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A Novel Mechanism on Multiple Waves of COVID-19 Pandemic by a Markov Chain Modeling and an Application for Turkey*

Markov Zincir Modellemesi ile COVID-19 Pandemisinin Çoklu Dalgaları Üzerine Yeni Bir Mekanizma ve Türkiye Uygulaması

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Abstract: The coronavirus, also known as COVID-19, which first confirmed in Wuhan, Hubei province, China on December 8, 2019, has spread rapidly to many countries, including Turkey. Moreover, the World Health Organization declares it as a pandemic on March 11, 2020. Related to this phenomenon, since the beginning, many papers have started to estimate the (single) peak time and possible ending time of the daily new cases for different countries. However, recently the studies on the potential second or third waves have been gaining importance. In contrast to the studies focusing on a single peak, this paper provides a novel mechanism on multiple waves of COVID-19 pandemic by a Markov Chain modeling. Moreover, we apply our model to Turkish data to check if there is a possibility for a second wave or not for Turkey. In our model, we use two reversing time-dependent parameters called ‘protection (isolation)’ and ‘deisolation’ rates. The number of protected or isolated people can quickly increase by the measures taken early by governments. These preventions help us to end the first peak relatively rapidly. On the other hand, the opposite can also be true. Governments can loosen the measures before the risk has gone and people may stop taking precautions. Then the number of protected or isolated people goes down and of course, this implies an increase in the number of susceptible cases who are the healthy population susceptible to COVID-19. Therefore, this can cause a second wave. Of course, this logic can be easily generalized to multiple waves. Besides generating multiple waves, the proposed model can be used for projections and simulations based on scenario analyses for policy implications.

Structured Abstract: Introduction and Purpose

After the rapid spread of coronavirus (COVID-19) from China to many countries, including Turkey, a large number of academic studies have started trying to find answers to the questions about the spreading rate of COVID-19. All these studies aim to predict and then control the spread of the disease; therefore, making it easier to choose better policies to prevent society from its harmful effects. Since the disease first appeared,

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many papers have started to estimate the (single) peak time and possible ending time of the daily new cases for different countries. However, recently many researchers are taking attention to the possible second or third waves. In contrast to the studies, which are focusing on a single peak, the subject of our study is the prediction of the second or third waves of the COVID-19 pandemic in its complete spreading period. This study develops and proposes a mathematical model for this prediction problem of multiple waves. Moreover, we utilize our model by using Turkish data, whether to check if the second wave will be experienced or not in Turkey.

Methodology

Our methodological approach in this paper is simulating a version of the Markov Chain model, namely extended SEIR model. Therefore, we provide a novel mechanism for generating multiple waves of COVID-19 pandemic by a Markov Chain modeling. As a theoretical contribution, we further extend the generalized SEIR model by adding two reversing time depending parameters, which are controlling the isolation and deisolation rates, called ‘protection (isolation) rate’ and ‘deisolation rate’. Thus, our model explores the ability of time-dependent isolation/deisolation rates to generate multiple waves. With our model, we show that by using these parameters, it is possible to match the second wave or the other waves which may occur later.

The number of protected or isolated people can quickly increase by the measures taken early by governments. These preventions help us to end the first peak rapidly. On the other hand, the opposite can also be true. Governments can loosen the measures before the risk has gone and people may stop taking precautions. Then the number of protected or isolated people goes down and of course, this implies an increase in the number of susceptible cases who are the healthy population who are susceptible to COVID-19. Therefore, this can cause a second wave. Of course, this logic can be easily generalized to multiple waves.

Another critical novel feature of the model is the addition of an “intensive care” state. We add this state into SEIR models to monitor the sufficiency of the health care system in the country. This state is crucial because if the number of people in this state exceeds some threshold (which can differ from country to country), the health care system will not work properly. Therefore, it is crucial to project the number of people in this state when making policy decisions.

There are two groups of parameters in the model. For the first group, we can infer the value of parameters directly from the data. The second group includes the parameters that we cannot directly obtain from the data, such as the rate of protection (i.e., isolation) and deisolation. Given the first group of parameters, we simulate the model and find the second group's parameter values by best fitting the model results to actual data.

Results and Discussion

We compare the actual daily cases and estimate daily cases via our model. Standard SEIR models can capture only a single peak. This implies that in these types of models, after the first peak, actual daily new cases decrease monotonically and converge to zero after a while. In terms of our model, this happens if the isolation rate is greater than or equal to the deisolation rate. This corresponds the most of the models in the literature, which can generate only a single peak. On the other hand, after a while, if the deisolation rate is sufficiently higher than the isolation rate, then the model can have a second upward sloping and second wave.

Our findings show that by using time-dependent isolation/deisolation rates, it is possible to match the second wave or the other waves, which may occur later. For this purpose, we simulate our model for Turkey to check whether the model can match the second upward slope which may or may not be a signal of the second wave. We conclude that it is possible to generate multiple waves with the proposed model.

Besides generating multiple waves, the model can be used for projections and simulations based on scenario analyses for policy implications. Implementing such scenario analyses for Turkey is left for future studies. Other possible future studies would be applications of our proposed extended model to other countries' data and comparing the results for verifying the robustness and applicability of the model.

Keywords: Markov Chain Modeling, Simulation, Generalized SEIR Model, COVID-19 Pandemic, Second Wave

Öz: Çin'in Hubei eyaleti, Wuhan kentinde 8 Aralık 2019'da ilk kez rastlanan ve COVID-19 olarak da bilinen koronavirüs hastalığı, Türkiye dahil birçok ülkeye hızla yayılmıştır. Dahası, bu hastalık 11 Mart 2020'de Dünya Sağlık Örgütü tarafından “pandemi (yaygın / salgın hastalık)” olarak ilan edilmiştir. Bu konuyla ilgili olarak farklı ülkeler için yapılan birçok çalışmada yeni / günlük vaka sayıları için tek bir zirve / pik zamanı ve olası bitiş tarihi tahmin edilmeye çalışılmıştır. Ancak zaman ilerledikçe potansiyel ikinci veya üçüncü dalga çalışmaları önem kazanmıştır. Bu makale, tek bir zirveye odaklanan çalışmaların aksine, Markov Zinciri modellemesi kullanarak birden fazla yaşanabilecek COVID-19 pandemi dalgalarını tahmin etmeye yönelik yeni bir mekanizma önermektedir. Ayrıca, bu çalışmada Türkiye’de ikinci dalgaya yönelik bir sinyal olup olmadığını belirlemek için Türkiye verileri kullanılarak da simülasyonlar gerçekleştirilmiştir. Modelimizde birbirinin tersi olarak çalışan koruma (veya izolasyon) oranı ve korumanın (veya izolasyonun) azalma oranı adında zamana bağlı iki parametre kullanılmaktadır. Korunan veya izole edilmiş kişilerin sayısı, hükümetler tarafından erken alınan tedbirlerle kolayca artırılabilir. Bu önlemler vaka sayısı bağlamında ilk zirveye hızla ulaşıp bu tepe noktasından dönülmesine yardımcı olur. Öte yandan, tam tersi de geçerlidir: Hükümetler risk tamamen geçmeden önlemleri gevşetebilir ve insanlar önlem almayı bırakabilirler. Bu durum da, korunan veya izole edilmiş kişilerin sayısını azaltır ve elbette bu durum henüz enfekte olmamakla birlikte COVID-19'a duyarlı sağlıklı nüfusun yani duyarlı vakaların sayısında da bir artış anlamına gelir. Bu da ikinci bir dalgaya neden olabilmektedir. Elbette, kurulan bu mantık ikinciden sonra oluşabilecek çoklu dalgalar için de genelleştirilebilir. Bu model, çoklu dalga yaratabilmenin dışında gelecek projeksiyonlarında ve politika çıkarımları yapmak üzere senaryo temelli simülasyonlarda da kullanılabilir.

Anahtar Kelimeler: Markov Zinciri Modellemesi, Simülasyon, Genelleştirilmiş SEIR Modeli, COVID-19 Pandemisi, İkinci Dalga

Introduction

The most discussed topic in the world nowadays is how to control the spread of coronavirus (COVID-19) pandemic¹ and how to reduce its harmful effects in all countries. After its confirmation, firstly in Wuhan, Hubei province, China, on December 8, 2019; the disease has spread rapidly to many countries, including Turkey. After the appearance of the first case in Turkey, on March 11, 2020, Turkish authorities had rapidly taken some measures, as well. To prevent society from its harmful effects and decrease the velocity of its spread, the only methods known so far are; the minimization of contact with each other in society (social distancing), using masks, and ensuring maximum hygiene in our daily lives. To guarantee this, governments have applied some restrictive policies to implement isolation in society, especially for some age groups. These can be grouped as “movement restrictions”, “lockdowns”, and “social distancing”; which include measures such as domestic and international flight restrictions, curfews, school closing, etc.

In Turkey, policies were applied to reduce the spread of the disease without completely stopping the flow of life, such as promoting social distance, partial travel restrictions, and partial curfews. However, these measures have serious negative impacts on the economy and social life. Therefore, they are not sustainable for a long time. For some most recent analyses of the economic impacts of the Covid-19 pandemic and related economic policies applied in Turkey; see Gülhan (2020), Durmuş & Şahin (2020), and Nakiboğlu & Işık (2020), among others. After a certain time of the first peak, many countries loosen the measures and the “normalization” periods have started (The Humanitarian Data Exchange, Acaps, 2020; The Declaration of Presidency of the Republic of Turkey, 04.05.2020 The COVID-19 Normalization Plan; also see Table 3 below). During this “normalization” period, the projection of the second, third, and repeated waves has become important.

Since the disease first appeared, there have been many academic studies and forecasts about these issues: How the disease will spread, and how these different policies affect the spread of disease? A literature review related to these issues is given in the following section. With these

¹ Coronavirus is declared as “pandemic” by the World Health Organization on March 11, 2020.

studies' help, it would be easier to choose better policies to reduce the pandemic's harmful effects. Due to the importance and urgency of the COVID-19 pandemic, many studies have developed mathematical models and implemented simulations using freely available data sets (CDC, 2020; ECDC, 2020; WHO, 2020; John Hopkins Visual Data, 2020; Our World in Data, 2020).

While the first studies and simulations focused on forecasting the first waves of the spread in many countries, researchers recently began taking attention to the possible second or third waves. In contrast to the studies which focus on a single peak, our paper provides a novel mechanism on multiple waves of COVID-19 pandemic by a Markov Chain Modeling. Moreover, we apply our model to Turkish data to check if the second wave will be experienced or not in Turkey.

Our main findings show that by using time-dependent isolation/deisolation rates, it is possible to match the second wave or the other waves. Therefore, it is possible to generate multiple waves with the proposed model. We also simulate our model for Turkey to check whether the model can match the second upward slope or not. We find a second upward slope, which can be a potential sign of the second wave.

The rest of the paper is structured as follows. A literature review and the model description follows the introduction. After describing the proposed model formally, we present the model results, and then finally, we conclude.

Literature Review

The models for the spread of infectious diseases in populations have been analyzed mathematically and applied to specific diseases, as stated in Hethcote (2000). An approach for the prediction of outbreaks is made by using the transitions between states, i.e., the individuals' epidemiological status (e.g., infected, recovered, death, etc.) of the disease's life-span in a dynamic environment. Therefore, it can be treated as a dynamic network model structure in mathematics. For a general definition of the similarity of a dynamic network topology for the spread of the outbreak, see Gross (2006), among others. The most widely used method in predicting outbreaks in the literature is based on simulations of Markov Chain Modeling. In epidemiology, these models are known as “compartmental models” where the analogy of “compartments of a train” is used instead of states (Brauer, 2008).

The first models that predicted how the outbreaks would follow (using Markov Chains, that is, switching between states in a dynamic environment) were 'SIR (Susceptible-Infected-Recovered or alternatively Removed)' models, which are based on the study of Kermack and McKendrick (1927). Since SIR models are not enough for modeling complicated disease states, extended models called 'SEIR (Susceptible-Exposed-Infected-Recovered or alternatively Removed)' models have been developed and proposed in the literature (Diekmann, 2012; Keeling & Rohani, 2011). In these abbreviations, "S" denotes the number of people susceptible to the disease (those who are not yet infected). "E" is the number of people who are infected but are not yet infectious, and "I" is the number of people who are infected and infectious. "R" is the total of people who recover or die. In other words, people in the “R” class do not infect the disease. In summary, in diseases analyzed by the SIR model, it is assumed that there is no state “E”, that is, an incubation period. However, it is clear that the "E" status is necessary to make more proper analyses.

It is essential to establish a unique model for each specific epidemic or infectious disease, which captures its own characteristics. For this reason, to model specific outbreaks for the COVID-19 virus (and viruses similar to this virus family), ‘generalized SEIR model’ is proposed recently in the literature. These models contain three additional classes -compared to SEIR models- that are important for the analysis of the outbreak: "P", "Q" and "D". In this epidemic, P (Insusceptible cases, the number of people who will not get the disease because they are isolated) has been added to carry the critical importance of isolation (e.g., staying at home). Q (Quarantined cases) shows the number

of quarantined people after the confirmation of the positive test result. For example, Zhang, et.al. (2020) named their model as “SEIQR” since they developed five states (susceptible-exposed-infectious-quarantine-recovered) to simulate the models which are including interventions such as social distancing and epicenter lockdown.

The closest approach to our model's background can be found in Peng, et. al. (2020). Our model and analysis added two additional states on top of this study. First, the number of intensive care cases have been added to the model because, in this epidemic, it has an important place in the health system. Secondly, protection (isolation rate) is assumed to be time-dependent in order to reflect a more realistic situation. Therefore, the model is a system of 9 different states (differential equations), which will be explained formally in the following section.

One of the first reviews on COVID-19 models is given in Rhodes, et.al. (2020). Besides mathematical models based on the Markov Modeling approach, statistical or machine learning models also developed in the literature to predict the COVID-19 pandemic. For comprehensive reviews of epidemiology or mathematical/statistical modeling of Covid-19 spread, please see Park et al. (2020); Loyal & Chen (2020); Mohamadou et al. (2020).

As stated in the Introduction section, mathematical models have been developed to spread disease, and simulations have been implemented based on them. In the first months of the COVID-19 pandemic, two essential simulations have been prepared for the USA and the United Kingdom (University of Washington USA Simulation, 2020; Imperial College, 2020). In these simulations, desired information to be learned by the society and policymakers is as follows: i) at which point the curves will reach “(single) peak point” and start to fall, and ii) according to these estimation results whether the health infrastructure will be sustainable or not. These simulations helped policymakers in the early stage of the pandemic to decide the measures for prevention from the disease. The technical details for the simulation done for Imperial College is given in Walker et. al. (2020).

Afterward, in many countries and research centers, simulations have been implemented to predict the disease's spread with such models worldwide. Two prestigious simulations among them are the ones implemented by the Singapore University of Technology (2020) and Design and Robert Koch Institute (2020).

As one of the first applications, Tang et. al. (2020) develop a deterministic compartmental model based on the clinical progression of the disease, and intervention measures. They used likelihood and model-based estimation to determine the basic reproduction number, which helps determine the disease's transmission potential and, therefore, the severity of the outbreak for the first periods in China.

On the other hand, in SIR, SEIR, and similar models, initial parameter values or assumptions such as infection rates, latent, quarantine times, etc. have to be determined. Some of them can be estimated internally while the model is executed; however, others can only be taken from other clinical-studies externally. For this aim, there also exist studies on the estimation of parameters used in the models. For example, in Verity et.al. (2020), case / infection fatality ratios, the mean duration from onset of symptoms to death, the proportion of infected individuals who are likely to require hospitalized have been estimated from the individual-case data collected for patients who died from COVID-19 in Hubei, China in February 2020.

All these models and estimations aim to help the public and decision-makers derive strategies to prevent the disease's harmful effects. Atkeson (2020) and Atkeson et al. (2020), intended to introduce economists to a simple SIR model of the progression of COVID-19 in the United States over the one / one and a half years' perspective and tried to answer the question that how country-based mitigation measures influence the course of the COVID-19 epidemic. Moreover, Anderson et.

al. (2020), briefly reviews the studies and attempts to predict disease in the first months of disease spreading related to the government inventions.

The proposed model in this paper has the same purpose: Developing a model to predict the spread of disease more clearly and help the decision-makers and the society in their decisions to reduce the adverse effects of the COVID-19 pandemic. For this aim, it includes nine states to capture the characteristics of COVID-19 more appropriately and realistically, although -as mentioned above- SIR, SEIR, and generalized SEIR models include three, four, and seven states, respectively. More clearly, we add three new states to the generalized SEIR model as a contribution to the literature: "IC (intensive care, the number of people taken into intensive care from quarantine)", " R_1 (recovery from quarantine before moving to intensive care state) and R_2 (the number of those recovering from intensive care). It is important to add the number of intensive care units to the model because intensive care units will determine the sustainability of the health system. It is also important to differentiate between R_1 and R_2 since we know from the data that only a certain rate will go to intensive care after quarantine and the other part will recover.

Besides, all of the studies mentioned above have used methods to predict only one wave of the epidemic. Although there exist some attempts such as Faranda & Alberti (2020); for the best of our knowledge, no study applies extended SEIR models to estimate a second wave of the spread of the pandemic by adding new states (e.g., intensive care) and adding new parameters (e.g., isolation / deisolation) to the existing models. These new features developed in this study help capture the multiple waves and contribute to the existing literature. Our model uses two reversing time-dependent parameters called 'protection (isolation) rate' and 'deisolation rate'. The number of protected or isolated people can quickly increase by the measures taken early by governments. These preventions help us to end the first peak rapidly. On the other hand, the opposite can also be true. Governments can loosen the measures before the risk has gone and people may stop taking precautions. Then the number of protected or isolated people goes down and of course, this implies an increase in the number of susceptible cases who are the healthy population who are susceptible to COVID-19. Therefore, this can cause a second wave. Of course, this logic can be easily generalized to multiple waves. The proposed model is explained formally and in more detail in the following section.

Model

It is important to establish a unique model for each specific epidemic or infectious disease, which captures its characteristics. Therefore, we propose and characterize a version of the Markov chain model by extending the generalized SEIR model for COVID-19.

Model Environment

In a closed population with no births and deaths -other than caused by COVID-19, the population is set to a constant, N . At each moment of the time, t , the population, N , is divided into nine states. These nine states/variables and parameters/functions of the model are summarized in Table 1 and 2, respectively:

Table 1: Definition of States / Variables

States / Variables	Definition
S(t): Susceptibles cases	A healthy population that is susceptible to COVID-19 (not infected yet).
P(t): Insusceptibles cases	A healthy population that is not susceptible to COVID-19 (e.g., by isolation).
E(t): Exposed cases	Infected but not yet be infectious (latent period).
I(t): Infectious cases	Infected with infectious capacity and not yet be quarantined.
Q(t): Quarantined cases	Infected and confirmed by tests.
IC(t): Intensive care cases	People who switch from quarantined cases to intensive care cases.
R ₁ (t): Recovered cases from quarantine	Recovered people (from quarantined cases) who are assumed to be no longer contagious.
R ₂ (t): Recovered cases from intensive care	Recovered people (from intensive care cases) who are assumed to be no longer contagious.
D(t): Death cases	Death people who are assumed to be no longer contagious.
N	Population (constant)

Table 2: Definition of Parameters / Functions

Parameters/Functions	Definition
$\alpha_{S-P}(t)$	Protection (isolation) rate
$\alpha_{P-S}(t)$	Deisolation rate
β	Infection rate
γ^{-1}	Average latent time
δ^{-1}	Average quarantine time
$\lambda_1(t)$	Cure function I (transmission to R ₁ from Q, time-dependent)
$\lambda_2(t)$	Cure function II (transmission to R ₂ from IC, time-dependent)
	IC function (transmission to the IC from Q, time-dependent)
$\mu(t)$	
$\kappa(t)$	Mortality function (time-dependent)

In the model, the protection (isolation) rate shows the ratio of a healthy population that is not susceptible to COVID-19 (for example, due to staying at home) to the total population where $0 \leq \alpha_{S-P}(t) \leq 1 \forall t$. Deisolation rate shows the ratio of a healthy population that is not isolated anymore and susceptible to COVID-19 (however, not infected yet) where $0 \leq \alpha_{P-S}(t) \leq 1 \forall t$. Infection rate ($0 \leq \beta \leq 1 \forall t$) is the rate at which susceptible individuals get infected. γ^{-1} and δ^{-1} are denoting the average latent time and average quarantine time, respectively, and they are both expressed in terms of the number of days. Cure functions and related parameters of these functions are determining the rate at which infected individuals recover. IC function and related parameters of this function is determining the rate at which quarantined people are switching to intensive care. Finally, mortality function and related parameters of this function determine the rate at which infected individuals die.

Figure 1 summarizes and illustrates the proposed Markov Chain model.

Figure 1. The Proposed Markov Chain (Generalized SEIR) Model for COVID-19

The generalized SEIR model utilized in this paper is defined with the following equations (1)-(15):

$$\frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N} - \alpha_{S-P}(t)S(t) \quad (1) \text{ or } \frac{dS(t)}{dt} = -\beta \frac{S(t)I(t)}{N} + \alpha_{P-S}(t)S(t) \quad (1')$$

$$\frac{dE(t)}{dt} = \beta \frac{S(t)I(t)}{N} - \gamma E(t) \quad (2)$$

$$\frac{dP(t)}{dt} = \alpha_{S-P}(t)S(t) \quad (3) \text{ or } \frac{dP(t)}{dt} = -\alpha_{P-S}(t)S(t) \quad (3')$$

Equation (1) simply tells that at each moment of time, some people in state S switches to state E (see also equation 2) depending on the magnitude of parameter β , which is defined as the infection rate. Some other portion of this population in state S switches to state P depending on the magnitude of parameter α_{S-P} (see also equation 3) because this population is socially isolated (e.g., staying at home). Similarly, equation (1') implies that (after loosening the measures), some people in state P switches to state S depending on the magnitude of parameter α_{P-S} (see also equation 3').

$$\frac{dI(t)}{dt} = \gamma E(t) - \delta I(t) \quad (4)$$

Equation (4) tells us that at each instant of time, some people in state E switches to state I, depending on the magnitude of the parameter, γ^{-1} , which is defined as the average latent time. Moreover, some people who are in the state I leave this state since they are quarantined after the confirmation of a positive test result.

Equation (5) tells us that at each instant of time some people in state Q switches to state R₁ (see also equation 7) depending on the magnitude of function $\lambda_1(t)$, and some other portion of this population switches to state IC (see also equation 6) depending on the function $\mu(t)$.

$$\frac{dQ(t)}{dt} = \delta I(t) - \lambda_1(t)Q(t) - \mu(t)Q(t) \quad (5)$$

$$\frac{dIC(t)}{dt} = \mu(t)Q(t) - \lambda_2(t)IC(t) - \kappa(t)IC(t) \quad (6)$$

Equation (6) tells us that at each instant of time some people in state IC switches to state R₂ (see also equation 8) depending on the magnitude of function $\lambda_2(t)$, and some other portion of this population switches to state D (see also equation 9) depending on the function $\kappa(t)$.

$$\frac{dR_1(t)}{dt} = \lambda_1(t)Q(t) \quad (7)$$

$$\frac{dR_2(t)}{dt} = \lambda_2(t)IC(t) \quad (8)$$

$$\frac{dD(t)}{dt} = \kappa(t)IC(t) \quad (9)$$

Equation (7)-(9) shows the time-varying cure and mortality functions, respectively.

Equation (10) captures the change in isolation/deisolation policies such as promoting social distancing, staying at home, wearing facemasks, etc.

$$\alpha_i(t) = \alpha_{i0}(1 - e^{-\alpha_{i1}t}) \quad (10)$$

where $i = S - P, P - S$.

Equation (11)-(14) implies that recovery and mortality rates are time-dependent.

$$\lambda_1(t) = \lambda_0(1 - e^{-\lambda_1t}) \quad (11)$$

$$\lambda_2(t) = \lambda_0(1 - e^{-\lambda_1t}) \quad (12)$$

$$\kappa(t) = \kappa_0 e^{-\kappa_1t} \quad (13)$$

$$\mu(t) = \mu_0 e^{-\mu_1t} \quad (14)$$

At each instant of time, the total number of people in these nine states should add up to a constant population, N :

$$N = S(t) + P(t) + E(t) + I(t) + Q(t) + IC(t) + R_1(t) + R_2(t) + D(t) \quad \forall t \quad (15)$$

Application and Results

Our model explores the ability of time-dependent isolation/deisolation rates to generate multiple waves. With our model, we show that by using these parameters, it is possible to match the second wave or the other waves, which may occur later.

The underlying mechanism leading to multiple waves is as follows:

- At the beginning of the pandemic, in many countries, including Turkey, the number of protected or isolated people were increasing due to measures taken by governments. In model terms, this is captured by a positive difference of $\alpha_{S-P}(t) - \alpha_{P-S}(t)$. Actually, at this stage of the pandemic, we normalize $\alpha_{P-S}(t)$ to zero. Therefore, $\alpha_{S-P}(t)$ shows the net number of people who are switching from state S state to state P.

- However, after the (first) peak, since the new daily cases start to decrease, governments loosen the measures and people are beginning disobeying the preventions. In the model, this is captured by a positive difference of $\alpha_{P-S}(t) - \alpha_{S-P}(t)$. Actually, at this stage of the pandemic, we normalize $\alpha_{S-P}(t)$ to zero. Therefore, $\alpha_{P-S}(t)$ shows the net number of people who are switching from state P to state S. If $\alpha_{P-S}(t)$ is sufficiently big, then this causes a second wave. This logic can be easily applied to multiple waves.

We apply our model to Turkish data to test whether the second wave will be experienced or not in Turkey. We use data tables for coronavirus cases, called “Coronavirus Table of Turkey”, which have been released daily by the Republic of Turkey Ministry of Health (<https://covid19.saglik.gov.tr/>). Simulations are implemented by MATLAB, and the MATLAB code is written by the authors.

Here we need to mention some important dates (i.e., milestones for COVID-19 spread and government measures taken in Turkey) and these are presented in Table 3. Moreover, for a recent review and analysis of the Republic of Turkey's presidential decrees released in the Official Gazette and the decisions of ministries and other institutions, see Erdem (2020).

Table 3: Milestones for COVID-19 Spread and Government Measures in Turkey

Date	Milestones for COVID-19 Spread or Government Measures
March 11, 2020	The confirmation of the first coronavirus case
March 16, 2020	Introduction of measures
March 17, 2020	Total number of cases reached 98
April 11, 2020	The peak for new/daily cases (5138 new cases)
May 11, 2020	The beginning of “normalization” period
June 1, 2020	Phase-out measures

*Source: The Humanitarian Data Exchange, Acaps, 2020; The Declaration of Presidency of the Republic of Turkey, 04.05.2020 The COVID-19 Normalization Plan.

First, we begin by presenting the actual new daily cases (blue curve) starting from March 17 until June 16 in Figure 2. Since the cumulative cases reached nearly 100 by March 17, we take this date as a starting point of our analysis. As seen in Table 3 and Figure 2 there is a peak on April 11 by 5138 new cases. This same figure also depicts the 7-day moving average of new daily cases (red curve). Since April 11, the new daily cases have a downward trend until June 8. However, after June

8, once again, there is an upward trend in 7-day moving average new daily cases, which may or may not be a sign of the second wave.

Figure 2: Daily New Cases (17.03.2020-16.06.2020)

In this paper, our concern is to generate a second upward slope for the 7-day moving average of actual daily cases. Therefore, in figure 3, we only concentrate on the recent stage of the pandemic, after May 1.

Figure 3: Daily New Cases versus Model Results (01.05.2020-16.06.2020)

Figure 3 presents the actual new daily cases (red curve), predicted daily cases 1 (blue curve), and predicted daily cases 2 (black dashed curve).² Predicted daily cases 1 depicts model results that can capture only a single peak. This implies that in these models, after the first peak, actual daily new cases decrease monotonically and converge to zero after a while (please see blue curve). In terms of our model, this happens while the difference between isolation and deisolation rates ($\alpha_{S-P}(t) - \alpha_{P-S}(t)$) is always positive or zero. This corresponds the most of the models in the literature, which can generate only a single peak. On the other hand, if after a while $\alpha_{P-S}(t) - \alpha_{S-P}(t)$ is sufficiently big, then the model can have a second upward sloping and second wave (please see black dashed curve).

The calculated mean absolute percentage error for the standard model, which can generate only one peak, is 22,5%. On the other hand, the calculated mean absolute percentage error for the proposed model, which can generate multiple waves, is 12,4%. These results indicate that the proposed model in this paper gives better results in predicting actual data. The model which can generate multiple peaks is a generalization of the standard models and should be used to match multiple potential waves during a pandemic.

Conclusion

In this study, as a theoretical contribution, we further extend the generalized SEIR model by adding two reversing time-depending parameters that control the isolation and deisolation rates. With our model, we show that by using these parameters, it is possible to match the second wave or the

² Please see the appendix A for the details of parameter values. Please see the appendix B for the numerical values of Figure 3.

other waves, which may occur later. For this purpose, we simulate our model for Turkey to check whether the model can match the second upward slope which may or may not be a signal of the second wave. We conclude that it is possible to generate multiple waves with the proposed model.

One another important novel feature of the model proposed in this paper is the addition of “intensive care” state to the SEIR model. This state is crucial because if the number of people in this state exceeds some threshold (which can differ from country to country), the health care system will not work properly. Therefore, it is crucial to project the number of people in this state when making policy decisions.

Last but not least, besides generating multiple waves, the proposed model can be used for projections and simulations based on scenario analyses for policy implications. Implementing such scenario analyses for Turkey is left for future studies.

Other possible future studies would be applications of our extended model to other countries’ data and comparing the results, to verify robustness and strengthen the applicability of the model.

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Appendix A: Parameter Values

There are two groups of parameters in the model. For the first group, we can infer the value of parameters directly from the data. The second group includes the parameters that we cannot directly obtain from the data, such as the rate of protection (i.e., isolation) and deisolation. Given the first group of parameters, we simulate the model and find the second group's parameter values by best fitting the model results to actual data. Average latent time and average quarantine time are assumed to be constant over time. Average latent time (5 days) and average quarantine time (14 days) are directly taken from the actual reports. Among others, please see “COVID 19 Rehberi (2020)” published by the Ministry of Health, Republic of Turkey. Therefore, values for γ and δ are equal to 0.20 and 0.07, respectively (1/average latent time and 1/average quarantine time). The infection rate (β) is also assumed to be constant over time. β is chosen as 0.99, and it is the estimated value to match the actual data and the model results. Cure functions I and II, IC function and mortality function are assumed to be time-dependent and take different values at each moment of time. We assume that both “Cure functions” are gradually increasing with time, while the IC and mortality functions decrease over time. These assumptions are raised by the increasing experience of health workers, the assistance of other emergency medical teams, the application of new drugs, etc. The crucial parameters of the model are the protection (isolation rate) and the deisolation rate. The model's estimates for these parameters are, on average, 0.17 and 0.20, respectively. The estimation is based on minimizing the difference between the actual data and model results. Therefore, these parameters are the ones that match the model results with actual data in the best manner. We use the Optimization Toolbox in Matlab for this minimization problem. Specifically, we use the “lsqcurvefit” solver with the “Trust-region-reflective” algorithm. Table 4 summarizes the parameter values.

Table 4: Parameter Values

Parameters/Functions	Values
$\alpha_{S-P}(t)$	0.17 (on average)
$\alpha_{P-S}(t)$	0.20 (on average)
β	0.99
γ^{-1}	5
δ^{-1}	14
$\lambda_1(t)$	gradually increasing with time
$\lambda_2(t)$	gradually increasing with time
$\mu(t)$	gradually decreasing with time
$\kappa(t)$	gradually decreasing with time

Appendix B: Table 5. Numerical Values of Figure 3.

May.01	2188	2401	2401
May.02	1983	2325	2325
May.03	1670	2250	2250
May.04	1614	2177	2177
May.05	1832	2105	2105
May.06	2253	2035	2035
May.07	1977	1967	1967
May.08	1848	1900	1900
May.09	1546	1835	1835
May.10	1542	1773	1773
May.11	1114	1711	1711
May.12	1704	1652	1652
May.13	1639	1595	1595
May.14	1635	1539	1539
May.15	1708	1485	1485
May.16	1610	1433	1433
May.17	1368	1382	1382
May.18	1158	1333	1333
May.19	1022	1286	1286
May.20	972	1240	1240
May.21	961	1196	1196
May.22	952	1153	1153
May.23	1186	1112	1112
May.24	1141	1072	1072
May.25	987	1034	1030
May.26	948	997	1000
May.27	1035	961	981
May.28	1182	927	966
May.29	1141	893	956
May.30	983	861	933
May.31	839	830	920
Jun.01	827	800	890
Jun.02	786	771	871
Jun.03	867	743	843
Jun.04	988	717	801
Jun.05	930	691	790
Jun.06	878	666	853
Jun.07	914	642	925
Jun.08	989	619	1024
Jun.09	993	596	1035
Jun.10	922	575	1124

Jun.11	987	554	1184
Jun.12	1195	534	1264
Jun.13	1459	515	1318
Jun.14	1562	496	1436
Jun.15	1592	478	1543
Jun.16	1467	461	1612