NUMERICAL SIMULATION OF CORONAVIRUS DISEASE EPIDEMIC BASED ON ESTABLISHED SUSCEPTIBLE-EXPOSED-INFECTIOUS-RECOVERED-UNDETECTABLE-SUSCEPTIBLE MODEL

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ABSTRACT

Coronavirus (COVID-19) is the virus which has killed so many people in the world. The spread of COVID-19 within a region in South East Asia has been modelled using a compartment model called SEIR (Susceptible, Exposed, Infected, Recovered). Actual number of sick people needing treatments, or the number active case data was used to obtain realistic values of the model parameter such as the reproduction number (R0), incubation, and recovery periods. It is shown that at the beginning of the pandemic where most people were still not aware, the R0 was very high as seen by the steep increase of people got infected and admitted to the hospitals. Few weeks after the lockdown of the region was in place and people were obeying the regulation and observing safe distancing, the R0 values dropped significantly and converged to a steady value of about 3. Using the obtained model parameters, fitted on a daily basis, the maximum number of active cases converged to a certain value of about 2500 cases. It is expected that in the early June 2020 that the number of active cases will drop to a significantly low level. We Implement SEIR model to enumerate the infected Population and the number of casualties of this pandemic. Numerical Simulations was carried out to set off the analytical results in investigating the effect of the implementation of Isolation and social distancing as a function of time. The initial number of exposed individuals and infected people, the incubation, infectious period and the fatal rate. The analysis shows how the observatory procedures, Isolation measures, social distancing and knowledge of the spreading conditions help us to understand the dynamic of the pandemic, hence it is important to quantify the process to verify the efficiency and effectiveness due to absence of restorative vaccine at the moment. The mathematical models equation also provides a good fit to the data but some of the results may not realistic, therefore an accurate determination of the fatality rate and characteristics of the pandemic is subject to knowledge of the precise bounds of the parameters of the (SEIR) models.

Keywords: Numerical Simulations, Seirus model, Coronavirus pandemic incubation, Isolation, Social distancing. parameter identification, statistical methods

INTRODUCTION

The outbreak of coronavirus 2019 (COVID-19) has created a global health crisis that has had a deep impact on the way we perceive our world and our everyday lives, Not only the rate of contagion and patterns of transmission threatens our sense of agency, but the safety measures put in place to contain the virus. The most abundant species in nature are viruses, they are parasites, since they cannot replicate themselves. Upon replication, some viruses cause serious infectious diseases in human and\or animals are medically, socially and economically. Pandemic are large scale outbreaks of infectious disease that can greatly increase morbidity and mortality over a wide geographic area and cause significant economic, social and political disruption. Evidence suggest the likelihood of pandemics has increased over the past century because of increased global travel and integration., urbanization, changes in land use, and greater exploitation of natural environment (Jones etal., 2008). An outbreak of a corona virus disease was first identified in Wuhan, China, in December 2019. What follows is an increasing number of reported cases internationally with travel histories related to Wuhan, China(http://virological.org/t/epidemiological-data-from-the-ncov-2019-outbreak-early-descriptions- from-publicly-available-data/337/3). This new corona virus has been designated as COVID-19 and later officially named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)by WHO (https://www.who.int/dg/ speeches/detail/who-director-general-s-remarks-at-the-media-briefing-on-2019-ncov-on-11-february-2020. 2020). Due to its worldwide spread, COVID- 19, as it is more well-known, has been de- clared as a world pandemic by WHO(https://www.who.int/news-room/detail/30-01- Governments around the world have been trying to implement various control measures to contain the virus. Researchers, on the other hand, do whatever they can to help giving information to the governments, as well as helping front liners and societies. One of the most important pieces of information regarding the outbreak of the virus is the estimation of how many people may get infected, fall sick, need treatments, and how health care systems can cope with that. This information is important to be able to de- velop and evaluate control measures as well as for future prevention (Prem *et al.,* 2020; Wang *et at.,* 2020).

Many researchers have done various modeling efforts using data to model the spread of viruses. As reported in literatures, the model approaches cover stochastic transmission model (Kucharski *et al.,* 2020), polynomial chaos-based nonlinear Bayesian approach(Bavdekar & Mesbah, 2016; San- tonja & Chen-Charpentier, 2012), stochastic Galarkin method(Harman & Johnston, 2016), and various compartmental based models such as SEIR (Fang *et al.,* 2020), SIR (Chen-Charpentier & Stanescu, 2010), or SUQC(Zhao & Chen, 2020).

The most commonly used model is what is called as compartmental based models which was developed and used a lot within epidemiological communities to predict the spread of the virus and its severity. Out of many variations of the compartmental based models, such as Susceptible, Exposed, Infectious, Recovery (SEIR), has been used as a general model to work with and modified further SEIR model is a population balance type of model where people are moving from one compartment to another compartment. Compartment "S" stands

for Susceptible, which is the population that may get infect- ed. Compartment "E" or exposed is the population that are exposed or infected by the virus, but there is no sign of illness yet. They are still in the incubation period. Compartment "I" or Infected population is the population that are infected and fall ill and needs treatment. The compartment "R" or recovered population is the population that has recovered from the illness caused by the Virus.

There are few observations that justify the use of SEIR model to better represent the spread of the virus. It is a known fact that people in compartment "E" may not fall sick or just show very light symptoms that they themselves do not notice. This group of people is commonly called as "carrier" where they are moving around spreading the viruses to people with lower level of immunities. This observation is the basis of having the compartment "E". It is also known that there is no passive or maternal immunity against this virus. Hence, other compartment "M" or population with ma- ternal/passive immunities is not included in the model. And lastly, it is widely assumed that the recovered people have permanent immunity against COVID-19. This assumption necessitates the Recovered group of people and they are not getting back to being ill. Hence, based on these observations and assumptions, the most appropriate model to use is the SEIR model. This model has been used widely and it has been used to model the actual case in China (Fang *et* a/., 2020). Some of the advanced versions of the model can be found online (https://covid19-scenarios.org).

METHODOLOGY

In this work, the SEIR model was fitted against the number of active cases or the number of infected people needing treatment at hospitals on a daily basis. This data fitting was to find the realistic values for the model parameters considering local circumstances of the affected community as mentioned previously. In this model, it was assumed that everybody has the same virus spreading capacity and the same immunity level. We consider the SEIR pandemic model which is categorized into four classes namely: Susceptible S(t), Exposed E(t), Infectious I(t), Recovered R(t) and Undetectable U(t) where t is the time variable. The governing equations are:

$$\frac{dS(t)}{dt} = \pi + \mu S \qquad\qquad (1)$$

$$\frac{dE(t)}{dt} = S - (\mu + B)E \qquad\qquad (2)$$

$$\frac{dI(t)}{dt} = BE - (\sigma + \mu + \varphi)I \qquad\qquad (3)$$

$$\frac{dR(t)}{dt} = \sigma I - (\rho + \mu + \varpi)R \qquad\qquad (4)$$

$$\frac{dU(t)}{dt} = \rho R - (\mu + \varepsilon)U \qquad\qquad (5)$$

Where

$$N(t) = S(t) + E(t) + I(t) + R(t) + U(t) \qquad (6)$$

Such that t denotes time differentiation, the equation 1-6 are subject to the initial conditions S(0), E(0), I(0), R(0) and U(0). The parameters are defined as:

$S(t)$	Number of susceptible population at time t
$E(t)$	Number of exposed population at time t
$I(t)$	Number of infected population at time t
$R(t)$	Number of infected population quarantined and expecting recovery at time t
$U(t)$	Number of recovered adults satisfying undetectable criteria at time t
μ	Natural death rate of the population
α_0	Maximum death rate due to COVID-19 coronavirus. ($\alpha \le \alpha_0$)
α	Death rate of infected population due to COVID-19 coronavirus
φ	Disease induced death rate of infected population not quarantined
ϖ	Disease induced death rate of infected receiving quarantined
T	Maximum lifespan after infection ($T \ge 14\ days$)
k	Efficacy of Quarantine ($0 \le k \le 1$)
ρ	Rate of recovery
β	rate of transmission
σ	Proportion of infected population in quarantine per unit time (Treatment rate)
π	Proportion of population from susceptible to exposed/latent class
ε	Proportion of removed population still being observed and being moved to susceptible class
$B(t)$	Incidence rate or force of infection in the population

The following diagram describes the dynamic of SEIRUS framework, and will be useful in the formulation of model equations
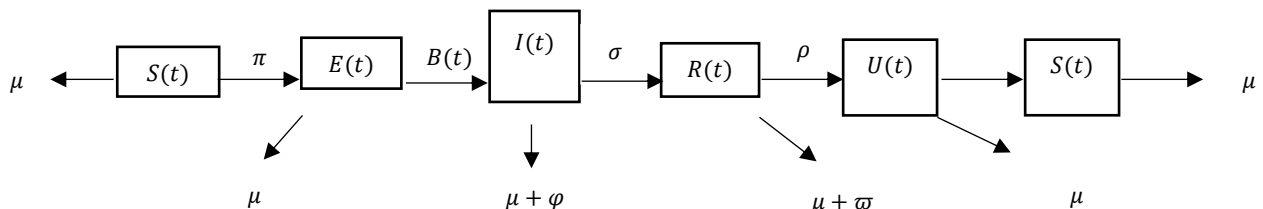
The transformed model Equation into Proportions is given by:

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} + \frac{dU(t)}{dt} \qquad (7)$$

$$\frac{dN(t)}{dt} = \pi + \mu S + S - \mu E - (\mu + \varphi)I - (\mu + \varpi)R - (\mu + \varepsilon)U \qquad (8)$$

$$s = \frac{S}{N}, e = \frac{E}{N}, i = \frac{I_1}{N}, r = \frac{R}{N}, u = \frac{U}{N} \qquad (9)$$

Then the rationalized system follows as:

$$\frac{ds}{dt} = \frac{1}{N}\left[\frac{dS(t)}{dt} - s\frac{dN(t)}{dt}\right]$$

Substituting (1) and (9) and using (10)

$$\frac{ds}{dt} = \frac{\pi(1-s)}{N} + \mu s - \mu s^2 - ss^2 + \mu se + (\mu + \varphi)si + (\mu + \varpi)sr + (\mu + \varepsilon)su \qquad (10)$$

Similarly,

$$\frac{de}{dt} = \frac{1}{N}\left[\frac{dE(t)}{dt} - e\frac{dN(t)}{dt}\right]$$

Substituting Equations (2) and (9) and using (10)

$$\frac{de}{dt} = s - (\mu + B)e - \frac{e\pi}{N} - \mu se - es + \mu e^2 + (\mu + \varphi)ei + (\mu + \varpi)er + (\mu + \varepsilon)eu \qquad (11)$$

Next we have;

$$\frac{di}{dt} = \frac{1}{N}\left[\frac{dI(t)}{dt} - i\frac{dN(t)}{dt}\right]$$

Substituting Equation (3) and (9) and using (10)

$$\frac{di}{dt} = Be - (\sigma + \mu + \varphi)i - \frac{i\pi}{N} - i\mu s - is + \mu ie + (\mu + \varphi)i^2 + (\mu + \varpi)ir + (\mu + \varepsilon)iu \qquad (12)$$

And

$$\frac{dr}{dt} = \frac{1}{N}\left[\frac{dR(t)}{dt} - r\frac{dN(t)}{dt}\right]$$

Substituting Equation (4) and (9) and using (10)

$$\frac{dr}{dt} = \sigma i - (\rho + \mu + \varpi)r - \frac{r\pi}{N} - \mu rs - rs + \mu re + (\mu + \varphi)ri + (\mu + \varpi)rr + (\mu + \varepsilon)ru \qquad (13)$$

And finally;

$$\frac{du}{dt} = \frac{1}{N}\left[\frac{dU(t)}{dt} - u\frac{dN(t)}{dt}\right]$$

Substituting Equation (5) and (9) and using (10)

$$\frac{du}{dt} = \rho r - (\mu + \varepsilon)u - \frac{u\pi}{N} - u\mu s - us + \mu u(\mu + \varphi)ui + (\mu + \varpi)ur + (\mu + \varepsilon)uu \qquad (14)$$

However,

$$s + e + i + r + u = 1 \qquad (15)$$

Equations (11) to (15) are the model equations in proportions, which define prevalence of infection.

RESULTS AND DISCUSSION

We Implement SEIR model to enumerate the infected Population and the number of casualties of this pandemic and the numerical results were obtained with the implementation of the MATLAB programme. Fitting active case data until mid of April 2020 is shown in Figure 2. It is a fact that every community has different response and preparedness towards the virus, different socio-cultural behavior, and so on, which may make these model parameters unique. From this fitted data, the model parameters of reproduction number (RO), incubation, and recovery periods are obtained. Hence, by fitting the model into the actual data, the obtained model parameters really reflect the actual local reality.

Figures 3 and 4 show the estimated Susceptible, Exposed, Infected, and Recovered populations using the parameters obtained by fitting the active case data until mid of April 2020. In Figure 3, the shape of the curves shows that many of the exposed population may not need treatment at the hospital and can recover by themselves. Their number is indeed very high, reaching above 20 thousand people. However, only about 2500 people need hospital treatment as shown in the infected population (or number of active cases, in this example).

Figure 5 shows several values of RO de- pending on the time frames of the fitted da- ta. It can be seen that at late March 2020, when most people were not fully aware of how this virus spreads and still moving around, the obtained R0 values were very high. This means that when people were still freely moving, the virus is spread very rapidly. One infected person can infect 6 or more people before the 25th of March 2020. The RO number even went up to about 10 during late March 2020. The last week of March as the time when lock do n was ordered. Once it was ordered, people were rushing to their hometowns, highways were jammed, and many crowds were at public transportation hubs. That was the perfect situation where the virus spread very rapidly. Then, about two weeks after the lockdown was commenced, situation got calm, people are obeying the lockdown situation, the R0 values are dropping substantially until it reaches a steady value of around 3.

Figure 6 shows the expected number of active cases using the parameters obtained from Figure 5. It can be seen that for the first two points in Figure 5 corresponds to the two highest peaks in Figure 6. With high R0 values, many people can get infected, fall sick, and then need further treatments in the hospitals. Few weeks after the lock- down, the number of infected people re- duces and the number of active cases also reduces. The maximum active cases are somewhat converging to a fixed value of about 2500 people. By the end of June 2020, the number of active cases is predicted to be at the very low level.

As a general conclusion from the graph, it can be seen that the lockdown and the way it is being observed and controlled seems to be effective in reducing the spread of the virus. The predictions seem to converge consistently to a certain value may also mean that people are obeying this lockdown situation, excellent work done by the government in providing testing and treatment facilities, and amazing work performed by front liners in treating people and maintaining the death ratio lower and relatively constant.
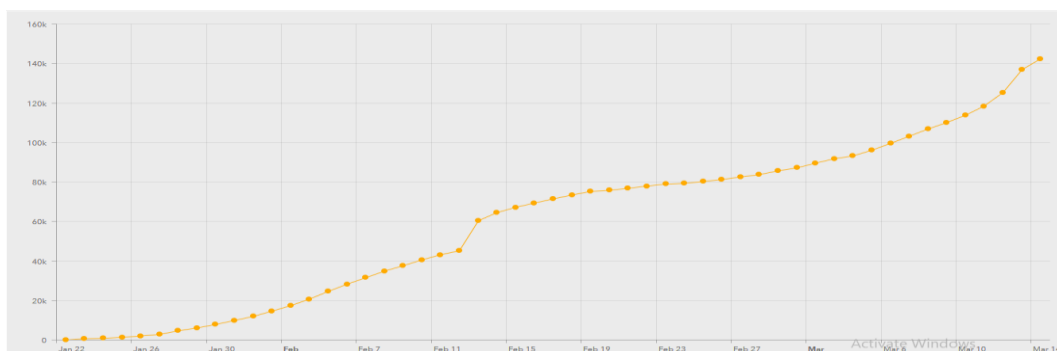

Figure 1: A Case by date of report chart showing the number of cases with a COVID-19 coronavirus case
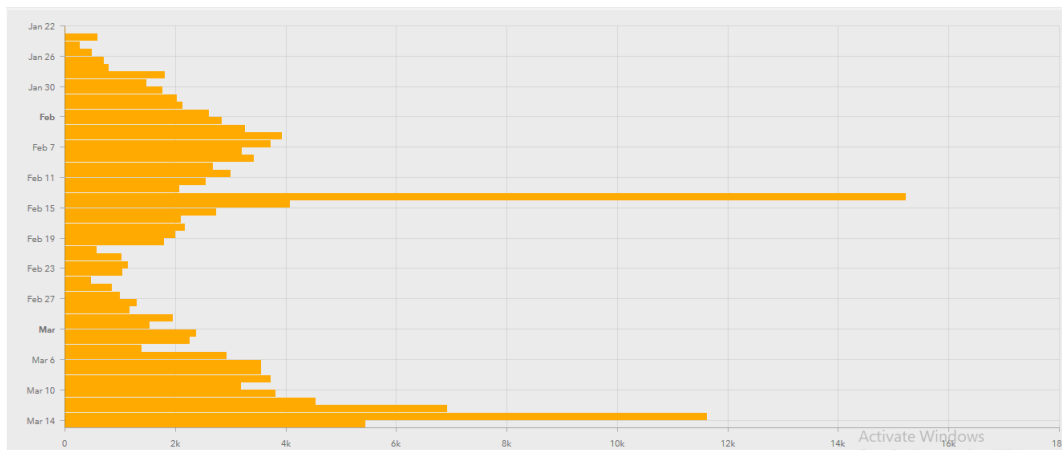
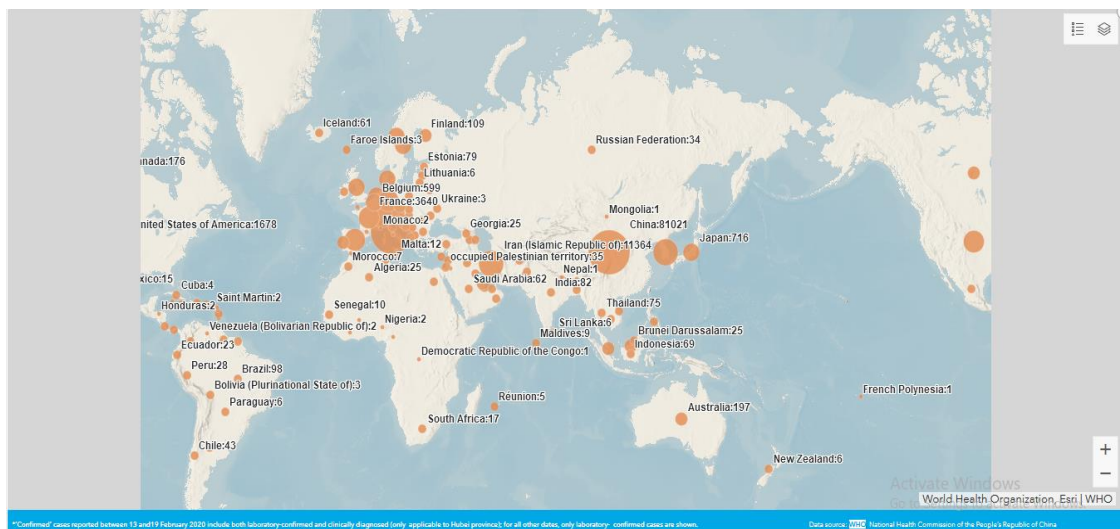Figure 2: A Cumulative Case chart showing the number of cases with a COVID-19 coronavirus case

Figure 3: A World Map showing the number of cases per each country with a COVID-19 coronavirus case

The age-structured deterministic model $(11) - (15)$ was solved numerical using Runge-Kutta-Fehllberg 4-5th order method and implemented using Maple Software. The model equations were first transformed into proportions, thus reducing the model equations to ten differential equations. The parameters used in the implementation of the model are shown in Table 1 below. Parameters were chosen in consonance with the threshold values obtained in the stability analysis of the disease free equilibrium state of the model.

**Table 1: Estimated values of the parameters used in the Numerical experiments**

Parameters	Values	Data Source	Parameters	Values	Data Source
$N(0)$	7.57bn	[10]	φ	0.000005	Assumed
$N(1)$	149, 292	[9]	ϖ	0.0000007	[12]
$s(0)$	1.0000	Estimation	T	14 days	[9]
$e(0)$	1.0000	Estimation	k	0.5	Assumed
$i(0)$	0.00002	[9]	ρ	0.000095	[12]
$r(0)$	0.000095	[12]	β	0.00002	[9]
$u(0)$	0.000095	[12]	σ	0.28404	Estimated
μ	0.000001	[10]	π	0.00567	Assumed
α_0	0.000011	[11]	ε	0.000095	[12]

Hence from Equation the Reproductive Number $R_0 = -0.009505 < 1$ means there is a 99% chances of secondary infection when an infected population interact by contact with the susceptible population.

Table 2: Estimated values of the parameters used in the Numerical experiments

Parameters	Values	Data Source	Parameters	Values	Data Source
$N(0)$	14,3bn	[10]	φ	0.000005	Assumed
$N(1)$	610, 292	[9]	ϖ	0.0000007	[12]
$s(0)$	1.0000	Estimation	T	14 days	[9]
$e(0)$	1.0000	Estimation	k	0.5	Assumed

$i(0)$	0.00003	[9]	ρ	0.000095	[12]
$r(0)$	0.000085	[12]	β	0.00002	[9]
$u(0)$	0.000085	[12]	σ	0.28404	Estimated
μ	0.000001	[10]	π	0.00567	Assumed
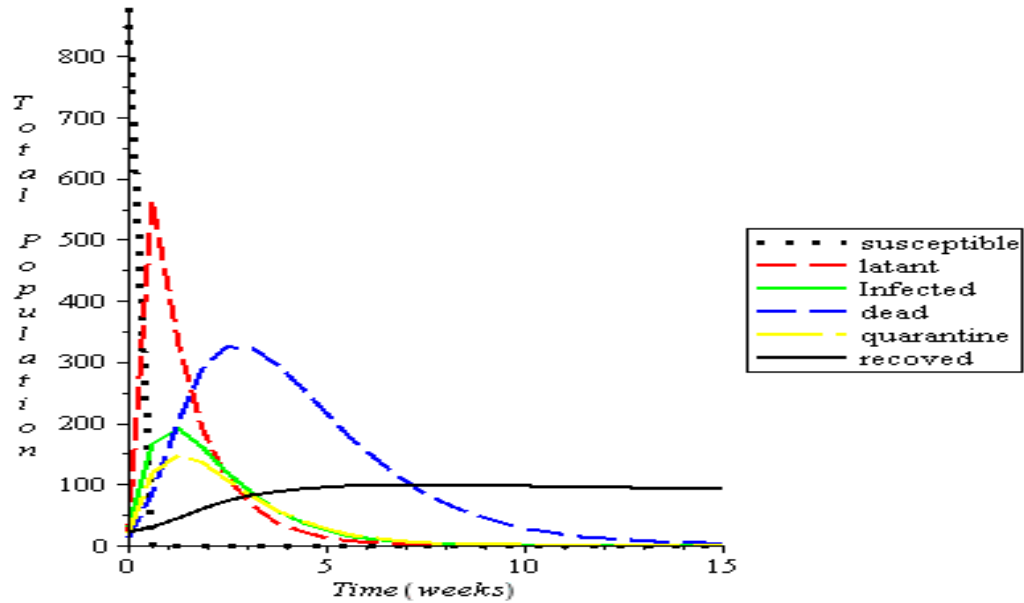
THE GENERAL BEHAVIOR OF EACH COMPARTMENT OVER TIME

Figure 4: The variation of the total population with time per week for the values of: $\Lambda = 0.06333, \mu = 0.011, \delta = 0.8, \kappa = 0.5189, \xi = 0.197, \eta = 0.3333, \phi = 0.17, \sigma = 0.5, \alpha_1 = 0.2605, \alpha_2 = 0.12$.
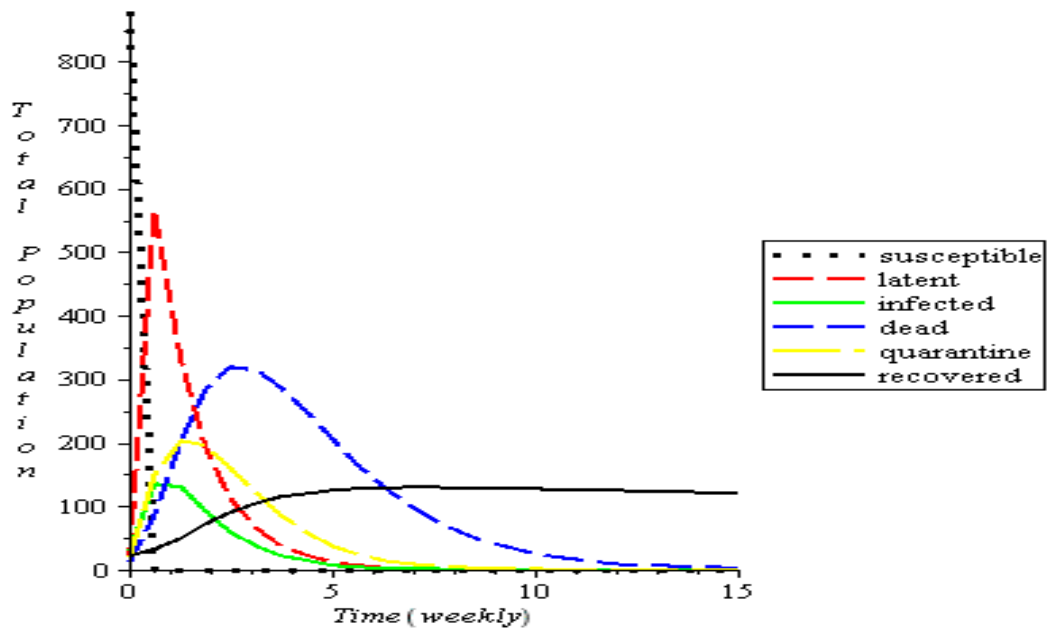
COMPARISON BETWEEN THE EFFECTS OF VARYING THE RATE OF QUARANTINING THE LATENT/INFECTED CLASS ON THE INFECTED CLASS

Figure 5: The simulation showing the effect of changes in the quarantine rate of infected on the infected group. $\Lambda = 0.06333, \mu = 0.011, \delta = 0.8, \kappa = 0.5189, \xi = 0.1, \xi = 0.5, \xi = 0.9, \eta = 0.3333, \phi = 0.17, \sigma = 0.5, \alpha_1 = 0.2605, \alpha_2 = 0.12$.
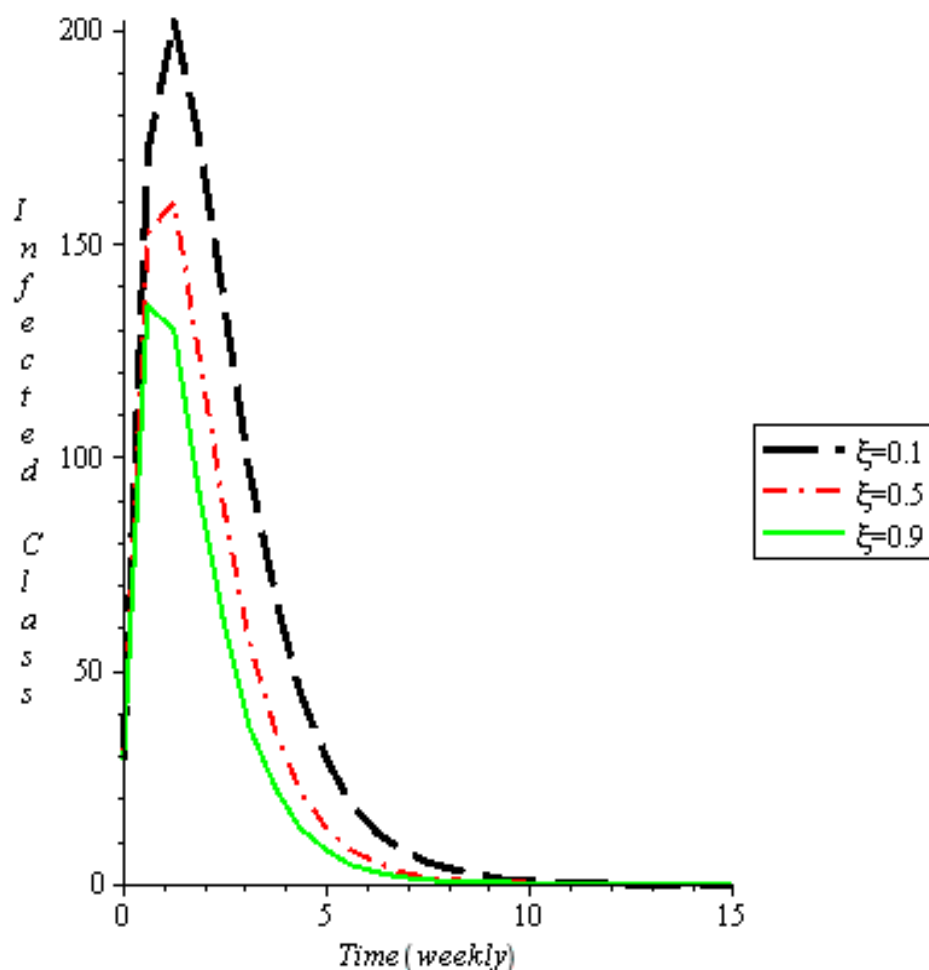
Figure 6: The simulation showing the effect of varying the rate at which the latent are quarantine on the infected group. $\Lambda = 0.06333, \mu = 0.011, \delta = 0.8, \kappa = 0.5189, \xi = 0.197, \eta = 0.1, \eta = 0.5, \ \eta = 0.9, \phi = 0.17, \sigma = 0.5, \alpha_1 = 0.2605, \alpha_2 = 0.12.$

CONCLUSION

A compartment model called SEIR has been described in this paper, demonstrating model for the number of active cases (number of sick people needing treatment) due to COVID19 in an area within South East Asia region. Actual active case data was used to obtain realistic number of the model parameters such as the reproduction number (R0), incubation, and recovery periods. It can be seen that at the beginning of the pandemic where most people were still not aware, the R0 was very high as seen by the steep increase of people got infected and admitted to the hospitals. Few weeks after the lockdown was in place and people were obeying the regulation and observing safe distancing practice, the R0 values dropped significantly and converged to a steady value of about 3. Using the obtained model parameters and fitting on a daily basis, the maximum number of active cases converged to a certain value. It is expected that in the early June 2020 that the number of active cases will drop to a low level. It is essential to simulate the process of infection and death in advance so as to apply adequate control measures and mitigate the risk of virus diffusion. One of the most commonly used mathematical algorithms to describe the diffusion of the pandemic is the SEIRUS model which we have applied to compute the number of infected, recovered, and undetectable individuals on the basis of number of contacts. In this research the $Def(J_{E_0}) = 0$ and $Trace(J_{E_0}) > 0$ does not satisfy the prescribed threshold criteria based on Gerald (2012), then the disease free equilibrium (E_0) for COVID-19 coronavirus does not satisfy the criteria for a locally or globally asymptotic stability. This implies that as a pandemic as declared by WHO (2020) the COVID-19 coronavirus does not have a curative vaccine yet and precautionary measures are advised through quarantine and observatory procedures.

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