac{y}{z} - 1\right)\right]$$

$$u' = u\left[(1-q)\alpha\left(\frac{y}{u} - 1\right)\right]$$

$$v' = v\left[\frac{\gamma_1 C_1}{R_1}\left(\frac{z}{v} - 1\right) + \frac{\gamma_1 I_1}{R_1}\left(\frac{u}{v} - 1\right)\right]$$

$$...... (12)$$

We define the Lyapunov function as
$$V_1 = S_1(x - 1 - \ln x) + E_1(y - 1 - \ln y) + C_1(z - 1 - \ln z)$$
$$+ I_1(u - 1 - \ln u) + R_1(v - 1 - \ln v) \tag{13}$$

The derivative of $V_1$ is given by
$$V_1' = S_1 \frac{x-1}{x} x' + E_1 \frac{y-1}{y} y' + C_1 \frac{z-1}{z} z' + I_1 \frac{u-1}{u} u' + R_1 \frac{v-1}{v} v' \tag{14}$$

$$V_1' = (x-1)\left[ (\Lambda + (1-p)A)\left(\frac{1}{x} - 1\right) - \beta S_1 C_1(z-1) - \frac{\beta_1 S_1 I_1}{(1+mI_1)}\left(\frac{1+mI_1}{1+mI} u - 1\right) + \epsilon R_1\left(\frac{v}{x} - 1\right)\right]$$
$$+ (y-1)\left[ \beta S_1 C_1\left(\frac{xz}{y} - 1\right) + \frac{\beta_1 S_1 I_1}{(1+mI_1)}\left(\frac{1+mI_1}{1+mI} \cdot \frac{xu}{y} - 1\right)\right]$$
$$+ (z-1)\left[ pA\left(\frac{1}{z} - 1\right) + q\alpha E_1\left(\frac{y}{z} - 1\right)\right] + (u-1)(1-q)\alpha I_1\left(\frac{y}{u} - 1\right)$$
$$+ (v-1)\left[ \gamma_1 C_1\left(\frac{z}{v} - 1\right) + \gamma_2 I_1\left(\frac{u}{v} - 1\right)\right]$$

Furthermore, by simplifying the resulting terms, we get that
$$V_1' = (\Lambda + (1-p)A)\left(2 - x - \frac{1}{x}\right) + pA\left(2 - z - \frac{1}{z}\right) + \beta S_1 C_1\left(x + z - y - \frac{xz}{y}\right)$$
$$+ \frac{\beta_1 S_1 I_1}{(1+mI_1)}\left[\frac{1+mI_1}{1+mI}\left(u - \frac{xu}{y}\right) + x - y\right] + \epsilon R_1\left(v - x - \frac{v}{x} + 1\right)$$
$$+ q\alpha E_1\left(y - z - \frac{y}{z} + 1\right) + (1-q)\alpha I_1\left(y - u - \frac{y}{u} + 1\right)$$
$$+ \gamma_1 C_1\left(z - v - \frac{z}{v} + 1\right) + \gamma_2 I_1\left(u - v - \frac{u}{v} + 1\right)$$

Since the arithmetical mean is greater than, or equal to, the geometrical mean, then
$2 - x - \frac{1}{x} \le 0$ for $x > 0$ and $2 - x - \frac{1}{x} = 0$ if and only if $x = 1$; $2 - z - \frac{1}{z} \le 0$
for $z > 0$ and $2 - z - \frac{1}{z} = 0$ if and only if $z = 1$; $x + z - y - \frac{xz}{y} \le 0$ for $x, y, z > 0$ and
$x + z - y - \frac{xz}{y} = 0$ if and only if $x = y = z = 1$; $\frac{1+mI_1}{1+mI}\left(u - \frac{xu}{y}\right) + x - y \le 0$ for $x, y, u > 0$ and
$\frac{1+mI_1}{1+mI}\left(u - \frac{xu}{y}\right) + x - y = 0$ if and only if $x = u = 1$; $v - x - \frac{v}{x} + 1 \le 0$ for $x, v > 0$ and
$v - x - \frac{v}{x} + 1 = 0$ if and only if $x = v = 1$; $y - z - \frac{y}{z} + 1 \le 0$ for $y, z > 0$ and $y - z - \frac{y}{z} + 1 = 0$
if and only if $y = z = 1$; $y - u - \frac{y}{u} + 1 \le 0$ for $y, u > 0$ and $y - u - \frac{y}{u} + 1 = 0$ if and only if
$y = u = 1$; $z - v - \frac{z}{v} + 1 \le 0$ for $z, v > 0$ and $z - v - \frac{z}{v} + 1 = 0$ if and only if $z = v = 1$; $u - v - \frac{u}{v} + 1 \le 0$ for $u, v > 0$ and $u - v - \frac{u}{v} + 1 = 0$ if and only if $u = v = 1$.
Therefore, $V_1' \le 0$ for $x, y, z, u, v > 0$ and $V_1' = 0$ if and only if $x = y = 1, z = u = v = 1$. The maximum invariant set of model (1) on the set $\{(x, y, z, u, v): V_1' = 0\}$ is the singleton $(1,1,1,1,1)$. Thus, for model (1), the pandemic equilibrium $e_1$ is globally asymptotically stable if $\mathcal{R}_0 > 1$, by LaSalle Principle [18].

## 6. Local bifurcation analysis

In this section, the effect of varying the parameter values on the dynamical behavior of model (1) near the equilibrium points is studied. It is well known that the existence of non-hyperbolic equilibrium point of the system is a necessary but not sufficient condition for bifurcation to occur. Therefore, in the following, the parameter that makes the equilibrium point of model (1) as a non-hyperbolic equilibrium point is considered as a candidate bifurcation parameter for the system. Now, we rewrite model (1) in the form:
$\frac{dX}{dt} = F(X)$, where $X = (S, E, C, I, R)^T$ and $F = (f_1, f_2, f_3, f_4, f_5)^T$, with $f_i; i = 1,2,3,4,5$ represent the interaction function in the right hand side of model (1). Then, straightforward computation on the Jacobian matrix of model (1), with any non-zero vector $V = (v_1, v_2, v_3, v_4, v_5)^T$, gives the following second directional derivative

$$D^2F(S,E,C,I,R)(V,V) = \begin{bmatrix} -2\left\{\beta v_1 v_3 + \frac{\beta_1 v_1 v_4}{(1+mI)^2} - \frac{\beta_1 mS}{(1+mI)^3}v_4^2\right\} \\ 2\left\{\beta v_1 v_3 + \frac{\beta_1 v_1 v_4}{(1+mI)^2} - \frac{\beta_1 mS}{(1+mI)^3}v_4^2\right\} \\ 0 \\ 0 \\ 0 \end{bmatrix} \qquad (15)$$

### 6.1 The Local Bifurcation Analysis Near $e_0$

**Theorem (6):** Under the sufficient condition $\mathcal{R}_0 = 1$, the model (1) undergoes a transcritical bifurcation, but neither saddle node bifurcation nor pitchfork bifurcation can occurs at disease-free equilibrium point $e_0$ when the following condition holds

$$(\alpha + \mu + \sigma_1)(\mu + \gamma_2 + \theta + \sigma_2) \neq (1-q)\alpha\beta_1 S_0 \qquad (16a)$$
$$\in m_4 \neq \beta^* S_0 m_2 + \beta_1 S_0 m_3 \qquad (16b)$$

**Proof:** According to the Jacobian matrix of model (1) at $e_0$, has zero eigenvalue (say $\lambda_0^* = 0$) when $\mathcal{R}_0 = 1$ and hence, by substituting the value of $\mathcal{R}_0$ and simplifying the resulting terms, we obtain the following positive quantity at

$$\beta = \beta^* = \frac{(\mu+\gamma_1+\theta)[(\alpha+\mu+\sigma_1)(\mu+\gamma_2+\theta+\sigma_2)-(1-q)\alpha\beta_1 S_0]}{q\alpha S_0(\mu+\gamma_2+\theta+\sigma_2)} \qquad (17)$$

Hence, $e_0$ is a nonhyperbolic point at $\beta = \beta^*$. Recall that the Jacobian matrix of model (1) at $e_0$ and $\beta = \beta^*$ can be represented by

$$J(e_0) = \begin{pmatrix} -\mu & 0 & -\beta^* S_0 & -\beta^* S_0 & \epsilon \\ 0 & -(\alpha+\mu+\sigma_1) & \beta^* S_0 & \beta^* S_0 & 0 \\ 0 & q\alpha & -(\mu+\gamma_1+\theta) & 0 & 0 \\ 0 & (1-q)\alpha & 0 & -(\mu+\gamma_2+\theta+\sigma_2) & 0 \\ 0 & 0 & \gamma_1 & \gamma_2 & -(\epsilon+\mu) \end{pmatrix}$$

Now, let $V^{[0]} = \left(v_1^{[0]}, v_2^{[0]}, v_3^{[0]}, v_4^{[0]}, v_5^{[0]}\right)^T$ be the eigenvector corresponding to the eigenvalue $\lambda_0^* = 0$. Thus $(J_0^* - \lambda_0^*)V^{[0]} = 0$, gives that $V^{[0]} = \left(\bar{n}_1 v_2^{[0]}, v_2^{[0]}, \bar{n}_2 v_2^{[0]}, \bar{n}_3 v_2^{[0]}, \bar{n}_4 v_2^{[0]}\right)^T$,
where
$$\bar{n}_1 = \frac{\in m_4 - (\beta^* S_0 m_2 + \beta_1 S_0 m_3)}{\mu}, \quad \bar{n}_2 = \frac{q\alpha}{(\mu+\gamma_1+\theta)}, \quad \bar{n}_3 = \frac{(1-q)\alpha}{(\mu+\gamma_2+\theta+\sigma_2)},$$
$$\bar{n}_4 = \frac{[q\alpha\gamma_1(\mu+\gamma_2+\theta+\sigma_2)+(1-q)\alpha\gamma_2(\mu+\gamma_1+\theta)]}{(\epsilon+\mu)(\mu+\gamma_1+\theta)(\mu+\gamma_2+\theta+\sigma_2)} \text{ and } v_2^{[0]} \text{ represents any nonzero real number.}$$

Also, let $\Psi^{[0]} = \left[\psi_1^{[0]}, \psi_2^{[0]}, \psi_3^{[0]}, \psi_4^{[0]}, \psi_5^{[0]}\right]^T$ be the eigenvector associated with the eigenvalue $\lambda_0^* = 0$ of the matrix $J_0^{*T}$. Then from $(J_0^{*T} - \lambda_0^*)\Psi^{[0]} = 0$, by solving this equation for $\Psi^{[0]}$, we obtain
$$\Psi^{[0]} = \left[0, \psi_2^{[0]}, \bar{r}_1\psi_2^{[0]}, \bar{r}_2\psi_2^{[0]}, 0\right]^T$$
where
$$\bar{r}_1 = \frac{\beta^* S_0}{(\mu+\gamma_1+\theta)}, \quad \bar{r}_2 = \frac{\beta_1 S_0}{(\mu+\gamma_2+\theta+\sigma_2)}, \text{ and } \psi_3^{[0]} \text{ is any nonzero real number.}$$

Now, consider
$$\frac{\partial F}{\partial \beta} = F_\beta(X, \beta) = [-SC, SC, 0, 0, 0]^T \qquad (18)$$

Thus,
$$F_\beta(e_0, \beta^*) = [0,0,0,0,0]^T \text{ which gives } \left[\Psi^{[0]}\right]^T F_\beta(e_0, \beta^*) = 0 \qquad (19)$$

So, according to Sotomayor's theorem [19], for local bifurcation, model (1) has no saddle-node bifurcation at $\beta = \beta^*$. Furthermore, because we have

$$DF_\beta(X,\beta) = \begin{bmatrix} -C & 0 & -S & 0 & 0 \\ C & 0 & S & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

we can show that

$$\left[\Psi^{[0]}\right]^T \left[DF_\beta(e_0,\beta^*)V^{[0]}\right] = \left[0, \psi_2^{[0]}, \bar{r}_1\psi_2^{[0]}, \bar{r}_2\psi_2^{[0]}, 0\right]^T \begin{bmatrix} -S_0\bar{n}_2 v_2^{[0]} \\ S_0\bar{n}_2 v_2^{[0]} \\ 0 \\ 0 \\ 0 \end{bmatrix} \neq 0 \qquad (20)$$

Moreover, by substituting $e_0, \beta^*$ and $V^{[0]}$ in (12), we get

$$D^2F(e_0,\beta^*)\left(V^{[0]},V^{[0]}\right) = \begin{bmatrix} -2\left(v_2^{[0]}\right)^2 \{\beta\bar{n}_1\bar{n}_2 + \beta_1\bar{n}_1\bar{n}_3 - \beta_1 mS_0\bar{n}_4^2\} \\ 2\left(v_2^{[0]}\right)^2 \{\beta\bar{n}_1\bar{n}_2 + \beta_1\bar{n}_1\bar{n}_3 - \beta_1 mS_0\bar{n}_4^2\} \\ 0 \\ 0 \\ 0 \end{bmatrix} \qquad (21)$$

Hence, we obtain

$$\left[\Psi^{[0]}\right]^T\left[D^2F(e_0,\beta^*)\left(V^{[0]},V^{[0]}\right)\right] \neq 0 \qquad (22)$$

Thus, according to Sotomayor's theorem, model (1) at disease-free equilibrium point has a transcritical bifurcation as the parameter $\beta$ passes through the bifurcation value $\beta^*$, provided that $\mathcal{R}_0 = 1$, while pitchfork bifurcation cannot occur. $\qquad\square$

# 7. Numerical simulation

In this section, we illustrate some numerical solutions of model (1) for different values of the parameters. We use the following different initial points. We use the parameter values from real data available from February 24, 2020, to September 26, 2020, and present some numerical simulation of model (1) to illustrate our results in Table-1.

**Table 1-**Definitions and values of model (1) parameters

| Parameter | Definition | Value |
|:---:|:---:|:---:|
| $N$ | Total population | $40 \times 10^6$ |
| $\Lambda$ | Birth rate | 1541.8 |
| $A$ | Number of immigrants | 100 |
| $p$ | Fraction rate | [0,1] |
| $\beta$ | Contact rate between $S$ and $C$ | $5 \times 10^{-7}$ |
| $\beta_1$ | Contact rate between $S$ and $I$ | $2 \times 10^{-7}$ |
| $m$ | Saturated rate | 10 |
| $\mu$ | Natural death rate | $3.8545 \times 10^{-5}$ |
| $\epsilon$ | Loss of immunity | 0.1429 |
| $\alpha$ | Transmission rate | 0.2 |
| $\sigma_1$ | Quarantine rate of exposed subjects | 0.2 |
| $\sigma_2$ | Quarantine rate of infected subjects | 0.38 |
| $q$ | Fraction rate | [0,1] |
| $\theta$ | Death rate due to disease | 0.034 |
| $\gamma_1$ | Recovery rate of carriers | 0.033 |
| $\gamma_2$ | Recovery rate of infected subjects | 0.71 |

**Case 1:** When we take the parameters in Table 1, we have the dynamical behavior of model (1) approaching the disease-free equilibrium point $e_0$. This theoretical result is illustrated by Figure 2 which shows the solutions of model (1) with different initial points.

**Case 2:** When we take $p = 0.8$ and $\beta = 5 \times 10^{-6}$ with keeping the other parameters in Table 1, we have the dynamical behavior of model (1) approaching the pandemic equilibrium point $e_1$. Figure 3 confirms that the disease-free equilibrium point became unstable and the solution of model (1) approaches the endemic equilibrium $e_1$. Also, the value of $\mathcal{R}_0 = 0.79$ implies that the backward bifurcation occurs.

**Case 3:** When we take $\beta = 5 \times 10^{-3}$, $\beta_1 = 2 \times 10^{-3}$, and $p = 0.1$, with keeping the other parameters in table 1, we have the dynamical behavior of model (1) still approaching the pandemic equilibrium point $e_1$ with $\mathcal{R}_0 = 1.3$. The result is illustrated by Figure-4.
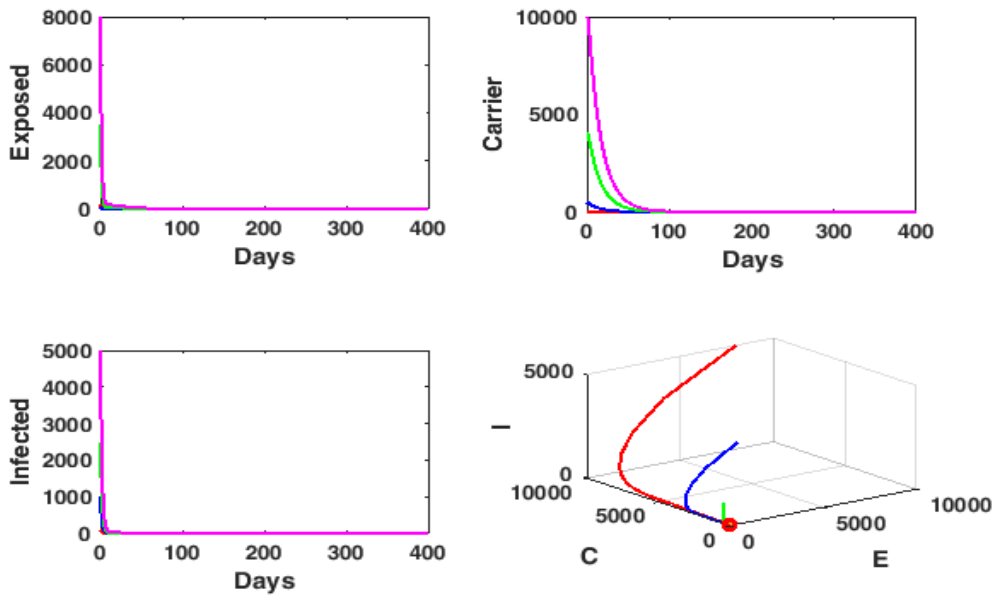


**Figure 2**-Global stability of disease-free equilibrium point of model (1) with $\mathcal{R}_0 = 0.754$.
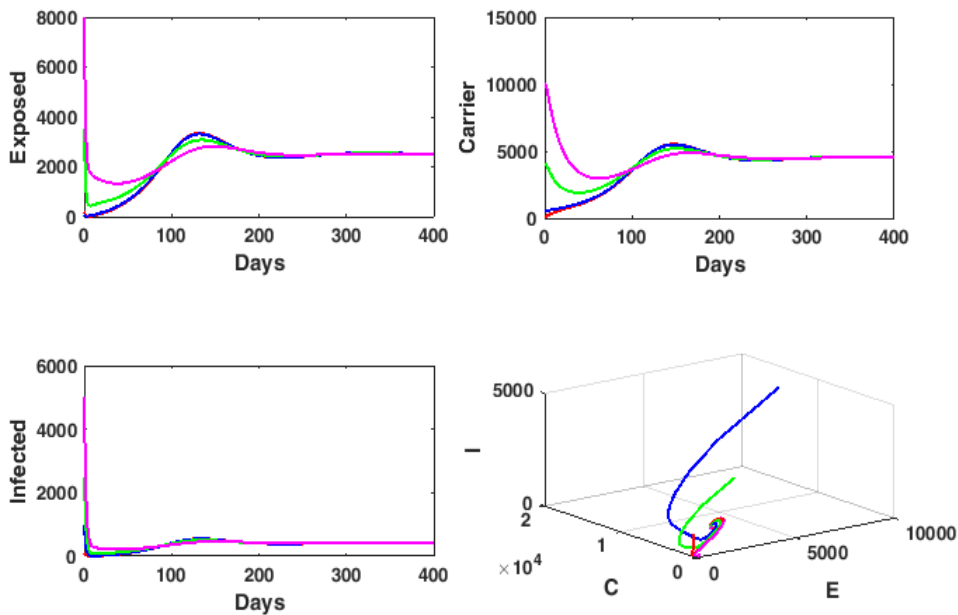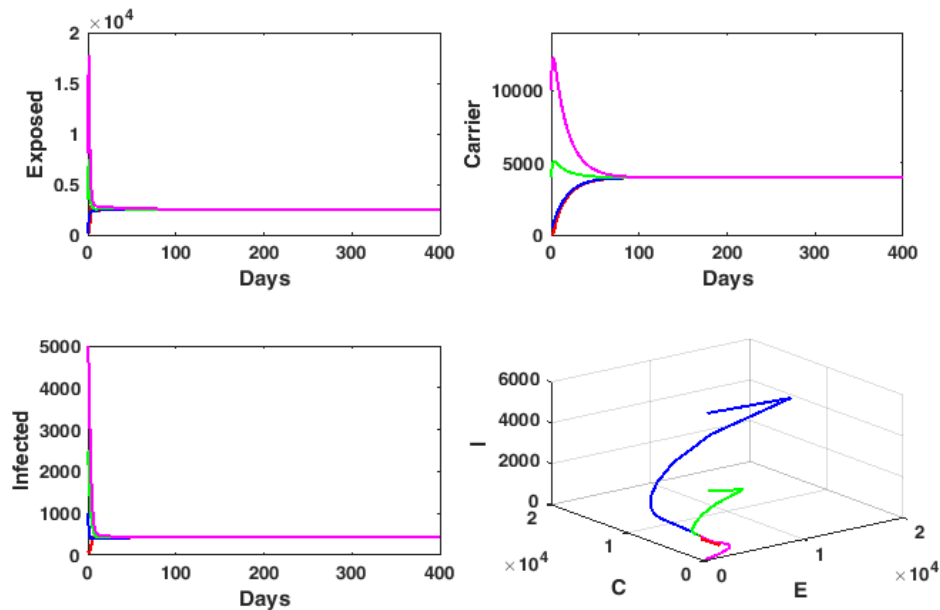


**Figure 3**-Global stability of pandemic equilibrium point of model (1) with $\mathcal{R}_0 = 0.79$.

**Figure 4-**Global stability of pandemic equilibrium point of model (1) with $\mathcal{R}_0 = 1.3$.

## 8. Discussion and Conclusions

In this work, a mathematical model of COVID-19 pandemic with immigrants was studied by dividing the total population into five classes, namely susceptible $S(t)$, exposed $E(t)$, carrier $C(t)$, infected $I(t)$ and recovered $R(t)$. The model incorporates the impact of infective immigrants, but without symptoms, with quarantine strategy. It has been noticed that the disease can spread if the number of immigrants increases. Thus, the dynamical behavior of the disease changes from the disease-free point to pandemic point. The model mainly accounts for the reduction in disease class due to social isolation or social spacing. While, we can say that the disease vanishes due to the proper application of quarantine measures. Our model has two biological equilibrium points, namely the disease-free and pandemic. If $\mathcal{R}_0 < 1$, we get that the disease-free equilibrium point is stable. Otherwise, this point becomes unstable when $\mathcal{R}_0 > 1$ and the solution of the model approaches the pandemic equilibrium point. The model does not have periodic dynamics but, instead, it approaches either the disease-free equilibrium point or pandemic equilibrium point. But model (1) near the disease-free equilibrium point has a transcritical bifurcation as the parameter $\beta$ passes through the bifurcation value $\beta^*$, provided that $\mathcal{R}_0 = 1$, while pitchfork bifurcation cannot occur.

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