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ORIGINAL RESEARCH

Mathematical modeling and stability of SARS-CoV-2 transmission dynamics among domestic tourists in Thailand

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Abstract
The defined epidemiological model system explaining the spread of infectious diseases characterized with SARS-CoV-2 is analysed. The resulting SEIQR model is analysed in a closed system. It considers the basic reproductive value, the equilibrium point, local subclinical stability of the disease-free equilibrium point and local subclinical stability of the endemic equilibrium point. This is examined and the asymptotic dynamics of the appropriate model system are investigated. Further, a sensitivity analysis supplemented by simulations is prepared in advance to impose how changes in parameters involve the dynamic behaviours of the model.

Keywords Stability · Basic reproductive number · Mathematical model · Numerical simulations · Asymptotic dynamics

Mathematics Subject Classification 65C20 · 34K20

1 Introduction

Coronaviruses be a group of viruses that cause illnesses such as respiratory or gastrointestinal illnesses. Respiratory illnesses range out of the common cold to more serious illnesses such as the Middle East Respiratory Syndrome (MERS-CoV). The

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severe acute Respiratory Syndrome (SARS-CoV). The novel coronavirus (nCoV) be a strain that has never been identified in humans. When scientists have tested and predicated exactly what type of coronavirus it is, they give it a name, such as in the case of COVID-19, contains the virus that causes the transmission of SARS-CoV-2 [1–6].

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by a new coronavirus called "SARS-CoV-2 virus". Most people infected with the virus will experience mild to moderate respiratory illness and recover without requiring special treatment. The World Health Organization (WHO) is responsible for monitoring and monitoring the spread of the coronavirus, as well as monitoring outbreaks that occur continuous and widespread outbreak of disease, which was the first searched in Wuhan, China, in late 2019. Since subsequently, it has been spread by travellers to well-nigh every country in the world, and was declared a pandemic by WHO on March 22, 2020 [1–6]. As of November 23, 2020, there are more than 59,002,152 confirmed cases of infection in 210 countries, more than 1,393,879 people have died from the pandemic, and more than 40,776,358 people have recovered (COVID-19 Dashboard, 2020). This COVID-19 outbreak has affected the health and lives of many people around the world, not including the economic damage that has occurred around the world [2–5]. The behaviour of COVID-19 It can range for mild to drastic. Someone recover clearly while others become seriously ill. If you test positive for COVID-19, you will have: Fever Cough, Sore throat, Shortness of breath. Some people are asymptomatic but can still spread the virus [5–8].

WHO describes "Quarantine of persons as the restriction of activities or separation of persons who are not ill, but who may have been exposed to an infectious agent or disease, with the primary objective of monitoring symptoms and the early detection of cases." Isolation, on the other hand, can be described as the parting of ill or infected persons from others, to avert the spread of infection or contamination. As an agreement in the public health sector, isolation is an effective approach in dealing with contagious diseases like COVID-19, which may spread from droplets in the air. It is also argued that compulsory quarantine and extensive travel restrictions may do more harm than good. Although the current estimated case fatality rate for this disease (approximately 3.4%) is much less than that of SARS (11%), its rate of transmission is much faster [12]. Hence, it is more likely to spread from one person to another. This rate, however, seems to be dependent on region and the average age of the community [1–7, 14–25].

COVID-19 outbreak drains health care resources. Not only in poor or developing countries. But it also affects developed countries, this causes a shortage of health resources both in terms of finances and readiness in all aspects related to medical care. Including utilities, consumer products and tourism for tourists. Therefore, early non-pharmaceutical preventive measures such as lockdown, social distancing are required and disease hygiene measures but later on the COVID-19 disease. This results in a shortage of medical equipment, shortage of medical personnel hospital bed Intensive care room (ICU room) Diagnostic safety equipment and oxygen tanks. In addition, factors such as the migration of large numbers of workers, unemployment, the education system, and the management of non-COVID- 19 crisis patients. It has become a concern amid the pandemic [6, 7, 9–11]. It is important to diagnose the infection

and the causative organism as early and accurately as possible so that the right intervention (including measures such as isolation and quarantine) can be put in place to confine the infection and prevent its spread [1–3, 5–9]. Preventive measures are the present strategy to limit the spread of disease. Screening is required, diagnosis, isolation, and treatment are necessary to prevent further spread. Prevention strategies focus on patient isolation and careful infection control. This including appropriate measures to be adopted during the diagnosis and the provision of clinical care to an infected patient. Measures to prevent and control COVID-19 disease Important in the community [1–3, 7–15].

From studying various impacts from the COVID-19 outbreak has seen the importance of economic and social impacts that directly affect tourism in all sectors related to national development. As a result of this impact, the number of both Thai and Domestic Tourists decreased rapidly. Compared to the past period, this causes a great loss to economic agility. In response to this many governments and international organizations have promoted domestic tourism as a strategy for economic recovery. By planning domestic tourism to outperform international tourism in many countries amid the pandemic. But there are many risks of COVID-19contamination, such as the relationship between population mobility and the spread of COVID-19, broad population movements and movement patterns, change tourism type and non-tourism type, etc.

Finally, the researcher studied mathematical models to create a model that predicts the actual situation and related factors that affect the spread of the disease for both Thai and foreign tourists. To be used in creating measures to prevent the spread of disease and control epidemics caused by this virus.

2 Materials and methods

In this section, we study a SEIQR ten dimensional COVID-19 transmission of infection in the model consisting of two groups of two populations, host humans in Thai and host humans in Domestic Tourists [8, 11–13, 16]. The host population is divides into five compartment: S_1 humans susceptible in Thai to COVID-19 infection at time t, E_1 humans exposed in Thai to COVID-19 infection at time t, I_1 humans infectious in Thai at time t, Q_1 humans quarantined in Thai to COVID-19 infection at time t, R_1 humans recovered in Thai at time t, S_2 humans susceptible in Domestic Tourists to COVID-19 infection at time t, E_2 humans exposed in Domestic Tourists to COVID-19infection at time t, I_2 humans infectious in Domestic Tourists at time t, Q_2 humans quarantined in Domestic Tourists to COVID-19infection at time t, R_2 humans recovered in Domestic Tourists at time t. The systems of ordinary differential equations (ODE) modelling the correspondence of two groups' populations with nonlinear event functions studied in [12–15, 17–23] follows;

$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = \mu N_h - \psi_1 S_1(I_1 + Q_1) - \delta_1 S_1 + \alpha_1 R_1$$
$$\frac{\mathrm{d}E_1}{\mathrm{d}t} = \psi_1 S_1(I_1 + Q_1) - \delta_1 E_1 - \frac{1}{IIP_1} E_1$$

$$
\begin{aligned}
\frac{\mathrm{d}I_1}{\mathrm{d}t} &= \frac{1}{IIP_1}E_1 - q_{1T}I_1 + q_{2T}Q_1 - (\delta_1 I_1 + \rho_1 I_1) \\
\frac{\mathrm{d}Q_1}{\mathrm{d}t} &= q_{1T}I_1 - q_{2T}Q_1 - \gamma_1 Q_1 - \delta_1 Q_1 \\
\frac{\mathrm{d}R_1}{\mathrm{d}t} &= \gamma_1 Q_1 - (\delta_1 + \alpha_1)R_1 \\
\frac{\mathrm{d}S_2}{\mathrm{d}t} &= CN_T - \psi_2 S_2(I_2 + Q_2) - (\delta_2 + \upsilon)S_2 + \alpha_2 R_2 \\
\frac{\mathrm{d}E_2}{\mathrm{d}t} &= \psi_2 S_2(I_2 + Q_2) - (\delta_2 + \upsilon)E_2 - \frac{1}{IIP_2}E_2 \\
\frac{\mathrm{d}I_2}{\mathrm{d}t} &= \frac{1}{IIP_2}E_2 - q_{1f}I_2 + q_{2f}Q_2 - (\delta_2 + \rho_2 + \upsilon)I_2 \\
\frac{\mathrm{d}Q_2}{\mathrm{d}t} &= q_{1f}I_2 - q_{2f}Q_2 - \gamma_2 Q_2 - (\delta_2 + \upsilon)Q_2 \\
\frac{\mathrm{d}R_2}{\mathrm{d}t} &= \gamma_2 Q_2 - (\delta_2 + \upsilon)R_2 - \alpha_2 R_2
\end{aligned} \tag{1}
$$

with initial densities:

$S_1(0) > 0,\ E_1(0) > 0,\ I_1(0) > 0,\ Q_1(0) > 0,\ R_1(0) > 0$ in Thai and
$S_2(0) > 0,\ E_2(0) > 0,\ I_2(0) > 0,\ Q_2(0) > 0,\ R_2(0) > 0$ in Domestic Tourists.

All the parameters and corresponding biological meaning are Table 1 given below.

We rescale the condition variables for the formulation model system (1) with normalizing as follows:

$$
\begin{aligned}
\frac{S_1}{N_h} &= S_1',\ \frac{E_1}{N_h} = E_1',\ \frac{I_1}{N_h} = I_1',\ \frac{Q_1}{N_h} = Q_1',\ \frac{R_1}{N_h} = R_1', \\
\frac{S_2}{N_T} &= S_2',\ \frac{E_2}{N_T} = E_2',\ \frac{I_2}{N_T} = I_2',\ \frac{Q_2}{N_T} = Q_2',\ \frac{R_2}{N_T} = R_2',
\end{aligned}
$$

So that $S' + E' + I' + Q' + R' = 1$ and $S_2' + E_2' + I_2' + Q_2' + R_2' = 1$. Thus, after discard of model system (1) leads to the following:

$$
\begin{aligned}
\frac{\mathrm{d}S_1'(t)}{\mathrm{d}t} &= \mu - \psi_1 S_1'(t)(I_1'(t) + Q_1'(t)) - \delta_1 S_1'(t) + \alpha_1 R_1'(t) \\
\frac{\mathrm{d}E_1'(t)}{\mathrm{d}t} &= \psi_1 S_1'(t)(I_1'(t) + Q_1'(t)) - \delta_1 E_1'(t) - \frac{1}{IIP_1}E_1'(t) \\
\frac{\mathrm{d}I_1'(t)}{\mathrm{d}t} &= \frac{1}{IIP_1}E_1'(t) - q_{1T}I_1'(t) + q_{2T}Q_1'(t) - (\delta_1 I_1'(t) + \rho_1 I_1'(t)) \\
\frac{\mathrm{d}Q_1'(t)}{\mathrm{d}t} &= q_{1T}I_1'(t) - q_{2T}Q_1'(t) - \gamma_1 Q_1'(t) - \delta_1 Q_1'(t) \\
\frac{\mathrm{d}R_1'(t)}{\mathrm{d}t} &= \gamma_1 Q_1'(t) - (\delta_1 + \alpha_1)R_1'(t)
\end{aligned}
$$

Table 1 The explanation of the state variables and parameters of the model

Description	Symbol
Recruitment term of the susceptible human in Thai	μ
Total Thai human population	N_h
Recruitment term of the susceptible human in domestic tourists	C
Total domestic tourists human population	N_T
Transmission rate of virus between human in Thai human	ψ_1
Transmission rate of virus between human in domestic tourists human	ψ_2
Per capita rate of progression of Thai human from the exposed state to the infectious state	IIP_1
Per capita rate of progression of domestic tourists human from the exposed state to the infectious state	IIP_2
Rate at which infected Thai human changed to quarantine Thai human	q_{1T}
Rate at which quarantine Thai human changed to infected Thai human	q_{2T}
Rate at which infected domestic tourists human changed to quarantine domestic tourists human	q_{1f}
Rate at which quarantine domestic tourists human changed to infected domestic tourists human	q_{2f}
Per capita recovery rate for humans in Thai from the infectious state to the recovered state	γ_1
Per capita recovery rate for humans in domestic tourists from the infectious state to the recovered state	γ_2
Natural death rate of Thai humans	δ_1
Natural death rate of domestic tourists humans	δ_2
Per capita rate of loss of immunity in Thai humans	α_1
Per capita rate of loss of immunity in domestic tourists humans	α_2
Rate at which domestic tourists humans move out the country	υ
Death rate due to COVID-19 of Thai human	ρ_1
Death rate due to COVID-19 of domestic tourists human	ρ_2

$$
\begin{aligned}
\frac{\mathrm{d}S_2'(t)}{\mathrm{d}t} &= C - \psi_2 S_2'(t)(I_2'(t) + Q_2'(t)) - (\delta_2 + \upsilon)S_2'(t) + \alpha_2 R_2'(t)\\
\frac{\mathrm{d}E_2'(t)}{\mathrm{d}t} &= \psi_2 S_2'(t)(I_2'(t) + Q_2'(t)) - (\delta_2 + \upsilon)E_2'(t) - \frac{1}{IIP_2}E_2'(t)\\
\frac{\mathrm{d}I_2'(t)}{\mathrm{d}t} &= \frac{1}{IIP_2}E_2'(t) - q_{1f}I_2'(t) + q_{2f}Q_2'(t) - (\delta_2 + \rho_2 + \upsilon)I_2'(t)\\
\frac{\mathrm{d}Q_2'(t)}{\mathrm{d}t} &= q_{1f}I_2'(t) - q_{2f}Q_2'(t) - \gamma_2 Q_2'(t) - (\delta_2 + \upsilon)Q_2'(t)\\
\frac{\mathrm{d}R_2'(t)}{\mathrm{d}t} &= \gamma_2 Q_2'(t) - (\delta_2 + \upsilon)R_2'(t) - \alpha_2 R_2'(t)
\end{aligned}
\tag{2}
$$

2.1 Positivity of solutions

In systems that the model Eqs. (2) are biologically and epidemiologically meaningful and well posed it is appropriate to show that the solutions of all the condition variables have non-negative for all time. Therefore, we possess the following proof theorem [12–15, 17–23].

Theorem 1 *The solution a group to set {S, E, I, Q, R} of the epidemiological for the Eqs. (2) with non-negative initial data when* $S_1(0) > 0$, $E_1(0) > 0$, $I_1(0) > 0$, $Q_1(0) > 0$, $R_1(0) > 0$ *and* $S_2(0) > 0$, $E_2(0) > 0$, $I_2(0) > 0$, $Q_2(0) > 0$, $R_2(0) > 0$ *still receive non-negative for all time non-negative* $t > 0$.

Proof of Theorem 1 Give that initial data $S_1(0)$, $E_1(0)$, $I_1(0)$, $Q_1(0)$, $R_1(0)$ and $S_2(0)$, $E_2(0)$, $I_2(0)$, $Q_2(0)$, $R_2(0)$ be non-negative. It is obvious for the first sub-equation of the Eqs. (2) thatso as

$$\frac{\mathrm{d}S_1'(t)}{\mathrm{d}t} + \left[\psi_1 S_1'(t)(I'(t)_1 + Q_1'(t)) + \delta_1 S_1'(t)\right] \geq 0$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\left[S_1'(t)\exp\left(\delta_1 t + \psi_1 \int_0^t I'_1(\zeta_1) + Q_1'(\zeta_1)\right)d\zeta_1\right] \geq 0 \tag{3}$$

Integrating (3) gives

$$S_1'(t) \geq S_1'(0)\exp\left[-\delta_1 t + \psi_1 \int_0^t I'_1(\zeta_1) + Q_1'(\zeta_1))d\zeta_1\right] > 0, \quad \forall t > 0 \tag{4}$$

In addition, only check for the second sub-equation of the Eqs. (2) that $\frac{\mathrm{d}E_1'(t)}{\mathrm{d}t}\left[\delta_1 E_1'(t) + \frac{1}{IIP_1}E_1'(t)\right] \geq 0$

so aswhere of on integration yields

$$\frac{\mathrm{d}}{\mathrm{d}t}\left[(E_1'(t)\exp\left(\delta_1 + \frac{1}{IIP_1}\right)\right] \geq 0$$

$$E_1'(t) \geq E'(0)\exp\left[\left(\delta_1 + \frac{1}{IIP_1}\right)t\right] - \geq 0, \quad \forall t > 0 \tag{5}$$

In addition, only check for the third sub-equation of the Eqs. (2) that

$$\frac{\mathrm{d}I_1'(t)}{\mathrm{d}t}\left[q_{1T}I_1'(t) + (\delta_1 I_1'(t) + \rho_1 I_1'(t))\right] \geq 0$$

so aswhere of on integration yields

$$\frac{\mathrm{d}}{\mathrm{d}t}\left[I_1'(t)\exp(q_{1T} + \delta_1 + \rho_1)\right] \geq 0$$

$$I_1'(t) \geq I_1'(0)\exp[-(q_{1T}+\delta_1+\rho_1)t] \geq 0, \quad \forall t > 0 \tag{6}$$

In addition, only check for the fourth sub-equation of the Eqs. (2) that

$$\frac{\mathrm{d}Q_1'(t)}{\mathrm{d}t}\left[q_{2T}\,Q_1'(t)+\gamma_1\,Q_1'(t)+\delta_1\,Q_1'(t)\right] \geq 0$$

so aswhere of on integration yields

$$\frac{d}{dt}\left[Q_1'(t)\exp(q_{2T}+\gamma_1+\delta_1\right] \geq 0$$

$$Q_1'(t) \geq Q_1'(0)\exp[-(q_{2T}+\gamma_1+\delta_1)t] \geq 0, \quad \forall t > 0. \tag{7}$$

In addition, only check for the fifth sub-equation of the Eqs. (2) that

$$\frac{dR_1'(t)}{dt}[\delta_1 R_1'(t)+\alpha_1 R_1'(t)] \geq 0$$

so as

$\frac{d_1}{dt}[R_1'(t)\exp(\delta_1+\alpha_1] \geq 0.$

Where of on integration yields

$$R_1'(t) \geq R_1'(0)\exp[-(\delta_1+\alpha_1)t] \geq 0, \quad \forall t > 0 \tag{8}$$

Within a resembling homologous, it can be shown that $S_2'(t) > 0$, $E_2'(t) > 0$, $I_2'(t) > 0$, $Q_2'(t) > 0$ and $R_2'(t) > 0$ for all time $t > 0$. This concludes the proof. It is decisive to note that model system (2) will be analysed in a practicable region Δ given by

$\Delta = \{(S_1, E_1, I_1, Q_1, R_1, S_2, E_2, I_2, R_2) \in \Re_+^{10} : S_1 + E_1 + I_1 + Q_1 + R_1 + S_2 + E_2 + I_2 + R_2 = 1\}$ (But divided into two groups $S_1 + E_1 + I_1 + Q_1 + R_1 = 1 and S_2 + E_2 + I_2 + R_2 = 1$. Whereof can be certainly endorsed to be positively invariant with consider to the Eqs. (2). In the following, systems (2) is epidemiologically and mathematically well-positioned in Δ.

Theorem 2 *The solution of the model system (1) are feasible for all $t > 0$, if they enter the invariant region $\Sigma = \Sigma_1 \times \Sigma_2$, where $\Sigma_1 = \{(S_1, E_1, I_1, Q_1, R_1 \in \Re_+^5 : 0 < N_h(t) \leq \frac{\mu N_h}{\theta_1}\}$ As $t \to \infty$, when $\theta = \min\{\delta_1, \delta_1+\rho_1\}$ and $\Sigma_2 = \{(S_2, E_2, I_2, Q_2, R_2 \in \Re_+^5 : 0 < N_T(t) \leq \frac{CN_T}{\theta_2}\}$ As $t \to \infty$, when $\theta_2 = \min\{\delta_2+\upsilon, \delta_2+\rho_2+\upsilon\}$.*

Moreover, every solution for systems (1) with initial states in Σ residues in Σ for all $t > 0$. Therefore, the dynamics of our model will be considered in Σ.

2.2 Analysis of the model

2.2.1 Basic reproduction number

The next generation matrix approach gives the following statute for the purpose of the basic number, R_0 (Van den Driessche and Watmough 2002). The number of secondary infections produced by a typical infectious individual in a completely susceptible two group population (in Thai and in Domestic Tourists), will be used to define the all systems behaviour of the model (2) [15–19, 24–28]. R_0 can be obtained as

$$R_0 = \sqrt{R_{0T} R_{0F}} \tag{9}$$

where

$$R_{0T} = \frac{(q_{1T} + q_{2T} + \gamma_1 + \delta_1)\mu\psi_1}{\delta_1(1 + II P_1\delta_1)(q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho_1))}$$

Describing the number of Thai infections population and

$$R_{0F} = \frac{C(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)\psi_2}{(\delta_2 + \upsilon)(1 + II P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))}$$

Describing the number of foreign infections population.

Lemma 1 *To encounter the basic reproduction number for our proposed this model (2). We take the assistance of next- generation matrix model [15–23, 31–35] formulation. Initially, we define* $\eta = (E_1', I_1', Q_1', R_1', S_1')^T$ *and* $\eta_1 = (E_2', I_2', Q_2', R_2', S_2')^T$. *The model (2) is rewritten in the following form*

$$\frac{dy}{dt} = F(y) - \upsilon(y).$$

where $F(y)$ *is the non-negative matrix of new infectious (Thai and Domestic Tourists populations) and* $\upsilon(y)$ *is the non-singular matrix for the transfers between the sections in the infective equations (Thai and Domestic Tourists populations). As follows;*

$$F(y) = \begin{bmatrix} \psi_1 S_1'(t)(I_1'(t) + Q_1'(t)) \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } \upsilon(y)$$

$$= \begin{bmatrix} \left(\delta_1 + \frac{1}{II P_1}\right) E_1'(t) \\ -\frac{1}{II P_1} E_1'(t) - q_{2T} Q_1'(t) + (q_{1T} + \delta_1 + \rho_1) I_1'(t) \\ -q_{1T} I_1'(t) + (q_{2T} + \gamma_1 + \delta_1) Q_1'(t) \\ -\gamma_1 Q_1'(t) + (\delta_1 + \alpha_1) R_1'(t) \\ -\mu + \psi_1 S_1'(t)(I_1'(t) + Q_1'(t)) + \delta_1 S_1'(t) - \alpha_1 R_1'(t) \end{bmatrix}$$

in Thai.

$$F(y) = \begin{bmatrix} \psi_2 S_2'(t)(I_2'(t) + Q_2'(t)) \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } \upsilon(y) = \begin{bmatrix} \left(\frac{1}{IIP_2} + \delta_2 + \upsilon\right) E_2'(t) \\ -\frac{1}{IIP_2} E_2'(t) - q_{2f} Q_2'(t) \\ +(q_{1f} + \delta_2 + \rho_2 + \upsilon) I_2'(t) \\ -q_{1f} I_2'(t) \\ +(q_{2f} + \gamma_2 + \delta_2 + \upsilon) Q_2'(t) \\ -\gamma_2 Q_2'(t) + (\alpha_2 + \delta_2 + \upsilon) R_2'(t) \\ -C + \psi_2 S_2'(t)(I_2'(t) + Q_2'(t)) \\ +(\delta_2 + \upsilon) S_2'(t) - \alpha_2 R_2'(t) \end{bmatrix}$$

and in Domestic Tourists.

The basic reproductive number (R_0) is the threshold for the stability of the disease free equilibrium B_0. It can be calculated by $R_0 = \rho(F\upsilon^{-1})$. Where, $F\upsilon^{-1}$ is called the next generation matrix and $\rho(F\upsilon^{-1})$ is the spectral radius of the matrix $F\upsilon^{-1}$. Then we get reproduction number (R_0) where,

$$R_0 = \left(\frac{(q_{1T} + q_{2T} + \gamma_1 + \delta_1)\mu\psi_1}{\delta_1(1 + IIP_1\delta_1)(q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho_1))}\right) \cdot \left(\frac{C(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)\psi_2}{(\delta_2 + \upsilon)(1 + IIP_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))}\right) \quad (10)$$

In ordinary, the basic reproduction number R_0 of an epidemiological model can be imposed as "The anticipatory number of associated by cases occurring in an entirely vulnerable population by infected persons in general". Therefore, the R_0 value can predict whether the disease will last or disappear. As stated in all mathematical epidemiology, when $R_0 < 1$ the number of infected people decreases over time and the disease disappears. Populations converge under the augmented hypothesis. Toward a disease-free balance, there are no infected people. On the other hand, when $R_0 > 1$, the number of infected people increases. It peaks and then drops to 0 for the epidemic model or converge to endemic equilibrium for endemic models.

R_0 is the prominent eigenvalue of the matrix $R_0 = \rho(F\upsilon^{-1})$. By SEIQR model epidemic, consider a Susceptible-Exposed-Infected-Quarantined-Removed. Which the basic reproductive number, R0, has played a central role in epidemiological theory for SARS-CoV-2 because it provides an index of transmission intensity and establishes threshold criteria.

Finally, Routh–Hurwitz standard is used for setting the stabilities of the model system. If $R_0 > 1$, subsequently the endemic equilibrium is local asymptotically stable, but if $R_0 < 1$, subsequently the disease free equilibrium point is local asymptotically stable.

2.2.2 Equilibrium points

The standard method is used to analyse the model. The equilibrium points are found by setting the right-hand side of Eq. (2) equal to zero. By doing this, equilibrium points are obtained as follows [25–29]:

(A) The disease free equilibrium of the systems (2) exists and then given by

$$\phi_0(S_1, E_1, I_1, Q_1, R_1, S_2, E_2, I_2, Q_2, R_2) = \phi_0\left(\frac{\mu}{\delta_1}, 0, 0, 0, 0, \frac{C}{\delta_2+\upsilon}, 0, 0, 0, 0\right)$$

(The disease-free equilibrium is defined as the point at which no disease is present and shown as $E_1 = 0, I_1 = 0, Q_1 = 0, R_1 = 0, E_2 = 0, I_2 = 0, Q_2 = 0, R_2 = 0$.)

(B) The endemic equilibrium state of the model systems (2) contains with infection and then given by $\phi_1(S_1^*, E_1^*, Q_1^*, R_1^*, S_2^*, E_2^*, Q_2^*, R_2^*)$

$$\begin{aligned}
S_1^* &= \frac{I_1^* q_{1T}\gamma_1\alpha_1 + (q_{2T}+\gamma_1+\delta_1)(\alpha_1+\delta_1)\mu}{(\alpha_1+\delta_1)(\delta_1(q_{2T}+\gamma_1+\delta_1) + I_1^*(q_{1T}+q_{2T}+\gamma_1+\delta_1)\psi_1} \\
E_1^* &= \frac{\left(IIP_1\psi_1\left(I_1^* + \frac{I_1^* q_{1T}}{q_{2T}+\gamma_1+\delta_1}\right)\left(I_1^* q_{1T}\gamma_1\alpha_1 + (q_{2T}+\gamma_1+\delta_1)(\alpha_1+\delta_1)\mu\right)\right)}{((\alpha_1+\delta_1)(1+IIP_1\delta_1)(\delta_1(q_{2T}+\gamma_1+\delta_1) + I_1^*(q_{1T}+q_{2T}+\gamma_1+\delta_1)\psi_1))} \\
Q_1^* &= \frac{I_1^* q_{1T}}{q_{2T}+\gamma_1+\delta_1} \\
R_1^* &= \frac{I_1^* q_{1T}\gamma_1}{(q_{2T}+\gamma_1+\delta_1)(\alpha_1+\delta_1)} \\
S_2^* &= \frac{C + \frac{I_2^* q_{1f}\gamma_2\alpha_2}{(q_{2f}+\gamma_2+\delta_2+\upsilon)(\alpha_2+\delta_2+\upsilon)}}{\delta_2+\upsilon + I_2^*\left(\frac{q_{1f}}{q_{2f}+\gamma_2+\delta_2+\upsilon}\right)\psi_2} \\
E_2^* &= \frac{\left(IIP_2\psi_2\left(I_2^* + \frac{I_2^* q_{1f}}{q_{2f}+\gamma_2+\delta_2+\upsilon}\right)\left(C + \frac{I_2^* q_{1f}\gamma_2\alpha_2}{(q_{2f}+\gamma_2+\delta_2+\upsilon)(\alpha_2+\delta_2+\upsilon)}\right)\right)}{(1+IIP_2(\delta_2+\upsilon)\left(\delta_2+\upsilon + I_2^*\left(\frac{q_{1f}}{q_{2f}+\gamma_2+\delta_2+\upsilon}\right)\psi_2\right)} \\
Q_2^* &= \frac{I_2^* q_{1f}}{q_{2f}+\gamma_2+\delta_2+\upsilon} \\
R_2^* &= \frac{I_2^* q_{1f}\gamma_2}{(q_{2f}+\gamma_2+\delta_2+\upsilon)(\alpha_2+\delta_2+\upsilon)}
\end{aligned} \tag{11}$$

In the SEIQR model for SARS-CoV-2, the equilibrium points are typically identified as the points where the rates of change for each compartment (Susceptible, Exposed, Infected, Quarantined, Recovered) are equal to zero. These points represent stable states where the system remains unchanged over time. The specific equilibrium points can vary depending on the parameters and assumptions of the model being used.

2.3 Local asymptotically stability of disease—free equilibrium point

Theorem 3 *If $R_0 < 1$, then the disease free equilibrium point ϕ_0 of the model system (2) is local asymptotically stable and unstable otherwise [12–18, 26–29].*

Proof of Theorem 3 To determine the local stability of J_0, we determine the Jacobian matrix evaluated at disease free is given by

$$J_1 = \begin{vmatrix} -\delta_1 & 0 & -\psi_1 S_1'(t) & -\psi_1 S_1'(t) & \alpha_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\left(\delta_1 + \frac{1}{TIP_1}\right) & \psi_1 S_1'(t) & \psi_1 S_1'(t) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{TIP_1} & -(q_{1\gamma} + \delta_1 + \rho_1) & q_{2\gamma} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & q_{1\gamma} & -(q_{1\gamma} + \gamma_1 + \delta_1) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_1 & -(\delta_1 + \alpha_1) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\delta_2 + \upsilon) & 0 & -\psi_2 S_2'(t) & -\psi_2 S_2'(t) & \alpha_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\left(\delta_2 + \upsilon + \frac{1}{TIP_2}\right) & \psi_2 S_2'(t) & \psi_2 S_2'(t) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{TIP_2} & -(q_{1f} + \delta_2 + \rho_2 + \upsilon) & q_{2f} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & q_{1f} & -(q_{2f} + \gamma_2 + \delta_2 + \upsilon) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_2 & -(\delta_1 + \upsilon + \alpha_2) \end{vmatrix} = 0 \tag{12}$$

The eigenvalues of the J_0 are obtained by solving $Det(J_0 - \lambda I) = 0$. We obtain the characteristic equation, where λ is an eigenvalue of the matrix J_0. Therefore, root of the model system (2) i.e., eigenvalue of the matrix J_0 are

$$\begin{aligned}(\lambda + \delta_2 + \upsilon + \alpha_2)(\lambda + \delta_1 + \alpha_1)(\lambda + \delta_1)(\lambda^7 + A_1\lambda^6 \\ + A_2\lambda^5 + A_3\lambda^4 + A_4\lambda^3 + A_5\lambda^2 + A_6\lambda + A_7) = 0\end{aligned} \tag{13}$$

The third of tenth eigenvalues of (13) are $\lambda_1 = -\delta_2 - \upsilon - \alpha_2$, $\lambda_2 = -\delta_1 - \alpha_1$ and $\lambda_3 = -\delta_1$, which has negative real part. The seven eigenvalues, we check the stability of disease free equilibrium state by using the Routh–Hurwitz criteria required for all of the eigenvalues defined by (12) are negative real parts and the coefficients must satisfy all conditions, when A_1, A_2, A_3, A_4, A_5, A_6, $A_7 > 0$.This display for $R_0 < 1$, disease free equilibrium will be stable as is seen in Fig. 1.

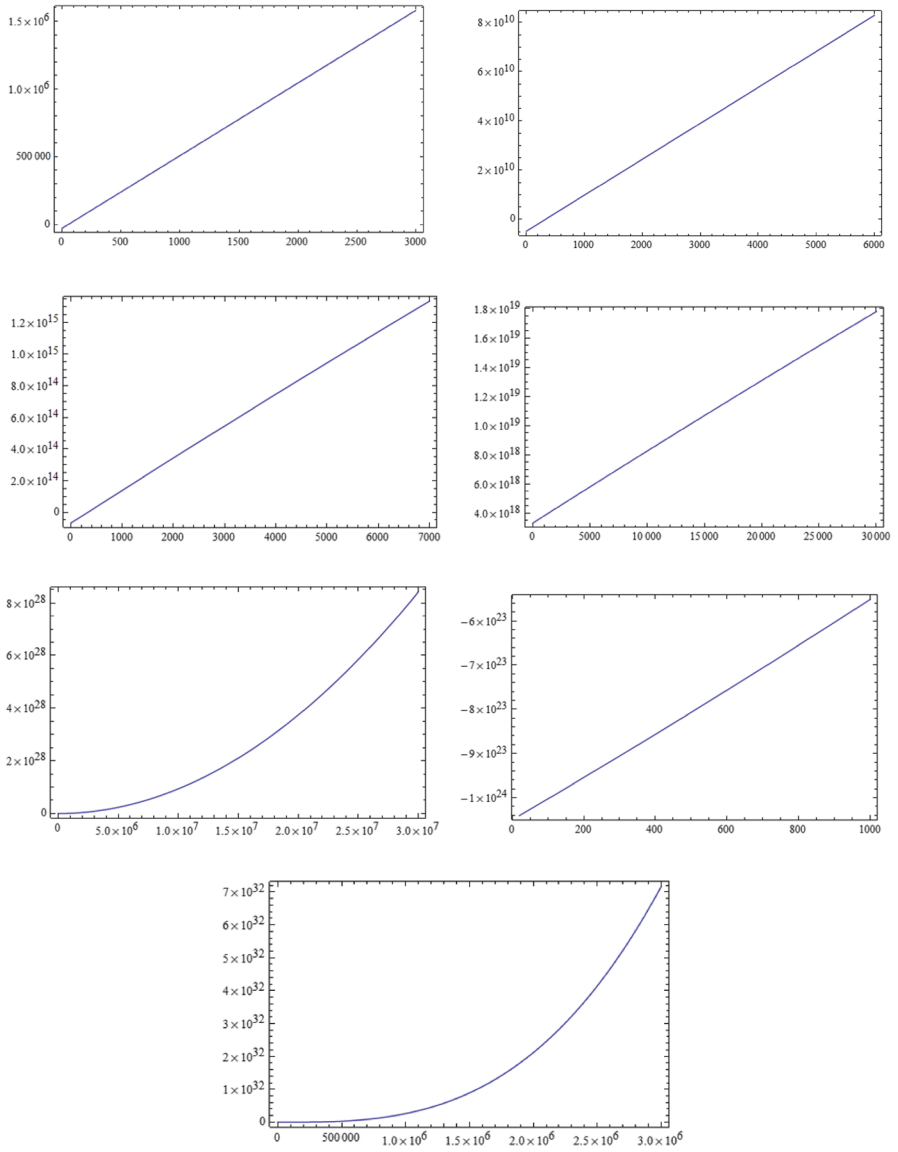

Fig. 1 The parameter spaces for disease free equilibrium state which satisfies the Routh–Hurwitz criteria with the value of parameters: respectively, for with $(\lambda^7 + A_1\lambda^6 + A_2\lambda^5 + A_3\lambda^4 + A_4\lambda^3 + A_5\lambda^2 + A_6\lambda + A_7) = 0$

In the SEIQR model, the disease-free equilibrium point is characterized by all compartments except for the susceptible compartment being empty. This means that there are no individuals in the Exposed, Infected, Quarantined, or Recovered compartments, and the disease is not present in the population. At this equilibrium point, the transmission of the disease has been effectively halted, and the population is considered disease-free.

For the disease-free equilibrium point in the SEIQR model to be locally sub clinically stable, the basic reproduction number (R_0) must be less than 1. The basic reproduction number is a measure of the average number of secondary infections produced by a single infected individual in a completely susceptible population, it indicates that the disease is not able to sustain itself in the population, leading to the disease-free equilibrium point being locally sub clinically stable. This means that small perturbations around the disease-free equilibrium point will not lead to an outbreak of the disease.

2.4 Local asymptotically stability of disease endemic equilibrium point

Theorem 4 *If $R_0 > 1$, then the endemic equilibrium point ϕ_1 of the model system (2) is local asymptotically stable and unstable otherwise [12–18, 26–29].*

Proof of Theorem 4 The Jacobian matrix of the Eqs. (2) at

$$J_0 = \begin{vmatrix} -\delta_1 & 0 & -\psi_1 S_1'(t) & -\psi_1 S_1'(t) & \alpha_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\left(\delta_1 + \frac{1}{IIP_1}\right) & \psi_1 S_1'(t) & \psi_1 S_1'(t) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{IIP_1} & -(q_{1\gamma} + \delta_1 + \rho_1) & q_{2\gamma} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & q_{1\gamma} & -(q_{2\gamma} + \gamma_1 + \delta_1) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma_1 & -(\delta_1 + \alpha_1) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\delta_2 + \upsilon) & 0 & -\psi_2 S_2'(t) & -\psi_2 S_2'(t) & \alpha_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\left(\delta_2 + \upsilon + \frac{1}{IIP_2}\right) & \psi_2 S_2'(t) & \psi_2 S_2'(t) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{IIP_2} & -(q_{1f} + \delta_2 + \rho_2 + \upsilon) & q_{2f} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & q_{1f} & -(q_{2f} + \gamma_2 + \delta_2 + \upsilon) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_2 & -(\delta_1 + \upsilon + \alpha_2) \end{vmatrix} = 0 \tag{14}$$

The endemic equilibrium point (ϕ_1) exists and is positive, if $R_0 > 1$. The eigenvalues of J_1 are obtained by solving $Det(J_1 - \lambda I) = 0$. The characteristic equation is as follows:

$$\begin{aligned} &(g_{11}g_8q_{1f}\gamma_2\alpha_2 + (-g_{15} - \lambda)(-q_{1f}(g_{11}g_{12}g_9 + g_{10}g_8q_{2f} + g_{10}g_9q_{2f} + g_{11}g_{12}\lambda + g_{10}q_{2f}\lambda \\ &+ g_8q_{2f}\lambda + g_9q_{2f}\lambda + q_{2f}\lambda^2) + (-g_{14} - \lambda)(-g_{11}(-g_{12}g_9 - g_{12}\lambda) + (-g_{13} - \lambda)(g_{10}g_8 + g_{10}g_9 \\ &+ g_{10}\lambda + g_8\lambda + g_9\lambda + \lambda^2))))(g_1g_4q_{1T}\gamma_1\alpha_1 + (-g_7 - \lambda)(-q_{1T}(g_1g_2q_{2T} + g_3g_4\delta_1 + g_2q_{2T}\delta_1 \\ &+ g_3g_4\lambda + g_1q_{2T}\lambda + g_2q_{2T}\lambda + q_{2T}\delta_1\lambda + q_{2T}\lambda^2) + (-g_6 - \lambda)(-g_4(-g_3\delta_1 - g_3\lambda) \\ &+ (-g_5 - \lambda)(g_1g_2 + g_2\delta_1 + g_1\lambda + g_2\lambda + \delta_1\lambda + \lambda^2)))) = 0 \end{aligned} \tag{15}$$

where.

$g_1 = \psi_1(I_1^* + Q_1^*)$, $g_2 = \frac{1}{IIP_1} + \delta_1$, $g_3 = \psi_1 * S_1^*$, $g_4 = \frac{1}{IIP_1}$, $g_5 = q_{1T} + \delta_1 + \rho_1$, $g_6 = q_{2T} + \gamma_1 + \delta_1$, $g_7 = \delta_1 + \alpha_1$, $g_8 = \psi_2(I_2^* + Q_2^*)$, $g_9 = \delta_2 + \upsilon$, $g_{10} = \frac{1}{IIP_2} - g_9$,

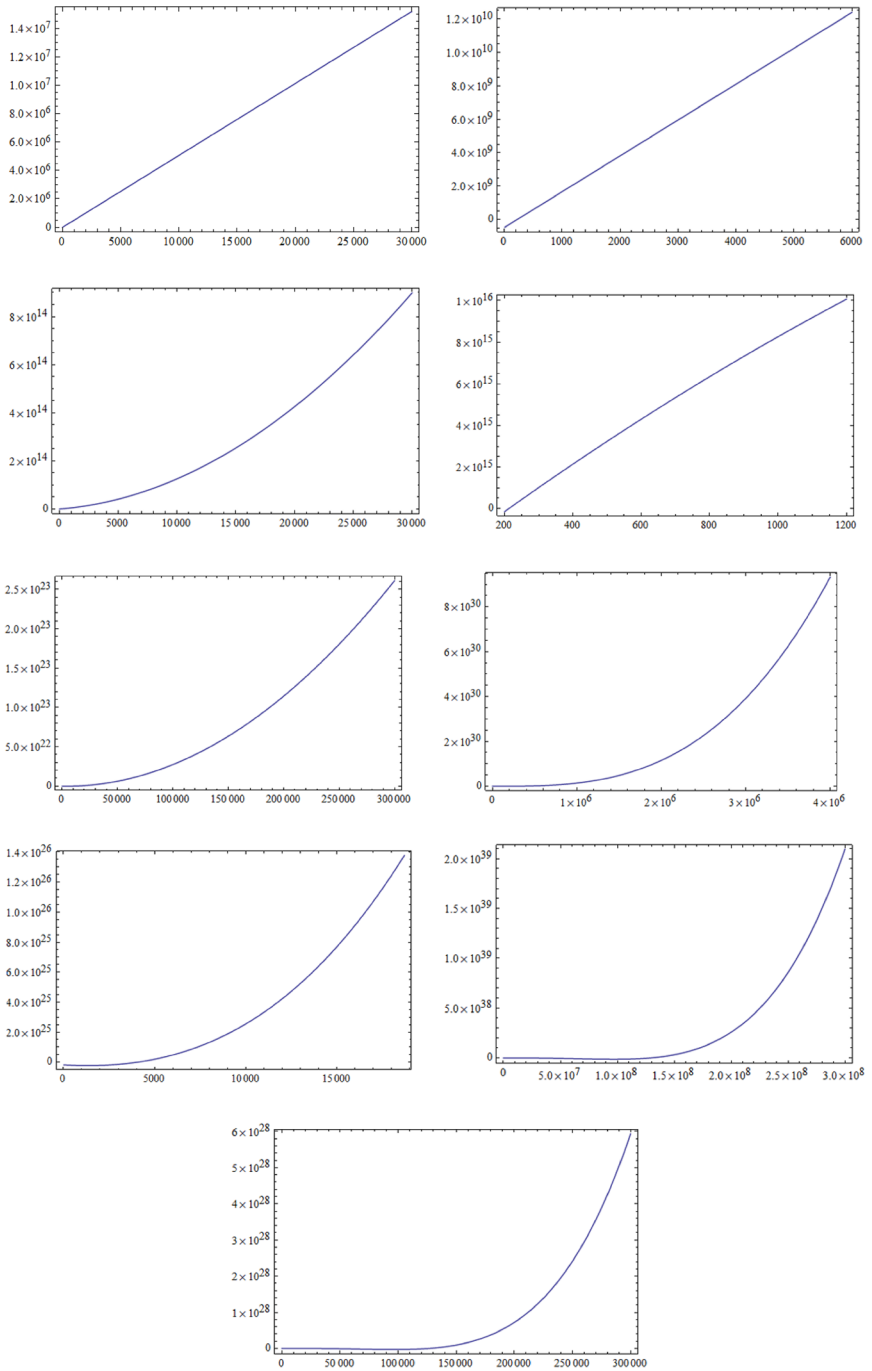

Fig. 2 The parameter spaces for endemic equilibrium point which satisfies the Routh–Hurwitz criteria with the value of parameters: respectively, for with $\lambda^{10} + W_1\lambda^9 + W_2\lambda^8 + W_3\lambda^7 + W_4\lambda^6 + W_5\lambda^5 + W_6\lambda^4 + W_7\lambda^3 + W_8\lambda^2 + W_9\lambda^1 + W_{10} = 0$

$g_{11} = \frac{1}{IIP_2}$, $g_{12} = \psi_2 * S_2^*$, $\frac{1}{IIP_2}$, $g_{13} = q_{1f} + \delta_2 + \rho_2 + \upsilon$, $g_{14} = q_{2f} + \gamma_2 + \delta_2 + \upsilon$, $g_{15} = \delta_2 + \upsilon + \alpha_2$.

We obtain the characteristic equation.

$\lambda^{10} + W_1\lambda^9 + W_2\lambda^8 + W_3\lambda^7 + W_4\lambda^6 + W_5\lambda^5 + W_6\lambda^4 + W_7\lambda^3 + W_8\lambda^2 + W_9\lambda^1 + W_{10} = 0$. Where λ is an eigenvalue of the matrix J_1. To determine the local stability of the endemic equilibrium state, we check the stability of endemic equilibrium state by using the Routh–Hurwitz criteria required for all of the eigenvalues defined by (14) are negative real parts and the coefficients must satisfy all condition, when W_1, W_2, W_3, W_4, W_5, W_6, W_7, W_8, W_9, $W_{10} > 0$. When this display for $R_0 > 1$, endemic equilibrium point will be stable as is seen in Fig. 2.

In the SEIQR model, the endemic equilibrium point is characterized by a stable state where the disease persists in the population at a constant level over time. At this equilibrium point, all compartments (Susceptible, Exposed, Infected, Quarantined, and Recovered) have non-zero values, indicating that the disease is circulating within the population. The endemic equilibrium point represents a balance between the transmission of the disease and the recovery or removal of individuals from the infected compartments, leading to a steady state of disease prevalence.

For the endemic equilibrium point in the SEIQR model to be locally subclinically stable, the basic reproduction number (R_0) must be greater than 1. The basic reproduction number is a measure of the average number of secondary infections produced by a single infected individual in a completely susceptible population. When R0 is greater than 1, it indicates that the disease is able to sustain itself in the population, leading to the endemic equilibrium point being locally sub clinically stable. This means that small perturbations around the endemic equilibrium point will not lead to the extinction of the disease, and the disease prevalence will remain constant over time.

3 Numerical results

In this study, we show the numerical simulations of the impacts of the system control strategies on COVID-19 transmission. The parameter and values used in the numerical solution are shown in Table 2. Data and collected form the official website of the Ministry of Public Health and World Health Organization (WHO) [1–6, 18–31].

Table 2 Values of the parameter of the model system (2) on COVID-19 transmission

Parameter	Description	Value/range (units)	References
δ_1	Natural death rate of Thai humans	0.057	[2, 9, 16]
δ_2	Natural death rate of domestic tourists humans	0.087	[1, 9–11]
α_1	Per capita rate of loss of immunity in Thai humans	0.017	Assumed
α_2	Per capita rate of loss of immunity in domestic tourists humans	0.008	Assumed
IIP_1	Per capita rate of progression of Thai human from the exposed state to the infectious state	0.056	Assumed
IIP_2	Per capita rate of progression of domestic tourists human from the exposed state to the infectious state	0.34	Assumed
q_{1T}	Rate at which infected Thai human changed to quarantine Thai human	0.0006	Assumed
q_{2T}	Rate at which infected Thai human changed to quarantine Thai human	0.000078	Assumed
q_{1f}	Rate at which infected domestic tourists human changed to quarantine domestic tourists human	0.0075	Assumed
q_{2f}	Rate at which quarantine domestic tourists human changed to infected domestic tourists human	0.095	Assumed
γ_1	Per capita recovery rate for humans in Thai from the infectious state to the recovered state	0.0078	Assumed
γ_2	Per capita recovery rate for humans in domestic tourists from the infectious state to the recovered state	0.050	Assumed
ρ_1	Death rate due to Covid-19 of Thai human	0.0054	[1, 2, 9, 16]
ρ_2	Death rate due to Covid-19 of domestic tourists human	0.083	[1, 9–11]
ψ_1	Transmission rate of virus between human in Thai human	0.74	Assumed
ψ_2	Transmission rate of virus between human in domestic tourists human	0.45	Assumed
υ	Rate at which domestic tourists humans move out the country	0.0089	[1, 9–11]

To determine the local asymptomatic stability of the disease-free equilibrium point in the SEIQR model, one common method is to analyze the eigenvalues of the jacobian matrix evaluated at the disease-free equilibrium point. The jacobian matrix arrest the differential equations dynamics of a system around the equilibrium point and provides information about the system's stability. Especially, the stability of disease-free equilibrium can be assessed by calculating the eigenvalues of the jacobian matrix. If all eigenvalues have negative real parts the equilibrium point is asymptotically stable. This indicates that small perturbations around the disease-free equilibrium point will not cause disease outbreaks. Jacobian matrix eigenvalue analysis is an important method used in mathematical epidemiology to determine the stability properties of the equilibrium point in partition models such as the SEIQR model.

To determine the local asymptomatic stability of the endemic equilibrium point in the SEIQR model, methods such as linear stability analysis are often used and calculation of jacobian matrices. Linear stability analysis involves linearizing a system of differential equations around a local equilibrium point and analysis of the eigenvalues of the resulting jacobian matrix. The eigenvalues provide information about the stability of the equilibrium point. The negative real part indicates stability, and a positive real part indicates instability. The jacobian matrix is a matrix of partial derivatives that describes how small changes in individual parts affect the rate of change of the parts in the system by estimating the eigenvalues of the jacobian matrix at the local equilibrium point. The researchers were able to determine that the equilibrium point is asymptotically stable.

3.1 Sensitivity analysis

To determine dependencies between inputs parameter affect the transmission and spread of the COVID-19 disease and results of the model. The sensitivity analysis of the model system (2) is taken out in the realize of [28–33].

Definition 1 The normalized forward sensitivity index of the variable (φ), that depend differential on a parameter, ζ is defined as:

$$E_{\delta}^{\varphi} = \frac{\partial \varpi}{\partial \delta} x \frac{\delta}{\varpi}$$

The apparent expression of R_0 is given follow:

$$\begin{aligned} R_0 = (((&C(q_{1T} + q_{2T} + \gamma_1 + \delta_1) \\ &.\mu(q_{2f} + q_{1f} + \gamma_2 + \delta_2 + \upsilon)\psi_1\psi_2))/((\delta_1(1 + IIP_1\delta_1)(\delta_2 + \upsilon) \\ &(1 + IIP_2(\delta_2 + \upsilon))(q_{1T}(\gamma_1 + \delta_1) \\ &+ (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho_1))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\ &+ (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))) \end{aligned} .$$

In particular, sensitivity indices of the basic reproduction number (R_0), with respect to the system model depends on the nineteenth parameter are computed as below.

$$
\begin{aligned}
\Psi_{\delta_1}^{R_0} &= \left(\frac{\partial R_0}{\partial \delta_1}\right)\left(\frac{\delta_1}{R_0}\right) \\
&= (q_{1T}^2(\gamma_1 + 2IIP_1\gamma_1\delta_1 + \delta_1(2 + 3IIP_1\delta_1)) \\
&\quad + (q_{2T} + \gamma_1 + \delta_1)^2(\rho_1 + \delta_1(2 + 3IIP_1\delta_1 + 2IIP_1\rho_1)) \\
&\quad + q_{1T}((\gamma_1 + 2IIP_1\gamma_1\delta_1 + \delta_1(2 + 3IIP_1\delta_1))(\gamma_1 + 2\delta_1 + \rho_1) \\
&\quad + q_{2T}(\gamma_1 + 2IIP_1\delta_1 + \rho_1 + 2\delta_1(2 + 3IIP_1\delta_1 + IIP_1\rho_1)))) \\
&\quad /((q_{1T} + q_{2T} + \gamma_1 + \delta_1)(1 + IIP_1\delta_1)(q_{1T}(\gamma_1 + \delta_1) \\
&\quad + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho))) \\
\Psi_{\alpha_1}^{R_0} &= \left(\frac{\partial R_0}{\partial \alpha_1}\right)\left(\frac{\alpha_1}{R_0}\right) = 0 \\
\Psi_{IIP_1}^{R_0} &= \left(\frac{\partial R_0}{\partial IIP_1}\right)\left(\frac{IIP_1}{R_0}\right) = -1 + \frac{1}{1 + IIP_1\delta_1} \\
\Psi_{q_{1T}}^{R_0} &= \left(\frac{\partial R_0}{\partial q_{1T}}\right)\left(\frac{q_{1T}}{R_0}\right) \\
&= \frac{q_{1T}(q_{2T} + \gamma_1 + \delta_1)(\gamma_1 - \rho)}{(q_{1T} + q_{2T} + \gamma_1 + \delta_1)(q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho))} \\
\Psi_{q_{2T}}^{R_0} &= \left(\frac{\partial R_0}{\partial q_{2T}}\right)\left(\frac{q_{2T}}{R_0}\right) \\
&= \frac{q_{1T}q_{2T}(\gamma_1 - \rho)}{(q_{1T} + q_{2T} + \gamma_1 + \delta_1)(q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho))} \\
\Psi_{\gamma_1}^{R_0} &= \left(\frac{\partial R_0}{\partial \gamma_1}\right)\left(\frac{\gamma_1}{R_0}\right) \\
&= \frac{q_{1T}\gamma_1(q_{1T} + q_{2T} + \delta_1 + \rho)}{(q_{1T} + q_{2T} + \gamma_1 + \delta_1)(q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho))} \\
\Psi_{\rho}^{R_0} &= \left(\frac{\partial R_0}{\partial \rho}\right)\left(\frac{\rho}{R_0}\right) = \frac{(\gamma_1 + q_{2T} + \delta_1)\rho}{q_{1T}(\gamma_1 + \delta_1) + (q_{2T} + \gamma_1 + \delta_1)(\delta_1 + \rho)} \\
\Psi_{\psi_1}^{R_0} &= \left(\frac{\partial R_0}{\partial \psi_1}\right)\left(\frac{\psi_1}{R_0}\right) = 1 \\
\Psi_{\mu}^{R_0} &= \left(\frac{\partial R_0}{\partial \mu}\right)\left(\frac{\mu}{R_0}\right) = 1 \\
\Psi_{\delta_2}^{R_0} &= \left(\frac{\partial R_0}{\partial \delta_2}\right)\left(\frac{\delta_2}{R_0}\right) \\
&= (\delta_2(-(\delta_2 + \upsilon)(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon) \\
&\quad (1 + IIP_2(\delta_2 + \upsilon))(q_{1f} + q_{2f} + \gamma_2 + 2(\delta_2 + \upsilon) + \rho_2) \\
&\quad - IIP_2(\delta_2 + \upsilon)(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon) \\
&\quad (q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)) \\
&\quad + (\delta_2 + \upsilon)(1 + IIP_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon))
\end{aligned}
$$

$$
\begin{aligned}
&- (q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(1 + III P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&+ (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))))/((\delta_2 + \upsilon)(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon) \\
&(1 + III P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&+ (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2)))
\end{aligned}
$$

$$\Psi_{\alpha_2}^{R_0} = \left(\frac{\partial R_0}{\partial \alpha_2}\right)\left(\frac{\alpha_2}{R_0}\right) = 0$$

$$
\begin{aligned}
\Psi_{III P_2}^{R_0} &= \left(\frac{\partial R_0}{\partial III P_2}\right)\left(\frac{III P_2}{R_0}\right) \\
&= -1 + \frac{1}{1 + III P_2(\delta_2 + \upsilon)}
\end{aligned}
$$

$$
\begin{aligned}
\Psi_{q_{1f}}^{R_0} &= \left(\frac{\partial R_0}{\partial q_{1f}}\right)\left(\frac{q_{1f}}{R_0}\right) \\
&= \frac{q_{1f}(q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\gamma_2 - \rho_2)}{(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))}
\end{aligned}
$$

$$
\begin{aligned}
\Psi_{q_{2f}}^{R_0} &= \left(\frac{\partial R_0}{\partial q_{2f}}\right)\left(\frac{q_{2f}}{R_0}\right) \\
&= \frac{q_{1f} q_{2f}(\gamma_2 - \rho_2)}{(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))}
\end{aligned}
$$

$$
\begin{aligned}
\Psi_{\gamma_2}^{R_0} &= \left(\frac{\partial R_0}{\partial \gamma_2}\right)\left(\frac{\gamma_2}{R_0}\right) \\
&= \frac{q_{1f}\gamma_2(q_{1f} + q_{2f} + \delta_2 + \upsilon + \rho_2)}{(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))}
\end{aligned}
$$

$$\Psi_{\rho_2}^{R_0} = \left(\frac{\partial R_0}{\partial \rho_2}\right)\left(\frac{\rho_2}{R_0}\right) = \frac{(q_{2f} + \gamma_2 + \delta_2 + \upsilon)\rho_2}{q_{1f}(\gamma_2 + \delta_2 + \upsilon) + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2)}$$

$$\Psi_{C}^{R_0} = \left(\frac{\partial R_0}{\partial C}\right)\left(\frac{C}{R_0}\right) = 1$$

$$\Psi_{\psi 2}^{R_0} = \left(\frac{\partial R_0}{\partial \psi_2}\right)\left(\frac{\psi_2}{R_0}\right) = 1$$

$$
\begin{aligned}
\Psi_{\upsilon}^{R_0} &= \left(\frac{\partial R_0}{\partial \upsilon}\right)\left(\frac{\upsilon}{R_0}\right) \\
&= (\upsilon(-(\delta_2 + \upsilon)(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(1 + III P_2(\delta_2 + \upsilon))(q_{1f} + q_{2f} + \gamma_2 + 2(\delta_2 + \upsilon) + \rho_2) \\
&\quad - III P_2(\delta_2 + \upsilon)(q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&\quad + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2)) + (\delta_2 + \upsilon)(1 + III P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&\quad + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2)) \\
&\quad - (q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon)(1 + III P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&\quad + (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2))))/((\delta_2 + \upsilon)((q_{1f} + q_{2f} + \gamma_2 + \delta_2 + \upsilon) \\
&\quad (1 + III P_2(\delta_2 + \upsilon))(q_{1f}(\gamma_2 + \delta_2 + \upsilon) \\
&\quad (q_{2f} + \gamma_2 + \delta_2 + \upsilon)(\delta_2 + \upsilon + \rho_2)))
\end{aligned}
$$

The parameters affect the effort to curtail the disease among the tourists, according to the sensitivity analysis are the parameter that have positive sign, i.e. $III P_1$, q_{1T}, q_{2T}, μ, ψ_1, $III P_2$, q_{1f}, q_{2f}, C and ψ_2 have a positive effect on R_0. We can estimate the sensitivity indices (S.I) of the basic reproduction number (R_0), with the respect to the parameter of the system model (2). The signs of S.I. are shows in the Table 3.

Table 3 The sensitivity index (S.I)

Parameter	S.I	Parameter	S.I
δ_1	Negative	δ_2	Negative
α_1	Negative	α_2	Negative
IIP_1	Positive	IIP_2	Positive
q_{1T}	Positive	q_{1f}	Positive
q_{2T}	Positive	q_{2f}	Positive
γ_1	Negative	υ	Negative
ρ	Negative	γ_2	Negative
μ	Positive	ρ_2	Negative
ψ_1	Positive	C	Positive
		ψ_2	Positive

The sensitivity indices (S.I) of the parameter that have positive sign, i.e. IIP_1, q_{1T}, q_{2T}, μ, ψ_1, IIP_2, q_{1f}, q_{2f}, C and ψ_2 have a positive effect on R_0. It determine that the increase in the number of two exposed human (E_1, E_2) and two infectious host human (I_1, I_2) with the value IIP_1, q_{1T}, q_{2T}, IIP_2, q_{1f}, q_{2f} may lead to an outbreak. On the other hand, the negative sign of the sensitivity indices (S.I) in the R_0 i.e. δ_1, α_1, γ_1, ρ, δ_2, α_2, υ, γ_2 and ρ_2 have a negative effect to the endemic of disease of system model (2). Thus, sensitivity indices (S.I) of the COVID-19 (2) supply a very good depth into the transmission the system of the disease. In particular, it helps the public health potentate in focusing on a reasonable interference strategy for preventing and controlling the spread of the disease. The purpose of conducting a sensitivity analysis in the context of the COVID-19 model, provide a suitable approach to reduce the number of infected people by identifying several factors that affect virus transmission and prevalence. This is determined by calculating the sensitivity index for each parameter of the model. It is related to basic reproductive values. Therefore, this index is used to identify parameters that influence basic reproductive costs in the COVID-19 epidemic and can also be used to design mitigation strategies to slow the spread of the disease by reducing reproductive costs. Basic, it also helps determine the level of change for incoming parameters to predict the desired parameters.

3.2 Parameter estimation, model inspection and prognosis

The nonlinear mathematic model in (1) can be solved using the numerical methods and we can observe the dynamics of the model. By means with respect to numerically solve the data we estimated the parameters first [1–4, 9–15, 24].

3.2.1 Case 1: Thailand population

The estimated model parameters and their sensitivity indices are given in Tables 2 and 3. To checking the model, we respect the real case of COVID-19 infection of Thailand. The values that affect the change of the model are as follows: q_{1T} (rate at

which infected Thai human change to become quarantine Thai human) and q_{2T} (rate at which infected Thai human changed to become quarantine Thai human). As for the other values of the model, they will have a decreasing effect on the duration of the COVID-19 epidemic, which is based on the spread for the patient's individual immunity, environment and surveillance of disease incidence in Thailand. Group I_1 (Infectious means showing symptoms of illness and can spread the disease). Both groups are prevalence of the COVID-19 pandemic and group Q_1 (dedicated to the quarantined population (hospitalized or isolated from the general population)).

3.2.2 Case 2: domestic tourists population

In this section, we are of broad interest to consider all countries and territories in the world for broad application and study our proposed model. Using parameters from Tables 2 and 3 with initial conditions. The system of equations can be solved by Runge—Kutta 4th order method of the model in Eq. (1), then graphs are generated to analyse the population dynamics affecting infection, exposure, and patient recovery. to understand the widespread outbreak. Therefore, we have the condition $1 = \mathrm{S} + \mathrm{E} + \mathrm{I} + \mathrm{Q} + \mathrm{R}$ is the population in each group. From Fig. 4, it can be seen that the virus COVID-19 spreads rapidly over time, thus affecting the increase in the number of infected people in the population. making it impossible to control the situation of the spread of COVID-19 By considering the parameters that cause the change of the dynamic system, namely q_{1f} (rate at which infected Domestic Tourists human changed to become quarantine Domestic Tourists human) and q_{2f} (rate at which quarantine Domestic Tourists human changed to become infected Domestic Tourists human). Group I_2 (Infectious means showing symptoms of illness and can spread the disease). Both groups are prevalence of the COVID-19 pandemic and group Q_2 (dedicated to the quarantined population (hospitalized or isolated from the general population)).

After that, numerical analysis revealed that the weak population was decreasing over time. But the number of people infected increases over time, which can lead to outbreaks in a short time and quickly. Using the parameters in Table 2, we can determine the base reproductive value $R_0 > 1$. Meaning that the COVID-19 outbreak is still occurring due to the effects of both parameters and other values, which is a factor in the spread of disease [18–25].

4 Conclusion and discussion

In this study, we have used the SEIQR mathematical model for the transmission dynamics of COVID-19 infection by dividing the spread among Thailand and Domestic Tourists (who are susceptible to the disease). By examining the impact of the factors that cause the change of the COVID-19 epidemic. We have analysed the basic reproductive number and we find that our model has a stable infection-free equilibrium when the basic reproduction number is less than one. The model indicated an existence of multiple endemic equilibrium. In epidemiological, the implication is always less than unity [16–28, 32–35].

The outbreak of the Covid-19 virus from the first outbreak in China and then spreading around the world leading to the suspension of both domestic and international commercial flights. Border crossing and emergency declaration to control the spread of COVID-19 by having every sector have measures to support the spread, such as social distancing, hygiene, a stay-at-home campaign to stop the spread of the virus, work from home, social responsibility as well as controlling the movement of citizens and close service establishments that are crowded with users or activities that cause contact and spread various diseases. Especially, tourist attractions, Department stores, amusement parks, entertainment venues, etc. With the fear of people around the world over the spread of the virus, the behaviour of people both in Thailand and abroad has changed. There have been changes in a short period of time. It has had a severe impact on the sudden disruption of tourism, both Thailand and the world refrain from traveling across countries. Suspension of both domestic and international flights. As a result, tourism came to a sudden halt. From the measures to refrain from traveling both domestically and internationally. Suspension of flights on all airlines, Cancellation of travel program. As a result, hotels, accommodations, restaurants, and various tourist attractions will lose income, including tourism businesses related to the production chain that will be affected by the shutdown of business. Continuously affecting the economy and government revenue collection. When examining the impact of Thailand populations and Domestic Tourists' populations, by considering for the dynamic of the COVID-19 epidemic. We used a mathematical model (1), a set of parameters derived from other recently published articles. This, while other parameters were assumed under epidemiology as listed in Table 2. Since, the researchers did not go to the data collections, then the assumed initial data were used in the model simulations basing on the actual environment of Thai and Domestic Tourists people in the health care in the of the transmission dynamics of COVID-19. From Figs. 1 and 2, show that the parameters in disease free equilibrium state and epidemic equilibrium point which satisfies the Routh – Hurwitz criteria with the value of parameters, see Figs. 3 and 4, show that numerical simulations of each human population for the disease-free state, we will see that the solutions converge to the disease free state and the disease state, we will see that the solutions converge to the endemic disease state. And Fig. 5, show that, the numerical projected onto the 2D and planes when there is no vertical transmission and equilibrium state the endemic state respectively [27–35]. Mathematical modelling plays as an important role in every field of epidemiology. This is because it helps explain the scope of the disease under consideration mathematical modelling, they help policy makers and public health planners in a variety of other ways. Models are used to formulate hypotheses and design experiments to test them. Interpret results Diagnosis based on observable symptoms and signs. It is a guideline for decision making and test results, etc. The model uses the results of numerical analysis to check the stability of the variables that affect the spread of the disease. To find an approximate answer to the equation that has been defined. Numerical analysis is a reliable method used to consider systems of equations for solving problems compared to standard techniques. Numerical analysis also helps to observe COVID-19 changes in the long run through the estimation of such models.

Sensitivity analysis of the basic reproductive number was performed to either of the parameters to define which parameter is more sensitive to dynamics systems than

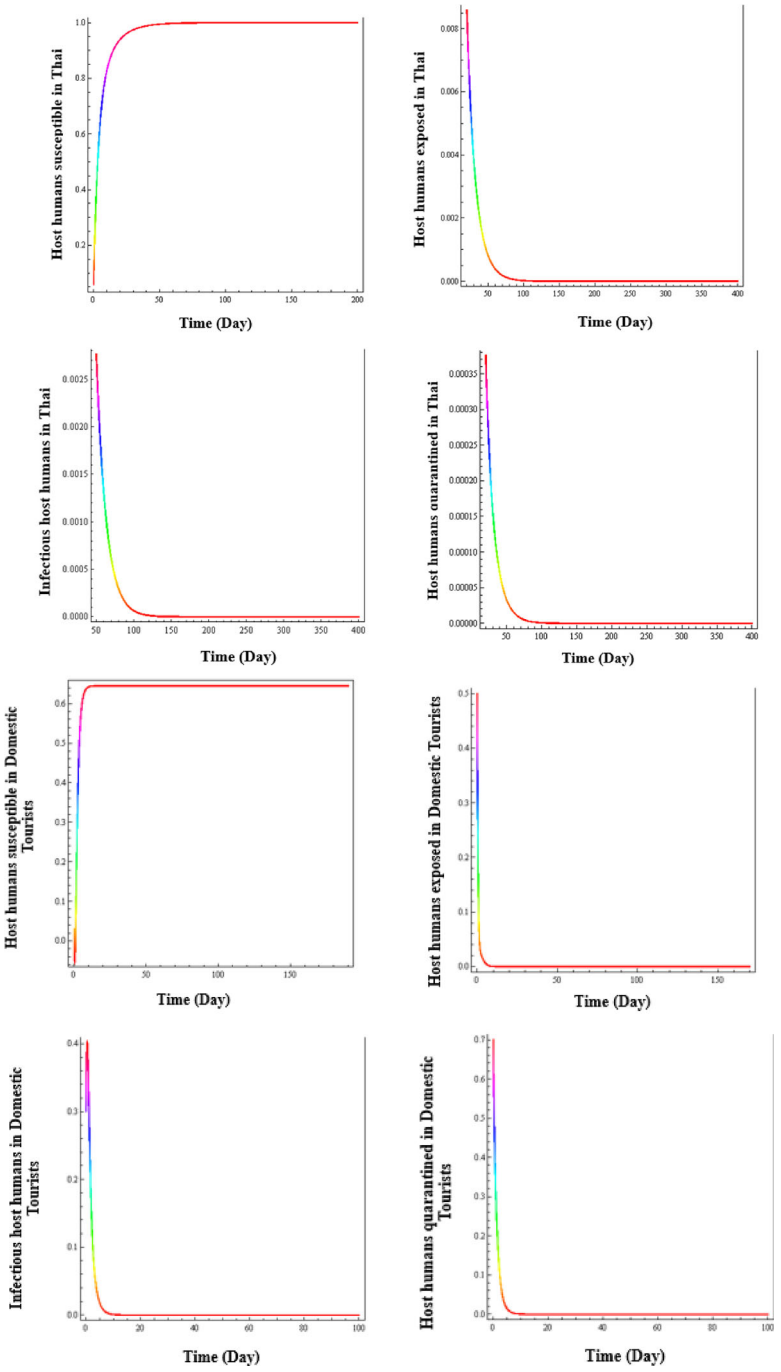

Fig. 3 Numerical simulations of each human population for the disease free state

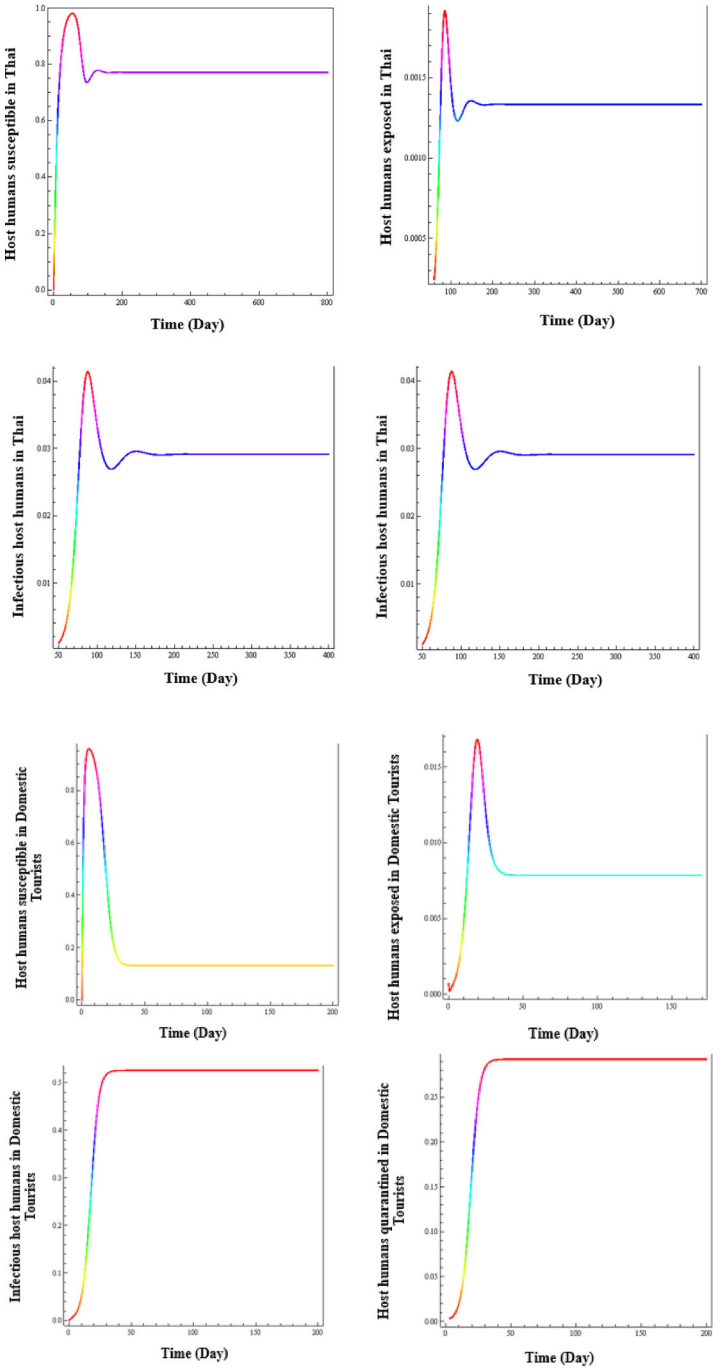

Fig. 4 Numerical simulations of each human population for the disease state

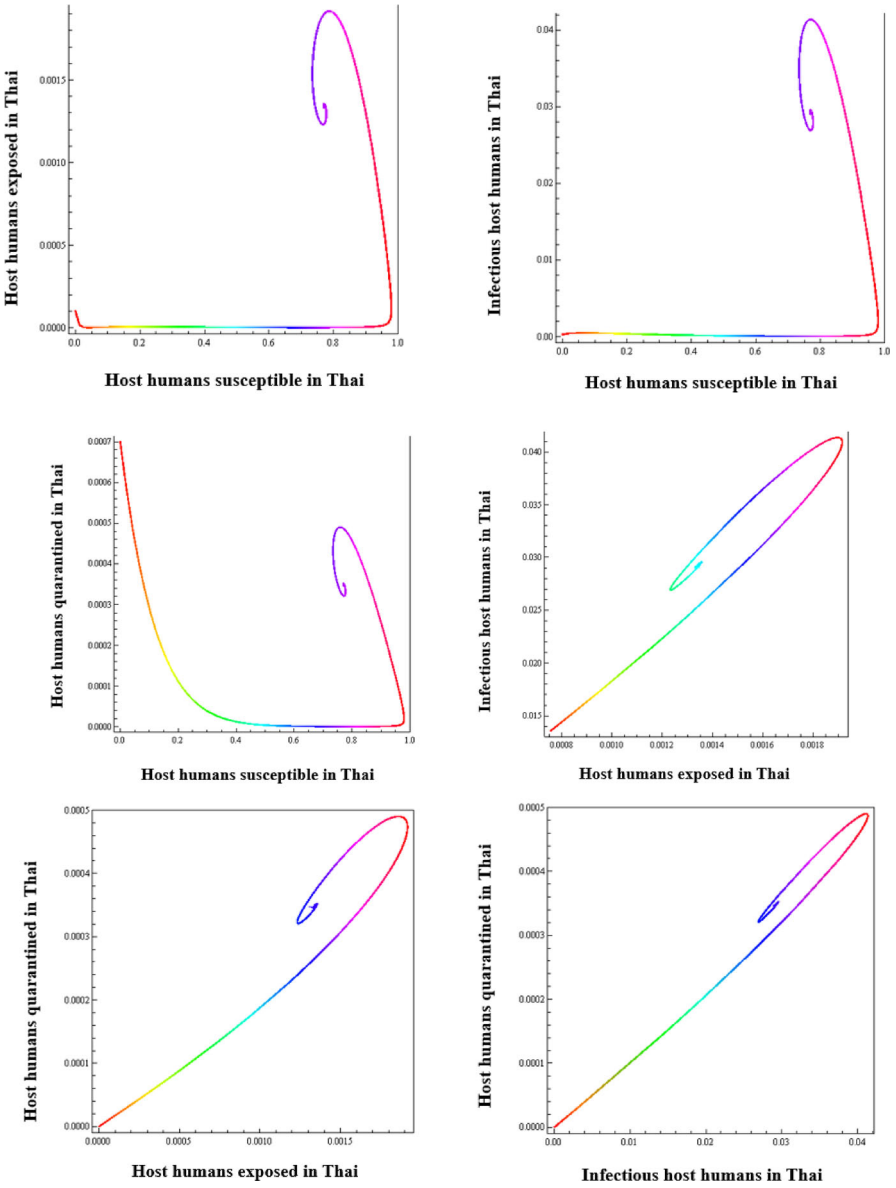

Fig. 5 The trajectories of the numerical projected onto the 2D (S_1, E_1), (S_1, I_1), (S_1, Q_1), (E_1, I_1), (E_1, Q_1), (I_1, Q_1), (S_2, E_2), (S_2, I_2), (E_2, I_2) and (E_2, Q_2) planes when there is no vertical transmission and equilibrium state the endemic state

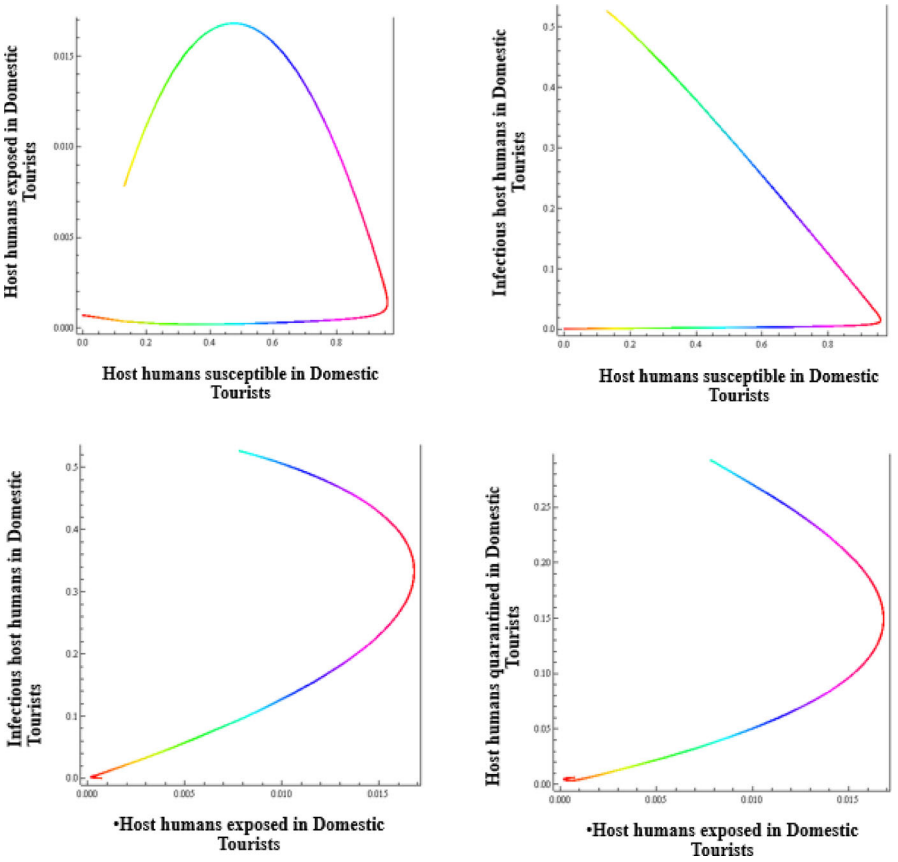

Fig. 5 continued

the other. Our analysis shows that the rate of recovery rate for Thailand and Domestic Tourists will decrease with recruitment rates and death rates. This results in an increasing the human recovery rate for Thailand and Domestic Tourists with recruitment rates and death rates would decrease the basic reproductive number. However, $III P_1$ (capita rate of progression of Thai human from the exposed state to the infectious state), $III P_2$ (capita rate of progression of Domestic Tourists human from the exposed state to the infectious state), q_{1T} (rate at which infected Thai human changed to quarantine Thai human), q_{2T} (rate at which infected Thai human changed quarantine Thai human), q_{1f} (rate at which infected Thai human changed to quarantine Thai human), q_{2f} (rate at which quarantine Domestic Tourists human changed infected foreign human), ψ_1 (transmission rate of virus between human in Thai human), ψ_2 (transmission rate of virus between human in Domestic Tourists human), μ (recruitment term of the susceptible human in Thai) and C (recruitment term of the susceptible human in Domestic Tourists) will affect the number of basic reproductive number will increase according to Table 3 [29–35]. Then, we can control significantly the number of new confirmed

cases, new infectious and thus can reduce the transmission risk. Form all the three control strategies considered in this study, we realized that the strategy which captures all the dependent control of the environment and factors affecting the epidemic yields better results. The results of the study, which parameters in the COVID-19 model affect the outbreak and control the spread of the disease. This result can be used as a strategy for creating disease control measures.

The basic reproductive value (R_0) plays an important role in determining the spread of SARS-CoV-2 in a closed system. R_0 represents the average number of secondary infections caused by a single infected person in a susceptible population. If an R_0 greater than 1 indicates that each infected person on average infects more than one other person. This leads to exponential growth of disease within the population. This results in the rapid spread of SARS-CoV-2 and a potential outbreak or epidemic. On the other hand, if R_0 is less than 1, it means that each infected person is spreading the virus on average less than the other people. In this case, the disease cannot survive in the population. The spread of SARS-CoV-2 will eventually decrease and die out. Therefore, basic reproductive value is an important factor in understanding and controlling the spread of SARS-CoV-2 in closed systems, as it directly influences the transmission potential and disease dynamics within a population. The impact of R_0 on the spread of SARS-CoV-2 in closed systems is critical to implementing effective public health measures, such as vaccination, social distancing, and quarantine, to control the spread of viruses and epidemic prevention. The basic reproductive value (R_0) in the SEIQR model is influenced by several factors. Including the rate of disease spread. Duration of the infection period, interpersonal contact rate the effectiveness of control measures, such as quarantine or vaccination, and the size and structure of the population. Together, these factors determine the likelihood that a disease will spread within a population and affect the overall dynamics of the epidemic. By understanding and quantifying these factors, researchers can estimate R_0 and assess the potential impact of control measures on controlling the spread of disease.

Local subclinical stability in the context of public health intervention for SARS-CoV-2 indicates that small perturbations around an equilibrium point, such as a disease-free or endemic equilibrium point will lead to a significant outbreak of the disease. This information can inform public health intervention, emphasizing the importance of maintaining control measures even when disease prevalence is low. Public health interventions such as vaccination campaigns testing and contact tracing and social distancing measures, it should be continued and adapted based on the stability of local asymptomatic disease. By understanding the stability of disease dynamics public health authorities can then make informed decisions about when to reinforce interventions to prevent potential outbreaks. Overall, local asymptomatic stability provides valuable insight into the ability to Resurgence of disease within a population and guide public health strategies to effectively control and manage the spread of SARS-CoV-2.

The asymptotic dynamics of the SEIQR model for SARS-CoV-2 depends on the specific parameters and assumptions of the model. In general, the models may exhibit different behaviours, such as convergence towards disease-free equilibrium. If the basic reproductive number (R_0) is less than 1, this eventually leads to the elimination of the disease from the population. Alternatively, if R_0 is greater than 1, the model may

exhibit oscillatory behaviour or converge to a local equilibrium point where disease persists at a constant level in the population. The exact asymptotic dynamics of the SEIQR model for SARS-CoV-2 can be analysed through mathematical modelling and simulation techniques.

The asymptotic dynamics in the SEIQR model help in understanding the long-term behaviour of SARS-CoV-2 spread by providing insights into the eventual outcomes and trends of the disease over time. By analysing the stability and behaviour of equilibrium points, such as the disease-free and endemic equilibrium points, researchers can predict how the spread of the virus will evolve in the long term. Understanding the asymptotic dynamics allows for the assessment of factors such as the effectiveness of control measures, the impact of vaccination campaigns, and the potential for recurrent outbreaks. By studying the long-term behaviour of SARS-CoV-2 spread through asymptotic dynamics, policymakers and public health officials can make informed decisions to mitigate the impact of the disease and protect public health.

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Data availability The data used to support the findings of this study are available from the corresponding author request.

Declarations

Conflict of interest The authors declare that there are no conflicts of interest regarding the publication of this paper.

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