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PREDICTION OF COVID-19 PANDEMIC SPREADING IN NORTH CYPRUS

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Abstract. During pandemics like COVID-19 major epidemiological parameters, that characterize the disease evolution, can be estimated using mathematical models. Numerous mathematical models assume that the population can be subdivided into multiple compartments that are categorized according to illness stage. It is the purpose of this work to create $SEICRD$ model of COVID-19 and fit it with time-dependent reproduction values and resource-dependent mortality rates to actual COVID-19 data with the intention of getting as near to the actual results as possible and to create precise estimates of expected future trends for Northern Cyprus.

Keywords: COVID-19, Compartmental model, Basic reproduction number, $SEICRD$ Model, Curve fitting.
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1 Introduction

For many years, the outbreak and spread of diseases have been questioned and studied. Indeed, Graunt was the first scientist to attempt systematic quantification of causes of death, and his analysis of causes of death resulted in a theory that is now widely accepted among contemporary epidemiologists. Bernoulli was the first mathematician to develop a mathematical model for the description of an infectious disease. In 1760, he modelled the spread of smallpox, a disease that was widespread at the time, and argued for the benefits of variolation. Kermack & McKendrick (1927) developed a simple deterministic (compartmental) model for predicting the behaviour of epidemic outbreaks. They proposed a nonlinear system of ordinary differential equations to describe the spread of diseases in their mathematical epidemic model, titled the Susceptible-Infected-Recovered (SIR) model.

According to Liu et al. (2020) , The International Committee on Taxonomy of Viruses designated the novel coronavirus strain SARS-CoV-2 as the fifth pandemic after the 1918 influenza pandemic. It originated in Wuhan, China, and has since expanded across the globe. Based on phylogenetic analysis, the coronavirus was given the name Severe Acute Respiratory Syndrome CoronaVirus 2 (SARS-CoV-2). The virus is genetically related to the SARS-CoV virus, which caused an outbreak of severe acute respiratory syndrome in 2002-2003. The World Health Organization identified SARS-CoV-2 as COVID-19 (short for coronavirus disease 2019). Due to the virus's great transmissibility, it continuously evolves and rapidly spreads across the human population.

On March 10, a resident of Northern Cyprus who had recently returned from a trip to Europe reported the first case. The first COVID-19-related mortality in the country occurred on March 28, 2020. Northern Cyprus has 5,746 confirmed cases, 4,922 recoveries, 28 deaths, and a death rate of 87 per million people as of April 21, 2021, which is one of the lowest rates in the world.

As of 16 April 2021, the observed case fatality rate in Northern Cyprus is 0.52 percent, which ranks it 139th globally.

In this work, we use $SEICRD$ model, the most extended SIR model, that takes into account changes in the basic reproductive number over time as well as limited resources due to patients filling up hospital beds. We then use a curve fitting model to determine the necessary parameters for our model that produce predictions that are most similar to the real data. Python programming language and its libraries are used for the implementation of proposed models.

The paper is organized as follows. Section 2 deals with the compartmental model in Epidemiology, develops the SIR model and focuses on some time-dependent parameters of the model. The $SEICRD$ model used for simulation is carefully explained in Section 3. This section details resource- and age-dependent fatality rates and provides reasoning for $SEICRD$ model. Section 4 focuses on the results obtained in the present work. The paper ends up with conclusions.

2 Research Method

2.1 Compartmental Models in Epidemiology

As Brauer et al. (2019) noticed, the tools and methods of mathematics play important role in modelling of epidemic diseases. Compartmental models are used in epidemiology to illustrate and investigate how an infectious illness spreads within a population and to enhance the effectiveness of disease-control measures in order to promote positive health policies. It can assist in forecasting both the number of infected people and the duration of an epidemic. In compartmental model, the population is classified into distinct compartments such as susceptible (S) - individuals susceptible to be exposed; exposed (E) - individuals exposed where the disease status is latent, and individuals are infected but not infectious yet; infected (I) - individuals actually infected and infectious; critical (C) infected individuals who need intensive care; recovered (R) - infected people who recover with an assumed lifelong immunity and do not return to the S compartment; and the absorbing state death (D). The choice of the compartment to be included in a model depends on the characteristics of the disease being modeled and the purpose of the model. Some compartments, e.g., the latent period, E, are often omitted, because they are not essential for the basic susceptible-infective interaction. Ordinary differential equations (ODEs) determine the rate of transfer between distinct compartments.

The backbone of any epidemiological model is interaction between S, I, and R compartments, often referred to as SIR model Cooper et al. (2020). SIR model is a simple yet useful mathematical description of the temporal dynamics of disease outbreak which is used by Alla et al. (2022), Sifriyani & Rosadi (2020) and Wahyudi & Palupi (2020). Most researchers directed their effort towards developing more fitting models by adding more compartments to the model. Acronyms for epidemiology models are often based on the flow patterns between the compartments such as SI, SIS, SIR, $SIRS$, $SEIR$, $SEIRS$, $SEIRD$, $SEICRD$, etc. According to Shang (2013), in the $SEIR$ model passively immune newborns first become susceptible, then exposed in the latent period, then infectious, and then removed with permanent immunity. An $SEIRS$ model would be similar, but the immunity in the compartment R would be temporary, so that individuals would regain their susceptibility when the temporary immunity ended.

2.2 SIR Model

The SIR model is the simplest compartmental model in epidemiology. Figure 1 illustrates the order of migration across compartments in SIR model. Below we detail the parameters involved in the SIR model introducing a running example.

Let p be the probability of catching a disease X by a healthy person from an infected individual. Assume that an infected person comes into daily contact with n individuals in

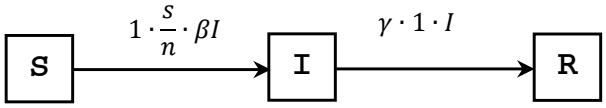

Figure 1: Schematic representation of the fundamental SIR model.

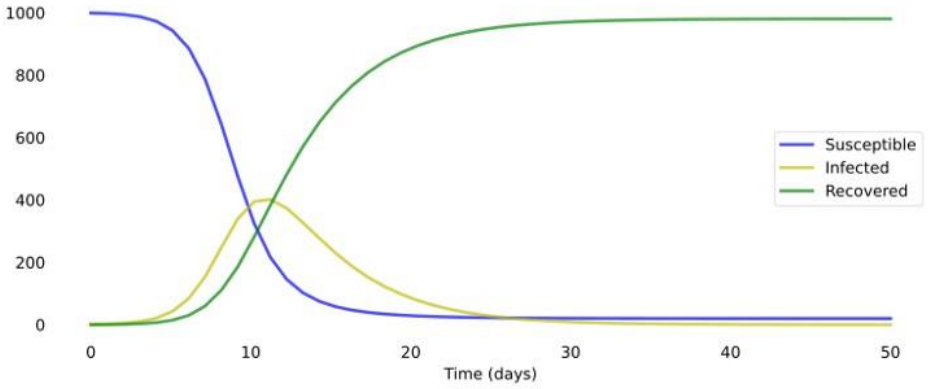

Figure 2: Visualization of the SIR model for a random population of 1000 people with a $\beta = 1$.

average, and remains infectious and being able to spread the disease during d days. The infectious rate in Epidemiology, written β, is the predicted number of individuals an infected person would infect per day. In our case, $\beta = p \cdot n$. The Basic Reproduction Number, written R_0, is the entire number of individuals that a sick individual infects. In our example, $R_0 = \beta \cdot d$. The recovery rate, γ, represents the fraction of infected individuals who recover per day and is represented by $\gamma = 1/d$. Thus, $R_0 = \beta/\gamma$.

Concerning the infected population, it is evident that susceptible individuals who become infected will move from the susceptible compartment to the infected compartment. However, we must consider the number of persons who are being removed because they are healing from the condition or passing away. After that we calculate the changes in recoveries based on the newly retrieved amount that is identical to what we determined previously. We can describe the change in number of susceptible, infected, and recovered individuals for the period of t days and for the population of N in terms of functions $S(t), I(t)$ and $R(t)$ introducing the following ODEs:

$$\frac{dS(t)}{dt} = -\beta I(t)\frac{S(t)}{N}$$

$$\frac{dI(t)}{dt} = \beta I(t)\frac{S(t)}{N} - \gamma I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t)$$

Figure 2 is a Python visualization of the SIR model for $N = 1000$, $\beta = 1$ and $\gamma = 0.25$. According to Figure 2, it takes approximately 10 days for nearly half of the population to get infected. Obviously, the disease depicted in this instance has an extremely high R_0 value of 4.0. Figure 3 demonstrates a significant alteration in the situation when reducing the number of people an infected individual infects per day from 1 to 0.5. We can deduct from Figures 2 and 3 that these ODEs are particularly sensitive to the starting settings. This is also the reason why it is so difficult to accurately simulate an outbreak of a new disease: we do not know the parameters, and even little modifications result in drastically different consequences.

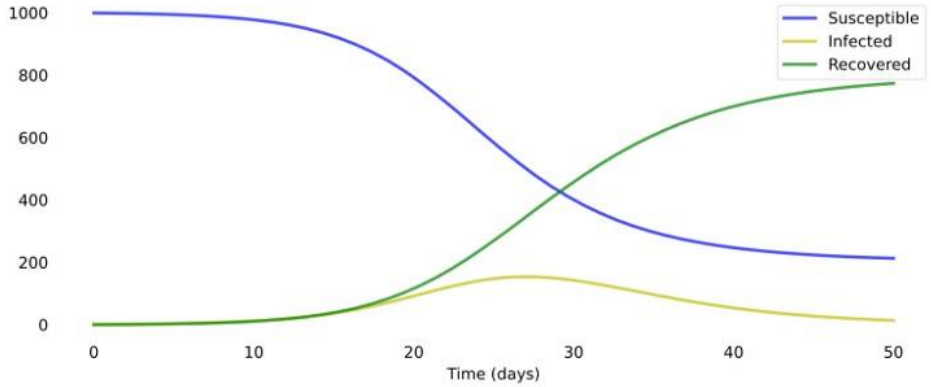

Figure 3: Visualization of the SIR model for a random population of 1000 people with a $\beta = 0.5$.

2.3 Basic Reproduction Number

The basic reproduction number, R_0, is an epidemiological metric used in epidemic research to assess the transmission capacity of a disease. The statistic shows the average number of secondary infections induced by a previously infected individual in a vulnerable group. This means that if R_0 for a certain disease is 5, each sick individual will, on average, infect five other people. Numerous factors influence R_0, including the extent to which the affected population is in contact, the risk of disease transmission during contact and the duration of an individual's infectiousness. A disease is said to be an epidemic in a population, if $R_0 > 1$. In an SIR-model, we have $R_0 = \frac{\beta}{\gamma}$.

2.4 Time-Dependent Variables

So far, we have only considered the evolution of the compartments over time. Which is highly implausible! Due to nationwide lockdowns, for instance, the value of R_0 cannot remain constant during the duration of a disease, as lockdowns reduce the number of individuals a sick individual infects. Naturally, in order to mimic realworld events more accurately, we must make our variables evolve with time.

2.4.1 Time-Dependent R_0

Events such as nationwide lockdowns and social isolation lower the number of others each sick individual infects, hence decreasing R_0. Consequently, R_0 evolves with time and cannot be a constant value. Therefore, there is a need to determine a time-dependent formula for R_0. For our purposes, we have employed a logistic function capable of capturing the continuous variations in R_0's value. Instead, we define a purpose-specific function

$$R_0(t) = \frac{R_{0_{start}} - R_{0_{end}}}{1 + e^{-k(-x+x_0)}} + R_{0_{end}},$$

where $R_{0_{start}}$ and $R_{0_{end}}$ stand for the values of R_0 on the first and the last days, respectively; x_0 is the x-value of the inflection point (i.e., the date of the greatest decrease in R_0, which may be considered the major "lockdown" date); k allows us to adjust the rate at which R_0 declines. The purpose of Figure 4 is to facilitate the understanding of the mentioned parameters.

2.5 Resource- and Age-Dependent Fatality Rates

Similar to R_0 the fatality rate α is presumably not constant for the majority of actual disorders. It could depend on a multitude of factors, e.g., resource- and age-dependence.

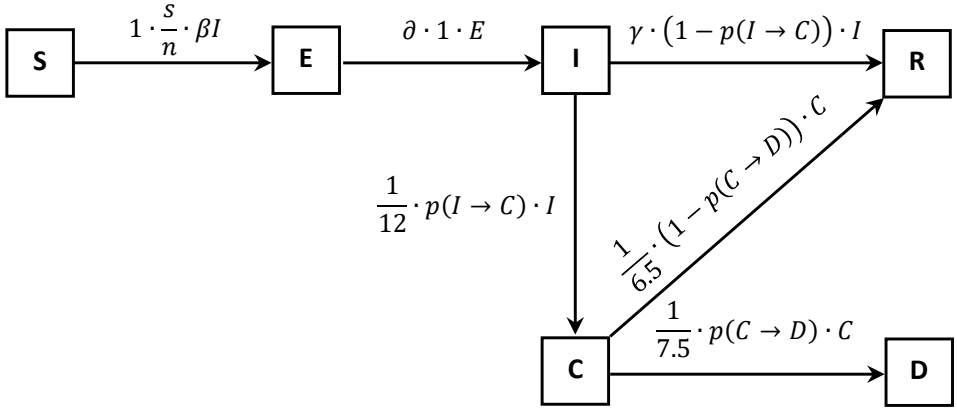

Figure 4: Visualization of time – dependent R_0 for $k = 0.1$, $k = 0.5$ and $k = 1$.

It is quite regular to expect a higher fatality rate when more persons are sick. Let us consider how this could be expressed as a function: we would likely require a "base" or "ideal" fatality rate for the scenario in which few individuals are sick (and hence receive optimal treatment) and a component that takes into consideration the fraction of the population that is now afflicted.

The function that implements these concepts is expressed as follows:

$$\alpha(t) = s \cdot \frac{I(t)}{N} + \alpha_{opt},$$

where α_{opt} is the ideal fatality rate; s is an arbitrary but fixed scaling factor that governs the fraction of infected individuals' effect.

Complex models might make the fatality rate dependent on the number of intensive care unit beds or ventilators, etc. It is more difficult to integrate age dependency into the model. To fully implement it, we would have to include separate compartments for every age group (e.g., infected compartment for 0–9-year-olds, another for 10–19-year-olds, etc.). That can be accomplished with a simple for-loop in Python, but the equations become a bit muddled. The following is a simplified strategy that is nonetheless capable of producing positive outcomes.

We operate with two variables that are fatality rates by age group and the proportion of the total population in that age group. For instance, we may have the following fatality rates and numbers of people by age group:

$$alpha\_by\_agegroup = \{"0-29" : 0.01, "30-59" : 0.05, "60-89" : 0.20, "89+" : 0.30\}$$

$$proportion\_of\_agegroup = \{"0-29" : 0.1, "30-59" : 0.3, "60-89" : 0.4, "89+" : 0.2\}$$

Now we calculate the overall average fatality rate by adding up the age group fatality rate multiplied with the proportion of the population in that age group as follows:

$$\alpha = 0.01 \cdot 0.1 + 0.05 \cdot 0.3 + 0.2 \cdot 0.4 + 0.3 \cdot 0.2 = 15.6\%.$$

If we want to use both our formulas for resource-dependency and age-dependency, we could use the resource-formula we just used to calculate α_{opt} and use that in above resource-dependent formula.

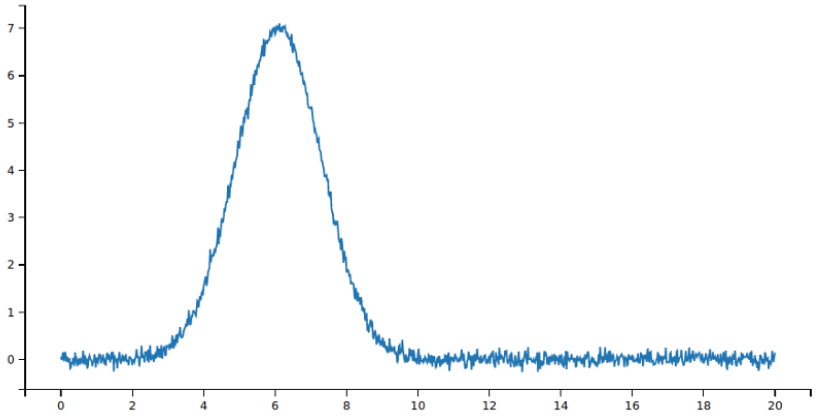

Figure 5: A normal distribution with some noise.

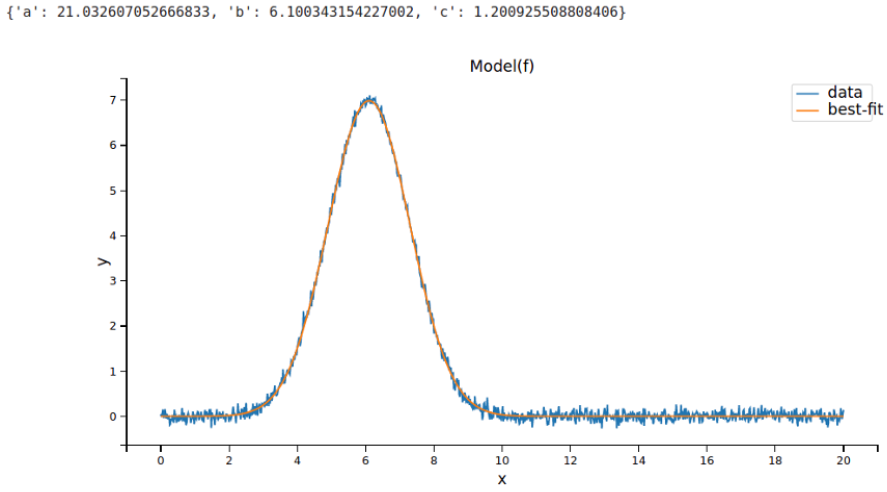

Figure 6: Example of Curve Fitting demonstrated for normally distributed random data with noice.

2.6 Curve Fitting

The Curve Fitting is a technique used to make forecasts that most closely mirror the actual data. The Curve Fitting allows to identify the model parameters that produce the most accurate predictions. In this work we use Python module lmfit to achieve realistic prediction by Curve Fitting. Below we illustrate of Curve Fitting for a Normal distribution. Figure 5 illustrates normally distributed random data with some noise. Now, we require a function that receives the x-value as the first argument, followed by the three fitting parameters (a, b, and c). This function will be used to fit the data, with the library for fitting curves adjusting the parameter until an acceptable fit is obtained. The lmfit package produces a Curve-Fitting model and accepts initial parameter guesses. Then, the data are fitted. Indicating that curve fitting methods in general do not guarantee the discovery of a global minimum and that initial assumptions regarding the parameters are necessary. Figure 6 is the output in which a, b, and c correspond closely to our data.

3 Results

3.1 Creating SEICRD Model for Fitting

In this section, we create more elaborate model which makes the fatality rate depend on the number of Intensive Care Unit (ICU) beds or ventilators available and we will be concerned with deriving our final model and feeding in the real-world COVID-19 data for North Cyprus. We focus on fitting an extended SIR model, which is $SEICRD$ model, with time-dependent R_0-values and resource-dependent mortality rates to actual COVID-19 data in order to come as near as feasible to the actual statistics and make accurate predictions on potential future changes of disease in North Cyprus.

We take the local characteristics of health care in North Cyprus into account and create a new category, Critical (C), to account for the group that requires intensive care. This is done to simulate overcrowded hospitals. Patients can only become critical if they are infected with the disease, hence we need a new transition from I to C. Based on methodology proposed by Hethcote (2000), we summarize the current general known and local to North Cyprus estimations:

- The number of days between infection and criticality is 12 (rate: 1/12)
- The number of days between critical and fatal is 7.5 (rate: 1/7.5)
- The number of days between critical and recovered is 6.5 (rate: 1/6.5)

Adding the new transition from I compartment to C compartment and with the above characteristics in mind we obtain the subsequent $SEICRD$ model which is shown in Figure 7.

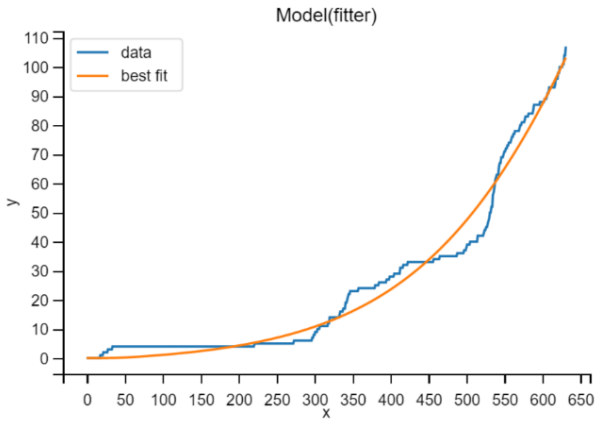

Figure 7: Schematic representation of the complete $SEICRD$ model.

3.2 Limited Resources

As a result of the growing number of COVID-19 patients, the majority of countries including North Cyprus face a shortage of hospital beds which is why we have taken into account the limited resources into our model as it is shown in Figure 8.

Let us consider the following running example to facilitate comprehension of the model. We assume a nation with K number ICU beds for treating severely unwell COVID-19 patients. If the number of critically sick patients (C, the critical compartment) exceeds K, all patients above K will be unable to be treated and would thus perish. For instance, if $K = 800$ and $C = 1000$, then 200 patients will perish due to a lack of treatment resources. This particularly means that $C - K$ individuals perish owing to shortages. Now, if we have more beds than critically

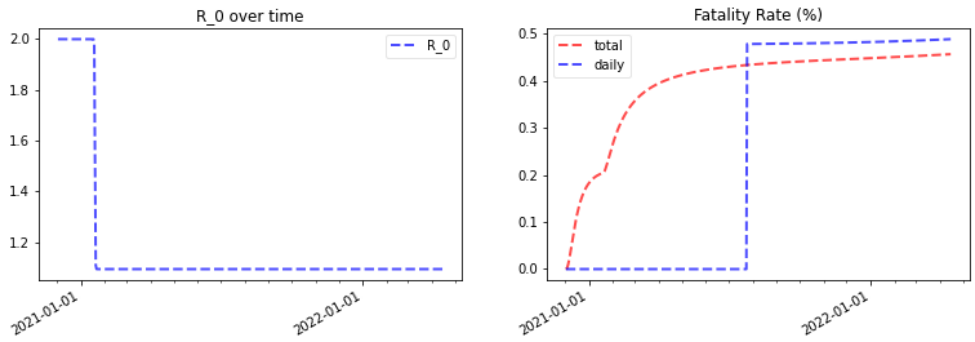

Figure 8: Schematic representation of the $SEICRD$ model taken limited resources into account.

sick patients, people will no longer die due to a lack of resources. Therefore, we conclude that maximum of $(0, C-K)$ number individuals die due to shortages (if $C < K$, that is, there are more beds than patients), then $C - K < 0$, so maximum $(0, C - B) = 0$, and 0 individuals die due to shortages; if $C > K$ (not enough beds), then $C-K > 0$, so maximum $(0, C-K) = C-K$, and $C - K$ individuals die due to shortages). Therefore, we must widen our transitions: from C, we must consider two populations: the $\max(0, C - K)$ individuals who will perish due to insufficient resources, and the remainder who will be treated. If $C > K$ (sufficient resources), then C individuals are treated. If $C > K$ (there are insufficient resources), then K people are treated. This indicates that the number of people receiving treatment is $\min(K, C)$.

The following are the ODEs for our $SEICRD$ model that takes restricted resources into consideration.

$$\frac{dS}{dt} = -\beta(t) I \frac{S}{N}$$

$$\frac{dE}{dt} = \beta(t) I \frac{S}{N} - \delta E$$

$$\frac{dI}{dt} = \delta E - \frac{p(I \to C) I}{12} - \gamma(1 - p(I \to C)) I$$

$$\frac{dC}{dt} = \frac{p(C \to D) I}{12} - \frac{p(C \to D)}{7.5} \min(Beds(t), C) - \max(0, C - Beds(t)) - \frac{(1 - p(C \to D))}{6.5} \min(Beds(t), C)$$

$$\frac{dR}{dt} = \gamma(1 - p(I \to C)) I + \frac{1 - p(C \to D)}{6.5} \min(Beds(t), C)$$

$$\frac{dD}{dt} = \frac{p(C \to D)}{7.5} \min(Beds(t), C) + \max(0, C - Beds(t))$$

3.3 Time-Dependent $R_0(t)$ and $Beds(t)$

Our $SEICRD$ model includes two time-dependent variables, namely, $R_0(t)$ (and thus $\beta(t)$ as $R_0(t) = \frac{\beta(t)}{\gamma}$) and $Beds(t)$. For $R_0(t)$ we use the logistic function

$$R_0(t) = \frac{R_{0_{start}} - R_{0_{end}}}{1 + e^{-k(-x + x_0)}} + R_{0_{end}}.$$

The logic behind of $Beds(t)$ is that as the virus spreads, the number of COVID-19 patients requiring hospital treatment increases. This is the reason why some countries begin constructing hospitals to augment their resources. Consequently, the quantity of available beds rises with time. The following equation represents $Beds(t)$:

$$Beds(t) = Beds_0 + s \cdot t \cdot Beds_0$$

where $Beds_0$ stands for the total number of available ICU beds and s is a scaling factor.

Table 1: Parameters used in the SEICRD model.

N	total population
$\beta(t)$	number of individuals an infected person is predicted to infect per day
γ	the proportion of infected individuals who recover per day ($\gamma = \frac{1}{D}$)
$R_{0_{start}}$	parameter in $R_0(t)$
$R_{0_{end}}$	parameter in $R_0(t)$)
x_0	variable in $R_0(t)$)
K	parameter in $R_0(t)$)
s	parameter in $Beds(t)$)
$Beds_0$	parameter in $R_0(t)$)
δ	length of incubation period
$p(I \to C)$	likelihood of becoming critically ill after becoming infected
$p(C \to D)$	probability of dying while in critical condition

3.4 Fitting the Model

We create the model under the following assumptions. The system of ODEs is particularly sensitive to initial conditions; even minor modifications can result in drastically different solutions. We assume population homogeneity, i.e., we do not account for some areas being initial hot spots and others enforcing limits earlier and more strictly. Deaths do not significantly alter the population structure. We calculate fatality rates a priori using the structure of the population before the outbreak and assume that death rates are not high enough to significantly alter the population structure. Due to a lack of available care, only life-threatening situations may fill hospitals, resulting in a greater death rate. All critically ill individuals who do not receive care perish. After regaining immunity, R_0 either decreases or remains constant but does not expand. Therefore, this model does not permit us to represent measures being loosened again; a different function for R_0 would be required for that. Scope of the parameters used in our model are indicated in Table 1 (all the variables in the equations plus the variables in the $R_0(t)$ and $Beds(t)$ functions)

We are able to determine N by determining the total population of Northern Cyprus. Similarly, the health ministry can provide the number of ICU beds in Northern Cyprus for Beds0. δ and γ are set to $\frac{1}{9}$ and $\frac{1}{3}$ respectively, which are the most accurate figures we could find after reading multiple study publications. It must be noticed that $\beta(t)$ is calculated using $R_0(t)$ and γ, therefore, there is no need to identify separate beta values.

3.5 Supplemental and COVID-19 Data

We have processed the data from the official government website https://saglik.gov.ct.tr/ of Northern Cyprus for age categories, ICU beds, and daily cumulative fatalities. The beds file lists the number of ICU beds per 10,000 residents in Northern Cyprus. The age groups file lists the population of Northern Cyprus by age groups. COVID-19 data is a massive database containing the number of Northern Cyprus fatalities every day beginning on 2020-03-10. We only use statistics regarding the number of deaths, not the number of reported cases. Because the reporting of confirmed cases is exceedingly noisy and highly dependent on the quantity of tests. From one day to the next, the number of cases could climb from 10,000 to 15,000, which could also be due to an increase of 5,000 tests. In general, the number of deaths reported is significantly more accurate; hence, the reported numbers are likely pretty close to the actual figures.

3.6 Fitting the Data in to the Model

Using the process of curve fitting, we validate the model, determining the model parameters that produce the most accurate predictions. As seen in Figure 9, the model is able to capture

Table 2: A posteriori determined parameters of the model.

$R0_{start}$	$R0_{end}$	K	$p(C \to D)$	$p(I \to C)$	S	x_0
4.0	1.066	1.607	0.581	0.062	0.009	11

the trend of the actual data and provide data points that were consistent with the actual data. As a result of the curve fitting, we determined the parameter values that are shown in Table 2.

According to our prediction model, the day with the greatest decrease in R_0 (the major lockdown date) is 11, which is January 11, 2021. According to official statistics, the primary lockdown date is the 10th of January, hence the predicted date is rather close to the actual date. We can also observe that the fatality rate is approximately 0.5 percent. The simulation results for rR_0 and fatality Rate for North Cyprus are illustrated in Figure 10.

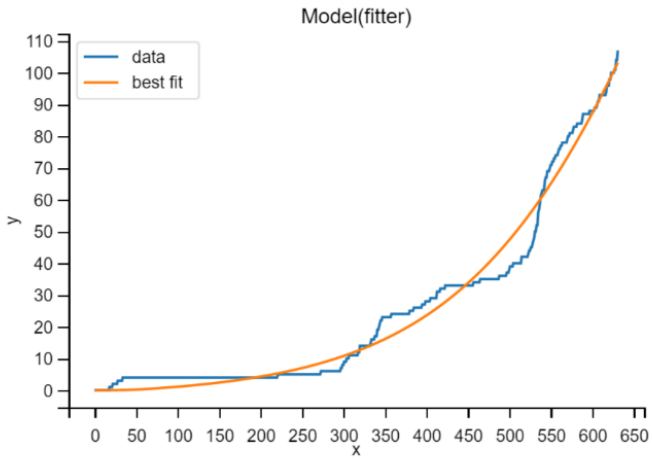

Figure 9: Fitting the model into daily cumulative fatalities in North Cyprus.

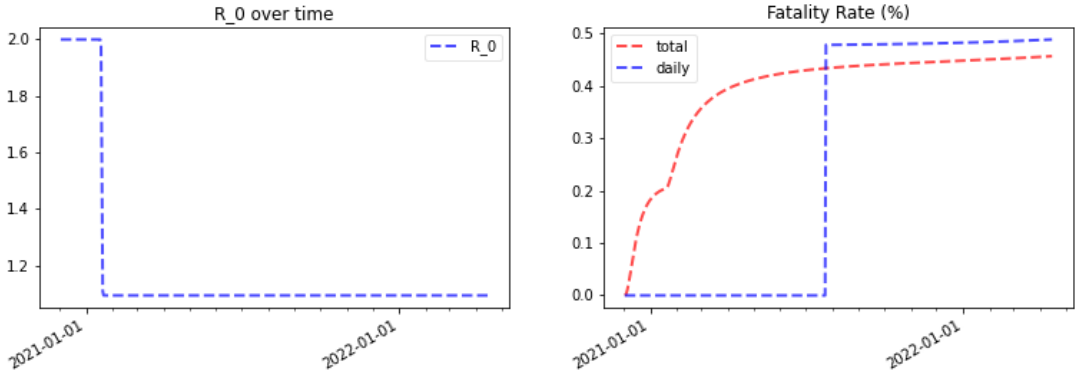

Figure 10: R_0 and the fatality rate of North Cyprus overtime.

4 Conclusion

We developed the extended COVID-19 model for a period of 500 days beginning on January 1, 2021, by fitting an extension of the SIR-model to actual Coronavirus data from Northern Cyprus. This extension of the SIR-model included time-dependent R_0-values and resource-dependent mortality rates. We can see that the curve begins to flatten around day 100, which indicates that, if the model is accurate, North Cyprus has already endured the worst of the pandemic, and

the number of deaths should begin to drop dramatically in the coming months. If the model is accurate, North Cyprus has already endured the worst of the pandemic. Evidently, our model anticipates that R0 will continue to hover around 1.066; however, if it rises when lockdowns are relaxed, we may expect the numbers to start climbing once more.

5 Further work

Numerous authors discussed importance of network science for modelling and behaviour prediction in epidemiology. The principles of application of networks for study of epidemic diseases are proposed by Newman (2002). Small & Cavanagh (2020) and Craig et al. (2020) particularly discussed several aspects and case studies.. As a further work, we are intended to use networks to study the COVID-19 dynamics in North Cyprus and then compare obtained results with the ones discussed in the present work.

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