# Applications of Non-linear Dynamics in Epidemic Modelling

Inti Benhur Rajavardhan, Ramakant Pal, Shreyas Chandgothia, Khagesh Vaidya, and Shashwat Chakraborty

Indian Institute of Technology, Bombay

## Abstract

This project report is concerned with nonlinear dynamical modeling and analysis of the COVID-19 pandemic. World Health Organization (WHO) declared the disease pandemic on March 11, 2020. The main objective is to develop a mathematical model consistent with actual dataset and explore non-linear dynamical behaviour. We have used a nonlinear susceptible, exposed, infectious and removed transmission model with added behavioral and government policy dynamics.

## 1  Introduction

Corona virus disease COVID-19 is an infectious disease currently ravaging the planet. Thus, the development of a mathematical model capable of explaining the characteristic features of COVID-19 spread is of prime importance. It has been seen that mathematical modelling is more efficient than statistical methods for studying epidemic dynamics. The key factors that govern the dynamics are the growth rate of the pathogen and the level of interaction between the pathogen and the host's immune response. Two characteristic parameters decide the strength of a disease:

- Reproduction number: It is the expected number of cases in population directly generated by one case, where all other individuals are susceptible to infection.

- Incubation Period: It is the time before the symptoms of a viral infection appears.

A basic but very powerful model used in general epidemic modelling is the Susceptible-Infected-Removed (SIR) model. People in the population who are not infected but are non-immune to the disease fall under the susceptible category. People who have acquired the disease fall under the infected category. The part of the population which got removed from the system due to the disease, i.e., the people who either died because of the disease or recovered with immunity fall under the removed category. The model can be visually represented using compartments and arrows. Transitions from one compartment to another are represented by arrows, and conventionally, the rate, the probability and the population are mentioned above it. Since, the
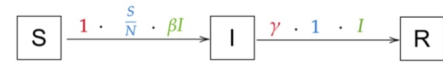


Figure 1: SIR model

COVID-19 spread is fairly complicated, a model as simple as the SIR model is incapable of appropriately explaining the dynamics involved because several other parameters need to be taken into account. Although, the SIR model cannot be used directly, it is a good base model to start working with.

A simple modification of the SIR model is the Susceptible - Exposed - Infected - Removed (SEIR) model, which is also commonly used. An individual who is infected, but exhibits no obvious symptoms and has low levels of the pathogen that is not high enough to sustain a transmission to other hosts falls under the exposed category. This small modification broadens the scope of the model because now it takes incubation period into account.



Figure 2: SEIR model

Sociological parameters such as governmental action and public response also play important role in determining the dynamics of COVID-19 spread. The level of complexity needs to be increased in a step by step

fashion to ultimately construct a mathematical model which appreciably close to the real data.

## 2    Description of model

We start with the SIR model, the visual representation of which has been shown in Figure 1. The governing equations are as follows:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

The above equation implies that the rate at which the susceptible part of the population changes, depends on the $S$-$I$interaction. $\beta$ is the transmission rate, which represents the rate of $S \to I$ transition.

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

Equation (2) indicates that the rate at which $I$ changes is enhanced by the $S$-$I$ interaction. The second term on the RHS represents the $I \to R$ transition, and $\gamma$ is the removal rate.

$$\frac{dR}{dt} = \gamma I \tag{3}$$

The $I \to R$ transmission can be thought of as an elementary first order transition with rate $\gamma$. The above model does not take into account the natural birth and death rates.

The first set of modifications needs to be made to take into account the following:

- Natural birth rate
- Natural death rate
- Incubation period

The natural birthrate is approximately constant in the short run, and a newly born individual is primarily susceptible. The natural death rate affects all the three equations because any individual can die a natural death irrespective of the category he/she belongs to. The incubation period of the infection can be taken into account by using SEIR model, i.e., introducing a new compartment $E$. Figure (2) shows the visual representation of the SEIR model. The equations after modification look like:

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S \tag{4}$$

Here, $\Lambda$ represents the natural birth rate and the last term on the right hand side, i.e., $\mu S$ represents the rate at which susceptible individuals die naturally.

$$\frac{dE}{dt} = \beta SI - \sigma E - \mu E \tag{5}$$

This equation governs the time evolution of the number of exposed individuals. Here, $\sigma$ is the incubation rate, and the last term $\mu E$ represents the rate at which exposed individuals naturally die. Similarly, the equations governing $I$ and $R$ are as follows:

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I \tag{6}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{7}$$

A strange characteristic feature of COVID-19 is that an exposed individual can infect other hosts. Thus, the path from $S$ to $E$ needs to be bifurcated, one representing contact with an infected individual ($CI$), and the other representing contact with an exposed individual ($CE$). The two paths will have two different transmission rates because the probability of a susceptible individual coming in contact with an infected individual naturally differs from that with an exposed individual. The modified set of equations is as follows:

$$\frac{dS}{dt} = \Lambda - \beta_1 SI - \beta_2 SE - \mu S$$

$$\frac{dE}{dt} = \beta_1 SI + \beta_2 SE + \sigma E - \mu E$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

The fixed points of the above four dimensional flow can be found by equating the time derivatives to zero and solving the system of linear equations. The trivial solution $(S_0^*, E_0^*, I_0^*, R_0^*) = (\frac{\Lambda}{\mu}, 0, 0, 0)$ corresponds to disease free equilibrium. The non-trivial solution is

$$E_1^* = \frac{\mu(\mu + \gamma)}{\beta_1 \sigma + \beta_2(\gamma + \mu)}(R_0 - 1)$$

$$R_1^* = \frac{\gamma \sigma}{\beta_1 \sigma + \beta_2(\gamma + \mu)}(R_0 - 1)$$

$$S_1^* = \frac{(\sigma + \mu)(\gamma + \mu)}{\beta_1 \sigma + \beta_2(\gamma + \mu)}(R_0 - 1)$$

$$I_1^* = \frac{\sigma \mu}{\beta_1 \sigma + \beta_2(\gamma + \mu)}(R_0 - 1)$$

Here $R_0$ is the reproduction number given by

$$R_0 = \frac{\Lambda[\beta_1 \sigma + \beta_2(\gamma + \mu)]}{\mu(\mu + \sigma)(\mu + \gamma)}$$

Stability analysis of endemic-equilibrium point helps in predicting whether the disease will persist or become extinct. The Jacobian matrix of the system is obtained as

$$
J = \begin{bmatrix}
-p_1 - \mu & -p_2 & -p_3 & 0 \\
p_1 & p_2 - (\mu + \sigma) & p_3 & 0 \\
0 & \sigma & -p_4 & 0 \\
0 & 0 & \gamma & -\mu
\end{bmatrix}
$$

with

$$
\begin{aligned}
p_1 &= (\beta_1 + \beta_2)S^* \\
p_2 &= \beta_2 S^* \\
p_3 &= \beta_1 S^* \\
p_4 &= \gamma + \mu
\end{aligned}
$$

The characteristic equation corresponding to the disease free equilibrium is

$$
(\lambda + \mu)(\lambda^2 + a_1\lambda + a_0) = 0 \tag{8}
$$

$$
\begin{aligned}
a_1 &= -\gamma - \sigma - 2\mu + 2\beta S_0^* \\
a_0 &= [\beta_1\sigma + \beta_2(\gamma + \mu)]\frac{\Lambda}{\mu}\frac{1 - R_0}{R_0}
\end{aligned}
$$

The roots of equation (8) are

$$
\begin{aligned}
\lambda_{1,2} &= \frac{-a_1 \pm \sqrt{a_1^2 - 4a_0}}{2} \\
\lambda_3 &= -\mu
\end{aligned}
$$

For stability, all roots of the characteristic equation should be negative. $\lambda_3$ is always negative, whereas $\lambda_{1,2}$ are negative if $R_0 < 1$, which is equivalent to

$$
\beta_1\sigma + \beta_2(\gamma + \mu) < \frac{\mu}{\Lambda}(\gamma + \mu)(\sigma + \mu)
$$

Similarly, the stability of endemic equilibrium can be analysed. The characteristic equation is

$$
a_0 + a_1\lambda + a_2\lambda^2 + \lambda^3 = 0 \tag{9}
$$

with

$$
\begin{aligned}
a_0 &= \mu(\gamma + \mu)(\sigma + \mu)(R_0 - 1) \\
a_1 &= p_4(a_2 + p_4) + \sigma p_3 + \frac{a_0 - p_3}{p_4} \\
a_2 &= \beta_2 S_0 - \mu(R_0 - 1) - (\gamma + \sigma + 3\mu)
\end{aligned}
$$

The roots of equation (9) are all negative if $R_0 > 1$. The above discussion helps us infer that the disease-free equilibrium is asymptotically stable if $R_0 < 1$, and the endemic-equilibrium is asymptotically stable if $R_0 > 1$.

To incorporate the effect of government policies, an infection function needs to be defined

$$
\Upsilon = (1 - \alpha)[\beta_1 SI + \beta_2 SE]
$$

Here, $\alpha$ represents the strength of governmental actions. The reason why it has been introduced this way is that the governmental policies tend to reduce the probability of interaction between susceptible individuals with exposed and infected individuals, which is why the older infection function $(\beta_1 SI + \beta_2 SE)$ gets scaled down. The previous analysis only slightly changes due to the introduction of $\alpha$. The new reproduction number $R_{00}$ is given by

$$
R_{00} = (1 - \alpha)R_0 = (1 - \alpha)\frac{\Lambda[\beta_1\sigma + \beta_2(\gamma + \mu)]}{\mu(\mu + \sigma)(\mu + \gamma)}
$$

Here $R_0$ is the old reproduction number. For endemic equilibrium to persist $R_{00}$ should be larger than 1. This implies $(1 - \alpha)R_0 > 0$. Finally, this gives

$$
0 < \alpha < 1 - \frac{1}{R_0}
$$

We define $\alpha_C := 1 - \frac{1}{R_0}$. Thus, the above condition can be equivalently written as $0 < \alpha < \alpha_C$. It justifies that a stronger governmental action implies better control over the spread of the infection. It also specifies a threshold value $\alpha_C$ as a function of transmission rates that would lead to complete control of the disease.

In the real world, public perception of risk plays an important role. Thus, we introduce a new state variable $D$, which represents public perception of risk. The intensity this perception is represented by the strength population response $\kappa$ and the proportion of severe cases $d$. The visual representation of this model is shown in figure (3).
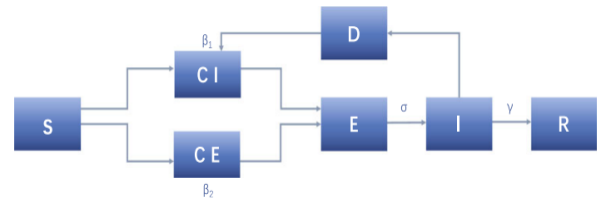


Figure 3: Modified SEIR model

The new infection function is

$$
\Upsilon = (1 - \alpha)[\beta_1 SI(1 - D)^\kappa + \beta_2 SE] \tag{10}
$$

The form of the infection function can be easily understood using the fact that public perception scales down

the susceptible-infected interaction term but doesn't affect the susceptible-exposed interaction term because people have no way of distinguishing between a susceptible and an exposed individual. The system of equations describing the dynamics of the model introduced above is

$$\frac{dS}{dt} = \Lambda - \Upsilon - \mu S$$
$$\frac{dE}{dt} = \Upsilon + \sigma E - \mu E$$
$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$
$$\frac{dD}{dt} = d\gamma I - \lambda D$$

The last equation describes the time evolution of the introduced state variable $D$. The first term on RHS qualitatively represents the proportion of severe cases of infection which got removed from the population, which increases public perception of risk as expected. The second term indicates that as the public becomes more cautious, the conditions become better, and hence the value of $D$ tends to go down. Here $\frac{1}{\lambda}$ is the mean period of public response and the model reflects the fact that public reaction would increase when more people get infected and would naturally diminish over time. This model is appreciably close to the real world scenario.
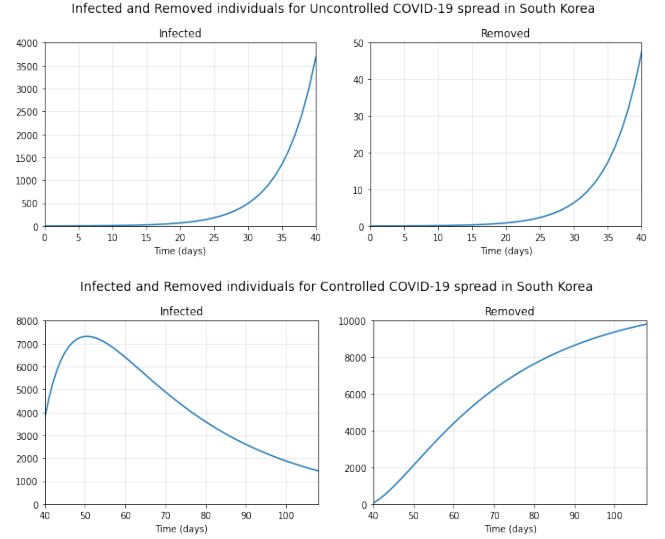
If we try to find out the fixed points of the 5D flow described above for any general $\kappa$, we obtain a system of transcendental equations which doesn't lead to explicit expressions of $S_p^*, E_p^*, I_p^*, R_p^*$, and $D_p^*$ ("$p$" in the subscript represents public response). Thus, we discuss the two limiting cases $\kappa = 0$ and $\kappa \to \infty$, and then try to infer about cases with other values of $\kappa$. The case with $\kappa = 0$ is identical to the SEIR model with governmental influence. For $\kappa \to \infty$, we get a non-trivial equilibrium point with

$$I_p^* = \frac{I_1^*}{R_0 - 1}[R_0 - 1 - \frac{\beta_1 \sigma}{\beta_2(\gamma + \mu)}]$$

## 3   Implementation

First we try to reproduce the results given in the paper. South Korean dataset was analysed in the reference paper which consisted data of a total of 108 days. No action was taken by the government in the first 40 days, but then COVID-19 related policies were made. Since we are considering the data of the early stage of COVID-19 spread, it is reasonable to disregard the

public perception state variable $(D)$ and associated parameters $(d, \kappa$ and $\lambda)$. The value of $(\beta_1, \beta_2, \gamma)$ for the uncontrolled and controlled conditions quoted in the reference paper are (0.4071399, 0.0626798, 0.0026) and (9.98E-07, 7.66E-06, 0.0329) respectively, and since they determine $\alpha$, it has not been included explicitly. $\sigma = 0.14$ which is the inverse of the incubation period and is fixed for COVID-19. Figures (4) and (5) show the obtained simulation plots.



Infected and Removed individuals for Uncontrolled COVID-19 spread in South Korea



Infected and Removed individuals for Controlled COVID-19 spread in South Korea

Next we analyse the evolution of the disease for different levels of governmental control and public response. The strength of governmental action $\alpha$, which ranges from 0 to 1. The strength of public response $\kappa$ ranges from 0 to $\infty$. Again we obtain a very good agreement with the results reported in the paper.



No Control ($\alpha = 0$, $\kappa = 0$)



Government Control ($\alpha = 0.75$, $\kappa = 0$)
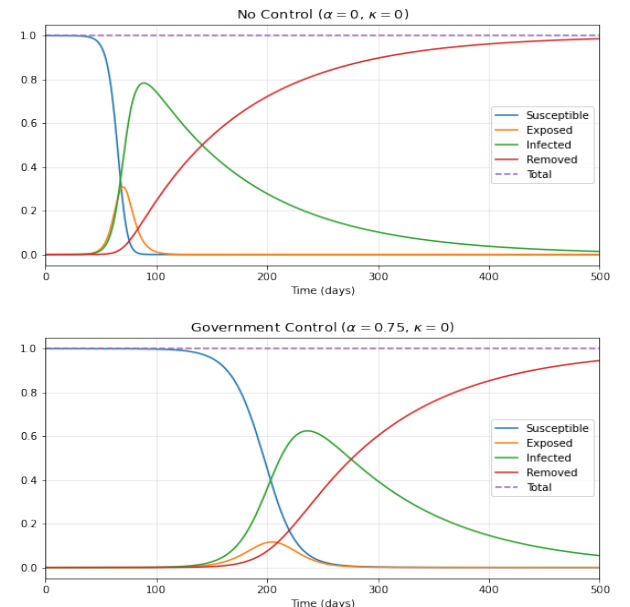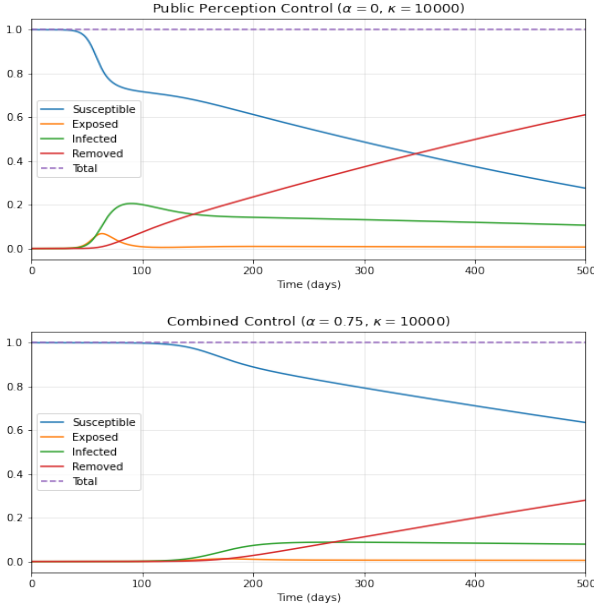
## 4   Modifications

The current model only predicts the number of Removed individuals in total, rather than explicitly provide the number of people recovering and dying. The main aim of epidemic management by the government is to reduce the total number of people dying. Thus, an absolutely important modification to be made is to separate the "Removed" compartment into two compartments namely "Recovered" and "Dead". We also get rid of the public perception compartment by using time-dependent parameters as explained later. The modified set of dynamical equations now becomes:

$$\frac{dS}{dt} = -\beta \cdot I \cdot \frac{S}{N}$$
$$\frac{dE}{dt} = \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E$$
$$\frac{dI}{dt} = \delta \cdot E - (1-\alpha) \cdot \gamma \cdot I - \alpha \cdot \rho \cdot I$$
$$\frac{dR}{dt} = (1-\alpha) \cdot \gamma \cdot I$$
$$\frac{dD}{dt} = \alpha \cdot \rho \cdot I$$

The list of all the variables and parameters in use is given by:

- $N$: Total population
- $S(t)$: Number of people susceptible on day t
- $E(t)$: Number of people exposed on day t
- $I(t)$: Number of people infected on day t
- $R(t)$: Number of people recovered on day t

- $D(t)$: Number of people dead on day t
- $\beta$: Expected amount of people an infected person infects per day
- $d$: Number of days an infected person has and can spread the disease
- $\gamma$: The proportion of infected recovering per day $(\gamma = \frac{1}{d})$
- $R_0$: The total number of people an infected person infects $(R_0 = \beta d = \frac{\beta}{\gamma})$
- $\delta$: Length of the incubation period
- $\alpha$: Fatality rate
- $\rho$: Rate at which people die (inverse of the expected number of days a person takes to die after being infected)

These set of equations can be represented in the form of a simple state transition diagram as follows:
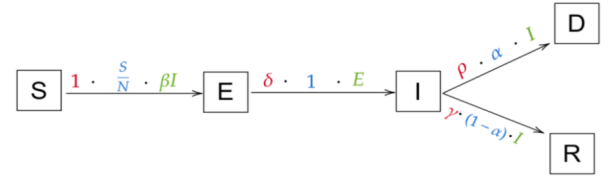


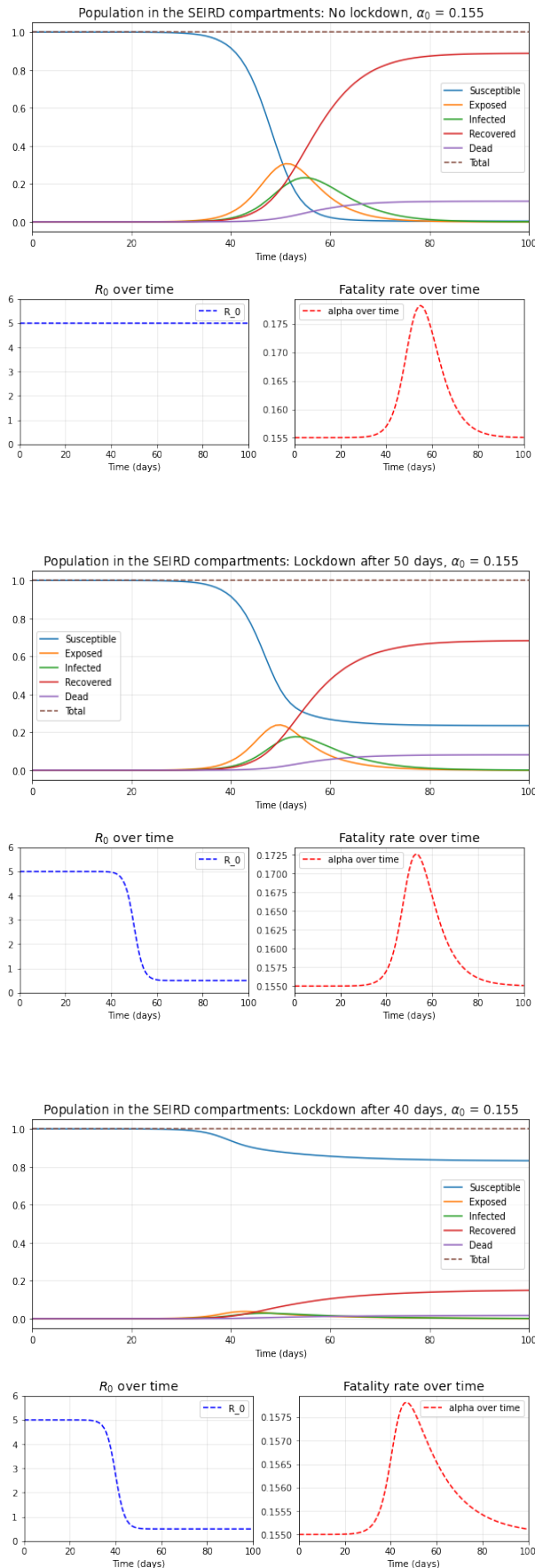Figure 4: SEIRD model

We make a couple of more modifications.

Firstly we make the paramater $R_0$ (reproduction number) time-dependent to incorporate the effect of a lockdown. Specifically we take a logistic function, where $R_0$ stays constant initially, decreases smoothly around the time of implementation of the lockdown, and reaches a minimum value where again it becomes constant.

$$R_0(t) = \frac{R_{0_{\text{start}}} - R_{0_{\text{end}}}}{1 + e^{-k(-t+t_0)}} + R_{0_{\text{end}}}$$

where $R_{0_{\text{start}}}$ and $R_{0_{\text{end}}}$ are the values of $R_0$ on the first and the last day, $t_0$ is the day of the inflection point (i.e. the main lockdown date) and $k$ is a factor controlling the decline rate of $R_0$. In the simulation ahead, we use $R_{0_{\text{start}}} = 5, R_{0_{\text{end}}} = 0.5, k = 0.5$ and $t_0 = [40, 50, \infty]$

Secondly, we make the parameter $\alpha$ (fatality rate) dependent on the available resources and the average age of the population. This can be done by simply scaling $\alpha$ in proportion to the infected fraction of the population. More infected people leads to lesser available health resources and thus, higher fatality rate.

$$\alpha(t) = s \cdot \frac{I(t)}{N} + \alpha_0$$

Population in the SEIRD compartments: No lockdown, $\alpha_0 = 0.155$



Population in the SEIRD compartments: Lockdown after 50 days, $\alpha_0 = 0.155$



Population in the SEIRD compartments: Lockdown after 40 days, $\alpha_0 = 0.155$

where $I(t)$ is the proportion of the infected population, $s$ is a scaling factor that controls the influence of $I(t)$ and $\alpha_0$ is the base fatality rate (i.e. when no one is infected and all hospital resources are available). $\alpha_0$ is calculated as the average fatality rate of different age groups (0-19 yrs, 20-39 yrs, 40-59 yrs, 60-79 yrs, 80+ yrs), weighted over their respective populations. For the simulation, we use $s = 0.1$ and $\alpha_0 = 0.155$.

On the left, we report simulation results for running the dynamical equations over a period of 100 days for different lockdown dates, with the following parameters: $N = 1e6, \gamma = 0.25, \delta = 0.2, \rho = 0.11$.

## Conclusions

In this project, we developed an SEIR model inclusive of sociological factors like governmental action and public response for the COVID-19 spread. We took the values of transmission and removal rates quoted in the reference paper, in which these parameter values were calculated using statistical estimation techniques on South Korean dataset. We first performed the non-linear dynamical analysis of the system, then attempted to enhance the scope of the model by making necessary modifications, and then developed a code framework to reproduce plots appreciably close to those given in the reference paper.

Through this project report we emphasise that the role of non-linear dynamics is quite crucial in epidemic modelling. Development of a mathematical model for a disease, and then fetching out information about the time evolution of the system through non-linear analysis, helps in deciding the plan of action to bring the situation under control. This is our code repository.

## References

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