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Research article

On the decomposition and analysis of novel simultaneous SEIQR epidemic model

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Abstract: In this manuscript, we are proposing a new kind of modified Susceptible Exposed Infected Quarantined Recovered model (SEIQR) with some assumed data. The novelty imposed here in the study is that we are studying simultaneously SIR, SEIR, SIQR, and SEQR pandemic models with the same data unchanged as the SEIQR model. We are taking this model a step ahead by using a non-helpful transition because it was mostly skipped in the literature. All sorts of features that are essential to study the models, such as basic reproduction number, stability analysis, and numerical simulations have been examined for this modified SEIQR model with decomposed other epidemic models.

Keywords: new SEIQR epidemic model; basic reproduction number; stability analysis; sensitivity analysis; pandemic model; quarantine strategy
Mathematics Subject Classification: 74H15, 34A07

1. Introduction

The rate in which the change in accordance with the time that occurs in everything always to be dealt with differential equations (DE). The differential equations play a predominant role in almost every emerging topic of engineering, science, and technology. Especially when we want to deal with

climatic changes its role is quite unavoidable. DE is further extended its application to the medical field in different aspects beginning with the formation of medicine to launching it to society's well-being. Moreover, why does one need medicine? The answer to this question is when there arise any diseases and medical treatment is obviously much more needed there arises the need for new medicines and new vaccines, etc. The pleasant surprise here is that the emergence and spread of all diseases can also be dealt with with the help of DEs. There are many classifications of DEs like ordinary differential equations (ODE), partial differential equations (PDE), Delay Differential Equations (DDE), etc., We are going to make use of ODE to present, study, and analyze our novel decomposable SEIQR epidemic model.

The earth is not only for human beings but also for all creatures. The ancient world begins human evolution in the wild environment. Initially, his physical and mental behavior is adopted to a wild lifestyle. But as time period passes he adopts himself to a different culture. He develops modern society, family life, agriculture, and training the animals for his work. This change in environment, lifestyle, and food style is also affecting the features of human immunity. Not only humans but also all the creatures in this world will be subject to immunity imbalance and stick on to new diseases. Epidemic diseases are different from diseases that cause to man due by food contamination, pollution, etc., Epidemic diseases are diseases that emerge in society and infect a few people with common symptoms like flu, diarrhea, etc., These epidemic diseases are transmitted from one human to another human. Sometimes the cure may be automatic by one's self-immunity but on many occasions, there is requiring a few more strategies like quarantine, Vaccination, and Medication. We are here by going to use the quarantine strategy and the mathematical background of our model will be described in the following section.

After Kermamack Mckendrick's work [9], most of the epidemic models are done as an application of fractional differential equations. We have obtained knowledge of epidemic modeling and framed our research in ordinary differential equations. Some of the research in the literature that motivated us highly are listed below. [1] Abboubakar et al. presented a "mathematical study of tuberculosis (TB) model with fractional derivatives". In [2] Adak et al. gave us a "mathematical perspective of COVID-19 pandemic with disease extinction criteria in deterministic and stochastic models." In [3]Adda and Cresson, have done the "novel works on fractional differential equations and the Schrodinger equation". In [4] Baleanu et al. went through the "new fractional model and optimal control of a tumor immune surveillance with non-singular derivative operator". In [6] Deo et al. had forecasted, "the transmission dynamics of COVID-19 in India Under Containment Measures-A Time-Dependent State-Space SIR Approach". In [10] Khan and Atangana modeled, "the dynamics of novel coronavirus (2019-nCov) with fractional derivative." In [12] Muhammad et al. analyzed and numerically found the "solution of SEIR epidemic model of measles with non-integer time fractional derivatives by using Laplace Adomian Decomposition Method." In [13–15] Prasantha et al. studied both, "fractional and non-fractional epidemic models with delay and without delay." In [22–24] Authors, used "the Homotopy perturbation method (HPM) to study the disease models". Rekha et al. [19, 20] used, "HPM to study the model of Dengue Fever, Listeriosis and Anthrax Diseases". Thamizh et al. [23, 24] done, "Mathematical modeling of Wastewater Treatment and Groundwater System Using Microbial growth by HPM method". Saranya et al. [22] derived, "Unprecedented HPM for nonlinear equations in the enzymatic reaction of glucose". Lee G et al. [11] presented, "a simple epidemic models along with segmentation." Carcione et al. [5] analyzed, "the simulation of a deterministic COVID-19 Epidemic

SEIR Model" whereas Rihan et al. [21] analyzed, "the time delay Stochastic SIRC epidemic model of COVID-19". Raid Kamel et al. [16] gave, "the dynamics of an epidemic model with two types of infectious diseases and Vertical Transmission". Recently papers are published [17, 18] with assumed data that closely match with corresponding diseases giving good analysis and helps society to predict the future occerances even without the actual scenario and corresponding data.

The arguments of the author for presenting our new work called SEIQR model is arranged in such a way that the mathematical background of model formulation in Section 2, decomposed systems in 3, equilibrium points and stability analysis in Section 4, numerical simulations in Section 5, and conclusion of the study in Section 6 are presented.

2. Mathematical background and epidemic model-formulation

Let us make use of the following considerations for building up the desired mathematical model. The background of the model is at a time of study once we observed there are few unnoticed cases of epidemic spread and control. There we noticed a few simultaneous changes in epidemic models and a few non-helpful transitions were also noticed. Let us explain them in detail with our model. Our model SEIQR is not like the model that was studied earlier by others in the literature. It's quite different. Here we do the simultaneous transitions from susceptible to recovered class. One transition passes directly from susceptible to infected at the rate of g and the second transition is that susceptible passes to Exposed at the rate of a and after that passes to Infected from exposed at the rate of c. Also, Exposed become quarantined by the rate b, and Exposed becomes infected by the rate of c, and after that infected become quarantined by the rate of f. Finally, we are introducing the concept of non-helpful transition on the simultaneous changes from Quarantined to recovered by the rate of u and also the Infected becoming quarantined at the same rate u. We say the quarantine factor is non-helpful here since assumed the same rate u from quarantined to recovered and as well as for infected to recovered. The most interesting factor and novelty of this manuscript are that our model not only behaves as SEIQR but also as SEQR, SEIR, SIQR, and SIR simultaneously. We assume that the parameters mentioned below are values with 3 decimal places, that a, b,c, u, f, g are taking the same scale since there are many diseases like common flu that are not spread to many people but are epidemic and requires quarantine also which notices one in thousand falls in each category. The remaining those thousand may be still healthy.

In Table 1, we are defining symbols and descriptions required for SEIQR model formulation (see Figure 1) and its decompositions such as SIR (see Figure 2), SEQR (see Figure 3), SEIR (see Figure 4), SIQR (see Figure 5).

SEIQR-Model-Formulation

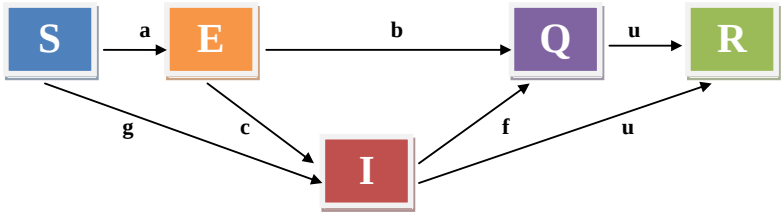

Figure 1. Model formulation.

Table 1. Symbols and descriptions (similar to [17, 18]).

S	Susceptible Population	—
E	Exposed Population	—
I	Infected Population	—
Q	Quarantined Population	—
R	Recovered Population	—
S_0	assumed Initial Susceptible population	10
E_0	assumed Initial Exposed population	10
I_0	assumed Initial Infected population	10
Q_0	assumed Initial Quarantined population	10
R_0	assumed Initial Recovered population	30
a	assumed rate of susceptible becoming exposed	0.006
b	assumed rate of exposed becoming quarnatined	0.005
c	assumed rate at which exposed become infected	0.007
u	assumed rate at which quarantined and infected become recovered	0.008
f	assumed rate at which infected become quarantined	0.002
g	assumed rate at which susceptible becoming infected	0.009

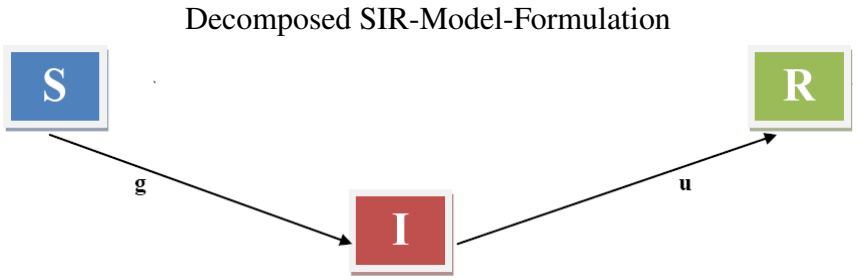

Figure 2. SIR model.

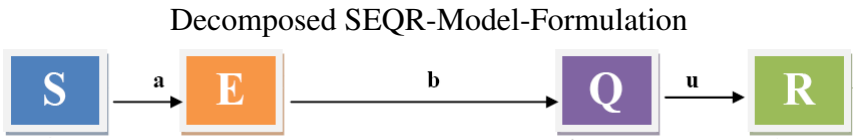

Figure 3. SEQR model.

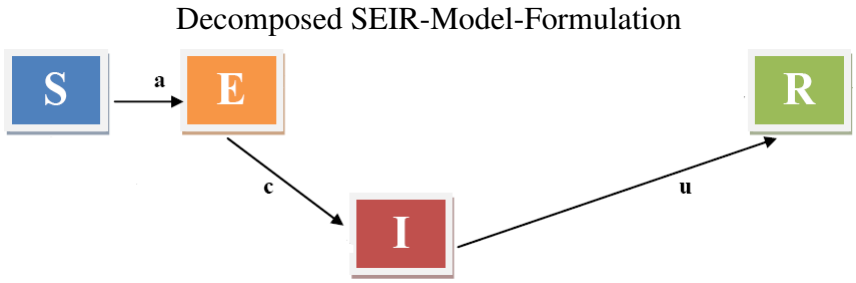

Figure 4. Model formulation.

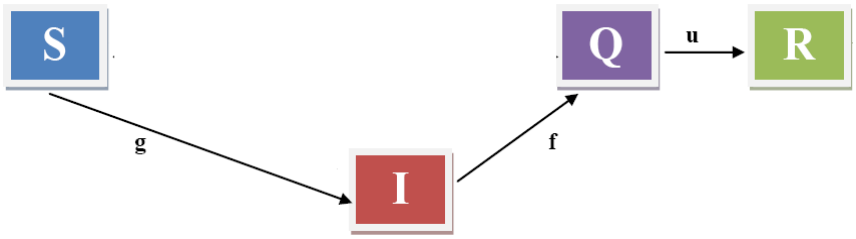

Figure 5. Model formulation.

$$\begin{aligned} S'(t) &= -aS(t)E(t) - gS(t)I(t), \\ E'(t) &= aS(t)E(t) - bE(t)Q(t) - cE(t)I(t), \\ I'(t) &= cE(t)I(t) - fI(t)Q(t)) - uI(t)R(t) + gS(t)I(t), \\ Q'(t) &= bE(t)Q(t) + fI(t)Q(t) - uQ(t)R(t), \\ R'(t) &= uQ(t)R(t) + uI(t)R(t). \end{aligned} \tag{2.1}$$

The total population for this SEIQR of size N will be $S(0) + E(0) + I(0) + Q(0) + R(0) = N$. But also we have few possible systems decomposed from the original systems such as SIR, SEIR, SIQR, and SEQR with

$$S(0) + I(0) + R(0) = N,$$

$$S(0) + E(0) + I(0) + R(0) = N,$$

$$S(0) + I(0) + Q(0) + R(0) = N,$$

$$S(0) + E(0) + Q(0) + R(0) = N.$$

Since we can decompose our model (2.1) in to various models the total population "N" will vary depending upon the kind of decomposition.

3. The decomposed systems from SEIQR

$$\begin{aligned} S'(t) &= -gS(t)E(t), \\ I'(t) &= gS(t)I(t) - uI(t)R(t), \\ R'(t) &= uI(t)R(t). \end{aligned} \tag{3.1}$$

The total population for this SIR of size N will be $S(0) + I(0) + R(0) = N$.

$$\begin{aligned} S'(t) &= -aS(t)E(t), \\ E'(t) &= aS(t)E(t) - bE(t)Q(t), \\ Q'(t) &= bE(t)Q(t) - uQ(t)R(t), \\ R'(t) &= uQ(t)R(t). \end{aligned} \tag{3.2}$$

The total population for this SEQR of size N will be $S(0) + E(0) + Q(0) + R(0) = N$.

$$\begin{aligned} S'(t) &= -aS(t)E(t), \\ E'(t) &= aS(t)E(t) - cE(t)I(t), \\ I'(t) &= cE(t)I(t) - uI(t)R(t), \\ R'(t) &= uI(t)R(t). \end{aligned} \tag{3.3}$$

The total population for this SEIR of size N will be $S(0) + E(0) + I(0) + R(0) = N$.

$$\begin{aligned} S'(t) &= -gS(t)E(t), \\ I'(t) &= gS(t)I(t) - fI(t)Q(t), \\ Q'(t) &= fI(t)Q(t) - uQ(t)R(t), \\ R'(t) &= uQ(t)R(t). \end{aligned} \tag{3.4}$$

The total population for this SEQR of size N will be $S(0) + E(0) + Q(0) + R(0) = N$.

4. Basic reproduction number, equilibrium points, stability analysis

4.1. Basic reproduction number (B_0)-estimation

Theorem 4.1. *Any epidemic model can be announced to*

(1) will not survive iff $B_0 < 1$,

(2) will survive and may lead to further waves iff $B_0 \geq 1$.

Proof. By this number, we can predict the count of occurring of new cases that transfers from an infected individual. The rate of infection leads to new susceptibility at time $t = 0$. The secondary susceptibility of our SEIQR model will be depending on two compartments namely $E(t)$ and $I(t)$. So we have to apply the concept of the next-generation matrix in order to find the basic reproduction number here. Let us consider,

$$\begin{aligned} E'(t) &= aS(t)E(t) - bE(t)Q(t) - cE(t)I(t), \\ I'(t) &= cE(t)I(t) - fI(t)Q(t) - uI(t)R(t) + gS(t)I(t). \end{aligned} \tag{4.1}$$

The Jacobian matrix of (4.1) is given by

$$F = \begin{pmatrix} aS(0) - bQ(0) - cI(0) & -cE(0) \\ cI(0)) & cE(0) - fQ(0) - uR(0) + gS(0) \end{pmatrix}. \tag{4.2}$$

Now, F can be decomposed as $F = F_1.F_2$ where

$$F_1 = \begin{pmatrix} aS(0) & 0 \\ 0 & 0 \end{pmatrix}, \tag{4.3}$$

and

$$F_2 = \begin{pmatrix} -bQ(0) - cI(0) & -cE(0) \\ cI(0)) & cE(0) - fQ(0) - uR(0) + gS(0) \end{pmatrix}. \tag{4.4}$$

Now, let us calculate X from $X = -F_2$ then

$$X = \begin{pmatrix} bQ(0) + cI(0) & cE(0) \\ -cI(0)) & fQ(0) + uR(0) - cE(0) - gS(0) \end{pmatrix}. \tag{4.5}$$

Now we have found $Adj.X$, $|X|$ and X as follows

$$Adj.X = \begin{pmatrix} fQ(0) + uR(0) - cE(0) - gS(0) & -cE(0) \\ cI(0) & -(bQ(0) + cI(0)) \end{pmatrix}. \tag{4.6}$$

$$|X| = ((bQ(0) + cI(0)).(fQ(0) + uR(0) - cE(0) - gS(0))) + ((cI(0)).(cE(0))) \tag{4.7}$$

$$X^{-1} = \frac{1}{|X|}(Adj.X)$$

$$F_1X^{-1} = \frac{\begin{pmatrix} \alpha S(0) & 0 \\ 0 & 0 \end{pmatrix}.\begin{pmatrix} fQ(0) + uR(0) - cE(0) - gS(0) & -cE(0) \\ cI(0) & -(bQ(0) + cI(0)) \end{pmatrix}}{((bQ(0) + cI(0)).(fQ(0) + uR(0) - cE(0) - gS(0))) + ((cI(0)).(cE(0)))}. \tag{4.8}$$

The Basic reproduction number is calculated from $B_0 = \rho F_1.X^{-1}$ where $\rho F_1.Y^{-1}$ is the spectral radius of the matrix $F_1.X^{-1}$ and is given by $\max(|\lambda_{B0}|)$ where, λ is the eigenvalue of the $F_1.X^{-1}$. The eigenvalues of $\lambda_{B0} = F_1.X^{-1} = (0.35503, 0.)$.

$B_0 = \max(|\lambda_{B0}|) = 0.35503$ is the basic reproduction number. Since the basic reproduction number $B_0 < 1$ the disease will not produce new secondary susceptible. □

4.2. Equilibrium points

The equilibrium points are found when the system undergoes no changes, i.e., $S'(t) = 0, E'(t) = 0, I'(t) = 0, Q'(t) = 0, R'(t) = 0$. By our calculation, we found a disease-free equilibrium point i.e., D_f and a disease dependence equilibrium points, i.e., D_d

$$D_f = (0, 0, 0, 0, 0),$$

where as if we want to find the diseases dependent equilibrium point, we have to choose which is fully dependent on infection. We know that Susceptible (S), Exposed (E), Quarantined are partially disease oriented if either they are symptomatic or asymptomatic but the populations I(t) and R(t) are purely infection dependent. So we found that the disease dependent equilibrium points are $S_0, E_0, I_0, Q_0, \frac{bE_0+fI_0}{u}$. i.e., now,

$$D_f = (0, 0, 0, 0, 0),\ D_d = (10, 10, 10, 10, 16.25).$$

4.3. Stability analysis

Theorem 4.2. *The system with the (2.1) is locally asymptotically stable when all the eigenvalues of characteristic polynomial obtained by the linearization of (2.1) are having negative real parts.*

Proof. Let us now consider the system (2.1). The linearized from of (2.1) can be presented using Jacobian matrix.

$$J = \begin{pmatrix} -aE(0) & -aS(0) & -gS(0) & 0 & 0 \\ aE(0) & aS(0) - bQ(0) - cI(0) & -cE(0) & -bE(0) & 0 \\ gI(0) & cI(0) & cE(0) + gS(0) & & \\ & & -fQ(0) - uR(0) & -fI0 & -uI(0) \\ 0 & bQ(0) & fI(0) & bE(0)+ & \\ & & & fI(0) - uR(0) & -uQ(0) \\ 0 & 0 & uR(0) & uR(0) & uI(0) + uQ(0) \end{pmatrix}. \tag{4.9}$$

On solving the above matrix by substituting the values of $S(0), E(0), I(0), Q(0), R(0)$ and also the required values of a, b, c, u, f, g, we found that the characteristic polynomial as

$$\lambda^5 + 0.32\lambda^4 + 0.0638\lambda^3 + 0.008008\lambda^2 + 0.00043152\lambda + 1.13981 \times 10^{-20} = 0.$$

The corresponding eigenvalues are found to be
$(-0.0428429 + 0.163821i, -0.0428429 - 0.163821i, -0.1171557 + 0.036387i, -0.117157 - 0.036387i, -2.64139 \times 10^{-17})$.

Since all the eigenvalues are having the negative real parts which is also shown in the Figure 6, the system we considered is locally asymptotically stable.

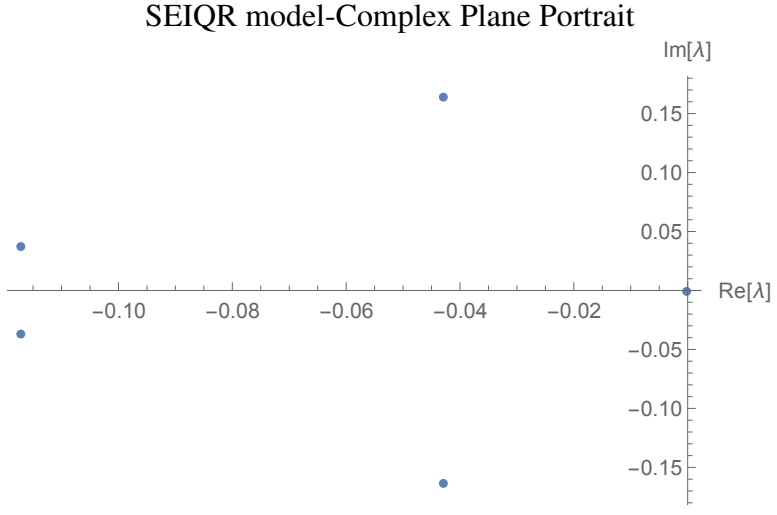

Figure 6. Complex plane-SEIQR.

□

Theorem 4.3. *The decomposed systems SIR, SEQR, SEIR, and SIQR of SEIQR model are at least marginally stable when the model SEIQR is asymptotically stable.*

Proof. Let us now consider the decomposed system SIR (3.1) obtained from (2.1). The linearized from of (3.1) can be presented using Jacobian matrix.

$$J = \begin{pmatrix} -gI(0) & -gS(0) & 0 \\ gI(0) & gS(0) - uR(0) & -uI(0) \\ 0 & uR(0) & uI(0) \end{pmatrix}. \tag{4.10}$$

On solving the above matrix by substituting the values of $S(0), I(0), R(0)$ and also the required values of a, b, c, u, f, g, we found that the characteristic polynomial as

$$4.21515 \times 10^{-21} - 0.0216\lambda - 0.16\lambda^2 - \lambda^3 = 0.$$

The corresponding eigenvalues are found to be

$$(-0.08 + 0.123288i, -0.08 - 0.123288i, 1.95146 \times 10^{-19}),$$

which is approximately equal to

$$(-0.08 + 0.123288i, -0.08 - 0.123288i, 0).$$

Since one of the eigenvalues is zero and the plot does not pass through the first or fourth quadrant the system we considered is marginally stable, which is also shown in the Figure 7.

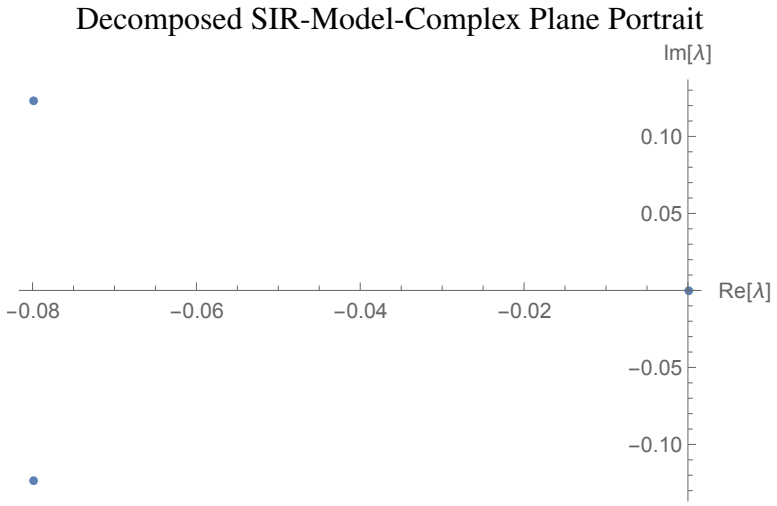

Figure 7. Complex plane- SIR.

Let us now consider the decomposed system SEQR (3.2) obtained from (2.1). The linearized form of (3.2) can be presented using Jacobian matrix.

$$J = \begin{pmatrix} -aE(0) & -aS(0) & 0 & 0 \\ aE(0) & aS(0) - bQ(0) & -bE(0) & 0 \\ 0 & bQ(0) & bE(0) - uR(0) & -uQ(0) \\ 0 & 0 & uR(0) & +uQ(0) \end{pmatrix}. \tag{4.11}$$

On solving the above matrix by substituting the values of $S(0), E(0), Q(0), R(0)$ and also the required values of a, b, c, u, f, g we found that the characteristic polynomial as

$$-7.75472 \times 10^{-21} + 0.00048\lambda + 0.015\lambda^2 + 0.16\lambda^3 + \lambda^4 = 0.$$

The corresponding eigenvalues are found to be

$$-0.054615 + 0.0804462i, -0.054615 - 0.0804462i, -0.0507701, 1.61557 \times 10^{-17}$$

which is approximately equal to

$$-0.054615 + 0.0804462i, -0.054615 - 0.0804462i, -0.0507701, 0.$$

Since one of the eigenvalues is zero and does not pass through first or fourth quadrant, the system we considered is marginally stable,which is also shown in the Figure 8.

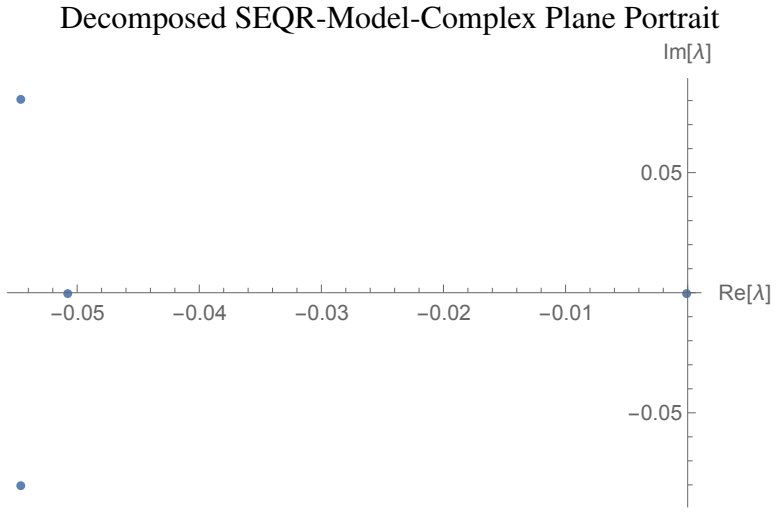

Figure 8. Complex plane-SEQR.

Let us now consider the decomposed system SEIR (3.3) obtained from (2.1). The linearized from of (3.3) can be presented using the Jacobian matrix.

$$J = \begin{pmatrix} -aE(0) & -aS(0) & 0 & 0 \\ aE(0) - cI(0) & aS(0) - cI(0) & -cE(0) & 0 \\ 0 & cI(0) & cE(0) - uR(0) & -uI(0) \\ 0 & 0 & uR(0) & +uI(0) \end{pmatrix}. \tag{4.12}$$

On solving the above matrix by substituting the values of $S(0), E(0), I(0), R(0)$ and also the required values of a, b, c, u, f, g we found that the characteristic polynomial as

$$2.35459 \times 10^{-21} + 0.000672\lambda + 0.021\lambda^2 + 0.16\lambda^3 + \lambda^4 = 0.$$

The corresponding eigenvalues are found to be

$$-0.0590719 + 0.112096i, -0.0590719 - 0.112096i, -0.0418563, -3.50385 \times 10^{-18}.$$

Since all the eigenvalues are having negative real parts, which is also shown in the Figure 9, the system we considered is locally asymptotically stable.

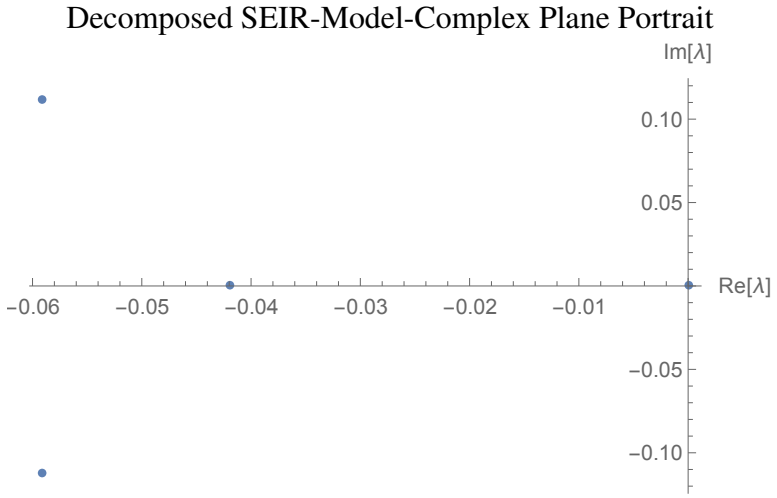

Figure 9. Complex plane SEIR.

Let us now consider the decomposed system SIQR (3.4) obtained from (2.1). The linearized form of (3.4) can be presented using the Jacobian matrix.

$$J = \begin{pmatrix} -gI(0) & -aS(0) & 0 & 0 \\ gI(0) & gS(0) - fQ(0) & -fI(0) & 0 \\ 0 & fQ(0) & fI(0) - uR(0) & -uQ(0) \\ 0 & 0 & uR(0) & +uQ(0) \end{pmatrix}. \tag{4.13}$$

On solving the above matrix by substituting the values of $S(0), I(0), Q(0), R(0)$ and also the required values of a, b, c, u, f, g we found that the characteristic polynomial as

$$6.9205 \times 10^{-21} + 0.000288\lambda + 0.0066\lambda^2 + 0.16\lambda^3 + \lambda^4 = 0.$$

The corresponding eigenvalues are found to be

$$-0.125724, -0.0171378 + 0.044688i, -0.0171378 - 0.044688i, -2.40295 \times 10^{-17}.$$

Using all the Eqs (4.1)–(4.8) and other equations, we found that, since all the eigenvalues are having negative real parts, which is also shown in the Figure 10, the system we considered is locally asymptotically stable. Hence it is now proved that the decomposed systems of asymptotically stable systems are at least marginally stable.

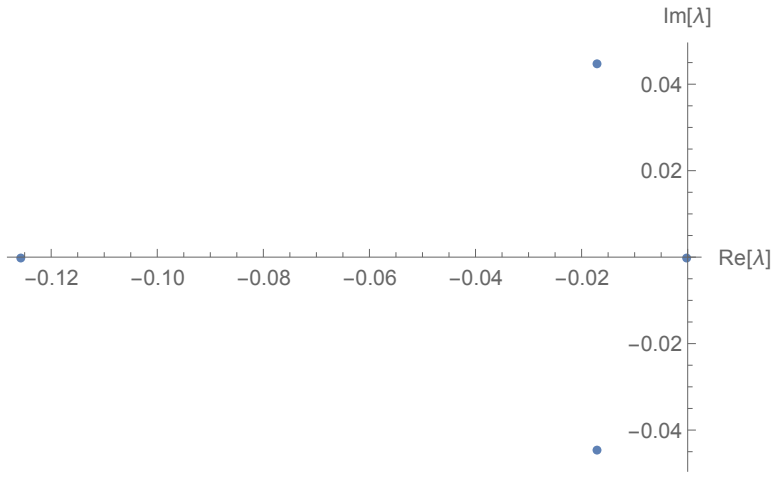

Figure 10. Complex plane- SIQR.

□

5. Numerical simulations

For our system (2.1) (SEIQR), and for the decomposed systems (3.1)–(3.4) (SIR, SEQR, SEIR, and SIQR) the numerical simulations are presented below respectively in Figures 11–15.

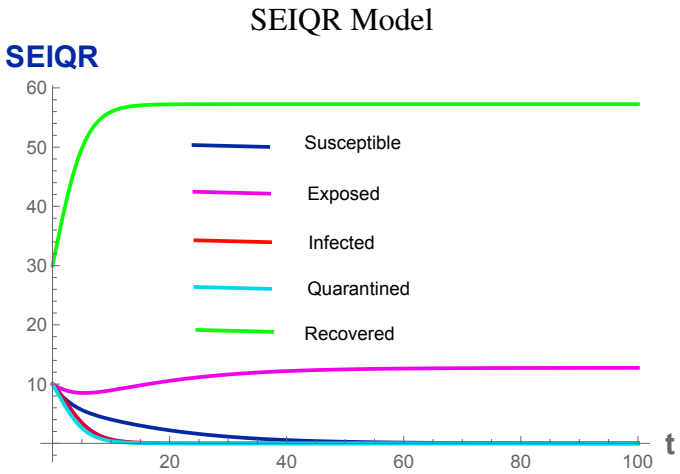

Figure 11. Plot of S, E, I, Q, and R.

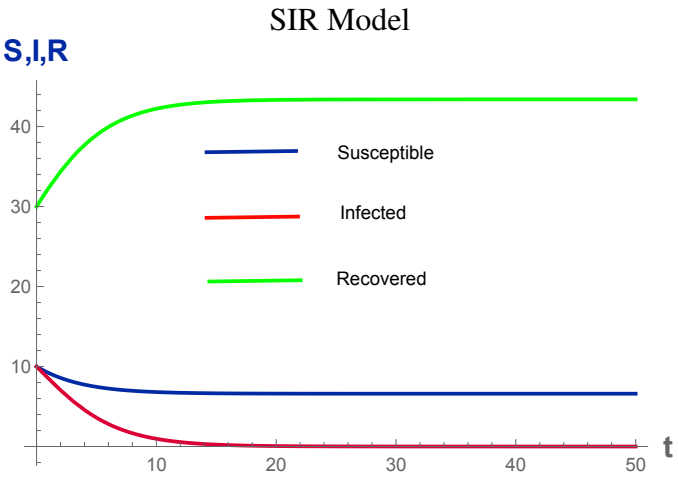

Figure 12. Plot of S, I, and R.

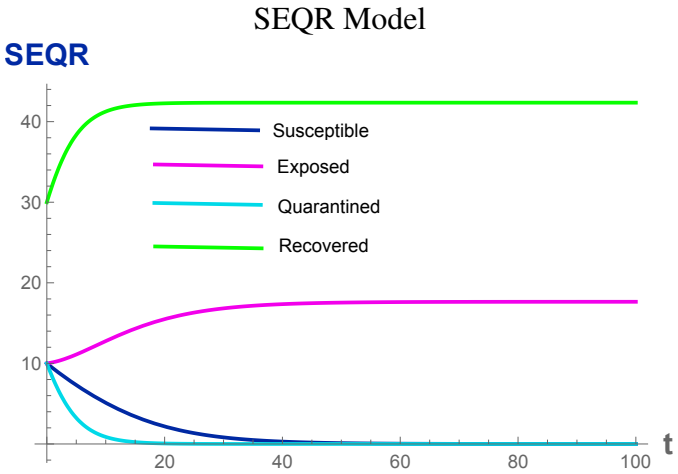

Figure 13. Plot of S, E, Q and R.

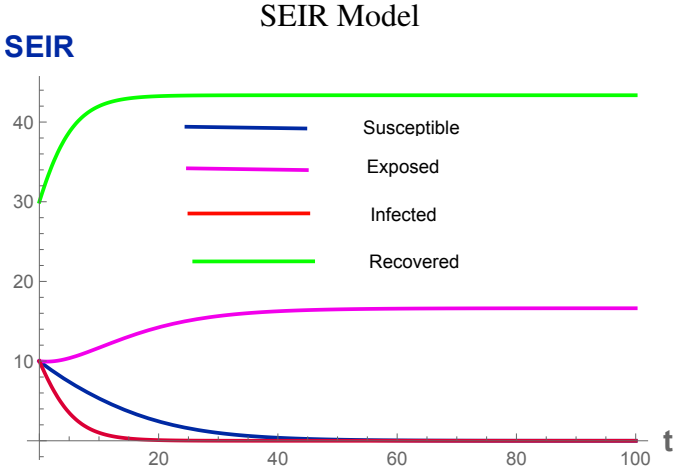

Figure 14. Plot of S, E, I, and R

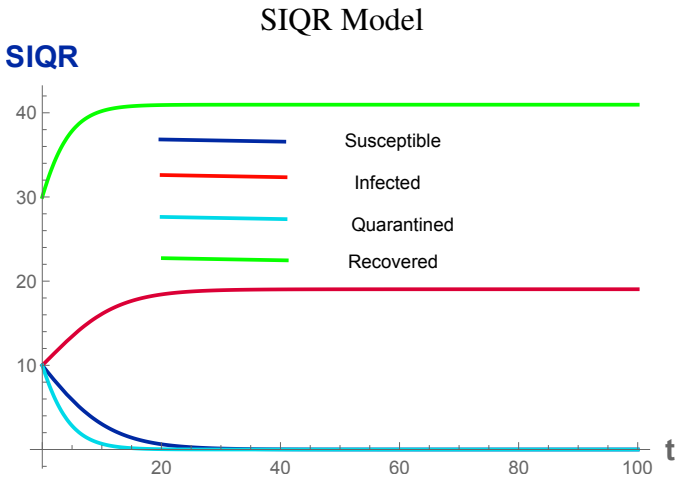

Figure 15. Plot of S, E, I, and R.

6. Conclusion and discussion

We have done a very new kind of developing epidemic model i.e., a model with simultaneous decomposed models. By theorem, we have proved that our SEIQR model is asymptotically stable. By using another theorem we have established that the decomposed models are at least marginally stable or almost asymptotically stable but they will never be unstable. Also, the numerical simulations are also supporting our results. Since this study is very new to the literature on the epidemic models we hope that this model will create much more impact in studying the diseases like HIV, cancer, etc., which will create additional opportunistic diseases like TB. On that occasion, instead of the strategy quarantine as a parameter, we need to include opportunistic diseases as a parameter. Also, we would like to consider a new version of the modified SEIQR model in the future study since many recent works investigated the SEIR model in a new way are very inspiring, e.g., Beddington–DeAngelis functional response in [7], the generalized nonlinear incidence [8].

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Conflict of interest

The authors declare no conflict of interest.

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