

Modeling COVID-19 Spread in Chile: Integrating Spatial Population Dynamics within the SIR Framework

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1 Introduction

Since its onset in 2020, COVID-19 has inflicted widespread devastation, claiming over 6.9 million lives globally. Throughout the pandemic, the Centers for Disease Control and Prevention (CDC) repeatedly extended shelter-in-place directives, fostering the population's growing distrust in scientific and governmental institutions. This erosion of trust has direly affected patient outcomes, as individuals increasingly disregarded CDC regulations, leading to heightened fatalities, especially in communities with lower access to healthcare facilities [1]. To mitigate this crisis, there is an urgent need for significant advancements in epidemic modeling to enhance our ability to predict infection rates and refine prevention strategies.

This study introduces a mathematical framework for examining the progression dynamics of the COVID-19 pandemic during its early stages in Chile. We propose a spatial-temporal epidemiological mathematical model tailored to approximate the pandemic's initial phase in the country, incorporating the spatial and temporal diffusion patterns of SARS-CoV-2. The model categorizes the population into susceptible, infected, and recovered individuals based on their COVID-19 progression status. Calibration of the model is conducted using real-world data on reported daily cases spanning 28 weeks (March 10, 2020-September 15, 2020) across Chile's 16 regions. We pre-process this data by organizing it into weekly new infections to facilitate data smoothing, a standard practice in epidemiology.

2 Methods

Chile's geographical configuration resembles a slender strip nestled between the Pacific Ocean to the west and the towering Andes mountains to the east. Stretching 4,270 kilometers from north to south [2], its width averages only about 177 kilometers. Furthermore, the eastern side, dominated

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by the Andes, exhibits sparse population density [3]. Notably, the narrowest segment measures approximately 66 kilometers, marking Chile as one of the world's most distinctive territorial shapes. As of the 2017 census by the Instituto Nacional de Estadísticas of Chile, Chile's population is 17,574,003 people [4]. Given these geographic features, this study adopts a spatial-temporal mathematical model, integrating a single spatial variable representing Chile's latitude position.

Furthermore, in multiple countries, a trend emerged where individuals relocated from densely populated urban regions to sparsely populated rural areas seeking lower-risk environments of SARS-CoV-2 infection [5].

2.1 Spatial-temporal mathematical model

Let us present the spatial-temporal mathematical model. Consider a bounded domain Ω within \mathbb{R} with a smooth boundary denoted by $\partial\Omega$. Leveraging the insights from the preceding discussion and the dynamics of SARS-CoV-2 transmission within the population, we introduce a spatial-temporal mathematical model outlined as follows:

$$\begin{aligned}\frac{\partial S(x,t)}{\partial t} &= d_1 \frac{\partial^2 S(x,t)}{\partial x^2} - \beta(x,t) S(x,t) I(x,t), x \in \Omega, t > 0, \\ \frac{\partial I(x,t)}{\partial t} &= d_2 \frac{\partial^2 I(x,t)}{\partial x^2} + \beta(x,t) S(x,t) I(x,t) - \alpha I(x,t), x \in \Omega, t > 0, \\ \frac{\partial R(x,t)}{\partial t} &= d_3 \frac{\partial^2 R(x,t)}{\partial x^2} + \alpha I(x,t), x \in \Omega, t > 0.\end{aligned}\tag{1}$$

With initial conditions:

$$\begin{aligned}S(x,0) &= S_0(x), x \in \Omega, \\ I(x,0) &= I_0(x), x \in \Omega, \\ R(x,0) &= R_0(x), x \in \Omega.\end{aligned}\tag{2}$$

And the boundary condition given by:

$$\frac{\partial S(x,t)}{\partial x} = \frac{\partial I(x,t)}{\partial x} = \frac{\partial R(x,t)}{\partial x} = 0, x \in \partial\Omega, t > 0.\tag{3}$$

The state variables, parameters, and their descriptions are listed in Table 1. It is important to remark that the values and units of these parameters must be considered and determined carefully. Notice that the mathematical model (1) includes self-diffusion terms that represent the movements of individuals modulated by the population densities over the space x . The model, however, does not include cross-diffusion terms [6].

2.2 Initial conditions

Let us proceed first with some options that can be used for the initial conditions $S(x,0)$, $I(x,0)$ and recovered $R(x,0)$. The form of the initial condition is crucial for the dynamics since this affects the transient dynamics and, therefore, the early phase of the COVID-19 pandemic. There are many options for the initial conditions that are approximations of the real-world scenario. Let $N(x)$ be a function that relates to the initial population density of Chile where

$$N(x) = S(x,0) + I(x,0) + R(x,0).\tag{4}$$

Parameter/variable	Description
S	Susceptible population density
I	Infected population density
R	Recovered population density
d_1	Diffusion coefficient for the susceptible population
d_2	Diffusion coefficient for the infected population
d_3	Diffusion coefficient for the recovered population
γ	Parameter related to the infectious period of SARS-CoV-2
β	Transmission rate of SARS-CoV-2

Table 1: State variables, parameters, and their definitions for the spatial-temporal mathematical model described in (1).

Now, since in the beginning of the early phase of the COVID-19 pandemic, we have almost no infected or recovered individuals, then $R(x, 0) = 0$ and $I(x, 0) \approx 0$. Hence gets that $S(x, 0) \approx N(x)$. Through this work we will use these approximations for the numerical simulations and results.

Figure 1 shows an example of a piecewise cubic Hermite interpolating polynomial for the initial condition $N(x)$. Observing the pronounced gradients between areas, particularly noticeable between the Metropolitan and O'Higgins regions, we predict that this will give us computational issues. Indeed, as we utilize Matlab to address this model numerically and leverage the *pdepe* algorithm [10], we have a computational challenge since this solver with the given initial condition necessitates a denser grid. Moreover, the values of the integrals of the function $N(x)$ that represent the population in each region become inaccurate as time increases due to the compound effect of the large gradients and the diffusion between regions.

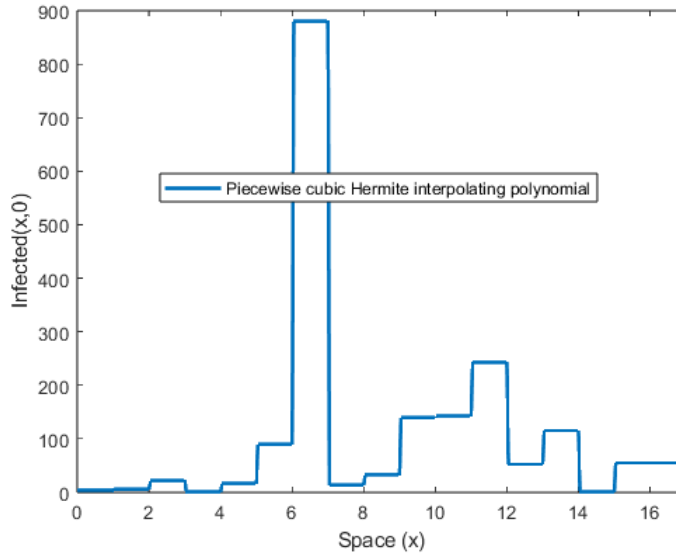


Figure 1: A piecewise cubic Hermite interpolating polynomial that approximates the initial condition of the infected population in Chile.

Another plausible modeling approach is to approximate the initial conditions by using a Gaussian function in each region where the integral of the Gaussian function approximates the initial subpopulations $S(x, 0)$, $I(x, 0)$ and recovered $R(x, 0)$. However, this has a main drawback since this approach generates several discontinuities in the boundaries between the regions in Chile, and numerical issues might arise. Nevertheless, a better modeling approach is to approximate the initial

conditions of the subpopulations by a sum of Gaussian functions where each function is centered in the midpoint or center of each region. This modeling approach solves the discontinuity aspect but generates an issue with regard to the approximation of the subpopulations in each region. This issue is because all the Gaussian functions overlap over the whole space that represents Chile. However, this computational issue can be partially addressed by selecting a variance such that the overlap between Gaussian functions is small [?]. The smaller the variance the less overlapping occurs. The variance helps to modulate the overlap and the separation between each region's main cities.

Therefore, in this study, one of the modeling approaches that we utilize for the initial condition is the following

$$N(x) = \sum_i^n N_i \sqrt{2/\pi} e^{-0.5(x-x_i)^2/\sigma_i^2}, \quad (5)$$

where n is the number of regions in Chile, x_i are the midpoints of each region i and N_i are the initial population of each region i . The main advantage of this approach is that the function $N(x)$ is continuous and differentiable. This allows us to guarantee the existence and uniqueness of the solution of the PDE system (1). In addition, it allows larger population densities in the middle of the regions in Chile and, therefore, more specific locations for the subpopulations.

3 Results

We present some numerical results when different mathematical modeling approaches are implemented. A variety of approaches are applied in order to get insight into the challenges of the mathematical modeling of the early phase of the COVID-19 pandemic in Chile. In this work, the mathematical modeling approaches vary depending on:

- The approximation of the initial conditions.
- The transmission rate.
- The diffusion coefficients.

To numerically solve the spatial-temporal mathematical model (1), as mentioned previously, we rely on the `pdepe` built-in Matlab function. It can be shown that in some cases, depending on the form of the initial conditions and the transmission rate $\beta(x, t)$, it is necessary to reduce the space step Δx and the time step Δt in the `pdepe` built-in Matlab function.

3.1 Space-variable transmission rate $\beta(x)$

We assume the transmission rate should depend on each region's population or population density [8, 7]. Thus, we assume an approximated standard bilinear incidence where the transmission rate in the PDE system (1) is replaced by

$$\beta(x, t) = \sum_i^n \frac{\beta}{N_i} \sqrt{2/\pi} e^{-0.5(x-x_i)^2/\sigma_i^2}, \quad (6)$$

where N_i is the total population of the region i . This form gives rise to a standard incidence, which implicitly assumes that an individual has a fixed number of contacts per unit time [9]. In some way, the terms N_i re-scale the Gaussian functions of each region, and therefore, for the regions with larger populations, the influence of β on the transmission is decreased.

Let us distribute the initial population by using the distribution function $N(x)$ given by a sum of Gaussian functions as presented in Eq. (4). Fig. 2 shows the dynamics of the infected population

density that results from the numerical simulation of the mathematical model (1) and the real data from Chile. It can be seen that this mathematical modeling approach is able to generate a significant amount of infected cases in each region by using a space-variable transmission rate $\beta(x)$ across the regions of Chile. Notice that the epidemic wave occurs in all the regions, but overestimates the real data. We have used a scale factor of $k = 3$ in order to adjust the peak of the model in the Metropolitan region to the real data. In some way, this scale takes into account the fact that there are asymptomatic cases that are not reported and, therefore, are not included in the real data. In the regions besides the highly dense Metropolitan region, there are large epidemic waves due to smaller population densities in the neighborhoods of the boundaries between regions. This latter aspect can be observed in Figure 3, where a great number of infected cases can be seen in those neighborhoods. For instance, at the first time step, we can see that the infected cases are distributed as Gaussian functions with mean values located at the middle of the regions, and then during the simulation, the infected cases shift to the boundaries where the transmission rate is higher. In the last time step of the simulation, we can see that the infected cases are now located at the boundaries between regions.

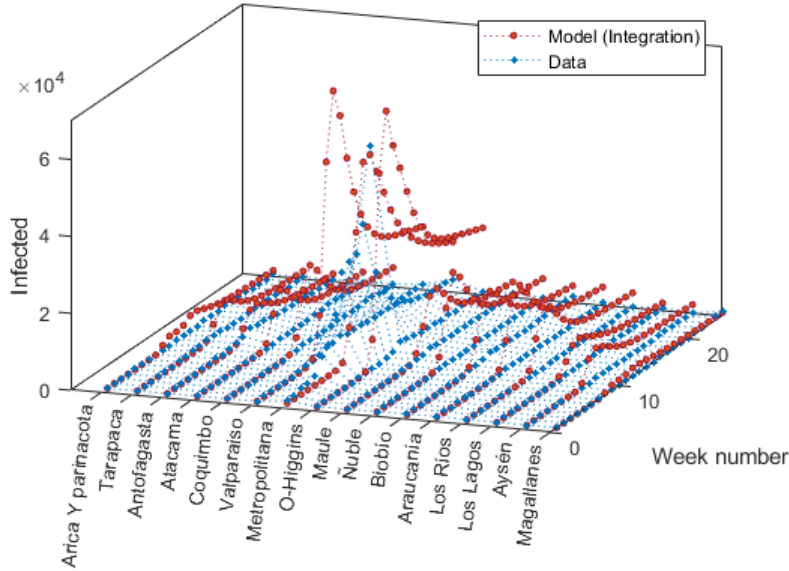


Figure 2: Numerical simulation of the spatial-temporal model (1) with space-variable transmission rate $\beta(x)$ and low diffusion rate.

3.2 Space-variable transmission rate $\beta(x)$ in terms of sum of scaled Gaussian functions

Here we assume that the transmission rate function $\beta(x)$ is given by a sum of scaled Gaussian functions. In this way, the transmission rate is larger in the middle of the regions and smaller in the boundaries. From a real-world viewpoint, this translates to there being more contacts in the cities and that the cities are closer to the middle of the region. Then the transmission rate function $\beta(x)$ is given by

$$\beta(x) = \beta \sum_i^n \frac{s_i}{N_i \sqrt{2/\pi}} e^{-18(x-x_i)^2}, \quad (7)$$

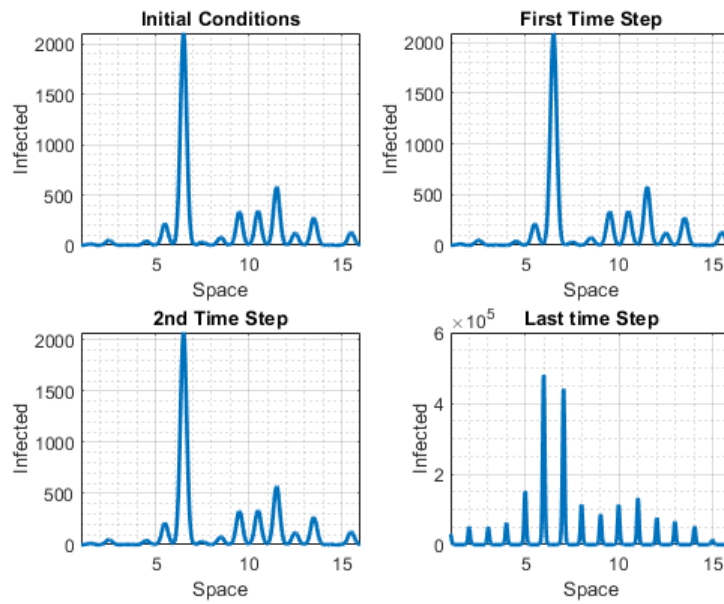


Figure 3: Numerical simulation of the spatial-temporal model (1) with space-variable transmission rate $\beta(x)$ and low diffusion rates.

where n is the number of regions in Chile, x_i are the midpoints of each region i and N_i are the initial population of each region i . Notice that the parameter β modulates the transmission rate over the whole space. Fig. 4 shows the transmission rate function $\beta(x)$. Notice that the transmission rate is larger in the middle of the regions and smaller in the boundaries. Using this modeling approach, the characterization of the dynamics of the early phase of the COVID-19 pandemic is improved. Despite all these improvements regarding the spatial-varying transmission rate, the model still presented some difficulties in describing the decay of the infected cases after reaching the peak of infected cases. Further improvements can be made by varying the transmission rate with regard to space and also with respect to time. For instance, the transmission rate can be varied for each region at different times. This would allow a reduction of infected cases after the peak of cases and with different decay rates.

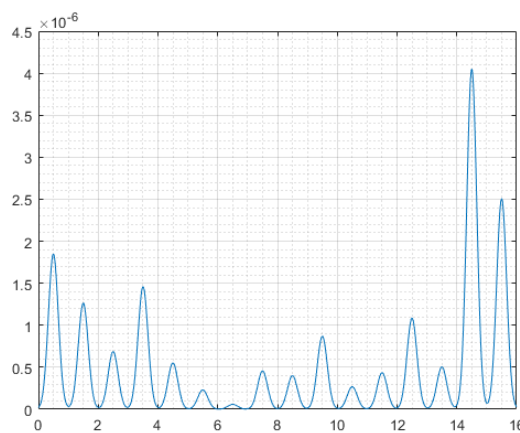


Figure 4: Space-variable transmission rate $\beta(x)$ in terms of sum of scaled Gaussian functions.

4 Conclusions

In this study, we proposed a spatial-temporal epidemiological mathematical model to approximate the dynamics of the early phase of the COVID-19 pandemic in Chile. The compartmental model divides the total population based on the COVID-19 disease progression status and also on the spatial location. In particular, the model considers susceptible, infected, and recovered individuals. A system of nonlinear first-order partial differential equations is used for the mathematical model in order to include spatial and temporal effects. We developed several mathematical modeling approaches to describe and explain the spatial-temporal data of Chile. The initial conditions were computed based on the population density of each region of Chile. We tested a variety of functional forms for the initial conditions. We found that the most suitable form was given by a continuous function that is composed of a sum of Gaussian functions. We assumed Neumann boundary conditions at the north and south of Chile due to travel restrictions during the early phase of the COVID-19 pandemic and the fact that the most southern region of Chile is bounded by the Antarctic Sea.

We studied a first mathematical modeling approach that considers a space-invariant SARS-CoV-2 transmission rate. In this approach, the mathematical model presented difficulties in describing and explaining the real data due to the implicit assumption that all regions have the same transmission rate. For the second modeling approach, we included a spatial-variant transmission rate, which provides more flexibility to the model and, at the same time, enables us to consider the possibility that the transmission rates vary depending on the region. Therefore, this approach improved the previous results obtained with a constant transmission rate. Nevertheless, the model still has difficulties describing the real epidemic data. We developed several modeling variations of the spatial-variant transmission rate in this second approach. For instance, we assumed the classical standard incidence where the transmission rate is inversely proportional to the population density of each location. This variation created some modeling issues in the boundaries between the regions since the population density was assumed to be low close to those boundaries. We implemented another variation by modifying the standard incidence with a scale factor that modulates the transmission rate of each region in such a way that the transmission rate becomes smaller close to the boundaries as it is expected in the real world. Despite all these improvements regarding the spatial-varying transmission rate, the model presented some difficulties in describing the decay of the infected cases after reaching the peak of cases.

Future works can include variations on the spatial-temporal transmission rate in order to allow the mathematical model to describe more accurately the real COVID-19 dynamics in Chile. For instance, a modeling approach that uses a transmission rate that varies with space and time can be more suitable. However, from a strictly mathematical point of view, it might present difficulties since the transmission rate becomes discontinuous with respect to time. This approach can be very useful since there are regions where the non-pharmaceutical interventions were not implemented at the same time, and people's reactions to these interventions were different depending on social factors. Therefore, this modeling approach is highly recommended despite the potential non-practical identifiability of the parameters due to the lack of enough detailed epidemic data.

To summarize, the use of heterogeneous transmission rates across the regions of Chile allows a better description of the early phase of the COVID-19 pandemic in Chile. In particular, the modeling approach with a spatial and time-varying transmission rate is the most suitable one. The results presented in this study show the advantages and challenges of the proposed mathematical approaches to describe the COVID-19 pandemic in Chile. In addition, the results suggest that the transmission rates of SARS-CoV-2 in the regions of Chile are different. The results provide additional insight into the study of COVID-19 pandemics since few studies have explored similar approaches and even less with real-world data. We have shown that the calibration of the mathe-

mathematical model under different scenarios could be very challenging due to the features of the model and the variety of parameters that affect the dynamics. This study gives further insight into the COVID-19 pandemic by means of a novel spatial-temporal mathematical modeling approach.

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