
Modelling COVID-19 dynamics using an extended SEIR model

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ABSTRACT

There is a long history of mathematical models in epidemiology. Most of these models, divide the population into classes defined by a rate of transmission between these compartments. SEIR is one such compartmental model. In this article, we study the chaotic dynamics of the SEIR model modified by the introduction of stochastic variations. The model is then further improved according to control strategies and used to study the evolution of the COVID-19 pandemic in Russia and Finland. Using this model, we are also able to calculate the mortality risk of individuals in need of critical care as well as analyse the effects of population size and the quality of healthcare systems on the evolution of the pandemic.

*Keywords: Dynamical systems · Chaos · SEIR model · COVID-19
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1. INTRODUCTION

Compartmental transmission models have become an invaluable tool to study the dynamics of an epidemic. Time and again, these models have proved their efficiency by predicting an accurate time evolution of past epidemics. In recent years, a large quantitative literature has been generated to explore the dynamical effects of such pandemic evolution. One of the simplest yet famous epidemic model employed to study the compartmental transmission and progress of an infectious disease is the SEIR epidemic model. This model will be the main focus of this article.

Epidemic evolution in nature is known to be chaotic and hence it is important that the model employed also incorporates such dynamics. The seasonally forced SEIR model presented in this article is one such model that generates an extremely rich spectrum of dynamical behaviour. The behaviour of this model is found to be sensitive to the added noise to the system. As we attempt to make this model more biologically realistic, the chaotic activity is found to be suppressed. Thus, we build an extended version of the SEIR model for the modelling of COVID-19.

Based on WHO statistics, since the detection of the first case of COVID-19 until December 25, 2020, the total number of confirmed cases worldwide is 80,133,093 and the number of deaths is 1,755,653 ([Khedher et al. \(2021\)](#)). The worrying spread of this infectious disease has invoked a need for various mathematical and machine learning models that will help predict the future of this pandemic in hopes of containing it. In this article, we use the extended version of the SEIR model to study the evolution of the pandemic in two countries; Russia and Finland by employing curve-fitting techniques on obtained data of the epidemic evolution until the 12th June, 2021. Finally, we also estimate to obtain parameters that govern the model. Finally, we also estimate the probability of the amount of the population of the country that will be in need of critical care and also the probability of their fatalities.

2. GENERALISED SEIR MODEL

In this section, we analyze the the generalised SEIR model (see, [Godio et al. \(2020\)](#)) that is based on epidemiological status of the individuals. The mathematical model is build on four compartments; the Susceptible, Exposed, Infectious and Removed (SEIR), as illustrated in figure: 1. It is the simplest case that can be used to model

infectious diseases. However, such a generalised model does not take into account the external influences that effect the population at a given time. Due to this, it is also not possible to find chaotic behaviour in such a general model.

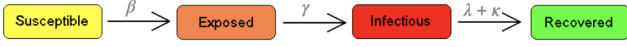


Figure 1. Generalised SEIR compartmental model.

The total (initial) population, N , is categorized into four classes, namely, susceptible, $S(t)$, exposed, $E(t)$, infected-infectious, $I(t)$ and recovered, $R(t)$, where t is the time variable. The governing differential equations depicting the generalised SEIR model are:

$$\begin{aligned}
 \frac{dS(t)}{dt} &= -\beta I(t) \cdot \frac{S(t)}{N} \\
 \frac{dE(t)}{dt} &= \beta I(t) \cdot \frac{S(t)}{N} - \gamma E(t) \\
 \frac{dI(t)}{dt} &= \gamma E(t) - (\lambda + \kappa) I(t) \\
 \frac{dR(t)}{dt} &= (\lambda + \kappa) I(t)
 \end{aligned} \tag{1}$$

The differential equations presented in equation: 1 are regulated by the parameters β , γ , λ and κ . Before the start of the pandemic, the Susceptible (S) compartment comprises of the whole population as it is the section of the population that is subjected to the infection. The fraction of the population that has been infected but has not shown any symptoms yet falls into the exposed (E) compartment. Then, the rate of transmission of the disease or the movement of the people from the susceptible to the exposed compartment is determined by the transmission rate β .

There is a latent period after which the exposed population move to the infected(I) compartment of the population and this is given by the parameter gamma. From the differential equations it can be noticed that the section of the population that is removed from the susceptible category has been added to the infectious category and similarly the removal from the exposed category results in the addition of the same amount in the infected category. Hence, the total amount of population at any given time is a constant and it is given by the sum of all the compartments:

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

Finally, the recovered (R) comprises of the individuals who have completely recovered from the disease. Depending on the pandemic being modelled, we may or may not reintroduce it back into the susceptible category; supposed that an individual cannot contract the disease again. Here, the R category also consists of the individuals who have died of the disease. λ and κ are the recovery rate and the death rate respectively. For the classical model, we do not consider the natural births and deaths of the population during the time span of the disease.

Taking into consideration, the complexity of the disease and the purpose for its modelling, there exists different variations of the classical SEIR model, regarding both the equations and the parameters, or managing different fitting techniques to make the model represent the reality as close as possible. In this article, we implement two such modifications. The former for the search of chaotic behaviour and the latter to implement curve-fitting techniques to acquired data.

3. MODIFIED SEIR MODEL FOR THE SEARCH OF CHAOTIC BEHAVIOUR

Epidemic modelling is often considered to be chaotic due to the the unanticipated addition of noises in nature. It is not truly possible to set a deterministic model to study the evolution of a pandemic due to its unpredictability. However, under several assumptions, we attempt to present a modified SEIR model that accounts for the chaotic nature of the evolution of an epidemic. In particular, we assume that the infection rate is time-dependent. We can consider scenarios such as a lockdown implementation that affects the number of contacts between people and a brings about a decrease in their overall mobility. This is implemented using the introduction of a stochastic variation to the rate of transmission β .

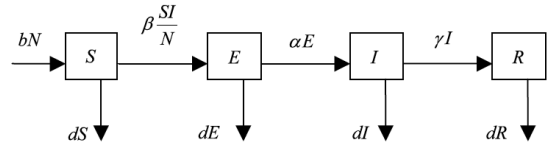


Figure 2. SEIR model for search of chaotic dynamics.

This model depicted in figure:2 (see, [Yi et al. \(2009\)](#)) is defined by the following set of differential equations:

$$\begin{aligned}
 s' &= b - bs - \beta si \\
 e' &= \beta si - (\alpha + b)e \\
 i' &= \alpha e - (\gamma + b)i \\
 r' &= \gamma i - br
 \end{aligned} \tag{2}$$

In this model, we assume N is constant and set it to one. We also reduce the variables such that, $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $r = \frac{R}{N}$. This implies $1 = s + e + i + r$. The new parameters b and d are the rate of natural birth and death respectively. This was neglected in the generalised model. In equation: 2, the rate at which the exposed individuals become infective is given by α and γ is the rate of recovery. In order to induce chaos in the generalised model, we introduce a seasonal forcing to the transmission rate β given by $\beta = \beta_0(1 + \beta_1 \cos 2\pi t)$.

3.1. Numerical Integration of the system

To integrate the system presented in equation:2, we use the Runge-Kutta fourth order integrator. The integration and simulation of the phase space is presented in the attached file `seir.py`. Using β as a varying parameter, we can analyse the dynamical behaviour of this system. The plots of the phase space given below are for the parameters, $b = 0.02$, $\alpha = 35.84$, $\gamma = 100$ and $\beta_0 = 1800$. The following cases are observed.

3.1.1. Periodic attractor

At a low value for $\beta_1 = 0.1$, we observe the presence of a periodic attractor characterised by its cyclic motion in phase space. The evolution of the system with time is also periodic and consistent as seen in figure: 4.

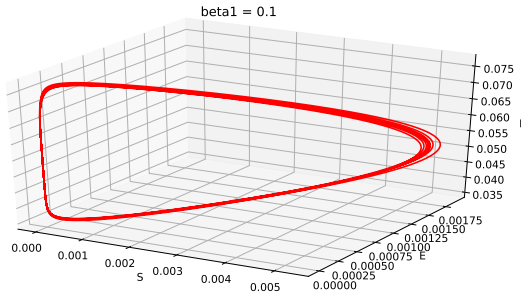


Figure 3. Periodic attractor for $\beta_1 = 0.1$.

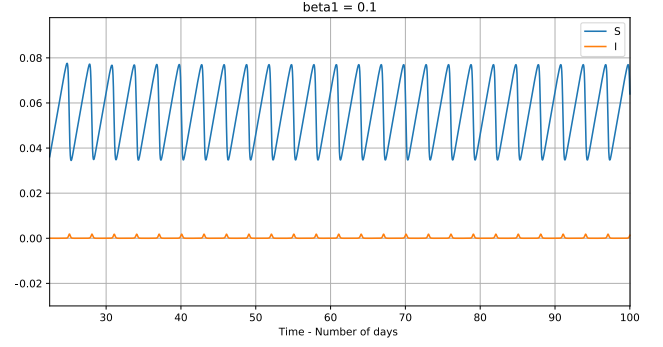


Figure 4. Evolution of the SEIR model for $\beta_1 = 0.1$.

3.1.2. Chaotic attractor

For a high value of $\beta = 0.9$, we observe the presence of chaotic behaviour of the dynamical system in the phase space as shown in figure: 5. This is a low dimensional chaotic attractor. There is also unexpected variations in the evolution of the model with time (figure: 6) due to the presence of chaos in the system.

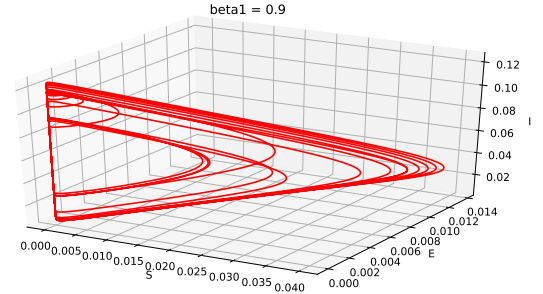


Figure 5. Chaotic attractor for $\beta_1 = 0.9$.

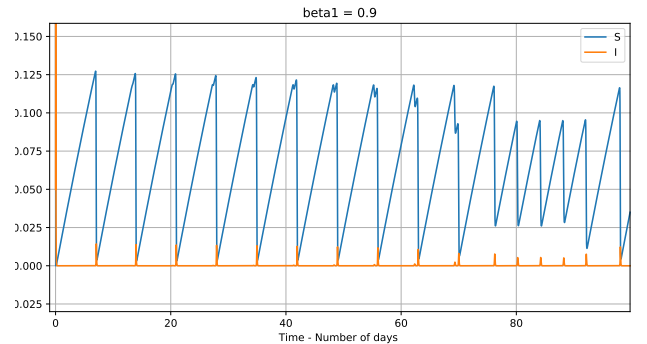


Figure 6. Evolution of the SEIR model for $\beta_1 = 0.9$.

3.1.3. Hyper-chaotic attractor

For the β values in the range of 0.25 to 0.35, we observe interesting behaviour of the dynamical system. This is shown in the figures: 7 & 8. The attractor of chaotic systems that may have two or more positive Lyapunov exponents is called hyperchaotic. Such dynamical behavior is similar to chaotic dynamical behavior. The projections of hyperchaotic attractor on a phase plane are of more complicated trajectories as compared to the low dimensional chaotic attractors.

Hyperchaos in epidemiological models imply the sudden break out of an epidemic and its gradual spread in a region at the period of the high incidence of the epidemic disease. This means that many people in the region will be infected by disease, and some of them could even lose their lives.

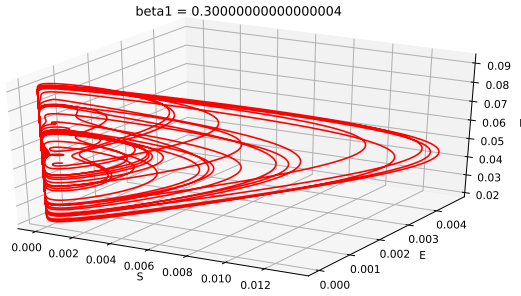


Figure 7. Hyper-Chaotic attractor for $\beta_1 = 0.3$.

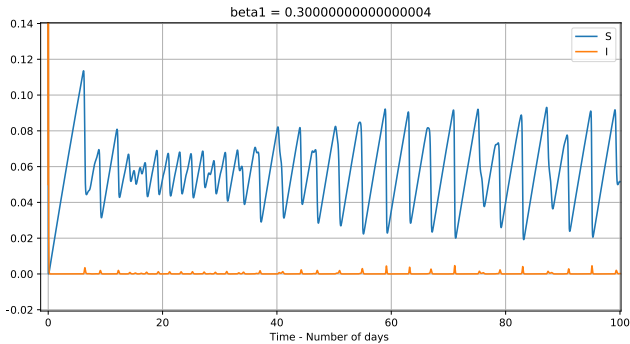


Figure 8. Evolution of the SEIR model for $\beta_1 = 0.3$.

The evolution of the hyper-chaotic attractor with time as depicted in 8 has several chaotic variations.

4. LYAPUNOV EXPONENTS

For the computation of the Lyapunov exponents of the system to confirm the presence of chaos, we use the QR

decomposition method (Felix et al. (1970)). The final Lyapunov exponents were calculated using equation: 3

$$\lambda = \frac{1}{kdt} \sum_{i=1}^n \log |J_{ii}| \quad (3)$$

where, dt is the time step of the integrator. The numerical simulation to calculate the Lyapunov exponents can be found in the file `lyapunov.py`.

For low values of β , such as 0.1, we have a periodic attractor. We find that one of the lyapunov exponents, $\lambda_1 \approx 0$, whereas the others are negative. For values of β that show chaotic dynamics in the phase space, we obtain either two or three positive Lyapunov exponents. Hence, we can confirm the presence of chaos in this modified SEIR model.

5. EXTENDED SEIR MODEL FOR MODELLING COVID-19

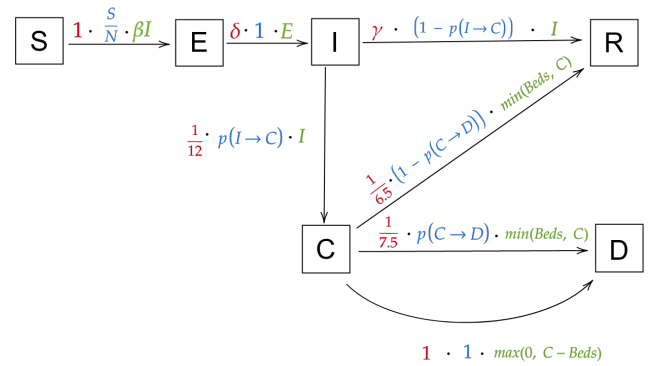


Figure 9. The Extended SEIR model

In order to adapt to the realistic evolution of an infectious disease such as COVID-19 and to carry out curve-fitting for the acquired data, we extend the SEIR model. The data used for the modelling of COVID-19 is obtained from the data repository for the Novel Coronavirus Visual Dashboard operated by the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE).

In the extended SEIR model, we add two additional compartments which are the section of the population in need of critical care and the section of the population that are deceased. The rate of transitions between these compartments are now mediated by the parameters as well as the probability of transition calculated from past statistical data. This model is illustrated in the figure 9.

Using this model, we are also able to calculate the probability of individuals requiring treatment in the

Table 1. Description of the parameters used in the Extended SEIR Model

Parameters	Description of the parameters
N	Total Population.
S(t)	Section of the population that is susceptible to the disease.
E(t)	Section of the population exposed to the disease but do not show any symptoms.
I(t)	Infected section of the population.
R(t)	Section of the population that has recovered from the disease.
C(t)	Section of the population under critical care.
D(t)	Section that has been removed from the population due to death.
β	Expected amount of people an infected person infects per day.
δ	Length of the incubation period.
γ	the proportion of infected recovering per day ($\gamma = 1/D$).
P(I \rightarrow C)	The probability of going into critical care.
P(C \rightarrow D)	The probability of disease becoming fatal for a patient in need of critical care.
Beds	The total number of beds available in the ICU at any given instant.
s	The initial amount of population susceptible to the disease.
R ₀	Reproduction number; the expected number of cases directly generated by one case in a population.
x ₀	The time of steepest descent in the reproduction number.
x	The day in consideration.
k	The logistic growth rate or steepness of the curve

Intensive Care Unit(ICU) and the probability of mortality risks at the ICU. We also estimate the effects of certain parameters onto the model and the importance of transition rates from one compartment to the other.

The extended SEIR model is implemented using the set of differential equations presented in equation: 4. The description for the set of parameters used is given in the table: 1

$$\begin{aligned}
 \frac{dS(t)}{dt} &= -\beta I(t) \frac{S(t)}{N} \\
 \frac{dE(t)}{dt} &= \beta I(t) \frac{S(t)}{N} - \delta E(t) \\
 \frac{dI(t)}{dt} &= \delta E(t) - \frac{1}{12} P(I \rightarrow C) I(t) - \gamma (1 - P(I \rightarrow C)) I(t) \\
 \frac{dC(t)}{dt} &= \frac{1}{12} P(I \rightarrow C) I(t) - \max(0, C - Beds(t)) \\
 &\quad - \frac{1}{7.5} P(C \rightarrow D) \min(Beds(t), C) \\
 &\quad - \frac{1}{6.5} (1 - P(C \rightarrow D)) \min(Beds(t), C) \\
 \frac{dD(t)}{dt} &= \frac{1}{7.5} P(C \rightarrow D) \min(Beds(t), C) \\
 &\quad + \max(0, C - Beds(t)) \\
 \frac{dR(t)}{dt} &= \gamma (1 - P(I \rightarrow C)) I(t) \\
 &\quad + \frac{1}{6.5} (1 - P(C \rightarrow D)) \min(Beds(t), C)
 \end{aligned}
 \tag{4}$$

For the modelling of the COVID-19 epidemics, we choose some standard values for the parameters. The average number of days that takes an infectious individual to require critical care is known to be 12 days. A critical patient will take an average of 6.5 days to recover or 7.5 days when the disease becomes fatal. At any given time, the rate of transition of the population out of the critical care compartment depends on the number of beds available at that given instant. This is given by the equation; $Beds(t) = (\frac{Beds \text{ per } 100k}{100k \times N}) + s(\frac{Beds \text{ per } 100k}{100k \times N}) * t$.

Hence, we compare the number of beds to the total number of critical patients under the assumption that all critical patients that do not get treatment due to the shortage of beds will die. Moreover we also consider that only critical cases fill up the hospitals and can lead to a higher fatality rate due to the shortage of available care. Similarly, the seasonally forced transition parameter β is dependant on the reproduction number R_0 that is, $\beta = R_0 * \gamma$.

The reproduction number R_0 , can be modelled using a logistic function instead of assuming it as a parameter that constantly decreases with the evolution of the pandemic, we assume that the reproduction number shows an exponential decrease after which it levels off showing the maximum sustainable population that is with another assumption that the recovered section of the population cannot contract the disease again. Thus, the logistic function is a convenient mathematical description of a

population that levels off.

$$R_0 = \frac{R_{0\text{initial}} - R_{0\text{final}}}{1 + e^{-k(-x+x_0)}} + R_{0\text{final}}$$

Similar to the generalised SEIR model, we assume a constant population N at any given time with the total number of natural deaths and natural births not being high enough to significantly change the structure of the population.

6. RESULTS AND DISCUSSIONS

From the obtained dataset ([Covid-Dataset \(2021\)](#)), we isolate the data for the sum of the total number of affected and infected population in Russia over the time series. The choice of country is arbitrary and only taken in the interest of the shape of the graph and it's simplicity to apply least squares fitting on to the extended SEIR model presented in equation: 4. The simulations carried out on this extended model can be found in the attached file `covid19.ipynb`.

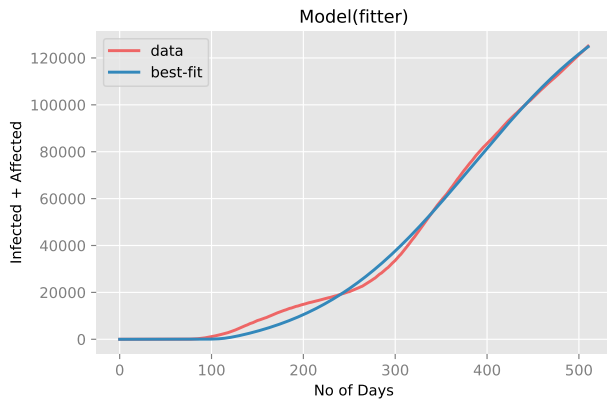


Figure 10. Curve fitting the acquired data for Russia onto the extended SEIR model.

The curve fitting is carried out using the least-squares method of the built-in Python module `lmfit`. We are able to determine the best parameters using the fit shown in figure: 10. We obtain the following values for the parameters; $R_{0\text{init}} \approx 6$, $k \approx 5$, $x \approx 108$, $R_{0\text{final}} \approx 1.27$, $\text{prob}(I \rightarrow C) \approx 0.03$, $\text{prob}(C \rightarrow D) \approx 0.1$ and $s \approx 0.1$.

Using these parameters obtained from fit, we can plot the evolution of the COVID 19 epidemic in Russia. The time series of this evolution over a period of 600 full days is shown in figure: 11

As we can see from the figures: 11 and 12, the pandemic takes more than 600 days to recede. The bell-shaped

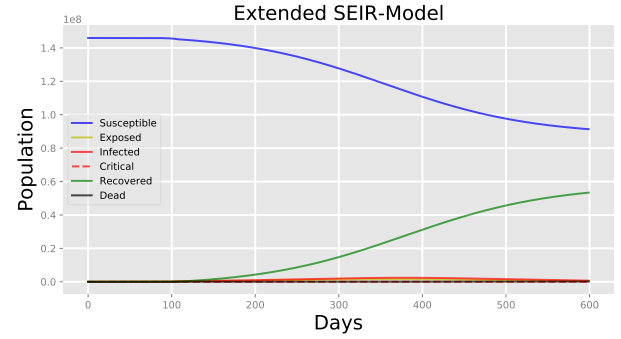


Figure 11. Evolution of COVID-19 in Russia over a period of 600 full days

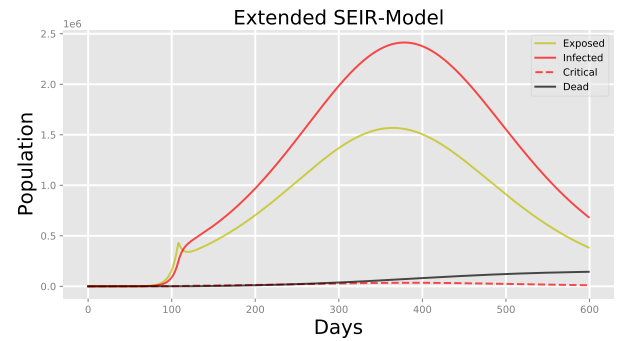


Figure 12. Evolution of the exposed, infected, critical and dead sections of the population over a period of 600 full days in Russia

models show that the number of positive cases shown by the red line, increases day by day, as is that of deaths. Initially, the amount of the susceptible population is the highest, but this slowly decreases since the recovered population is not reintroduced into this category under the assumption that recovered individuals acquire immunity to COVID-19. This can also be taken as the reason for the decline of the epidemic. Using this model, we were also able to estimate the percentage of people who go into critical care which was found to be approximately 2.7 percent of the population in Russia. We have also calculated that approximately 10 percentage of the individuals in need of critical care will expire.

According to the data obtained for the total number of beds availability in Russia, we can observe that there is never a case of over-capacity (figure: 13) of the hospitals in Russia. Moreover, the logistic decrease of the reproduction number can be observed in the figure: 14. This shows a sharp decline in the reproduction number after 100 full days of the pandemic evolution, after which it levels to a value 1.27.

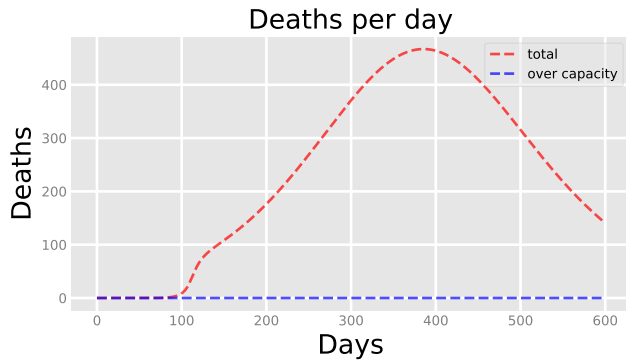


Figure 13. Total number of deaths per day.

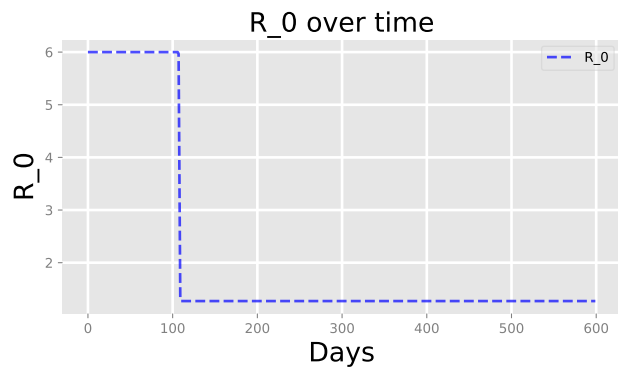


Figure 14. Evolution of the reproduction number with time.

Assuming that the parameters determined from the least squares method, remain fairly constant with the change in the size of the population, we also model the evolution of the pandemic in Finland. Using the plots in figures, 15 and 16, we can compare the difference in the evolution of the COVID-19 epidemic in Finland and Russia. The difference in population size and the health care facilities in both the countries is clearly visible in these figures.

Unlike in Russia, the epidemic takes only around 300 full days to completely die down. There is a peak in the total number of positive cases around 150 days, also accounting for the sharp decline in the susceptible category of the population. This also indicates that the pandemic is unable to evolve over a longer time period due to a reduction in the susceptible population and a drop in the reproduction number around the same time. However, from the figure: 17 we observe that, unlike the health care units in Russia, Finland has an over-capacity of the health care units after about 150 days which is the peak of the pandemic. The largest number of deaths also occur during this period.

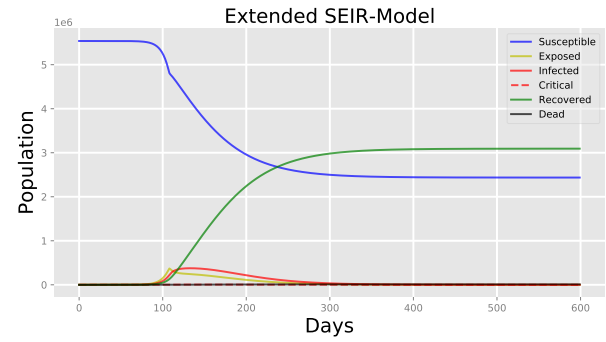


Figure 15. Evolution of COVID-19 in Finland over a period of 600 full days.

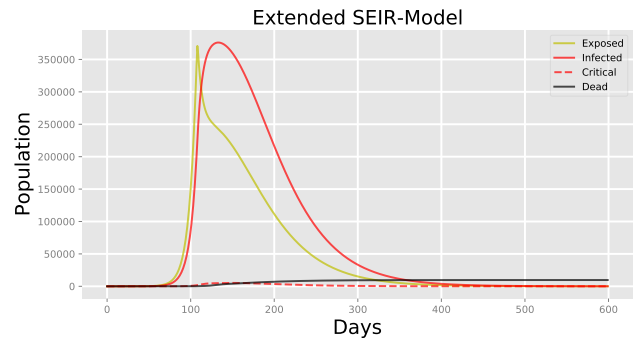


Figure 16. Evolution of the exposed, infected, critical and dead sections of the population over a period of 600 full days in Finland.

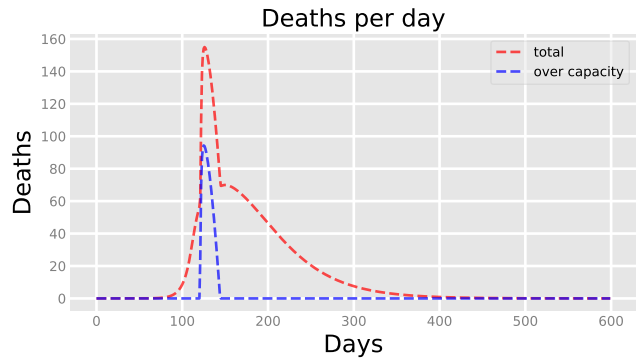


Figure 17. Over-capacity of the health care units in Finland.

Finally, we can also discuss the effects of the parameters such as γ , β and δ . For the simulations, γ was taken to be 14 days accounting for the initial quarantine period estimated for COVID. However, it is now known that this period can be decreased do about an average of 10 days after which the infected individual becomes completely free of the disease. The decrease of this parameter yields faster decline of the pandemic. Moreover,

the transmission parameter plays a huge role in the evolution of the pandemic. When policies such as lockdowns and social distancing is implemented, we are able to decrease the possibility of transmission of the disease between individuals. This can be taken into account for further extending the present model and studying the effects of such policies on containing the pandemic.

Novel Coronavirus (COVID-19) Cases Data;
<https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases>

7. CONCLUSION

Chaotic behaviour exists in several models used in epidemiological modelling and they account for the sudden breakouts and spread of infectious diseases. It is thus imperative to study the chaotic nature of commonly used models in epidemiology such as the famous SEIR model.

We applied two different approaches for solving the equations of the SEIR model to describe the evolution of the epidemic phenomenon. The former model analyzes the chaotic behaviour of the system whereas the extended model allows ease of curve-fitting of the acquired data. Both models incorporate a stochastic variation of parameters that accounts for dynamical behaviour of the model.

The main purpose of this article was to review the chaotic properties of the SEIR model and make aware its ability to be an efficient tool in modelling the current epidemic and support the policymakers in their decision about the action to minimize the impact of the disease. However, it must be kept in mind that the analysis of such modelling goes beyond the mathematical interpretations and requires wide-scale evaluations on all the possible socio-economic and political factors.

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