Modified SEIR model for Covid-19

Hesham Mleah[1☯], Mohd Saiful Islam[2☯], Nuri Jannatul[3☯]

Faculty of Applied Computer Sciences and Bio-sciences, Applied Mathematics for Network and Data Sciences, Mittweida University of Applied Sciences, 09648, Mittweida, Germany.

Author to whom correspondence should be addressed:
1. hmleah@hs-mittweida.de
2. mislam2@hs-mittweida.de
3. njannatu@hs-mittweida.de

☯These authors contributed equally to this work.

Abstract

In this report, we study a proposed modification to the basic SEIR model for COVID-19 in a published paper that uses data from Hubei province in China. A great number of COVID-19 related papers and articles are published analyzing its dynamic, but this paper looks into the effects of control measures taken by health authorities such as medical intervention, hospitalized patients, and quarantine. It is important to note that the paper is concerning the early period of the pandemic before the availability of vaccines. In the said report, we will take a look at the methodology of the proposed modifications of the SEIR model that adds compartments to the basic model for the control strategies mentioned earlier, while also accounting for external input in the form of outsiders entering the province. Then we perform a study on stability analysis for a disease-free equilibrium. Moreover, we will also use a method called the next generation matrix or in short NGM to calculate the basic reproduction number R_0 using the points of the disease-free equilibrium. Finally, we have a discussion that aims to illustrate the results of our simulation of the COVID-19 epidemic in using the given data for the SEIR model, as well as what changes in the simulation when we change the value of R_0 and some criticism for implementation of the model.

Introduction

The first case of a Novel Coronavirus was discovered in Wuhan, China, in December 2019. It was given the temporary name "2019-nCoV"by the World Health Organization (WHO) in January 2020. On February 11, 2020, the WHO officially designated the virus as "COVID-19"(Coronavirus disease 2019). Since that time, the disease has quickly spread over the globe, causing the COVID-19 pandemic. COVID-19 is a single-stranded, good attitude, enclosed virus that is a member of the RNA coronaviridae family [2, 3].

To stop the outbreak, researchers from many disciplines looked at COVID-19 from various angles and some of the factors are sociological aspects, pathology, the process of infection, and forecasting [4–9]. Since diseases can strike at any time, it might be challenging to control an epidemic. Statistical simulations can be used to locate, understand, and predict an epidemic. The paper has listed several statistical simulations [1].

The spread of a pandemic is influenced by numerous factors. Before vaccines were developed, governments took a number of tactics to stop the spread of COVID-19, including rigorously limiting social connections, imposing lockdowns, shutting down institutions, and restricting travel across the country. The interaction of many of these well-known aspects has a big effect on how quickly the virus spreads. Additionally, there are a few undetected, subtle elements that support the virus's unintentional transmission.

It is difficult to determine how to create an appropriate epidemiological model for these epidemics. For forecasting and modeling purposes, some scientists consider the spread of diseases as a complex network [10, 11]. At the moment, there are numerous models, including SIS, SIR, and SEIR, for simulating epidemics. Numerous research studies have been published and it demonstrates how effectively these models capture the dynamics of various epidemics. These models have been applied to the COVID-19 simulations in the interim [12, 13].

Even though there are numerous models, we attempt to propose an SEIR model to simulate the COVID-19 process, in this study. The SEIR model features four variables, and the initials S, E I, and R stand for Susceptible, Exposed, Infectious, and Recovered respectively. Therefore, a susceptible person transitions to an exposed phase before going to the infectious phase. Different writers define these dynamics differently based on their objectives to keep matters simple.

In this study, our objective is to investigate COVID-19 spreading capabilities by implementing the SIER model and mathematically analysing it. We will have a better understanding of the process as we continue to study it, which will help us to better comprehend why we utilize SEIR models to depict infectious diseases. We will calculate disease-free equilibrium points and comprehend them. We will examine the fundamental reproduction number R_0 using the Next Generation Matrix Method (NGM), which is an important predictor of how a disease would behave over the long run. R_0 is a well-known epidemiological notion for estimating the transmission of an infectious disease.

Methodology

In the standard SEIR model, four compartments of the system represented as the following S (Susceptible), E (Exposed), I (Infectious), and R (Recovered). In addition, the total population can be presented as its own compartment and calculated to be: $N = S + E + I + R$. The basic notion is that individuals will assume a role in the four compartments as time progresses as a natural course for an epidemic, which goes: $S \to E \to I_1 \to R$, and the changes in each compartment are shown by equations that demonstrate the rats of increasing or decreasing numbers of individuals in each compartment. However, there are some limitations of this model. That is why three new compartments were proposed by the researchers of the original paper [1], this addition will enable the simulation to take into account in addition to the natural course of the pandemic. The effects of containment efforts imposed at the population, this yield a new course for the model that goes hand to hand with the original on as: $S \to Q \to I_2 \to H \to R$. So this makes the system of equations to the new SEIR model and it's compartments denoted as: [1]

$$\frac{dS}{dt} = -\frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_1 Q - \rho_2 S + \alpha R \tag{1}$$
$$\frac{dE}{dt} = \frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) - \theta_1 E - \theta_2 E \tag{2}$$
$$\frac{dI_1}{dt} = \theta_1 E - \gamma_1 I_1 \tag{3}$$
$$\frac{dI_2}{dt} = \theta_2 E - \gamma_2 I_2 - \varphi I_2 + \lambda(\Lambda + Q) \tag{4}$$
$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 + \phi H - \alpha R \tag{5}$$
$$\frac{dH}{dt} = \varphi I_2 - \phi H \tag{6}$$
$$\frac{dQ}{dt} = \Lambda + \rho_2 S - \lambda(\Lambda + Q) - \rho_1 Q \tag{7}$$

Where the system variables are:

Table 1. A description of the system variables [1]

Variable	Description
S	Susceptible group
E	Exposed individuals
I_1	Infectious without treatment
I_2	Infectious with assistance
R	Recovered individuals
Q	Quarantined individuals
H	Hospitalized individuals

And the parameters are: [1]

- α: Rate of temporary immunity.
- β_1, β_2: The contact and infection rate of transmission per contact from infected group.
- χ: Probability of transmission from each contact with exposed individuals.
- θ_1, θ_2: Transition rate from the exposed class to the infected class.
- γ_1, γ_2: Recovery rate of infected people with symptoms to recover from the disease.
- φ: Hospitalization rate of infectious with symptoms.
- ϕ: Recovery rate of infected people under quarantines.
- λ: Rate of the quarantined group to the recovered group.
- ρ_1, ρ_2: Transition rate of quarantined exposed between the quarantined infected group and the broader community.
- Λ: External contributions from the foreign nations.

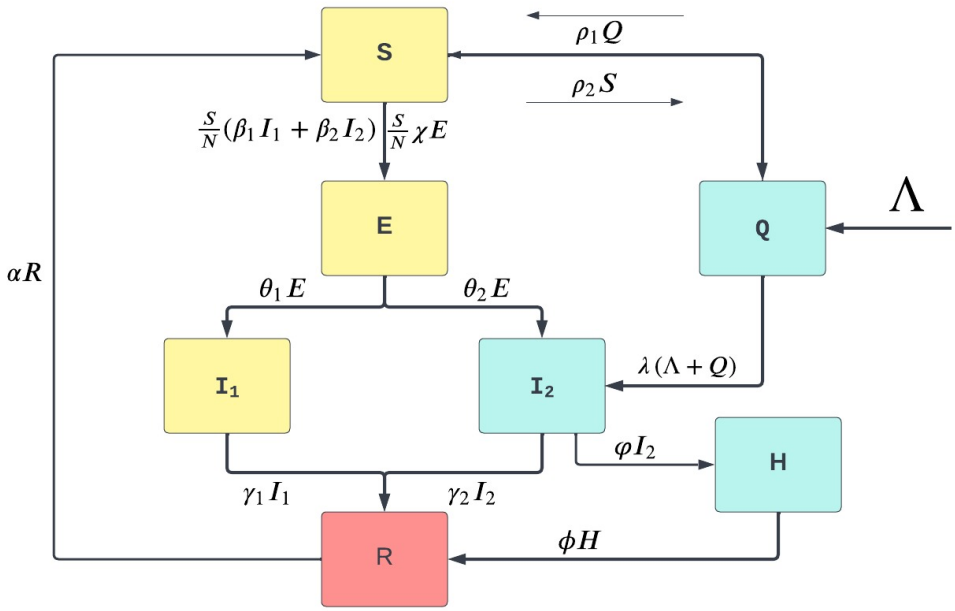

Fig 1. Flowchart of the suggested SEIR model

By expanding the number of compartments, the model needs to be illustrated to better show the dynamics and changes of the model this can be seen in the flowchart (1), where the compartments in the yellow color as will as the recovery compartment represent the above mentioned natural course of the disease while the cyan compartments are the new proposed changes. It is also important to observe that the total population N in this system is changing over time since there is an external output of individuals when $\Lambda \neq 0$ meaning when individuals are coming in to the controlled area from the outside world, but according to the Chinese government those individuals were getting quarantined immediately. In addition, there are many individuals who are under self-isolation, meaning that thanks to the last two factors the total population: $N \neq S + E + I_1 + I_2 + Q + R$, but it can be estimated by adding the final total number of deaths and recoveries.

Results

Disease free equilibrium

Equilibrium points are constant solutions to the differential equations (1), (2), (3), (4),(5), (6), (7), and to obtain said points we first start by setting
$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI_1}{dt} = \frac{dI_2}{dt} = \frac{dR}{dt} = \frac{dH}{dt} = \frac{dQ}{dt} = 0$

$$
\begin{aligned}
\frac{dS}{dt} &= -\frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_1 Q - \rho_2 S + \alpha R = 0 \\
\frac{dE}{dt} &= \frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) - \theta_1 E - \theta_2 E = 0 \\
\frac{dI_1}{dt} &= \theta_1 E - \gamma_1 I_1 = 0 \\
\frac{dI_2}{dt} &= \theta_2 E - \gamma_2 I_2 - \varphi I_2 + \lambda(\Lambda + Q) = 0 \\
\frac{dR}{dt} &= \gamma_1 I_1 + \gamma_2 I_2 + \phi H - \alpha R = 0 \\
\frac{dH}{dt} &= \varphi I_2 - \phi H = 0 \\
\frac{dQ}{dt} &= \Lambda + \rho_2 S - \lambda(\Lambda + Q) - \rho_1 Q = 0
\end{aligned}
$$

Now from equation (1) we derive the value of S as the following:

$$
\begin{aligned}
&-\frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_1 Q - \rho_2 S + \alpha R = 0 \\
&\implies \frac{S}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_2 S = \rho_1 Q + \alpha R \\
&\implies S[\frac{1}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_2] = \rho_1 Q + \alpha R \\
&\implies S = \frac{\rho_1 Q + \alpha R}{\frac{1}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) + \rho_2} \qquad (8)
\end{aligned}
$$

And in a similar fashion we can derive the following equations:

$$E = \frac{S(\beta_1 I_1 + \beta_2 I_2)}{N(\theta_1 + \theta_2 - \frac{\chi S}{N})} \qquad (9)$$

$$I_1 = \frac{\theta_1 E}{\gamma} \qquad (10)$$

$$I_2 = \frac{\theta_2 E + \lambda(\lambda + Q)}{\gamma_2 + \phi} \qquad (11)$$

$$R = \frac{\gamma_1 I_1 + \gamma_2 I_2 + \Phi H}{\alpha} \qquad (12)$$

$$H = \frac{\phi}{\Phi} I_2 \qquad (13)$$

$$Q = \frac{\rho_2 S + \Lambda(1 - \lambda)}{\rho_1 + \lambda} \qquad (14)$$

However, in this study we are focusing on the disease-free equilibrium preforming a stability analysis around said equilibrium. Therefore in order to study a disease-free system lets assume that there are no new infections happening among the population meaning that $I_1 = 0$ and $I_2 = 0$ thus from equations (9),(12), (13) E, R, and H are also equal to zero.
So by substituting these values in equation (8), we end up with:

$$S = \frac{\rho_1 Q + \alpha 0}{(\beta_1 0 + \beta_2 0 + \chi 0) + \rho_2}$$

$$\implies S = \frac{\rho_1}{\rho_2} Q \tag{15}$$

In addition substitution the values in equation (14) gives:

$$Q = \frac{\rho_2 \frac{\rho_1}{\rho_2} Q + \Lambda(1-\lambda)}{\rho_1 + \lambda}$$

$$\implies Q = \frac{\rho_1 Q + \Lambda(1-\lambda)}{\rho_1 + \lambda}$$

$$\implies Q - \frac{\rho_1}{\rho_1+\lambda} Q = \frac{\Lambda(1-\lambda)}{\rho_1+\lambda} \implies Q(1 - \frac{\rho_1}{\rho_1+\lambda}) = \frac{\Lambda(1-\lambda)}{\rho_1+\lambda}$$

$$Q(\frac{\lambda}{\rho_1+\lambda}) = \frac{\Lambda(1-\lambda)}{\rho_1+\lambda} \implies Q = \frac{\Lambda(1-\lambda)(\rho_1+\lambda)}{\lambda(\rho_1+\lambda)}$$

$$\implies Q = \frac{\Lambda(1-\lambda)}{\lambda} \tag{16}$$

And by introducing the new value of Q from equation (16) to (15), we have

$$S = \frac{\rho_1 \Lambda(1-\lambda)}{\rho_2 \lambda} \tag{17}$$

So the disease-free equilibrium point is:

$$E_0 = (\frac{\rho_1 \Lambda(1-\lambda)}{\rho_2 \lambda}, 0, 0, 0, 0, 0, \frac{\Lambda(1-\lambda)}{\lambda})$$

Stability of the disease-free equilibrium

In order to preform a stability analysis around E_0, the Jacobian matrix is required for the derivatives of the variables of the system of ODE's and it is defined as:

$$\frac{df(X)}{dx} = \begin{bmatrix} \frac{df(X)}{dx_1} & .... & \frac{df(X)}{dx_n} \end{bmatrix} = \begin{bmatrix} \frac{df_1(X)}{dx_1} & .... & \frac{df_1(X)}{dx_n} \\ \vdots & \ddots & \vdots \\ \frac{df_n(X)}{dx_1} & .... & \frac{df_n(X)}{dx_n} \end{bmatrix}$$

So adjusting for the variables in the system the matrix is:

$$\begin{bmatrix} \frac{-1}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) - \rho_2 & \chi & \frac{-S}{N}\beta_1 & \frac{-S}{N}\beta_2 & \alpha & \rho & 0 \\ \frac{1}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E) & \frac{S}{N}\chi - \theta_1 - \theta_2 & \frac{S}{N}\beta_1 & \frac{S}{N}\beta_2 & 0 & 0 & 0 \\ 0 & \theta_1 & -\gamma_1 & 0 & 0 & 0 & 0 \\ 0 & \theta_2 & 0 & -\gamma_2 - \varphi & 0 & 0 & 0 \\ 0 & 0 & \gamma_1 & \gamma_2 & -\alpha & 0 & \Phi \\ \rho & 0 & 0 & 0 & 0 & -\phi & 0 \\ 0 & 0 & 0 & \varphi & 0 & 0 & \Phi \end{bmatrix}$$

Thus the eigenvalues are the main diagonal elements of the matrix, and they are:

$$\frac{-1}{N}(\beta_1 I_1 + \beta_2 I_2 + \chi E), \frac{S}{N}\chi - \theta_1 - \theta_2, -\gamma_1, -\gamma_2 - \varphi, -\alpha, -\rho_1, \Phi$$

And around our disease-free equilibrium $E_0 = (\frac{\rho_1 \Lambda(1-\lambda)}{\rho_2 \lambda}, 0, 0, 0, 0, 0, \frac{\Lambda(1-\lambda)}{\lambda})$
The eigenvalues become:

$$-\rho_2, \frac{\rho_1 \Lambda(1-\lambda)}{N \rho_2 \lambda} - \theta_1 - \theta_2, -\gamma_1, -\gamma_2 - \varphi, -\alpha, -\rho_1, \Phi$$

And since there are still positive values in these eigenvalues, we draw the conclusion that the equilibrium is unstable.

Basic Reproduction Number

For quantifying the transmission of a contagious disease, the basic reproduction number R_0 is a familiar epidemiological concept. It is defined as the average number of secondary cases initiated by a single person in a given population, where none is immune or vaccinated.

It is specified at the opening time of an outbreak, and in particular, any public health measures are commenced. When a value of R_0 more significant than 1 follows that the number of cases of the disease in the population will prolong exponentially, while a value of R_0 less than 1 denotes the outbreak will stop after a shorter period [14].

A simpler explanation is that R_0 is the product of the infection rate and the mean duration of the infection [15]. However our model is a little more complex and have two infectious compartments that is why we use the Next Generation Matrix method below.

Computing R_0 using NGM

To calculate the reproduction number R_0 by the Next Generation Matrix method, a reduced system is needed where it only accounts for new infections that have been introduced or being introduced to the original system of the model, meaning that the reduced system is the one concerning the following equations (2), (3), (4). In addition all individuals are considered to be susceptible meaning that $S = N$ in order to see the potential of the disease to spreads in an entire population made of susceptible individuals, also for sake of simplicity the variables E, I_1, I_2 are going to be refereed to as x_1, x_2, x_3 respectively in this section. Therefore, the reduced system is:

$$\begin{aligned}
\frac{dx_1}{dt} &= \beta_1 x_2 + \beta_2 x_3 + \chi x_1 - \theta_1 x_1 - \theta_2 x_1 \\
\frac{dx_2}{dt} &= \theta_1 x_1 - \gamma_1 x_2 \\
\frac{dx_3}{dt} &= \theta_2 x_1 - \gamma_2 x_3 - \varphi x_3
\end{aligned}$$

Additionally the reduced system can be written as:

$$\frac{d\underline{x}}{dt} = F(\underline{x}) - V(\underline{x})$$

Where $F(\underline{x})$ is the matrix that represents new infections in the population, and $V(\underline{x})$ denotes the matrix of transmissions rats between the system compartments, as:

$$F = \left[\frac{\sigma F_i}{\sigma x_i}\right] = \begin{bmatrix} \chi & \beta_1 & \beta_2 \\ \theta_1 & 0 & 0 \\ \theta_2 & 0 & 0 \end{bmatrix}$$

$$V = \left[\frac{\sigma v_i}{\sigma x_i}\right] = \begin{bmatrix} -(\theta_1 + \theta_2) & 0 & 0 \\ 0 & \gamma_1 & 0 \\ 0 & 0 & -(\gamma_2 + \varphi) \end{bmatrix}$$

To find R_0, we now need to calculate the matrix: $F.V^{-1}$, and because of $V(\underline{x})$ is a diagonal matrix it is easy to calculate V^{-1}, and it is:

$$V^{-1} = \begin{bmatrix} \frac{-1}{-\theta_1+\theta_2} & 0 & 0 \\ 0 & \frac{1}{\gamma_1} & 0 \\ 0 & 0 & \frac{-1}{\gamma_2+\varphi} \end{bmatrix}$$

Thus $F.V^{-1}$ equals:

$$F.V^{-1} = \begin{bmatrix} \frac{-\chi}{\theta_1+\theta_2} & \frac{\beta_1}{\gamma_1} & \frac{\beta_2}{\gamma_2+\varphi} \\ \frac{-\theta_1}{\theta_1+\theta_2} & 0 & 0 \\ \frac{-\theta_2}{\theta_1+\theta_2} & 0 & 0 \end{bmatrix}$$

R_0 is the spectral radius of the matrix $F.V^{-1}$ meaning it is $\rho(F.V^{-1})$ (the largest absolute value of the eigenvalues).

$$\implies R_0 = \frac{\chi}{\theta_1 + \theta_2} \tag{18}$$

And as we have found earlier that the disease-free equilibrium is unstable this means that R_0 numerical value is greater than one and that is according to the following section.

Basic properties

Lemma 1:
Let P be a non-singular M-matrix and suppose G and PG^{-1} have the Z sign pattern. Then P is a non-singular M-matrix if and only if PG^{-1} is a non-singular M-matrix. [15]
Lemma 2:
Let P be a non-singular M-matrix and suppose $Q \geq 0$.Then,

(a) $(P-Q)$ is a non-singular M-matrix if and only if $(P-Q)P^{-1}$ is a non-singular M-matrix.

(b) $(P-Q)$ is a singular M-matrix if and only if $(P-Q)P^{-1}$ is singular M-matrix. [15]

Theorem:
Consider the disease transmission model like the one represented by equations (1) to (7) and satisfying the following five conditions:

(I) if $x_i \geq 0$ then $F(\underline{x}), V(\underline{x}) \geq 0$

(II) if $x \in E_0$ then $V_i^- = 0$

(III) $F_i = 0$ if $x \notin E_0$

(IV) if $x \in E_0$ then $F(\underline{x}) = 0$ and $V_i^+ = 0$

(V) finally if F($\underline{x}$) is set to zero then all eigenvalues of the Jacobian matrix have negative real parts.

Where V_i^+ is the rate of transferring individuals into compartment i, and V_i^- is the transfer rate out of compartment i.
Then, if E_0 is the disease-free equilibrium of the model, E_0 is locally asymptotically stable if $R_0 < 1$ and it is unstable if $R_0 > 1$.
Proof: Let

$$\frac{d\underline{x}}{dt} = F(\underline{x}) - V(\underline{x})$$

as $V(\underline{x})$ is a non-singular M-matrix and $F(\underline{x})$ is non negative,

$$\frac{-d\underline{x}}{dt} = V(\underline{x}) - F(\underline{x})$$

has Z sign pattern.
Thus, $S\frac{d\underline{x}}{dt} < 0 \iff \frac{-d\underline{x}}{dt}$ is a non-singular M-matrix, where $S\frac{d\underline{x}}{dt}$ represents the maximum real part of all the eigenvalues of the matrix $\frac{d\underline{x}}{dt}$ (the spectral abscissa of $\frac{d\underline{x}}{dt}$)

Since $F.V^{-1}$ is non-negative,

$$\frac{-d\underline{x}}{dt}V^{-1} = I - F.V^{-1}$$

also has the Z sign pattern. Following Lemma 1, with $P = V$ and

$$G = \frac{-d\underline{x}}{dt} = V(\underline{x}) - F(\underline{x})$$

we get, $\frac{-d\underline{x}}{dt}$ is a non-singular M-matrix $\iff I - F.V^{-1}$ is a non-singular M-matrix. At last, since $F.V^{-1}$ is non-negative, all eigenvalues of $F.V^{-1}$ have magnitude less than or equal to $\rho(F.V^{-1})$. Then,

$$I - F.V^{-1}$$

is a non-singular M-matrix,$\iff \rho(F.V^{-1}) < 1$. Hence,

$$S\frac{d\underline{x}}{dt} < 0$$

if and only if $R_0 < 1$. Similarly,we have,

$$S\frac{d\underline{x}}{dt} = 0$$

$\iff \frac{-d\underline{x}}{dt}$ is a singular M-matrix, $\iff I - F.V^{-1}$ is a singular M-matrix, $\iff$ $\rho(F.V^{-1}) = 1$. Following the second equivalence from Lemma 2,we get $P = V$ and $Q = F$. The rest of the equivalences follow as with non-singular case. Therefore,

$$S\frac{d\underline{x}}{dt} = 0$$

if and only if $\rho(F.V^{-1}) = 1$. It follows that

$$S\frac{d\underline{x}}{dt} > 0$$

if and only if $R_0 > 1$. □ [15]

Discussion

In this paper, we studied a mathematical model of the COVID-19 pandemic. Where also two more compartments were added for hospitalization (H) and quarantining (Q). The equilibrium point and basic reproduction number R_0 were calculated based on the modified SEIR model. In the stability section, we noticed that some eigenvalues are positive. Therefore, we concluded that the equilibrium is unstable. The effects of this are shown in our simulation as fast growth of the number of new infections, due to the relatively high reproduction number extracted from the data of the model. Despite that there was for example the number of infectious individuals without any treatment or intervention I_1 that was taking as a small fraction of the individuals that were actually under medical supervision I_2, that is according to the reports from Hubei province, which lead that numbers of I_1 to stay near zero, while in sharp contrast to this, the values of the recovered individuals seems to grow fast as more time goes by, accompanied naturally by the values of the Hospitalised individuals this is illustrated in the chart in Fig 2

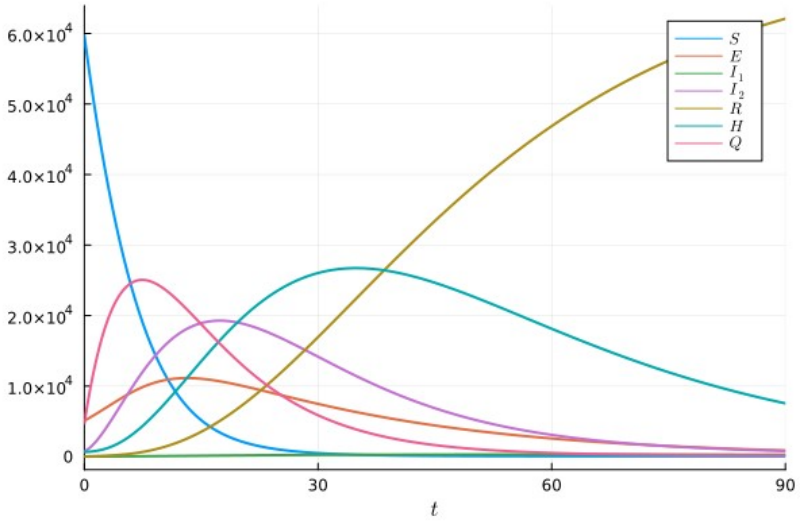

Fig 2. Simulation of the model with the original values of parameters

Additionally the number of susceptible individuals drop continuously, and approaches zero despite having a positive feedback loop from the individuals that have recovered from the infection but only had an immunity for short duration of time. Moreover, the infectious with intervention numbers I_2 as well as the number of Exposed individuals seems to grow fast in the initial phase of the disease, but with that rise we also spot the rise of number of quarantined people, followed by a decline in all three simulated numbers past that initial phase that is somewhere before the thirty days mark, indicating that the control measures in this model have a significant effects on curbing the spread of the disease locally.
Coming back to the value of the reproduction number it can be calculated using the values of the parameters from Table 3, as R_0 we found was:

$$R_0 = \frac{\chi}{\theta_1 + \theta_2}$$

And by substituting

$$\chi = 1.6221 \times 10^{-1}, \theta_1 = 9.5000 \times 10^{-4}, \theta_2 = 3.5412 \times 10^{-2}$$

Thus

$$R_0 \simeq 4.46$$

which is a high value that corresponds with the initial phase of the pandemic.
It is important to know that those values were calculated from the collected data of the Wuhan Municipal Health Commission, and the initial values of the model are:

Table 2. Initial values for the SEIR model [1]

Parameter	N	E	I_1	I_2	H	R	Q	Λ
Value	6.5563×10^4	5077	$I_2 \times 0.01$	729	658	32	4711	10

While the calculated parameter values are

Table 3. SEIR model system parameters [1]

Parameter	Values
β_1	1.0538×10^{-1}
β_2	1.0538×10^{-1}
χ	1.6221×10^{-1}
ρ_1	2.8133×10^{-3}
ρ_2	1.2668×10^{-1}
θ_1	9.5000×10^{-4}
θ_2	3.5412×10^{-2}
γ_1	8.5000×10^{-3}
γ_2	1.0037×10^{-3}
λ	9.4522×10^{-2}
α	1.2048×10^{-4}

And it is also worth mentioning that the value of φ and ϕ were estimated using the Particle Swarm Optimization (PSO) algorithm, where the most accurate values according to the original paper [1] are given as $\varphi = 0.0973$ and $\phi = 0.0416$
Lets assume that the value of R_0 is less than 1. This can be done by enlarging the value of the sum $\theta_1 + \theta_2$. So suppose we make the change to:

$$\theta_1 = 9.5000 \times 10^{-1}, \theta_2 = 3.5412 \times 10^{-2}$$

meaning that R_0 is actually now equal to $R_0 = 0.16$, then the differences can be seen in the chart in Fig 3

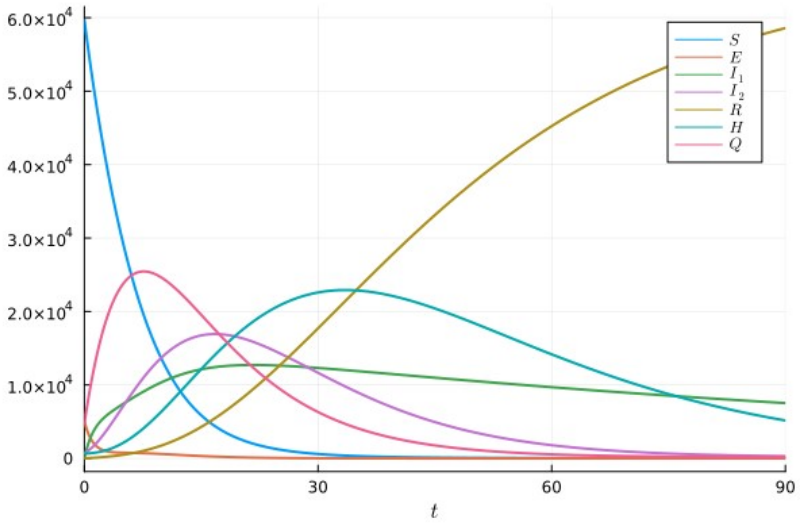

Fig 3. Simulation of the model with the manipulated values of parameters

And the main changes in the simulation comes most obviously from the progression of I_1 values over time, as now this kind of infection is more prolonged and instead of hovering near zero as in the original simulation we see that it decline very slowly after a peak in the initial phase. Furthermore, the Exposed cases do drop immediately meaning that the disease is almost likely now faster to spread, explaining why I_1 does not converge to zero, and why numbers of those who get treatment of the infectious I_2 converge to zero faster than the original model, and have slightly less peak in numbers.

Lastly, lets discuss some facts that we mentioned in this report, to control and prevent the pressure of the epidemic, the Wuhan Government declared to lockdown the

city from almost all outside world contact on January 23rd, 2020. Then the authorities of other cities in Hubei province also announced the "closure city"measure. We used the same data of the original report between January 24th and April 12th, since the COVID-19 epidemic situation in Hubei is comparatively steady after January 23rd, 2020, until the spring of 2020.

To critique the model, we may mention one critical point. The implementation of the proposed model fails to show that the exposed population is only temporarily immunized after gaining recovery. which is as we now know after three years to be the case for COVID-19, because record over time shows that infected people who recover from it have a descent chance of getting infected again by the virus and its multiple variants.

Conclusion

The world was under a partial shutdown when the COVID-19 virus spread rapidly, as the nature of this disease was unknown and unpredictable to everyone. Even after the availability of the vaccine, confirmed cases of coronavirus were increasing day by day.

The objective of the study was to realize and explore the behavior of the pandemic the world is facing. We tried to implement actual data in the mathematical model to observe the situation in different parameters and dynamics. Lastly, we discussed how the parameters influenced the system dynamics and introduced the control strategies. We have suggested some conventions which we suppose can be subsidiary to reducing the pandemic.

- The quarantine and treatment are more suitable for the dynamics of the epidemic of COVID-19.
- For untested people with symptoms, self-quarantine is most important.
- The susceptible class needed to test rapidly to identify infected numbers, as COVID-19 was new in nature and critical.
- In detecting the infected individuals, quarantine and isolation protocols must impose so that the infected do not spread the virus further.
- Since it is difficult to understand and predict the nature of a new variant of coronavirus, everyone should use face mask at a public gathering.
- Vaccination campaigns should implement around the globe, including in poor and developing countries.

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