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# A Mathematical Model of the Critical Coronavirus Disease (Covid-19) Situation in Thailand During March 2021 to August 2021

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**ABSTRACT**

In this article, the authors introduce a mathematical model of the critical Coronavirus Disease (Covid-19) situation in Thailand during March 2021 to August 2021. The work is divided into three parts. Firstly, the model is formulated with a description of the parameters defined in the model, the we compute the basic reproduction number ($R_0$) and study the locally asymptotically stability of its disease free equilibrium point, the existence of endemic equilibrium point, and locally and globally asymptotically stability of its endemic equilibrium point. Secondly, we present a strategy using fixed point iterative methods for solving a nonlinear dynamical problem in form of Green's function for analysis of the parameters, the existence and convergence theorems of solutions are shown by the fixed point theorem techniques. Finally, the authors show the numerical to predict the future situation of coronavirus disease in Thailand contain $R_0$ and give the conclusion of this work.

**Keywords:** Coronavirus; Equilibrium problem; Fixed point iteration; Green function

## 1. Introduction

A mathematical model is a description of real world functioning that uses mathematical symbols, equations, and formulas. Mathematical models are used in numerous fields. In 1927 Kermack and

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Mckendrick [1] presented the epidemiological models describing a virus or bacterial agent that is directly transmissible to a close population and comprising susceptible $S$, invectives $I$, and recovers $R$. For certain diseases, such as influenza and tuberculosis, through adequate contact with an infectious individual, a susceptible individual is exposed for a certain time, in other words infected but not contagious. Thus it is realistic to introduce a latent compartment usually denoted by $E$, leading to an SEIR model, a type of model that has been widely discussed in recent decades [2, 3]. In December 2019, the fatal global coronavirus pandemic, popularly known as COVID-19, erupted in the ancient town of Wuhan Hubei Province, China and spread to several countries by 2020.

In January 2020 the coronavirus (Covid-19) outbreak in Thailand has occurred, as Thailand surveillance of people traveling from China. And the virus epidemic has continued until now. Coronavirus disease 2019 is an emerging disease that has a wide impact both in the economy and society. Studies and research to develop the knowledge and innovations are required in virus prevention and treatment of coronavirus disease 2019.

In 2020, Chen et al [4] introduced a mathematical model for simulating the transmissibility of a coronavirus in Wuhan and estimating the basic reproduction number. In 2021 Idris et al [5], introduced a mathematical model of COVID-19 containing asymptomatic and symptomatic classes in Nigeria. A mathematical model using both the ordinary differential equation and fractional differential equation to estimate the basic reproduction number (See more model A. Hussain et al. in [6]). Recently Abukhaled and Khuri [7] and Muangchoo-in et al [8], present a strategy based on fixed point iterative methods to solve a nonlinear dynamical problem in a form of Green's function with boundary value problems.

Motivated by these works, this article is organized as follows: in Section 2, we present our model and formulate the model with a description of the parameters identified in the model. In Section 3, we obtain the invariant region. Moreover, we calculate the basic reproduction number $R_0$ and study the disease free equilibrium (DFE), local stability, the existence of endemic equilibrium $E_1$, local stability of the endemic equilibrium, and global stability of the endemic equilibrium. In Section 4, we introduce a strategy based on fixed point iterative methods to solve a nonlinear dynamical problem in the form of Green's function for analysis of the parameters; the existence and convergence theorems of solutions are shown via the techniques of fixed point theorems. In Section 5, we present the numerical model by using real data of Thailand (March 2021 - August 2021) to predict the future (1 September 2021 - 19 October 2021), all data calculate from Department of Disease Control, Thailand.

## 2. Model formulation

In this article, the coronavirus (COVID-19) model based on a simple transmission rate is considered. Let $N(t)$ be the total population of humans, divided into six classes: susceptible individuals $S(t)$, exposed individuals $E(t)$, asymptotically infected but reported individuals $I_A(t)$, symptomatic infected and reported individuals $I(t)$, quarantined Infected and reported individuals $Q(t)$, and individuals that have recovered/remove from COVID-19 $R(t)$. According to consideration, the total population is $N(t) = S(t)+E(t)+I_A(t)+I(t)+Q(t)+R(t)$, where $t \geq 0$.

The natural human natality and mortality rates are designated as $\wedge$ and $\delta$ respectively. Susceptible individuals $(S)$ get infected from enough contact with exposed individuals $(E)$ at the rate of $\eta$. The exposed individuals $(E)$ may get infected without symptoms (asymptomatic) $(I_A)$ or with symptoms (symptomatic) $(I)$ at the rates of $\theta$, where $\xi$ is incubation rate of exposed individuals. Also, those asymptomatic infected $(I_A)$ may be confirmed infected then move to quarantined individuals $(Q)$ at rate of $m_1$ or show symptoms then move to individuals $(I)$ at rate of $m_3$ or remove to $(R)$ at rate of $r_1$. Symptomatic individuals $(I)$ will move to quarantined individuals $(Q)$ at rate of $m_2$. When $(I)$ and $(I_A)$ were confirmed infected then move to quarantined individuals $(Q)$ then it able to recover at $(R)$ at rate of $r_2$, where $\nu$ is death rate due to COVID-19. Each class may decrease as a result of natural mortality $\delta$, while the class of individuals infected with symptoms $(I)$ and symptoms (asymptomatic) $(I_A)$ may also decrease as a result of death from the disease at the rate of $\nu$. The possibility of reinfection after recovery has not been considered in this model.

Fig. 1, below depicts the schematic diagram showing the spread of COVID-19.

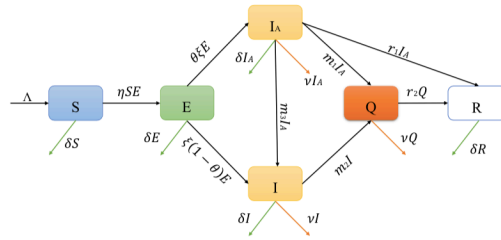


**Fig. 1.** Example how to insert figures.

The schematic diagram show in Fig. 1, a system of nonlinear differential equations is obtained and presented below (see Table 1):

$$\begin{cases} \dfrac{dS}{d(t)} = \wedge - \eta SE - \delta S, \\ \dfrac{dE}{dt} = \eta SE - (\delta + \xi)E, \\ \dfrac{dI_A}{dt} = \xi\theta E - (\delta + \nu + m_1 + m_3 + r_1)I_A, \\ \dfrac{dI}{dt} = \xi(1-\theta)E + m_3 I_A - (\delta + \nu + m_2)I, \\ \dfrac{dQ}{dt} = m_1 I_A + m_2 I - (r_2 + \nu)Q, \\ \dfrac{dR}{dt} = r_1 I_A + r_2 Q - \delta R, \end{cases} \tag{2.1}$$

subject to following initial condition :

$$S(0) \geq 0, E(0) \geq 0, I_A(0) \geq 0, I(0) \geq 0, \\ Q(0) \geq 0, R(0) \geq 0. \tag{2.2}$$

**Table 1.** Description of state variables.

| Compartment and Parameter | Description |
|---|---|
| $S$ | Susceptible Individuals |
| $E$ | Exposed Individuals |
| $I_A$ | Asymptomatic Infected Individuals |
| $I$ | symptomatic Infected Individuals |
| $Q$ | Quarantine Infected, detected and reported Individuals |
| $R$ | Recovered Individuals |
| $\wedge$ | Recruitment rate |
| $\delta$ | Natural death rate |
| $\nu$ | Death rate due to COVID-19 |
| $\eta$ | Transmission probability during contact |
| $\xi$ | Incubation rate of an exposed individuals |
| $\theta$ | Fraction of exposed individuals that becomes asymptomatic infected |
| $m_1$ | Rate of quarantine of asymptomatic infected individuals |
| $m_2$ | Rate of quarantine of symptomatic infected individuals |
| $m_3$ | Rate of transmission from asymptomatic to symptomatic infected individuals |
| $r_1$ | Natural recovery rate of asymptomatic individuals |
| $r_2$ | Recovery rate of quarantine individuals |

## 3. Analysis of the model

This section presents the computation and presentation of basic reproduction number for the proposed model (2.1) and studies the locally asymptotically stability of disease free equilibrium (Theorem 3.1), unique endemic equilibrium point (Theorem 3.2), locally asymptotically stability of unique endemic equilibrium point (Theorem 3.3), globally asymptotically stable (Theorem 3.4 and Theorem 3.5).

### 3.1 At invariant region

The model (2.1) state the parameters $S(t)$, $E(t)$, $Q(t)$, $I_A(t)$, $I(t)$, $R(t)$ are nonnegative for all $t \geq 0$. Solution with positive initial data remains positive for all $t \geq 0$ and are bounded. Let start systems (2.1) get $\frac{dN}{dt} = \wedge - \delta N(t) - \nu I(t)$ and $\sup_{t\to\infty} N(t) \leq \frac{\wedge}{\delta}$. So we study the system (2.1) in the following feasible region:

$$\Omega = \{(S(t), E(t), I_A(t), I(t), Q(t), R(t)) \in \mathbb{R}^6_+ : 0 \leq N(t) \leq \frac{\wedge}{\delta}\}. \tag{3.1}$$

(3.1) is now positive invariant in relation to (2.1). Meaning the proposed model (2.1) is epidemiologically well posed and all solutions of the system with all parameters in $\Omega$.

### 3.2 Disease free equilibrium point (DFE)

Set $E = I_A = I = Q = R = 0$ the disease free equilibrium is obtained :

$$DFE = (S_0, 0, 0, 0, 0) = (\frac{\wedge}{\delta}, 0, 0, 0, 0, 0). \tag{3.2}$$

Next, the basic reproduction number ($R_0$) is the expected value of infection rate per time unit. The infection occurs in a susceptible population. If, $R_0 < 1$ implies that disease will decline, $R_0 > 1$ implies that disease will persist and $R_0 = 1$ requires further investigation. $R_0$ is obtained using the next generation matrix approach [9].

We use the next generation matrix start from (2.1) only classes of $E, I_A, I, Q$:

$$\begin{cases} \frac{dE}{dt} = \eta SE - (\delta + \xi)E, \\ \frac{dI_A}{dt} = \xi\theta E - (\delta + \nu + m_1 + m_3 + r_1)I_A, \\ \frac{dI}{dt} = \xi(1-\theta)E + m_3 I_A - (\delta + \nu + m_2)I, \\ \frac{dQ}{dt} = m_1 I_A + m_2 I - (r_2 + \nu)Q. \end{cases} \tag{3.3}$$

From (3.3), the study generates matrix $\mathbb{F}$ and $\mathbb{V}$, i.e.

$$\mathbb{F} = \begin{pmatrix} \eta S(t)E(t) \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

and

$$\mathbb{V} = \begin{pmatrix} (\delta + \xi)E(t) \\ (\delta + \nu + m_1 + m_3)I_A(t) - \xi\theta E(t) \\ (\delta + \nu + m_2)I(t) - \xi(1-\theta)E(t) - m_3 I_A(t) \\ (\nu + r_2)Q(t) - m_1 I_A(t) - m_2 I(t). \end{pmatrix}$$

The Jacobian matrix of $\mathbb{F}$ and $\mathbb{V}$ at DFE, denoted by F and V is given as follows

$$\mathrm{F} = \begin{pmatrix} \eta\frac{\wedge}{\delta} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$\mathrm{V} = \begin{pmatrix} V_{11} & 0 & 0 & 0 \\ -\xi\theta & V_{22} & 0 & 0 \\ -V_{31} & -m_3 & V_{33} & 0 \\ 0 & -m_1 & -m_2 & V_{44} \end{pmatrix}$$

where, $V_{11} = \delta + \xi, V_{22} = \delta + \nu + m_1 + m_3, V_{31} = \xi(1-\theta), V_{33} = \delta + \nu + m_2, V_{44} = \nu + r_2$.

Then

$$\mathrm{FV}^{-1} = \begin{pmatrix} \frac{\eta\wedge}{\delta(\delta+\xi)} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Therefore, $\mathrm{FV}^{-1}$ is the next generation matrix of the model (3.3). So as described in [9], $R_0 = \rho(\mathrm{FV}^{-1})$ where $\rho$ stands for spectral radius of the next generation matrix $\mathrm{FV}^{-1}$. Thus,

$$\rho(\mathrm{FV}^{-1}) = R_0 = \frac{\eta\wedge}{\delta(\delta+\xi)} > 0. \quad (3.4)$$

### 3.3 Local stability analysis of disease free equilibrium.

**Theorem 3.1.** *if $R_0 < 1$ then the disease free equilibrium point is locally asymptotically stable.*

*Proof.* The Jacobian matrix with respect to the system (2.1) is given by

$$J = \begin{pmatrix} J_{11} & -\eta S & 0 & 0 & 0 & 0 \\ \eta E & J_{22} & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & -J_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & -V_{33} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & -V_{44} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta \end{pmatrix},$$

where $J_{11} = -\eta E - \delta, J_{22} = \eta S - (\delta + \xi), J_{33} = (\delta + \nu + m_1 + m_3 + r_1)$, which implies at DFE

$$J_{DFE} = \begin{pmatrix} -\delta & -\eta\frac{\wedge}{\delta} & 0 & 0 & 0 & 0 \\ 0 & JJ_{22} & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & -J_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & -V_{33} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & -V_{44} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta \end{pmatrix},$$

where, $JJ_{22} = \eta\frac{\wedge}{\delta}(\delta + \xi)$.

The characteristic polynomial of the Jacobian matrix at DFE is given by $det(J_{DFE} - \lambda I) = 0$, where $\lambda$ is the eigenvalue and I is a $6 \times 6$ identity matrix. Thus, $det(J_{DFE} - \lambda I)$ is

$$\begin{vmatrix} -\delta-\lambda & -\eta\frac{\wedge}{\delta} & 0 & 0 & 0 & 0 \\ 0 & D_{22} & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & D_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & D_{44} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & D_{55} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta-\lambda \end{vmatrix},$$

where, $D_{22} = JJ_{22} - \lambda, D_{33} = -J_{33} - \lambda, D_{44} = -V_{33} - \lambda, D_{55} = -V_{44} - \lambda$.

Simplifying and solving for $\lambda$, gives

$$\begin{aligned} \lambda_1 &= -\delta < 0 \\ \lambda_2 &= -J_{33} = -(\delta + \nu + m_1 + m_3 + r_1) < 0 \\ \lambda_3 &= -V_{33} = (\delta + \nu + m_2) < 0 \\ \lambda_4 &= -V_{44} = -(r_2 + \nu) < 0 \\ \lambda_5 &= -\delta < 0 \\ \lambda_6 &= V_{11}(R_0 - 1) = (\delta + \xi)(R_0 - 1) < 0. \end{aligned} \quad (3.5)$$

Then $R_0 < 1$ this completes the proof.

□

### 3.4 Existence of endemic equilibrium point.

We focus the existence of endemic equilibrium point. Let $E_1 = (S^*, E^*, I_A^*, I^*, Q^*, R^*)$ is the endemic equilibrium point. For simplicity, $S(t) = S, E(t) = E, I_A(t) = I_A, I(t), I, Q(t) = Q$ and $R(t) = R$, then endemic equilibrium satisfies

$$\begin{cases} 0 = \wedge - \eta S^* E^* - \delta S^*, \\ 0 = \eta S^* E^* - (\delta + \xi) E^*, \\ 0 = \xi\theta E^* - (\delta + \nu + m_1 + m_3 + r_1) I_A^*, \\ 0 = \xi(1-\theta) E^* + m_3 I_A^* - (\delta + \nu + m_2) I^*, \\ 0 = m_1 I_A^* + m_2 I^* - (r_2 + \nu) Q^*, \\ 0 = r_1 I_A^* + r_2 Q^* - \delta R^*, \end{cases} \quad (3.6)$$

From the first Equation of (3.6), we obtain

$$S^* = \frac{\wedge}{\eta E^* + \delta}. \tag{3.7}$$

Inserting (3.7) in the second equation of (3.6), we get

$$E^* = \frac{\delta}{\eta}(R_0 - 1), \tag{3.8}$$

substituting $E^*$ in (3.7), yields

$$S^* = \frac{V_{11}}{\eta}. \tag{3.9}$$

Using (3.8) and (3.9) in the third equation (3.6), gives

$$I_A^* = \frac{\xi\theta\delta}{\eta J_{33}}(R_0 - 1). \tag{3.10}$$

Substituting (3.8) and (3.9) in the fourth equation (3.6), gives

$$I^* = \frac{\xi\delta((1-\theta)J_{33} + m_3\theta)}{\eta V_{33} J_{33}}(R_0 - 1). \tag{3.11}$$

Inserting equations (3.10), (3.11) in (3.6), we get

$$Q^* = \frac{\xi\delta[m_1 V_{33} + Q_1 + Q_2 J_{33}]}{\eta V_{44} J_{33} V_{33}}(R_0 - 1), \tag{3.12}$$

where $Q_1 = m_2 m_3 \theta, Q_2 = m_2(1-\theta)$.

Bringing equations (3.10), (3.11) and (3.12) into the last equation (3.6), yields

$$\begin{aligned} R^* &= \xi \frac{r_1\theta V_{44} V_{33}}{\eta V_{44} J_{33} V_{33}} \\ &\times \frac{r_2\{m_1 V_{33} + Q_1 + Q_2 J_{33}\}}{\eta V_{44} J_{33} V_{33}} \\ &\times (R_0 - 1). \end{aligned} \tag{3.13}$$

Thus, we get a conclusion in the follwing theorem.

**Theorem 3.2.** *The system (2.1) has unique endemic equilibrium point given by*

$$\begin{aligned} E_1 = \Big(&\frac{\delta+\xi}{\eta}, \frac{\delta}{\eta}(R_0-1), a(R_0-1), b(R_0-1), \\ &\big(\frac{am_1 + bm_2}{\nu + r_2}\big)(R_0-1), \big(\frac{r_1 a + r_2 c}{\delta}\big)(R_0-1)\Big), \end{aligned}$$

*where* $R_0 > 1$ *and*

$$a = \frac{\xi\theta\delta}{\eta(\delta + \nu + m_1 + m_3 + r_1)},$$

$$b = \frac{\xi\delta((1-\theta)(\delta + \nu + m_1 + m_3 + r_1) + m_3\theta)}{\eta(\delta + \nu + m_2)(\delta + \nu + m_1 + m_3 + r_1)},$$

$$c = \frac{am_1 + bm_2}{\nu + r_2}.$$

### 3.5 Local stability analysis of the endemic equilibrium $E_1$

**Theorem 3.3.** *If* $R_0 > 1$*, the endemic equilibrium* $E_1$ *is locally asymptotically stable.*

*Proof.* The Jacobian matrix with respect to the system (2.1) is

$$J = \begin{pmatrix} J_{11} & -\eta S & 0 & 0 & 0 & 0 \\ \eta E & J_{22} & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & -J_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & -V_{33} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & -V_{44} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta \end{pmatrix}$$

which implies at $E_1$

$$J_{E_1} = \begin{pmatrix} -\delta R_0 & -V_{11} & 0 & 0 & 0 & 0 \\ JE_{21} & 0 & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & -J_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & -V_{33} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & -V_{44} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta \end{pmatrix}$$

where $JE_{21} = \delta(R_0 - 1)$.

The characteristic polynomial of the Jacobian matrix at $E_1$ is given by $det(J_{E_1} - \lambda I) = 0$, where $\lambda$ is the eigenvalue and I is $6 \times 6$ identity matrix. Thus, $det(J_{E_1} - \lambda I)$ is

$$= \begin{vmatrix} E_{11} & -V_{11} & 0 & 0 & 0 & 0 \\ JE_{21} & -\lambda & 0 & 0 & 0 & 0 \\ 0 & \xi\theta & E_{33} & 0 & 0 & 0 \\ 0 & V_{31} & m_3 & E_{44} & 0 & 0 \\ 0 & 0 & m_1 & m_2 & E_{55} & 0 \\ 0 & 0 & r_1 & 0 & r_2 & -\delta-\lambda \end{vmatrix}$$

where $E_{11} = -\delta R_0 - \lambda, E_{33} = -J_{33} - \lambda, E_{44} = -V_{33} - \lambda, E_{55} = -V_{44} - \lambda$

$$\begin{aligned} &=[\lambda^2 + \lambda\delta(R_0-1) + \lambda\delta + \delta(R_0-1)V_{11}] \\ &\quad [-J_{33}-\lambda] \\ &\quad [-V_{33}-\lambda][-V_{44}-\lambda][-\delta-\lambda] \\ &=[\lambda^2 + \lambda\delta(R_0-1) + \lambda\delta + \delta(R_0-1)(\delta+\xi)] \\ &\quad [-(\delta+\nu+m_1+m_3+r_1)-\lambda] \\ &\quad [-(\delta+\nu+m_2)-\lambda][-(r_2+\nu)-\lambda][-\delta-\lambda]. \end{aligned}$$

Simplifying the characteristic polynomial and solving for $\lambda$, gives

$$\begin{aligned} &\lambda_1 = -\delta < 0 \\ &\lambda_2 = -(r_2+\nu) < 0 \\ &\lambda_3 = -(\delta+\nu+m_2) < 0 \\ &\lambda_4 = -(\delta+\nu+m_1+m_3+r_1) < 0. \end{aligned}$$

The quadratic $\lambda^2 + \lambda\delta(R_0-1) + \lambda\delta + \delta(R_0-1)(\delta+\xi)$ has all positive terms and thus, its root must all be negative. Then $\lambda_5$, $\lambda_6 < 0$, completes the proof. □

### 3.6 Global stability analysis of the endemic equilibrium $E_1$

**Theorem 3.4.** *The endemic equilibrium $E_1$ for the system* (2.1) *is globally asymptotically stable whenever $R_0 > 1$.*

*Proof.* To show global stability at $E_1$ of the system, consider the Lyapunov function,

$$\begin{aligned} U(S,E,I_A,I,Q,R) =& \frac{1}{3}(S-S^*+E-E^*+I_A \\ &- I_A^*+Q-Q^*+R-R^*)^3. \end{aligned}$$

It easy to see that $U$ is positive for any point and equal to zero at the endemic equilibrium $E_1$ if $S = S^*, E = E^*, I_A = I_A^*, I = I^*, Q = Q^*$ and $R = R^*$. Then consider,

$$\begin{aligned} \frac{dU}{dt} &= (S-S^*+E-E^*+I_A-I_A^*+Q-Q^* \\ &\quad + R-R^*)^2(\wedge - \delta S - \delta E - (\delta+\nu+m_3)I_A \\ &\quad + m_2 I - \nu Q - \delta R) \\ &= -(S-^*+E-E^*+I_A-I_A^*+Q-Q^* \\ &\quad + R-R^*)^2(M-N), \end{aligned}$$

where $M = \delta S+\delta E+(\delta+\nu+m_3)I_A+\nu Q+\delta R$ and $N = \wedge + m_2 I$.

So $\frac{dU}{dt} < 0$ if and only if $M > N$ and $\frac{dU}{dt} = 0$ if and only if $S = S^*, E = E^*, I_A = I_A^*, I = I^*, Q = Q^*$ and $R = R^*$. Then the endemic equilibrium $E_1$ is globally asymptotically stable.

□

### 3.7 Global stability analysis at disease free equilibrium

**Theorem 3.5.** *The disease free equilibrium for the system* (2.1) *is globally asymptotically stable whenever $R_0 < 1$.*

*Proof.* To show global stability at DFE of the system, consider the Lyapunov function,

$$\begin{aligned} U(S,E,I_A,I,Q,R) =& \frac{1}{3}(S-S_0+E-E_0+I_A \\ &- I_{A_0}+Q-Q_0+R-R_0)^3. \end{aligned}$$

It easy to see that $U$ is positive for any point and equal to zero at disease free equilibrium point($S = S_0, E = I_A = I = Q = R = 0$). Then consider,

$$\begin{aligned} \frac{dU}{dt} &= (S-S_0+E-E_0+I_A-I_{A_0}+Q-Q_0 \\ &\quad + R-R_0)^2(\wedge - \delta S - \delta E - (\delta+\nu+m_3)I_A \\ &\quad + m_2 I - \nu Q - \delta R) \\ &= -(S-S_0+E-E_0+I_A-I_{A_0}+Q-Q_0 \\ &\quad + R-R_0)^2(M-N) \end{aligned}$$

where $M = \delta S + \delta E + (\delta + \nu + m_3) I_A + \nu Q + \delta R$ and $N = \wedge + m_2 I$.

So $\frac{dU}{dt} < 0$ if and only if $M > N$ and $\frac{dU}{dt} = 0$ if and only if $S = S_0, E = E_0, I_A = I_{A_0}, I = I_0, Q = Q_0$ and $R = R_0$. Then, the disease free equilibrium is globally asymptotically stable. □

## 4. Green's Function of the Model

### 4.1 Overview of Green's function for first order differential equation

Consider the first order differential equation decomposed into a linear term $L(y)$ and a nonlinear(or linear) term $f(t, y)$ as follow

$$L[y] \equiv y' + p(t)y = f(t, y), \text{ for } t > a, \tag{4.1}$$

subject to a homogeneous initial condition, $B[y] \equiv y(a) = 0$.

The Green function $G(t|z)$ is defined as the solution to

$$L[G(t, z)] = \delta(t - z) \text{ subject to } G(a, z) = 0.$$

A particular solution to $y' = f(t, y, y')$ is expressed in terms of $G$ and is given by the following structure

$$y(t) = \int_a^{\infty} G(t, z) f(t, y(t)) dt. \tag{4.2}$$

Now we consider the qualitiative behavior of the Green function. For $t \neq z$, the Green function is simply a homogeneous solution of the differential equation; however at $t - z$ we expect some singular behavior. $G'(t, z)$ will have a Dirac delta function type singularity. This means that $G(t, z)$ will have a jump discontinuity at $t = z$.

$$G(z^+, z) - G(z^-, z) = 1 \tag{4.3}$$

The homogeneous solution of the differential equation is

$$y_h = e^{-\int p(t) dt}.$$

Since the Green function satisfies the homogeneous equation for $t \neq z$, it will be a constant times this homogeneous solution for $t < z$ and $t > z$.

$$G(t, z) = \begin{cases} c_1 e^{-\int p(t) dt} & \text{for } a < t < z, \\ c_2 e^{-\int p(t) dt} & \text{for } z < t, \end{cases}$$

where $p(t)$ coefficient function of $y(t)$. In order to satisfy the homogeneous initial condition $G(a, z) = 0$ and the jump condition, gives us the constraint $G(z^+, z) = 1$. We can use the Green function in term

$$G(t, z) = e^{-\int_z^t p(x) dx}. \tag{4.4}$$

### 4.2 Construct Green's Picard iteration

The Green's function apply to Picard iterative method, we recall the following differential equation

$$L[y] + N[y] = f(t, y), \tag{4.5}$$

where $L[y]$ is a linear operator in $y$, $N[y]$ is a nonlinear operator in $y$, and $f(t, y)$ is a linear or nonlinear function in $y$. Let $y_p$ be a particular solution of (4.5). We define the linear integral operator in terms of the Green's function and the particular solution $y_p$ as

$$K[y_p] = \int_a^b G(t, z) L[y_p] dz. \tag{4.6}$$

Here $G$ is the Green's function corresponding to the linear differential operator $L[y]$. For convenience we set $y_p(t) = v(t)$. Adding and subtracting $N[v] - f(z, v)$ from within the integral in (4.6) yields

$$\begin{aligned}K[v] &= \int_a^b G(t,z)\big(L[v]+N[v]-f(z,v)\big)dz \\ &\quad + \int_a^b G(t,z)\big(f(z,v)-N[v]\big)dz, \\ &= v + \int_a^b G(t,z)\big(L[v]+N[v] \\ &\quad - f(z,v)\big)dz.\end{aligned} \tag{4.7}$$

We apply Picard iterative form

$$v(t_{n+1}) = K[v(t_n)], \tag{4.8}$$

where $n \geq 0$. That is,

$$\begin{aligned}K[v(t_n)] &= \int_a^b G(t_n,z)\big(L[v(t_n)]+N[v(t_n)] \\ &\quad - f(z,v(t_n))\big)dz + \int_a^b G(t_n,z) \\ &\quad \big(f(z,v(t_n)) - N[v(t_n)]\big)dz, \\ &= v(t_n) + \int_a^b G(t_n,z)\big(L[v(t_n)] \\ &\quad + N[v(t_n)] - f(z,v(t_n))\big)dz.\end{aligned} \tag{4.9}$$

Next, we construct all parameter sequences of (2.1) to Green's Picard iteration

$$\begin{aligned}S(t_{n+1}) &= S(t_n) + \int_a^\infty G_S(t_n,z)\big[S'_{t_n}(z) \\ &\quad + (\eta E_{t_n}(z)+\delta)S_{t_n}(z) - \wedge\big]dz, \\ E(t_{n+1}) &= E(t_n) + \int_a^\infty G_E(t_n,z)\big[E'_{t_n}(z) \\ &\quad - (\eta S_{t_n}(z) - \delta - \xi)E_{t_n}(z)\big]dz, \\ I_A(t_{n+1}) &= I_A(t_n) + \int_a^\infty G_{I_A}(t_n,z)\big[I'_{A_{t_n}}(z) \\ &\quad + (\delta+\nu+m_1+m_3+r_1)I_{A_{t_n}}(z) \\ &\quad - \xi\theta E_{t_n}(z)\big]dz, \\ I(t_n) &= I(t_n) + \int_a^\infty G_I(t_n,z)\big[I'_{t_n}(z) \\ &\quad + (\delta+\nu+m_2)I_{t_n}(z) - \xi(1-\theta)E_{t_n}(z) \\ &\quad - m_3 I A_{t_n}(z)\big]dz, \\ Q(t_n) &= Q(t_n) + \int_a^\infty G_Q(t_n,z)\big[Q'_{t_n}(z) \\ &\quad + (r_2+\nu)Q_{t_n}(z) - m_1 I_{A_{t_n}}(z) \\ &\quad - m_2 I_{t_n}(z)\big]dz, \\ R(t_{n+1}) &= R(t_n) + \int_a^\infty G_R(t_n,z)\big[R'_{t_n}(z) \\ &\quad + \delta R_{t_n}(z) - r_1 I_{A_{t_n}}(z) - r_2 Q_{t_n}(z)\big]dz.\end{aligned} \tag{4.10}$$

For $n \geq 0$, and

$$\begin{aligned}G_S(t_n,z) &= e^{-\int_z^{t_n}(\eta E_{t_n}(x)+\delta)dx}, \\ G_E(t_n,z) &= e^{-\int_z^{t_n}(\delta+\xi-\eta S_{t_n}(x))dx}, \\ G_{I_A}(t_n,z)) &= e^{-\int_z^{t_n}(\delta+\nu+m_1+m_3+r_1)dx}, \\ G_I(t_n,z) &= e^{-\int_z^{t_n}(\delta+\nu+m_2)dx}, \\ G_Q(t_n,z) &= e^{-\int_z^{t_n}(r_2+\nu)dx}, \\ G_R(t_n,z) &= e^{-\int_z^{t_n}\delta dx}.\end{aligned} \tag{4.11}$$

### 4.3 Existence and convergence theorems for Green's Picard iteration

In Theorem 4.1 we define and prove that the operator $P_{G_\Omega}$ is a contraction mapping. Then all sequences defined by Picard iteration converge strongly to the fixed point of $P_{G_\Omega}$. Now, we introduce the following continuous functions $P_{G_\Omega}$, defined by

$$\begin{aligned}P_{G_S}(t_{n+1}) &= S(t_n) + \int_0^{t_n} G_S(t_n,z)\big[S'_{t_n}(z) \\ &\quad - f(z,S_{t_n})\big]dz, \\ P_{G_E}(t_{n+1}) &= E(t_n) + \int_0^{t_n} G_E(t_n,z)\big[E'_{t_n}(z) \\ &\quad - f(z,E_{t_n})\big]dz,\end{aligned}$$

$$
\begin{aligned}
P_{G_{I_A}}(t_{n+1}) &= I_A(t_n) + \int_0^{t_n} G_{I_A}(t_n, z)\big[I'_{A_{t_n}}(z) \\
&\quad - f(z, I_{A_{t_n}})\big]dz, \\
P_{G_I}(t_{n+1}) &= I(t_n) + \int_0^{t_n} G_I(t_n, z)\big[I'_{t_n}(z) \\
&\quad - f(z, I_{t_n})\big]dz, \\
P_{G_Q}(t_{n+1}) &= Q(t_n) + \int_0^{t_n} G_Q(t_n, z)\big[Q'_{t_n}(z) \\
&\quad - f(z, Q_{t_n})\big]dz, \\
P_{G_R}(t_{n+1}) &= R(t_n) + \int_0^{t_n} G_R(t_n, z)\big[R'_{t_n}(z) \\
&\quad - f(z, R_{t_n})\big]dz.
\end{aligned} \tag{4.12}
$$

Where $t = t_n \in [0, T]$ and $n \geq 0$. $B([0, T], \mathbb{R})$ is the Banach space of all continuous real-valued function equipped with the norm defined by

$$
\begin{aligned}
|(S, E, I_A, I, Q, R)| &= |S(t)| + |E(t)| + |I_A(t)| \\
&\quad + |I(t)| + |Q(t)| + |R(t)|,
\end{aligned}
$$

where

$$
\begin{aligned}
|S(t)| &= \sup_{t\in[0,T]} |S(t)|, |E(t)| = \sup_{t\in[0,T]} |E(t)|, \\
|I_A(t)| &= \sup_{t\in[0,T]} |I_A(t)|, |I(t)| = \sup_{t\in[0,T]} |I(t)|, \\
|Q(t)| &= \sup_{t\in[0,T]} |Q(t)|, |R(t)| = \sup_{t\in[0,T]} |R(t)|.
\end{aligned}
$$

**Theorem 4.1.** *Assume $f$ is a function, which appears in the definition of the operator $P_{G_\Omega}$, is such that $C = K_G C_c < 1$, where $K_G = \max_{t\in[0,T]} \int_0^t |G_\Omega(t_n, z)|dz$ and $C_c = \max_{t\in[0,T]} |f'(u(t))|$. Then $P_{G_\Omega}$ is a contraction and hence, the sequence $\{u_n\} \in \Omega$ defined by Picard iteration converges to fixed point of $P_{G_\Omega}$.*

*Proof.* We will prove all operator of the sequences $S(t), E(t), I_A(t), I(t), Q(t), R(t)$ that they are contraction mapping.

Forming integration by part the Eqs. (4.9) - (4.12) the product is

$$
\begin{aligned}
P_G(S) &= S - \int_0^t G_S(t, z) f(z, S)dz, \\
P_G(E) &= E - \int_0^t G_E(t, z) f(z, E)dz, \\
P_G(I_A) &= I_A - \int_0^t G_{I_A}(t, z) f(z, I_A)dz, \\
P_G(I) &= I - \int_0^t G_I(t, z) f(z, I)dz, \\
P_G(Q) &= Q - \int_0^t G_Q(t, z) f(z, Q)dz, \\
P_G(R) &= R - \int_0^t G_R(t, z) f(z, R)dz.
\end{aligned} \tag{4.13}
$$

Direct calculations (4.11) imply that

$$
\begin{aligned}
\int_0^t G_S(t_n, z)dz &= \left[\frac{1}{\eta E(t) + \delta}\right], \\
\int_0^t G_E(t_n, z)dz &= \left[\frac{1}{\delta + \xi - \eta S(t)}\right], \\
\int_0^t G_{IA}(t_n, z))dz &= \left[\frac{1 - e^{-(\delta+\nu+m_1+m_3+r_1)t}}{\delta + \nu + m_1 + m_3 + r_1}\right], \\
\int_0^t G_I(t_n, z)dz &= \left[\frac{1 - e^{-(\delta+\nu+m_2)t}}{\delta + \nu + m_2}\right], \\
\int_0^t G_Q(t_n, z)dz &= \left[\frac{1 - e^{-(r_2+\nu)t}}{r_2 + \nu}\right], \\
\int_0^t G_R(t_n, z)dz &= \left[\frac{1 - e^{-\delta t}}{\delta}\right],
\end{aligned} \tag{4.14}
$$

since (3.1) and (4.14), we get $\max_{t\in[0,T]} \int_0^t |G_\Omega(t_n, z)|dz$ is $K_G$, then

$$
\int_0^t |G_\Omega(t_n, z)|dz \leq K_G.
$$

Let $u, v \in \Omega$ thus

$$\begin{aligned}|P_{G_\Omega}(u) - P_{G_\Omega}(v)| &= |\int_0^t G_\Omega(t,z)[f(z,u) \\ &\quad - f(z,v)]dz| \\ &\leq (\int_0^t |G_\Omega(t,z)|dz) \\ &\quad (\int_0^t |f(z,u) - f(z,v)|dz) \\ &\leq K_G \int_0^t |f(z,u) - f(z,v)|dz.\end{aligned}$$

By using the mean value theorem for $f(u)$ and using the condition that $C_c = \max_{t\in[0,T]} |f'(u(t))|$, we consider the last inequality that

$$\begin{aligned}|P_{G_\Omega}(u) - P_{G_\Omega}(v)| &\leq K_G \max_{t\in[0,T]} |f(u(t)) - f(v(t))| \\ &\leq K_G C_c \|u - v\| \\ &\leq C\|u - v\|,\end{aligned}$$

where $\|u - v\| = \max_{t\in[0,T]} |u(t) - v(t)|$ and $C = K_G C_c < 1$. So we obtain the following

$$\|P_{G_\Omega}(u) - P_{G_\Omega}(v)\| \leq C\|u - v\|,$$

such $0 \leq C < 1$. Hence $P_{G_\Omega}$ is a contraction mapping. □

## 5. Modeling estimation

Aim of this section is using real data of Thailand (March 2021 - August 2021) to forecast the future (1 September 2021 - 19 October 2021) of this model to study behavior of all sequences $S(t), E(t), I_A(t), I(t), Q(t), R(t)$. All data in Table 2 calculate from Department of Disease Control, Thailand.

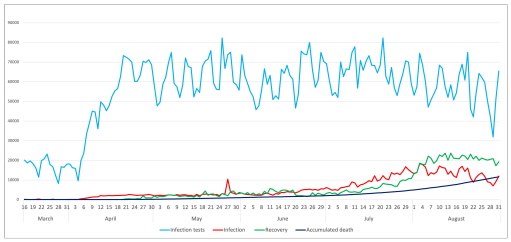


**Fig. 2.** The daily report of Thailand Coronavirus (16 March - 31 August 2021).

**Table 2.** The value of the parameters used in the model

| Parameters | Value | Units |
|---|---|---|
| $\wedge$ | $3.068e^{-5}$ | 100,000 units |
| $\delta$ | $1.89e^{-5}$ | 100,000 units |
| $\nu$ | $8.963e^{-3}$ | $day^{-1}$ |
| $\eta$ | 0.271830 | $day^{-1}$ |
| $\xi$ | 0.200000 | $day^{-1}$ |
| $\theta$ | 0.700000 | $day^{-1}$ |
| $m_1$ | 0.883876 | $day^{-1}$ |
| $m_2$ | 0.990948 | $day^{-1}$ |
| $m_3$ | $3.5714e^{-3}$ | $day^{-1}$ |
| $r_1$ | 0.071428 | $day^{-1}$ |
| $r_2$ | 0.991037 | $day^{-1}$ |

For all parameters in Table 2, we can calculate the basic reproduction number $R_0 = 2.2061 > 1$; it explains that at this time, Thailand is continue at infection period. In the next part we will forecast the future situation of Thailand.

### 5.1 Numerical simulation

The purpose of this section is to forecast behavior of all compartments. Consider the differential Eqs. (4.10)-(4.11). Based on this consideration, let $S$ be number of infection tests in (16 March - 31 August 2021) = 9,336,014 units and $E$ be number of infection in (16 March - 31 August 2021) = 1,153,837 units. Then the initial condition is $S(0) = 1, E(0) = 0.12359, I_A(0) = I(0) = Q(0) = R(0) = 0$.

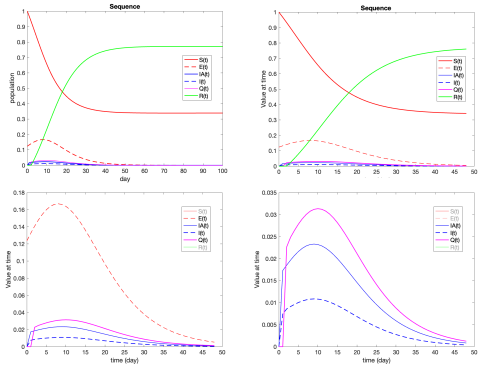


**Fig. 3.** Prediction behavior of all compartments of the model.

Fig. 3 shows the dynamic of all compartments, and explains that all compartments will converge to normal situation at $t = 50$ days. Infection will maximum spread at $E(9) = 0.166847$ and decrease until normal situation, that is this case number of infection will increase to be 1,557,685 units in 9 days after that number of infection will decrease to 0.

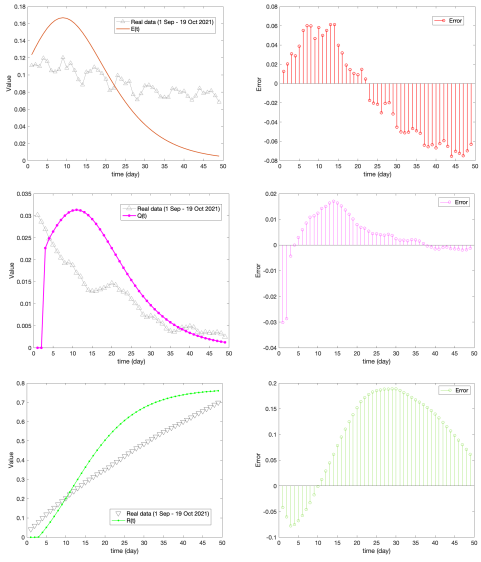


**Fig. 4.** Prediction behavior and error compare $E(t), Q(t), R(t)$ with real data.

Fig. 4 explains the comparison between the dynamic of $E(t), Q(t), R(t)$ with real data (1 September 2021 to 19 October 2021) to show the error value (Error = approximate value - real Value) of $E(t), Q(t)$ and $R(t)$. By the gray lines is real data and the color lines is approximate value of each compartment.

## 6. Conclusion

This paper presents a mathematical model of the Coronavirus Disease (Covid-19) of Thailand by using parameters from real data (16 March 2021 to 31 August 2021). The authors compute the basic reproduction number $R_0 = 2.2061 > 1$, it explain that at this time, Thailand is continue at infection period and the disease free equilibrium (DFE), local stability, the existence of endemic equilibrium ($E_1$), local stability, global stability of the endemic equilibrium. Next the existence and convergence theorems of solutions are shown via the techniques of fixed point theorems in from of Green's function. Finally, the authors show numerical to forecast the future of the Coronavirus Disease (Covid-19) in Thailand (1 September 2021 to 19 October 2021) in Figs. 3 and 4. Note that the authors can not find minimum error value because this model fix the parameters in Table 2 all times and all system is closed condition. The author wants to develop a model for open condition in the future.

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