

Article

A Mathematical Model for the COVID-19 Pandemic in Tokyo through Changing Point Calculus

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Abstract: The great social and economic impact that the COVID-19 pandemic has had on a global level has encouraged the development of new mathematical models that make it possible to better manage this and future pandemics. Here, we propose an extension of the classical epidemiological compartmental model SIR, the SEIAMD model (Susceptible–Exposed–Identified–Asymptomatic–iMmunized–Deceased), which considers the appearance of new virus variants, the use of vaccines, the existence of nonidentified asymptomatic individuals, and the loss of immunity acquired by infection or vaccination. Using an optimization model coded in Python that allows us to determine the change points that represent different behaviors of infected people, the SEIAMD model calculates, from official data, the different effective contact rates that were observed during the first seven waves of the COVID-19 pandemic in Tokyo due to the application of Non-Pharmaceutical Interventions (NPIs) and social habits. The closeness of the results obtained with our model and the real data, as well as the accuracy of predictions and observations, confirm the suitability of our model for studying the evolution of the COVID-19 pandemic in Tokyo.

Keywords: SARS-CoV-2; COVID-19; pandemic; epidemiological compartmental model; effective contact rate; Non-Pharmaceutical Interventions (NPIs)



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1. Introduction

On 11 February 2020, the International Committee on Taxonomy of Viruses (ICTV) named the virus that in December 2019 had produced an outbreak of pneumonia in Wuhan, China, as *severe acute respiratory syndrome coronavirus 2* (SARS-CoV-2). The same day, the World Health Organization (WHO) named the disease caused by this new coronavirus as COVID-19. On 11 March 2020, the WHO declared the outbreak of COVID-19 a pandemic. According to WHO data [1], since the first case of COVID-19 was detected in December 2019, until March 2023, the date on which we wrote this article, more than 750 million cases of COVID-19 have been confirmed worldwide, and more than 6.8 million people have died as a result of this disease.

The COVID-19 pandemic has had a high impact on economics, social relations, and physical and mental health all over the world [2]. This has prompted researchers from different countries to develop mathematical models that allow them to determine which measures are most appropriate to deal with the pandemic. When we develop a mathematical model, the objective is to ensure that the model represents real data with high fidelity so that the parameters obtained from the model can be used to draw conclusions from the real world. The main technical issue in the construction of such mathematical model is that there is no primitive function that describes the behavior of the COVID-19 pandemic data; so, the development of a more complex mathematical model is necessary. The relative simplicity of the SIR model makes it suitable for rapidly assessing an epidemic when data on virus parameters are scarce. However, as pointed out in [3], the application

of the classical SIR model to the COVID-19 pandemic has given poor results. Several characteristics of the SARS-CoV-2 virus can explain this fact, including a relatively high latency period, the existence of asymptomatic individuals, and the possibility of reinfection due to loss of acquired immunity. Thus, to overcome the limitations that the SIR model presents when modeling the characteristics of this new virus, several SIR-based models have been proposed, some of which we discuss below. We must keep in mind that better mathematical models provide us with tools to understand the evolution of the COVID-19 pandemic and, therefore, enable us to better confront future pandemics caused by viruses that have characteristics similar to the SARS-CoV-2 virus.

One of the strategies used in the development of new models, the one we have followed, is to expand the number of compartments of the SIR model. Following this approach, authors in [4] model the COVID-19 pandemic with the SEIRD model (Susceptible, Exposed, Infective, Recovered, and Deceased), which expands the SIR model with two new compartments, Exposed and Deceased. Although with the Exposed compartment the authors take into account the latency period of the SARS-CoV-2 virus, they do not consider the asymptomatic individuals or the loss of immunity. Similarly, in [5], the researchers propose a seven compartmental model—Susceptible, Exposed, Infected, Asymptomatic, Quarantined, Fatal, and Recovered (SEIAQFR)—which takes into account both the latency period and the existence of asymptomatic individuals. However, it does not consider the loss of immunity and, therefore, reinfections.

Following a different approach, the authors in [6] propose three time-dependent modified SIR models (SIR-T, SIRD-T, and SIAR-T), and in [7], researchers propose an age-structured SIR model. A study that, like ours, models the pandemic in Tokyo uses a combination of SIR models to fit the data [3]. They obtain effective contact rate values similar to those we obtain when applying our model. However, the characteristics of its procedure make it unfeasible as a tool for evaluating Non-Pharmaceutical Interventions (NPIs).

To model the spread of COVID-19, other alternatives different from SIR models have also been explored, such as the use of Cellular Automaton (CA) [8,9]. Specifically, CA has been used to model the effects of the lockdowns [10] or also to model the variants of the SARS-CoV-2 virus [11]. In other approaches, the combination of SIR like models with CA and optimization models allows not only an estimation of the parameters but the creation of a digital twin of the pandemic situation [12]. However, solutions based in CA are complex and require large computation times.

In this paper, we propose to study the evolution of the COVID-19 pandemic in Tokyo by using the SEIAMD model (Susceptible–Exposed–Identified–Asymptomatic–iMmunized–Deceased), an extension of the SIR model that considers the appearance of new virus variants at different times, the use of several rounds of vaccination in the population, the existence of nonidentified asymptomatic individuals, and the loss of immunity, acquired by infection or vaccination, after a certain period of time.

As we detail later, our model makes it possible to determine points of change in the behavior of the population under study, making it especially appropriate to assess the impact of Non-Pharmaceutical Interventions (NPIs) carried out by the authorities. Japanese legislation does not allow for limiting the mobility of citizens; therefore, lockdowns have not occurred in Japan as in other parts of the world, with states of emergency decreed by the authorities being mere recommendations to the population. However, the social discipline that characterizes Japanese society and the extensive use of masks, both in children and adults, has meant that the incidence of the COVID-19 pandemic in Tokyo is considerably lower than in other parts of the world, especially if we take into account the large number of inhabitants (14 million) and the high population density of the prefecture (6408 persons per square kilometer).

The results obtained by executing the model we propose highly fit with the official data, and the predictions and observations regarding the NPIs were accurate. Moreover, the values obtained for the effective contact rate are similar to those obtained in other studies [3] and explain the relatively low number of COVID-19 cases registered in Tokyo.

The results, therefore, demonstrate that our mathematical model is adequate to study the evolution of the COVID-19 pandemic in Tokyo, and can be useful to study other epidemics.

In summary, the main contributions of this work are as follows. First, we study the spread of COVID-19 in Tokyo from the perspective of mathematical modeling—namely, fitting data in explanatory and predictive equations. Second, we propose the addition of new compartments to the classical SIR model to allow us to model viruses with a significant latency period, reinfection, and asymptomatic individuals. Third, we contribute the implementation of an adjustment procedure that allows us to determine when a change in behavior of the population affects the spread of the virus under study.

The remainder of the paper is organized as follows. In Section 2.1, we describe the compartments, parameters, and equations that constitute the SEIAMD model. In Section 2.2, we detail how we have implemented this model. In Section 3, we present the results obtained. Finally, in Section 4, we discuss the implications of our results, as well as the conclusions obtained and future work.

2. Materials and Methods

2.1. Conceptual Model

2.1.1. Model Compartments

The SIR model is a compartmental model used in the field of epidemiology that describes the transmission process of an infectious disease through a system of differential equations. As we can see in Figure 1, the total population is divided into three mutually exclusive compartments, namely Susceptible (S), Infected (I), and Recovered (R) [13]. Individuals move from one compartment to another as time passes based on different transfer rates.

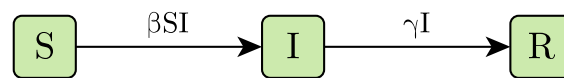


Figure 1. Compartments of the SIR epidemic model (Susceptible–Infected–Recovered) and associated parameters.

The SEIAMD model that we propose is an extension of the SIR model and it consists of six compartments: Susceptible, Exposed, Identified, Asymptomatic, iMmunized, and Deceased (see Figure 2).

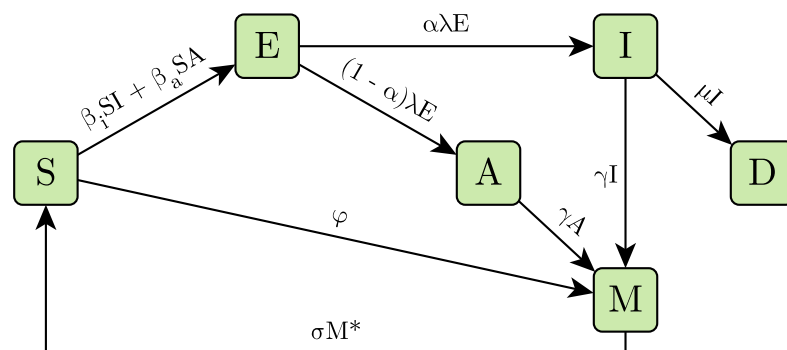


Figure 2. Compartments of the SEIAMD epidemic model (Susceptible–Exposed–Identified–Asymptomatic–iMmunized–Deceased) and associated parameters.

The Susceptible compartment (S) contains the susceptible individuals of the population, i.e., those who can be infected by the virus. The Exposed compartment (E) contains the individuals who have been exposed to the virus by being in contact with infected individuals. The addition of this compartment to the basic SIR model allows our proposed model to take into account the virus latency period.

Although it is difficult to quantify the incidence of asymptomatic individuals with certainty, several studies have shown their importance [14]. Therefore, we decided to split

the original I defined in SIR into our I and A compartments. Thus, the infected individuals are in the Identified (I) and Asymptomatic (A) compartments. The I compartment contains the infected individuals that have been identified as positive for SARS-CoV-2, and the A compartment contains those individuals who are infected but do not have symptoms, i.e., they are asymptomatic, so they have not been tested and, therefore, have not been identified as positive.

The Immunized compartment (M) contains those individuals who are immunized. An individual can be immunized after being infected (identified or asymptomatic) or after being vaccinated. We create this compartment to contemplate the immunity loss of the population and the subsequent reinfection possibility. Thus, over time, immunization declines, and individuals become susceptible again.

Finally, as the population must be constant in time, and this virus causes the death of some infected individuals, who logically will not be reinfected or infect other individuals, such unfortunate deaths must be taken into account in the model. We, therefore, define the Deceased compartment (D) to contain those individuals who have died. Here, we assume that all people who have died have been identified as positive.

As is shown in Figure 2, different parameters determine the number of individuals who move from one compartment to another. We define these parameters in the next section.

2.1.2. Model Parameters

The effective contact rate (β) is defined as the product of the total contact rate and the transmission risk, i.e., the rate at which the contact between a susceptible individual and others infected will cause the susceptible individual to become infected. The parameters β_i and β_a represent the effective contact rate for the identified and for the asymptomatic, respectively. Considering the results obtained in [14], we assume that $\beta_a = 0.58\beta_i$. On the other hand, β_i is calculated by adjustment when running the model.

The parameter φ is the number of individuals immunized by vaccine. We obtained the official data of vaccinations from [15], and we calculated φ taking into account the results obtained in [16]. Thus, we suppose that 14 days after the first dose, only 52 percent of vaccinated individuals will be immunized, and 7 days after the second, third, fourth, and fifth doses, 95 percent of vaccinated individuals will be immunized.

The parameter σ represents the proportion of immunized individuals that are susceptible again after a period of time. From [17], we assume that $\sigma = 0.81$ for the B.1.1.529 (Omicron) variant and $\sigma = 0.15$ for the others variants. M_t is the number of immunized individuals at time t , and M^* is the number of individuals immunized at $t - p$, with p as the period of time needed for the loss of immunity; from [17], we assume that $p = 6$ months.

The parameter λ is the latency rate, and we suppose that the incubation period ($1/\lambda$) is 5 days for the original variant of SARS-CoV-2 ($\lambda = 0.2$) [18], 4 days for the B.1.1.7 (Alpha) and B.1.617.2 (Delta) variants ($\lambda = 0.25$) [19,20], and 3 days for the B.1.1.529 (Omicron) variant ($\lambda = 0.33$) [21].

The parameter α represents the proportion of infected individuals that are identified, and we assume that nonidentified individuals are asymptomatic; therefore, taking into account the results obtained in [14], we suppose that $\alpha = 0.83$.

The parameter γ is the recovery rate, and it is calculated from the official data as follows:

$$\gamma = \frac{1}{f} \sum_{t=1}^f \frac{D_t - D_{t-1}}{G_t} = 0.1201 \sim 0.12, \quad (1)$$

where D_t is the number of discharged individuals at time t , and G_t is the number of individuals at time t that have tested positive, minus the number of individuals that have been discharged, and minus the number of deaths.

Finally, the parameter μ is the mortality rate. It is calculated, also from the official data, as follows:

$$\mu = \frac{1}{f} \sum_{t=1}^f \frac{H_t - H_{t-1}}{G_t} = 0.00095 \sim 0.001, \quad (2)$$

where H_t is the number of deaths at time t .

For the SIR model, implemented for comparative purposes, as the R compartment contains individuals that have recovered as well as individuals that have died, we recalculate the γ parameter so that it includes the deceased. Thus, the parameter γ for the SIR model is calculated from the official data as follows:

$$\gamma_{SIR} = \frac{1}{f} \sum_{t=1}^f \frac{(D_t + H_t) - (D_{t-1} + H_{t-1})}{G_t} = 0.12105 \sim 0.121. \quad (3)$$

2.1.3. Model Equations

The classical SIR model proposed by Kermack and McKendrick is expressed by the following system of differential equations [22]:

$$\begin{cases} \frac{dS}{dt} = -\beta IS, \\ \frac{dI}{dt} = \beta IS - \gamma I, \\ \frac{dR}{dt} = \gamma I. \end{cases} \quad (4)$$

When we consider, as in this case, that the population mixes at random, so that each individual has a small and equal chance of coming into contact with any other individual, the transmission of infection is represented by the term $\beta IS/N$ [23], where N is the total population. Thus, we have the following system of equations:

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta IS}{N}, \\ \frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I, \\ \frac{dR}{dt} = \gamma I. \end{cases} \quad (5)$$

Taking into account that the data regarding the COVID-19 pandemic are discrete, since the authorities publish the measures every day, it is more convenient to work with a discrete form of the SIR model. A fast and direct way to discretize the SIR model is by the forward Euler method [24], using the formula:

$$y_{n+1} = y_n + \Delta t f(t, y(t)), \quad \text{for } n = 0, 1, 2, \dots \quad (6)$$

Thus, applying Equation (6) to Equation (5), with $\Delta t = 1$ day, we obtain the following system of equations for the discrete SIR model:

$$\begin{cases} S_{t+1} = S_t - \beta I_t S_t / N_t, \\ I_{t+1} = I_t + \beta I_t S_t / N_t - \gamma I_t, \\ R_{t+1} = R_t + \gamma I_t, \end{cases} \quad (7)$$

where N_t is the total population in any given time t , and $N_t = S_t + I_t + R_t$.

Following the same reasoning, we decide to formulate the SEIAMD model as a discrete-time model. Thus, applying the same procedure described above, the resulting system of difference equations that rule the SEIAMD model behavior is:

$$\begin{cases} S_{t+1} = S_t - \beta_i S_t I_t / N_t - \beta_a S_t A_t / N_t - \varphi_t + \sigma M^*, \\ E_{t+1} = E_t + \beta_i S_t I_t / N_t + \beta_a S_t A_t / N_t - \lambda E_t, \\ I_{t+1} = I_t + \alpha \lambda E_t - \gamma I_t - \mu I_t, \\ A_{t+1} = A_t + (1 - \alpha) \lambda E_t - \gamma A_t, \\ M_{t+1} = M_t + \gamma I_t + \gamma A_t + \varphi_t - \sigma M^*, \\ D_{t+1} = D_t + \mu I_t, \end{cases} \quad (8)$$

where $N_t = S_t + E_t + I_t + A_t + M_t + D_t$. Furthermore, we consider N_t to be constant, and, calculating the mean value from official data [25], $N_t = 14,039,312$.

Taking into account the inputs and outputs of each compartment that is part of the SEIAMD model (see Figure 2), we can follow step by step the construction of the equations that we have just presented.

By doing so, we have that the Susceptible compartment (S) in time $t + 1$ contains the individuals that were in time t ($S_{t+1} = S_t \dots$), minus the individuals that have moved to the Exposed compartment (E), whose number depends on the parameters β_i and β_a ($-\beta_i S_t I_t / N_t - \beta_a S_t A_t / N_t$), minus the φ individuals that have moved to the Immunized compartment (M) ($-\varphi_t$), plus the individuals that have entered from the Immunized (M) compartment, whose number depends on the parameter σ ($+\sigma M^*$). Finally, combining all these factors, we obtain the Susceptible equation:

$$S_{t+1} = S_t - \beta_i S_t I_t / N_t - \beta_a S_t A_t / N_t - \varphi_t + \sigma M^*.$$

In the same way, we have that the Exposed compartment (E) in time $t + 1$ contains the individuals that were in time t ($E_{t+1} = E_t \dots$), plus the individuals that have moved from the Susceptible compartment (S), whose number depends on the parameters β_i and β_a ($+\beta_i S_t I_t / N_t + \beta_a S_t A_t / N_t$), minus the individuals that have moved to the Identified compartment (I) ($-\alpha \lambda E_t$), minus the individuals that have moved to the Asymptomatic compartment (A) ($-(1 - \alpha) \lambda E_t$). These last two factors can be simplified into λE_t , which are the individuals who have left the Exposed compartment (E). Combining all these factors, we obtain the Exposed equation:

$$E_{t+1} = E_t + \beta_i S_t I_t / N_t + \beta_a S_t A_t / N_t - \lambda E_t.$$

On the other hand, the Identified compartment (I) in time $t + 1$ contains the individuals that were in time t ($I_{t+1} = I_t \dots$), plus the individuals that have moved from the Exposed compartment (E) ($+\alpha \lambda E_t$), minus the individuals that have moved to the Immunized compartment (M) ($-\gamma I_t$), and minus the individuals that have moved to the Deceased compartment (D) ($-\mu I_t$). Combining all these factors, we obtain the Identified equation:

$$I_{t+1} = I_t + \alpha \lambda E_t - \gamma I_t - \mu I_t.$$

The Asymptomatic compartment (A) in time $t + 1$ contains the individuals that were in time t ($A_{t+1} = A_t \dots$), plus the individuals that have moved from the Exposed compartment (E) ($+(1 - \alpha) \lambda E_t$), minus the individuals that have moved to the Immunized compartment (M) ($-\gamma A_t$). Combining all these factors, we obtain the Asymptomatic equation:

$$A_{t+1} = A_t + (1 - \alpha) \lambda E_t - \gamma A_t.$$

The Immunized compartment (M) in time $t + 1$ contains the individuals that were in time t ($M_{t+1} = M_t \dots$), plus the individuals that have moved from the Identified compartment (I) ($+\gamma I_t$), plus the individuals that have moved from the Asymptomatic compartment (A) ($+\gamma A_t$), plus the φ individuals that have moved from the Suscepti-

ble compartment (S) ($+\varphi_t$), minus the individuals that have moved to the Susceptible compartment (S) ($-\sigma M^*$). Combining all these factors, we obtain the Immunized equation:

$$M_{t+1} = M_t + \gamma I_t + \gamma A_t + \varphi_t - \sigma M^*.$$

Finally, the Deceased compartment (D) in time $t + 1$ contains the individuals that were in time t ($D_{t+1} = D_t \dots$) plus the individuals that have moved from the Identified compartment (I) ($+\mu I_t$). Combining these factors, we obtain the Deceased equation:

$$D_{t+1} = D_t + \mu I_t.$$

2.2. Model Implementation

We coded the SEIAMD model in Python, using the function *optimize.least_squares* from the *SciPy* library to adjust the parameter β_i (see Supplementary Materials). Our application reads the officially published records of COVID-19 confirmed cases, discharged patients, deaths, and vaccinations [15,26]. It also reads a table with values for the other parameters of the model. All the obtained files are in the source format, unmodified; so, they will be read as they are provided by the source. The vaccination file is in the streaming JSON format (i.e., ND-JSON). The other files are in CSV format. Then, our code builds an object that will put together all available data for each day, as well as some calculated data (e.g., immunized and immunized by vaccine, which are fulfilled after all records are already created). A list with these records is used for adjusting the parameter β_i as follows.

First, our model is coded as a function that obtains values for the compartments for some time $t + 1$, given the values of the compartments for time t . This is a straightforward implementation of the equations of our model, as shown in Equation (8). Second, we implement a function that compares the values obtained by executing the previous function for some provided compartment values and the actual values that should be, as indicated by the record that corresponds to the day of the values introduced. This function returns the sum of differences for N (which should be 0), and the I , A , and D compartments.

Third, the second function is iteratively provided to the least squares function for each period indicated in the input table of periods. This function performs the adjustment, but it is not independent. Instead, the code joins the values obtained by executing the function of our model (the first function). This way, the least squares is actually adjusting the parameter β_i for some time period provided the behavior of the model in the previous time period, which, in turn, is adjusted considering the previous time period, and so on until the first time period is reached. This ensures that the resulting function is less artificial and thus closer to the real behavior measured and provided in the input files.

We executed this fitting procedure several times. Each execution allowed us to identify a point of change, which will become a point of parameter adjustment for the next execution of the fitting procedure. This way, after all needed change points have been identified, we obtained the fitting parameters required for our SEIAMD model to fit the behavior of the Tokyo population.

In addition to β_i and β_a , we also defined the parameters λ and σ during our fitting procedure (although they were not adjusted by least squares), taking into account the predominant variant of each period. Thus, we assumed, from [27], that the original strain was the dominant one in the first eleven periods, that the Alpha variant was dominant in periods 12 and 13, the Delta variant between periods 14 and 15 (both included), and the Omicron variant from period 19.

Finally, we implemented a function that calls the first function for subsequent days to obtain the projection of the I compartment on time. The resulting projection is shown in the next section.

3. Results

To showcase the feasibility of the proposed SEIAMD model to the COVID-19 pandemic in Tokyo, we used the implementation discussed in Section 2.2. The closer the calculated

data are to the official number of persons infected, the more suitable our SEIAMD model is for the purpose discussed in this paper. The nearness between the official and calculated data is shown in Figure 3. This figure shows the number of persons identified (y -axis) for each day (x -axis). The values of the plotted curve of the official data are obtained directly from the official data provided by health authorities [26]. The values of the plotted curve of the calculated data are obtained by executing the last function described in Section 2.2. As we can see, both curves are highly overlapped for most days.

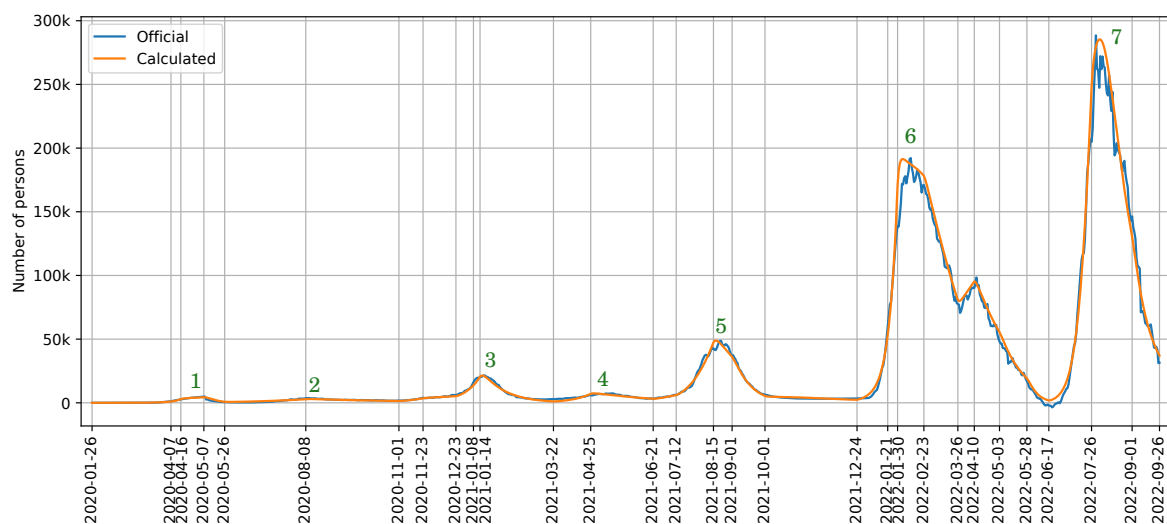


Figure 3. Official and calculated data of identified people obtained with the SEIAMD model in the prefecture of Tokyo during the first seven waves of the COVID-19 pandemic.

To assess numerically the accuracy of our model, we calculated the *MdAPE* (Median Absolute Percentage Error) value as follows [28]:

$$MdAPE = \left(\text{median} \left(\frac{|\text{official data} - \text{calculated data}|}{\text{official data}} \right) \right) \times 100. \quad (9)$$

By doing so, we obtained an *MdAPE* value of 9.3%, which indicates that the calculated data fit very well to the official data.

In order to compare the fit of our model to the data with the fit of the classical SIR model, we implemented the SIR model in Python following the same procedure described in Section 2.2 for the SEIAMD model, using the equations described in Equation (7), and the parameter γ_{SIR} shown in Equation (3). The resulting projection is shown in Figure 4.

The *MdAPE* value obtained for the SIR model was 60.6%, which indicates that the calculated data fit poorly to the official data. In view of these results, we can affirm that the SEIAMD model fits the official data better than the SIR model.

Table 1 shows the change points obtained with the SEIAMD model. We determined that on each of the dates listed in this table, there was a change in the behavior of Tokyo's inhabitants, which implies a change in the effective contact rate of the population. Between each pair of change points, there is a period with consistent (similar) behavior, which is justified by showing the good fitting of the values obtained with our model. Table 2 shows these periods and the values obtained for the parameters β_i and β_a associated with each period. As mentioned above, our fitting procedure iterated among the periods to obtain the value of β_i and β_a .

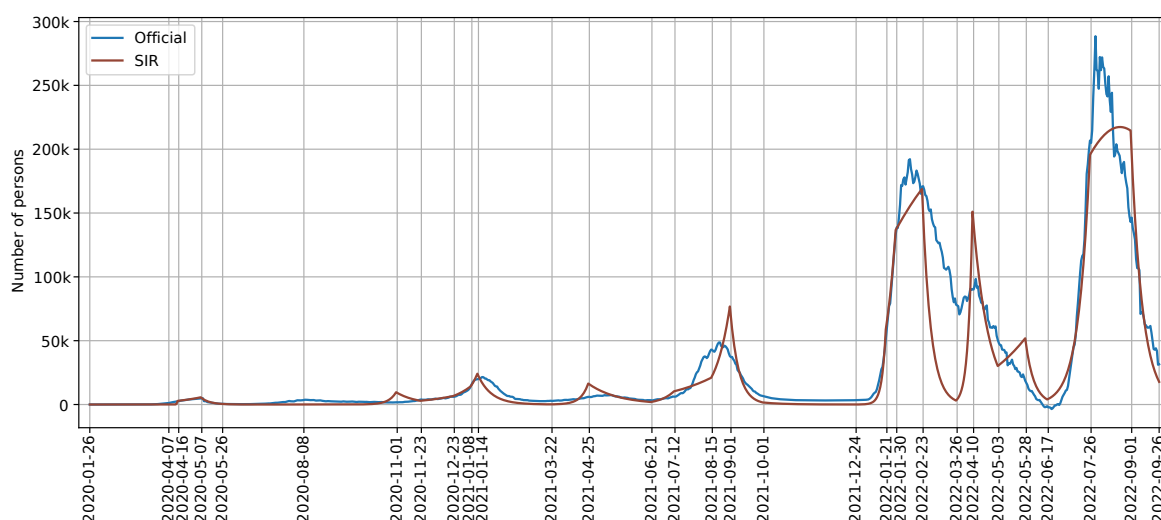


Figure 4. Official and calculated data of identified people obtained with the SIR model in the prefecture of Tokyo during the first seven waves of the COVID-19 pandemic.

Table 1. Change points in the behavior of the Tokyo population, shown in Figure 3.

Date	Event
2020-04-07	Declaration of state of emergency in Tokyo [29].
2020-04-16	Declaration of state of emergency in Japan [30].
2020-05-07	Extension of the state of emergency (planned end: 6 May) [30].
2020-05-26	First day after the end of the state of emergency [30].
2020-08-08	Obon Festival.
2020-11-01	Resumption of cross-border travel [31].
2020-11-23	Labor Thanksgiving Day.
2020-12-23	First case of Alpha variant [32].
2021-01-08	Declaration of state of emergency in Tokyo [33].
2021-01-14	Extension of the state of emergency to other prefectures [34].
2021-03-22	First day after the end of the state of emergency [35].
2021-04-25	Declaration of state of emergency in Tokyo [36].
2021-06-21	First day after the end of the state of emergency [37].
2021-07-12	Declaration of state of emergency in Tokyo [38].
2021-08-15	Obon Festival.
2021-09-01	Disaster Prevention Day.
2021-10-01	First day after the end of the state of emergency [39].
2021-12-24	First community transmission of Omicron variant [40].
2022-01-21	Establishment of quasi-emergency measures [41].
2022-01-30	Weekend.
2022-02-23	The Emperor's Birthday.
2022-03-26	Hanami (cherry blossom viewing).
2022-04-10	Weekend.
2022-05-03	Golden Week holidays.
2022-05-28	Weekend.
2022-06-17	Friday.
2022-07-26	Summer vacation.
2022-09-01	Disaster Prevention Day.

As we can see in Table 1, the change points obtained with the SEIAMD model can be linked to actual events related to the Tokyo population, most of which can be identified as Non-Pharmaceutical Interventions (NPIs) or events clearly related to the habits of the population such as holidays and weekends. This strengthens the validity of the assumptions we considered while defining our SEIAMD model, as well as the validity of the SEIAMD model as a tool for evaluating the effectiveness of NPIs.

Table 2. Effective contact rates obtained with the SEIAMD model.

Period	Dates	β_i	β_a
(1)	2020-01-26 → 2020-04-06	0.36	0.21
(2)	2020-04-07 → 2020-04-15	0.45	0.26
(3)	2020-04-16 → 2020-05-06	0.15	0.09
(4)	2020-05-07 → 2020-05-25	0.00	0.00
(5)	2020-05-26 → 2020-08-07	0.17	0.10
(6)	2020-08-08 → 2020-10-31	0.11	0.07
(7)	2020-11-01 → 2020-11-22	0.21	0.12
(8)	2020-11-23 → 2020-12-22	0.14	0.08
(9)	2020-12-23 → 2021-01-07	0.26	0.15
(10)	2021-01-08 → 2021-01-13	0.26	0.15
(11)	2021-01-14 → 2021-03-21	0.06	0.03
(12)	2021-03-22 → 2021-04-24	0.23	0.13
(13)	2021-04-25 → 2021-06-20	0.10	0.06
(14)	2021-06-21 → 2021-07-11	0.19	0.11
(15)	2021-07-12 → 2021-08-14	0.29	0.17
(16)	2021-08-15 → 2021-08-31	0.14	0.08
(17)	2021-09-01 → 2021-09-30	0.08	0.04
(18)	2021-10-01 → 2021-12-23	0.26	0.15
(19)	2021-12-24 → 2022-01-20	0.70	0.41
(20)	2022-01-21 → 2022-01-29	0.66	0.38
(21)	2022-01-30 → 2022-02-22	0.20	0.11
(22)	2022-02-23 → 2022-03-25	0.16	0.10
(23)	2022-03-26 → 2022-04-09	0.30	0.17
(24)	2022-04-10 → 2022-05-02	0.19	0.11
(25)	2022-05-03 → 2022-05-27	0.15	0.09
(26)	2022-05-28 → 2022-06-16	0.00	0.00
(27)	2022-06-17 → 2022-07-25	0.86	0.50
(28)	2022-07-26 → 2022-08-31	0.49	0.29
(29)	2022-09-01 → 2022-09-26	0.34	0.20

In Figure 3, we can notice that around the last months of 2020, there was a higher concentration of change points (i.e., the change points were closer to each other). This is explained by a fast change in the behavior of the population. Thus, people stressed by different and changing conditions ended up in disparate outcomes. However, just after that period, as is normal, the behavior of the population stabilized; therefore, there was a longer period with no change point. This also resulted in a quite long period with very sparse change points, even covering the totality of the fifth wave (around August 2021). At this moment, the population reacted more strictly to the NPIs, as demonstrated by the fact that the change points reflected the change in official policy.

The stable period ended around December 2021 with the first occurrence of the Omicron variant. This change point was succeeded by a higher concentration of change points, although never as close as the previous case. Our model experienced higher deviations, as shown at the end of January 2022. This is because of the high number of people infected, which made it more difficult to adjust with high precision. The same occurred around July 2022. However, the concentration of change points around both spikes was very different. There was a noticeably lower concentration of change points around the last spike in comparison to the previous spike, which means that people did not react to the rise in cases by changing their behavior; so, it is normal that this last spike resulted in a higher number of persons infected.

Regarding the periods and values of the effective contact rates shown in Table 2, it is worth noting the stability of the resulting values of the parameters. This is particularly important for the parameter β_i , which responds to the effective contact rate of people identified as infected, which was always lower than 0.9, although most values (75-percentile) were lower than 0.3 (the mean is 0.26, and the standard deviation is 0.2). These values are

aligned with the related work [3], which demonstrates the validity of the SEIAMD model and the fitting procedure we propose in this paper.

Table 3 shows the expected effects (predictions) of the NPIs on the effective contact rate (parameter β_i), contrasted with the observed effects on the same parameter. On the one hand, the predictions are based on supposing that establishing or extending a state of emergency makes people reduce the number of contacts, which will be translated into a decrease in parameter β_i . Similarly, lifting a state of emergency makes people increase their contact, which will end up in an increase in the parameter β_i . The observation was obtained by comparing the value of β_i from a specific period with the value of β_i from the period just before.

Table 3. Predicted effects of NPIs on the effective contact rate (β_i).

Date	Event	Prediction	Observation
2020-04-07	Declaration of state of emergency in Tokyo [29].	Decrease	Increase
2020-04-16	Declaration of state of emergency in Japan [30].	Decrease	Decrease
2020-05-07	Extension of the state of emergency (planned end: May 6th) [30].	Decrease	Decrease
2020-05-26	First day after the end of the state of emergency [30].	Increase	Increase
2020-11-01	Resumption of cross-border travel [31].	Increase	Increase
2021-01-08	Declaration of state of emergency in Tokyo [33].	Decrease	Equal
2021-01-14	Extension of the state of emergency to other prefectures [34].	Decrease	Decrease
2021-03-22	First day after the end of the state of emergency [35].	Increase	Increase
2021-04-25	Declaration of state of emergency in Tokyo [36].	Decrease	Decrease
2021-06-21	First day after the end of the state of emergency [37].	Increase	Increase
2021-07-12	Declaration of state of emergency in Tokyo [38].	Decrease	Increase
2021-10-01	First day after the end of the state of emergency [39].	Increase	Increase
2022-01-21	Establishment of quasi-emergency measures [41].	Decrease	Decrease

We see in the table that most predictions were right, as confirmed by the observations. The only exceptions were for 2020-04-07 (period 2), 2021-01-08 (period 10), and 2021-07-12 (period 15). The first exception can be explained by the lack of awareness in the population because it was the beginning of the pandemic. The second exception is a minor one because there is no change in the effective contact rate. The third exception can be explained by the fact that period 15 includes the duration of the Olympic Games in Tokyo (held from 23 July to 8 August 2021), which made people increase their contacts, even though the emergency state was declared.

In view of these results, we can affirm that the NPIs carried out in Tokyo were generally effective in mitigating the impact of the COVID-19 pandemic. This conclusion is aligned with the results obtained in other studies [42,43], which reinforces the validity of the proposed SEIAMD model.

4. Discussion

In this paper, we studied the application of the SEIAMD model to the evolution of the COVID-19 pandemic in Tokyo. As shown in Figure 3, the model that we propose fits

well with the official data, and with an *MdAPE* value of 9.3%, it significantly improves the projections made with the SIR model, with which an *MdAPE* value of 60.6% was obtained. Moreover, the values obtained for the effective contact rate (β_i) are similar to those obtained in other studies [3], and they explain the relatively low number of COVID-19 cases that have been registered in Tokyo. Therefore, we confirm that our mathematical model, built as an extension of the classical SIR model, is adequate for representing the evolution of the COVID-19 pandemic in Tokyo.

At this point, we should note that since our model fits the official data, the conclusions that we have obtained with our model depend on how well the data reflect reality. If data were missing or altered, our conclusions would be less reliable.

In the first five waves, the dates that have been identified as points of change in the behavior of the population coincide with the establishment, extension, or lifting of emergency measures by the authorities. Therefore, we claim that our model is a useful tool for evaluating the impact that Non-Pharmaceutical Interventions (NPIs) have had in Tokyo, and it can serve as a starting point for the development of future models that evaluate these types of measures in other epidemics.

On 21 March 2022, the quasi-emergency state in Tokyo was lifted and, on the dates included in our study, it was not established again. Therefore, there were no particular measures from that day until the end of our analysis. This lack of government measures justifies the low response of the population to the rise in new cases of COVID-19, which, as we discussed in the previous section, made the seventh wave higher than the previous ones. The decision to eliminate the restrictions imposed in Tokyo to mitigate the spread of COVID-19 was aligned with the global trend, as many countries lifted COVID-19 restrictions in March 2022. However, this decision was questioned by part of the scientific community, who considered it hasty [44]. Returning to the data from Tokyo, the large seventh wave of infections confirmed the fears of these scientists; therefore, we should be more cautious when lifting restrictions in future pandemics.

In our analysis, we should also consider that although the contact rate in the population did not increase, the appearance of more virulent strains of the virus also produced an increase in the number of cases, and that it is difficult, due to pandemic fatigue [45], to have the population adhere to strict measures for prolonged periods, even in highly aware societies, such as the Japanese. In this regard, studies should be carried out to analyze the responses that different societies have had to the NPIs, since a society like the Spanish may require more information to withstand the extension of the measures, while, on the contrary, in a society as aware as the Japanese, it is more effective to reduce the load of messages so that people feel less pressure and the authorities can prolong the restrictive measures.

Similarly, when studying NPIs, not only the social characteristics but also the legislation of each country must be taken into account. Thus, while mandatory lockdowns were carried out in Spain, in Japan, the legislation does not allow citizens to be confined; so, the emergency measures were the recommendation for citizens to stay at home, for businesses to work remotely, and limitations of maximum occupancy and business hours. Tokyo citizens followed these recommendations, causing the number of cases of COVID-19 to remain relatively low.

In summary, regarding the model, we found that the compartments that we defined in the SEIAMD model are required for modeling the COVID-19 pandemic in Tokyo, and that our fitting procedure allows us to assess the effectiveness of Non-Pharmaceutical Interventions (NPIs). Moreover, regarding the impact of the NPIs, we found that, in general, the behavior of the Tokyo population was aligned with the recommendations of the authorities; so, the NPIs were a key aspect in controlling the spread of COVID-19 in Tokyo.

In future work, we will apply our model to other populations, and we also plan to adapt it to study the population behavior in response to other viral outbreaks, as in the case of seasonal flu. Since our model has been developed taking into account the characteristics of the SARS-CoV-2 virus, we expect the SEIAMD model to fit well

to outbreaks of virus with similar characteristics. Since one in three influenza-infected individuals is asymptomatic [46], reinfection with the influenza virus is possible [47], and the latency period of the influenza virus, although shorter than that of the SARS-CoV-2 virus, is significant (1.6 days) [48], we expect the SEIAMD model to allow us to evaluate the impact that NPIs have on the spread of the influenza virus.

Supplementary Materials: The Python code for the SEIAMD model is available at: <https://doi.org/10.24433/CO.1462861.v1> (accessed on 7 November 2023).

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