REPORT #2: ESTIMATION OF MAXIMAL ICU BEDS DEMAND FOR COVID-19 OUTBREAK IN SANTIAGO, CHILE

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Abstract. In this document we propose a compartmental epidemiological model in order to estimate the maximal ICU (intensive care unit) beds capacity required by a city (Santiago, Chile) during the COVID-19 outbreak. The proposed model is a variation of such presented in Report # 1, which includes now an additional state variable: asymptomatic people or people with mild symptoms (not detected), who according to recent literature is a key group in the transmission of this disease. The maximal demand of ICU beds is presented as an output of our model, for different values of the basic reproductive number $\mathcal{R}_0$, which is interpreted as different scenarios after mitigation measures. For the sake of comparison we also show results obtained with a second model (provided by [2]) that includes an age-class structure.

Contents

1. Model formulation

The disease spread within a particular contaminated city (Santiago, Chile) is modeled by using a deterministic compartmental model (see, for instance [1]). We use this approach in our reports because the simplicity and the rapidity to obtain some results that can be used later for more complex models (e.g., stochastic, with interconnection between cities, etc.). The model proposed consists in a compartmental model, where the population is distributed into 8 groups corresponding to different stages of the disease:

- **Susceptible** (denoted by S): Persons not infected by the disease.
- **Exposed** (denoted by E): Persons in the incubation period after being infected by the disease. In this stage, persons **do not have symptoms but they can infect other people** with a lower probability than people in the infectious compartments described below.
- **Mild infected** (denoted by I^m): Persons infected that can infect other people. Persons in this stage are asymptomatic or present mild symptoms, **they are not detected and then not reported by authorities**. At the end of this stage, they pass directly to recovered state.
- **Infected** (denoted by I): Persons infected that can infect other people. Persons in this stage develop symptoms and **are detected and then reported by authorities**. People in this stage can recover or pass to some hospitalized state.
- **Recovered** (denoted by R): People that survive the disease, **is no longer infectious and have developed immunity to the disease**.
- **Hospitalized** (denoted by H): Persons hospitalized in basic facilities. People in this stage can infect other people. **After this stage, people recover or pass to use a ICU bed**.
- **Hospitalized in ICU beds** (denoted by H^c): People hospitalized in ICU beds. People in this stage can infect other people. After this stage, **people die or are hospitalized in basic facilities**.
- **Dead** (denoted by D): People who did not survive the disease.

The choice of the above stages and the transition between them (described below) is because our purpose is to estimate the maximal demand of ICU beds. For this reason we are modeling that all people that need a UCI bed will pass by stage H^c without any constraint of availability.

The total population is then

$$N = S + E + I^m + I + R + H + H^c. \tag{1}$$

As usual, these groups of stages are called state variables, so the vector of state variables is $x = (S, E, I^m, I, R, H, H^c, D)$. We omit to consider N as a state variable because of equality (1).

The (indirect) control variables to be considered in our reports are the rate of contacts with infectious people. We denote by $u_X(t)$ the rate of contact of susceptible people with a person in the stage $X \in \{E, I^m, I, H, H^c\}$ at time $t \geq t_0$ (t_0 the considered initial time).

The rates of contagious at time $t \geq t_0$ are given by

$$\beta_X(t) = p_X u_X(t) \qquad t \geq t_0,\ X \in \{E, I^m, I, H, H^c\}, \tag{2}$$

where p_X is the probability of a susceptible person (S) to be infected (i.e., to enter to the incubation stage E) after a contact with a person in the stage $X \in \{E, I^m, I, H, H^c\}$.

Notice that one should have

$$u_E(t) \approx u_{I^m}(t) \geq u_I(t) \geq u_H(t) \geq u_{H^c}(t) \approx 0, \tag{3}$$

because the contacts with people in incubation (E) or with mild symptoms (I^m) should be more frequent (because they do not know they are infected) than the contacts with infectious people with symptoms (I) or hospitalized (H or H^c), and we assume that people hospitalized are highly isolated. For this reason, we do not consider u_H and u_{H^c} as control variables, because we will assume these values are constant and near to zero.

Now, for each control strategy $u_X(\cdot)$, with $X \in \{E, I^m, I\}$, we consider reference values (to be calibrated) $u_X^{\text{ref}} > 0$. In the light of (3) we will assume

$$u_E^{\text{ref}} \approx u_{I^m}^{\text{ref}} \geq \frac{1}{2} u_I^{\text{ref}} \geq u_H^{\text{ref}} \geq u_{H^c}^{\text{ref}} \approx 0.$$

Hence, mitigation strategies focused in reducing the contact rates satisfy $u_X(t) \in [0, u_X^{\text{ref}}]$ for all $t \geq t_0$, with $X \in \{E, I^m, I\}$.

In Report #1 we present results using constant strategies $u_X(t) \equiv \alpha u_X^{\text{ref}}$ with $\alpha \in \{0.5, 0.75, 1\}$. **The objective of this report is to show the outcomes of the new model under different scenarios associated with different percentages of symptomatic people and some values for the basic reproduction number $\mathcal{R}_0$.** To consider different values of $\mathcal{R}_0$ will imply to modify the values u_X^{ref} for each scenario and to apply $u_X(t) \equiv u_X^{\text{ref}}$ for all $t \geq t_0$. For this reason, to consider **lower $\mathcal{R}_0$ is interpreted as stronger mitigation measures**[1].

We represent the scenarios related to different percentages of symptomatic people through the fraction of exposed people (E) that will present symptoms and then they will be detected. This people pass to the infected compartment (I) and not to (I^m). This fraction will be denoted by $\phi_{EI} \in [0, 1]$. If ϕ_{EI} is near to one means a large proportion of infected people presents symptoms.

[1]The basic reproduction number $\mathcal{R}_0$ is proportional to contact rates.

The evolution of state variables is described by the following system of ordinary differential equations:

$$
\left\{
\begin{array}{rcl}
\dot{S} &=& \mu_b N - S\overbrace{\left(\frac{\beta_E E+\beta_{I^m} I^m+\beta_I I+\beta_H H+\beta_{H^c} H^c}{N}\right)}^{\Lambda(x,u)\text{: rate of contagious}} - \mu_d S \\
\dot{E} &=& S\left(\frac{\beta_E E+\beta_{I^m} I^m+\beta_I I+\beta_H H+\beta_{H^c} H^c}{N}\right) - (\gamma_E+\mu_d)E \\
\dot{I^m} &=& (1-\phi_{EI})\gamma_E E - (\gamma_{I^m}+\mu_d)I^m \\
\dot{I} &=& \phi_{EI}\gamma_E E - (\gamma_I+\mu_d)I \\
\dot{R} &=& \gamma_{I^m} I^m + \phi_{IR}\gamma_I I + \phi_{HR}\gamma_H H - \mu_d R \\
\dot{H} &=& (1-\phi_{IR})\gamma_I I + (1-\phi_D)\gamma_{H^c} H^c - (\gamma_H+\mu_d)H \\
\dot{H^c} &=& (1-\phi_{HR})\gamma_H H - (\gamma_{H^c}+\mu_d)H^c \\
\dot{D} &=& \phi_D \gamma_{H^c} H^c.
\end{array}
\right. \tag{4}
$$

The above system (4) is represented also in Figure 1.

From (1) and (4) we obtain that the dynamics of the total population is

$$\dot{N} = (\mu_b - \mu_d)N - \phi_D \gamma_H H^c.$$

System (4) is a variation of the model introduced in Report # 1. We are including now the state I^m, a key group in the disease transmission [4] because the mobility of this people is not highly affected since they have mild symptoms and are not detected. This is inspired by the very recent technical reports [4] and [2]. The main difference with [4] is that they do not consider people in H^c can recover, because their objective is not the estimation of the maximal demand of ICU beds. On the other hand, in [2] they consider other state, the incubation of infectious asymptomatic people, that is, they divide our state E in two states (see Section 4). Also they divide the population in several age-classes, which is one of our objectives for future reports but with few age classes. The objetive of [2] is to estimate the maximal demand of ICU beds but it is not clear for us how to deduce a recommendation from the mitigation strategies they use. The authors of [2] are advising the French Government during the crisis and they shared with us their computational codes. In Section 4 we report the results obtained with their model.

2. Parameters

The parameters to be identified (literature and/or calibration) are

$$P = (p, \mu_b, \mu_d, \gamma, \phi, u^{\text{ref}}) \in [0,1]^5 \times \mathbb{R}_+ \times \mathbb{R}_+ \times [0,1]^5 \times [0,1]^3 \times \mathbb{R}_+^5 \subset \mathbb{R}^{20}. \tag{5}$$

The descriptions of these parameters are the following:

- $p = (p_E, p_{I^m}, p_I, p_H, p_{H^c})$ are the probabilities of contagious (see (2)) when a susceptible person is in contact with a person in stages E, I^m, I, H, and H^c.

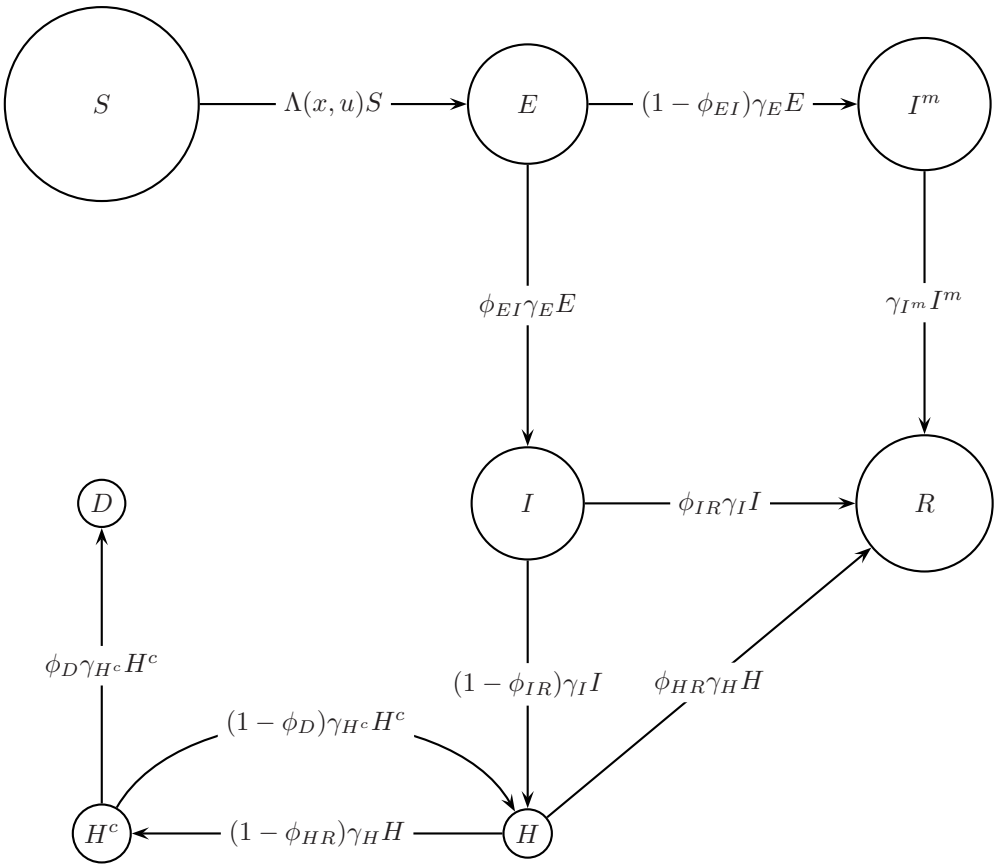

FIGURE 1. **Structure of the mathematical model for the dynamics of COVID-19 in an isolated city given by** (4)**.** Each circle represents a compartment. Susceptible individuals (S), and different disease states: exposed (E), mild infected (I^m), infected (I), recovered (R), hospitalized (H), hospitalized in ICU beds (H^c), and dead (D). Natural natality and mortality flows are not represented.

- μ_b is the natality rate in the city and μ_d is the mortality rate, both measured in $[\text{day}]^{-1}$;
- Parameters γ_X measured in $[\text{day}]^{-1}$ are the rate of transition from a disease stage $X \in \{E, I^m, I, H, H^c\}$ to the following stage, where γ_X^{-1} represents the mean duration of stage X;
- ϕ_{IR} is the fraction of infected people that recover;
- ϕ_{HR} is the fraction of hospitalized (in normal services) people that recover;
- ϕ_D is the fraction of hospitalized people in ICU beds that die;
- The vector $u^{\text{ref}} = (u_E^{\text{ref}}, u_{I^m}^{\text{ref}}, u_I^{\text{ref}}, u_H^{\text{ref}}, , u_{H^c}^{\text{ref}})$ contains references values of rates of contact.

Recall that $\phi_{EI} \in [0,1]$ is the fraction of exposed people that will present symptoms. These persons are identified and pass to the infected compartment (I) and not to (I^m) (see system (4) or Figure 1). This fraction may be consider as a parameter but in this report we do not do so, because the scenarios to be considered are related to assumptions on this unknown value.

For parameters listed above we consider a range of values taken from literature and consideration of the authors of this report. These ranges are presented in Table 1.

Notation	Unit	Range of values	References
p_E	dimensionless	$[0, 0.2]$	modeling team
p_{I^m}	dimensionless	$[0.6, 0.9]$	modeling team
p_I	dimensionless	$[0.6, 0.9]$	modeling team
p_H	dimensionless	$[0.6, 0.9]$	modeling team
p_{H^c}	dimensionless	$[0.6, 0.9]$	modeling team
μ_b	$[\text{day}]^{-1}$	$3.57 \cdot 10^{-5}$	INE-Chile (2017)
μ_d	$[\text{day}]^{-1}$	$1.57 \cdot 10^{-5}$	INE-Chile (2017)
γ_E	$[\text{day}]^{-1}$	$[1/7, 1/4]$	[2, 4, 8]
γ_{I^m}	$[\text{day}]^{-1}$	$[1/14, 1/3]$	[2, 4]
γ_I	$[\text{day}]^{-1}$	$[1/6, 1/2]$	[4, 7]
γ_H	$[\text{day}]^{-1}$	$[1/6, 1/2]$	[3, 5, 6]
γ_{H^c}	$[\text{day}]^{-1}$	$[1/15, 1/10]$	[2, 3]
ϕ_{IR}	dimensionless	$[0.95, 0.96]$	[3]
ϕ_{HR}	dimensionless	$[0.75, 0.95]$	[3, 5]
ϕ_D	dimensionless	$[0.005, 0.5]$	[4]/ modeling team
u_E^{ref}	dimensionless	$[0, 0.8]$	modeling team
$u_{I^m}^{\text{ref}}$	dimensionless	$[0, 0.8]$	modeling team
u_I^{ref}	dimensionless	$[0, 0.15]$	modeling team
u_H^{ref}	dimensionless	0.01	modeling team
$u_{H^c}^{\text{ref}}$	dimensionless	0.01	modeling team

TABLE 1. Range of values for parameters used in model (4).

For initial conditions we consider the total population in of Santiago (CENSO 2017), which is 5.624 millions people, and an estimation of cases until today. The values used are indicated in Table 2.

State	Value (individuals)
S_0	$5.624 \cdot 10^6$
E_0	1000
I_0^m	2000
I_0	1200
H_0	200
H_0^c	10
R_0	100
D_0	3

TABLE 2. Initial conditions for (4), considering the total population of Santiago and an estimation of cases until today.

3. Simulations and results

The scenarios to be simulated are related to choices of ϕ_{EI}, the fraction of infected people that presents symptoms and then is in the infected compartment (I) and not in (I^m). A high

value of ϕ_{EI} represents that a high percent of the Chilean population presents symptoms when is infected.

For each $\phi_{EI} \in \{0.2, 0.5, 0.75\}$ we simulate three sub-scenarios related to different values of the basic reproduction number $\mathcal{R}_0 \in \{1.5, 2, 3\}$. Different values of $\mathcal{R}_0$ are interpreted, as in [2], as different mitigation measures, because $\mathcal{R}_0$ depends proportionally on the contact rates. Also, we simulate a fourth sub-scenario corresponding to a choice of parameters that fit the daily reports published from March 3 for Santiago by authorities.

For a given scenario, that is, a choice of $\phi_{EI} \in \{0.1, 0.5, 0.75\}$ and $\mathcal{R}_0 \in \{1.5, 2, 3\}$, we calibrate the parameters described in Section 2 in the ranges indicated in Table 1 in order to obtain the given $\mathcal{R}_0$. Thus, we obtain a vector of parameters $P = (p, \mu_b, \mu_d, \gamma, \phi, u^{\text{ref}})$.

Also, for each $\phi_{EI} \in \{0.1, 0.5, 0.75\}$ we simulate a fourth sub-scenario as follows: For a vector of parameters P we compute the detected cases at day $d \in \{03/03, \ldots, \text{today}\}$ given by the model, that is

$$C(d, P) = \int_{t_0}^{d} \phi_{EI} \gamma_E E(t) dt,$$

and then, we chose parameters P in order to fit the above quantity to daily reports until today. The basic reproduction number obtained with these parameters is denoted by $\hat{\mathcal{R}}_0$ and is reported in tables 3, 4, and 5.

Thus, with these (four) choices of parameters, for each $\phi_{EI} \in \{0.2, 0.5, 0.75\}$, and the initial condition (see Table 2), we run the model and obtain the maximal demand of hospitalized in non complex services ($H_{\max}$), the maximal demand of ICU beds ($H^c_{\max}$) and the date when this demand is reached ($t_{\max}$). These values are reported in tables 3, 4, and 5. The evolution in time of hospitalized, the occupancy of UCI beds, and total deaths are depicted in figures 2, 3, and 2.

Few people are symptomatic ($\phi_{EI} = 0.2$)

$\mathcal{R}_0$	$H_{\max}$	$H^c_{\max}$	$t_{\max}$ (date)
3	4416	3017	May 14
2	2841	1740	May 23
1.5	1131	781	June 30
$\hat{\mathcal{R}}_0 = 2.49$	4557	4352	May 12

TABLE 3. Results with $\phi_{EI} = 0.2$ (20% of infected people present symptoms) for different values of the basic reproduction number $\mathcal{R}_0$ and for fitted parameters (from daily reports in Santiago) obtaining $\hat{\mathcal{R}}_0$.

Few people are symptomatic ($\phi_{EI} = 0.2$)

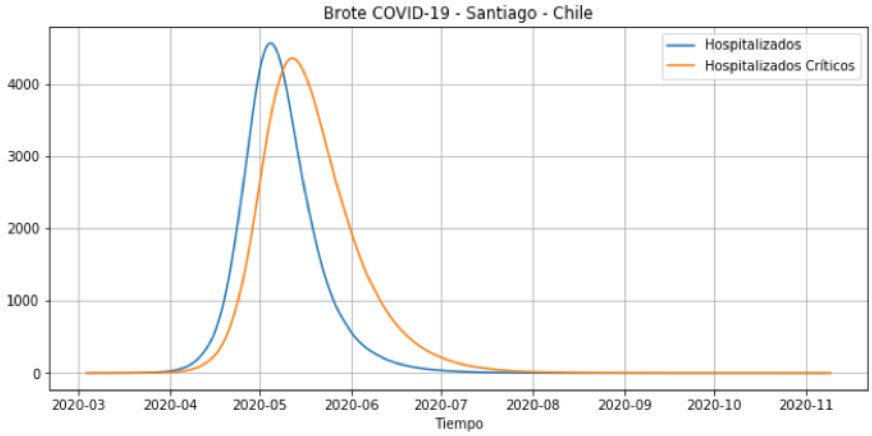

FIGURE 2. Demand of basic hospital facilities and UCI beds when few people are symptomatic ($\phi_{EI} = 0.2$) and $\mathcal{R}_0 = \hat{\mathcal{R}}_0 = 2.49$.

Half people are symptomatic ($\phi_{EI} = 0.5$)

$\mathcal{R}_0$	$H_{\max}$	$H^c_{\max}$	$t_{\max}$ (date)
3	13779	7070	May 19
2	6891	5597	May 25
1.5	3015	2868	June 24
$\hat{\mathcal{R}}_0 = 2.32$	24660	8512	May 29

TABLE 4. Results with $\phi_{EI} = 0.5$ (50% of infected people present symptoms) for different values of the basic reproduction number $\mathcal{R}_0$ and for fitted parameters (from daily reports in Santiago) obtaining $\hat{\mathcal{R}}_0$.

Half people are symptomatic ($\phi_{EI} = 0.5$)

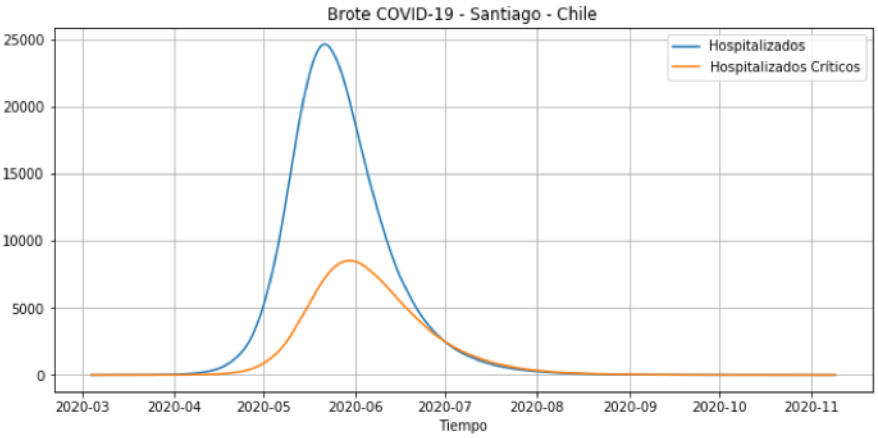

FIGURE 3. Demand of basic hospital facilities and UCI beds when half people are symptomatic ($\phi_{EI} = 0.5$) and $\mathcal{R}_0 = \hat{\mathcal{R}}_0 = 2.32$.

Many people are symptomatic ($\phi_{EI} = 0.75$)

$\mathcal{R}_0$	$H_{\max}$	$H^c_{\max}$	$t_{\max}$ (date)
3	19940	8204	May 20
2	8209	5255	May 31
1.5	4179	2859	June 19
$\hat{\mathcal{R}}_0 = 1.96$	7615	2140	June 12

TABLE 5. Results with $\phi_{EI} = 0.75$ (1 70% of infected people present symptoms) for different values of the basic reproduction number $\mathcal{R}_0$ and for fitted parameters (from daily reports in Santiago) obtaining $\hat{\mathcal{R}}_0$.

Many people are symptomatic ($\phi_{EI} = 0.75$)

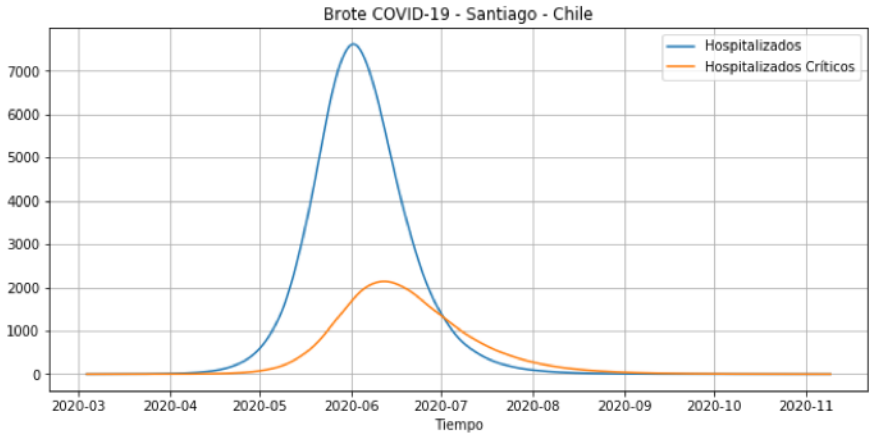

FIGURE 4. Demand of basic hospital facilities and UCI beds when many people are symptomatic ($\phi_{EI} = 0.75$) and $\mathcal{R}_0 = \hat{\mathcal{R}}_0 = 1.96$.

4. Model proposed in [2] and results

In this section we present a brief description of model [2] used by *Mathematical Modelling of Infectious Diseases* team (Institut Pasteur, France), who sent to us their computational codes. We report the results obtained for Santiago using this model.

The model consists in a compartmental model, where the population is distributed into 9 groups corresponding to different stages of the disease: Susceptible (S), infected asymptomatic and non-infectious (E_1), infected asymptomatic and infectious (E_2), mild infections (I^m), severe infections requiring hospitalization (I^{severe}), recovered (R), hospitalized (H), hospitalized requiring ICU beds (H^c), and dead (D) as direct consequence of COVID-19. The structure of this model is depicted in Figure 5.

These groups are divided into 17 5-year age-groups. This gives rise to a contact matrix $(\widetilde{c_{ij}}) \in \mathcal{M}_{17,17}(\mathbb{R})$ accounting for an age-dependent susceptibility and infectivity.

4.1. Model Parameters.

In order to state the model equations, several parameters need to be defined. First, age-dependent severity parameters are considered. These values were extracted for 5-year age-group from [9] and are shown in Table 6.

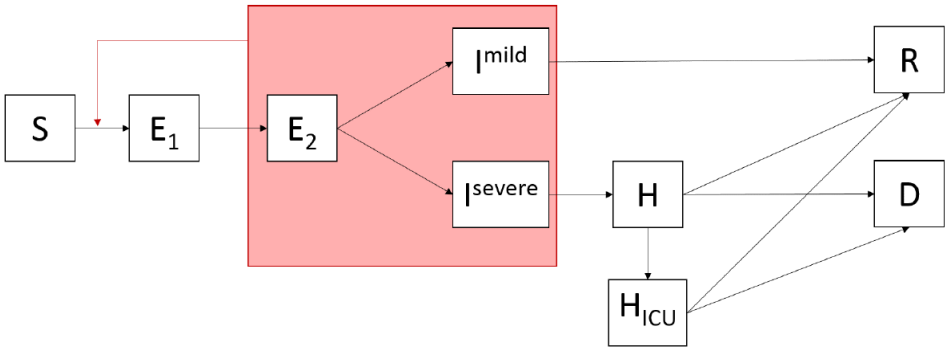

FIGURE 5. Compartmental model structure.

Age group	P[Hospitalization | Infection]	P[ICU / Infection]	P[Death | Hospitalization non ICU]
$0-4$	0.000744	$3.74E-05$	0.013448
$5-9$	0.000634	$3.18E-05$	0.013448
$10-14$	0.001171	$5.88E-05$	0.013448
$15-19$	0.002395	0.00012	0.013448
$20-24$	0.005346	0.000269	0.013448
$25-29$	0.01029	0.000517	0.013448
$30-34$	0.016235	0.000815	0.013448
$35-39$	0.023349	0.001243	0.014294
$40-44$	0.028945	0.001729	0.016159
$45-49$	0.038607	0.00288	0.020502
$50-54$	0.057735	0.005982	0.029395
$55-59$	0.072422	0.010822	0.044677
$60-64$	0.101602	0.022736	0.073315
$65-69$	0.11698	0.035911	0.112652
$70-74$	0.146099	0.056362	0.159727
$75-79$	0.176635	0.081467	0.217699
$80+$	0.18	0.1277	0.620944

TABLE 6. Age-dependent severity parameters.

Also, the mean time an individual spends in each stage of infection is considered in the model equations, which are obtained from the following assumptions considered in [2]:
The symptoms onset begins on average 5 days after infection and that an individual is on average infectious one day before symptoms onset and for 4 days. Hospitalized individuals spend on average 6 days in hospital before admission into intensive care units (ICUs). The mean time spent in hospital for patients that do not require an ICU admission is assumed to be 8 days. The mean time spent in intensive care units is assumed to be 15 days. This information is summarized in Table 7, where the related parameters g_1, g_2, g_3, g_{hosp}, g_{adm}, g_{dis}^{NC}, g_{dis}^{ICU} are defined.

Parameter	Value (days)
Mean time spent in the E_1 compartment (latent state)	$1/g_1 = 4$
Mean time spent in the E_2 compartment (asymptomatic and infectious)	$1/g_2 = 1$
Mean time spent in the I^{mild} compartment	$1/g_3 = 3$
Mean time spent in the I^{severe} compartment	$1/g_{\text{hosp}} = 3$
Mean time spent in hospital before ICU admission	$1/g_{\text{adm}} = 6$
Mean time spent in hospital when no ICU admission is required (before death/discharge)	$1/g_{\text{dis}}^{Nc} = 8$
Mean time spent in 1CU (before death/discharge)	$1/g_{\text{dic}}^{ICU} = 15$

TABLE 7. Mean time an individual spends in each stage.

Finally, a transmission rate β is subsequently set to satisfy a given reproduction number $\mathcal{R}_0$:

$$\beta = \frac{\mathcal{R}_0}{1/g_2 + 1/g_3} \cdot \max(Eigenval(\widetilde{c_{ij}})).$$

4.2. **Simulation and Results.** The evolution of the system described in Figure 5 was simulated considering a total population of 5.624 millions people, and as an initial condition the entire population is considered healthy (S compartment) and 1 infected in the E_{i1} compartment per age-group. The remaining compartments start with zero population.

Three different scenarios are simulated for the following values of the reproduction number $\mathcal{R}_0$: $\mathcal{R}_0 = 3$, $\mathcal{R}_0 = 2$ and $\mathcal{R}_0 = 1.5$. For each scenario we obtain the evolution from day 1 (initial condition) of the people requiring hospitalization (with no critical state) and people requiring hospitalization in intensive care units, as it is depicted in figures 8, 7, and 6.

Also we compute the maximal demand of hospitalized in non complex services ($H_{\max}$) and the maximal demand of ICU beds ($H_{\max}^c$), as shown in Table 8.

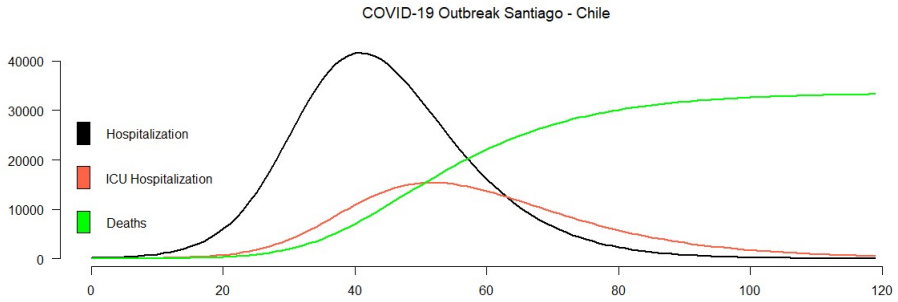

FIGURE 6. Number of non-critic hospitalizations, hospitalizations requiring ICU and deaths due to COVID-19 in Santiago de Chile, from the first day of infection, for $\mathcal{R}_0 = 3$.

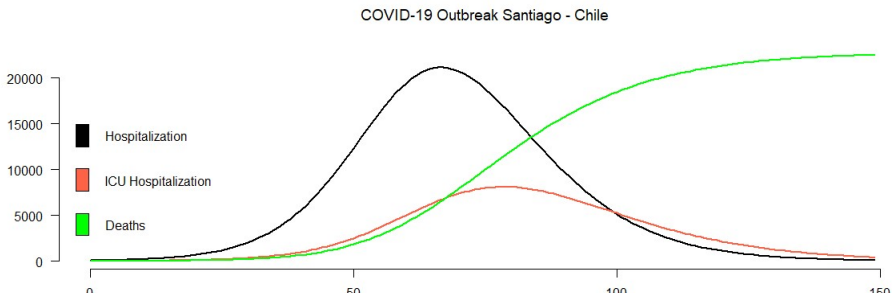

FIGURE 7. Number of non-critic hospitalizations, hospitalizations requiring ICU and deaths due to COVID-19 in Santiago de Chile, from the first day of infection, for $\mathcal{R}_0 = 2$.

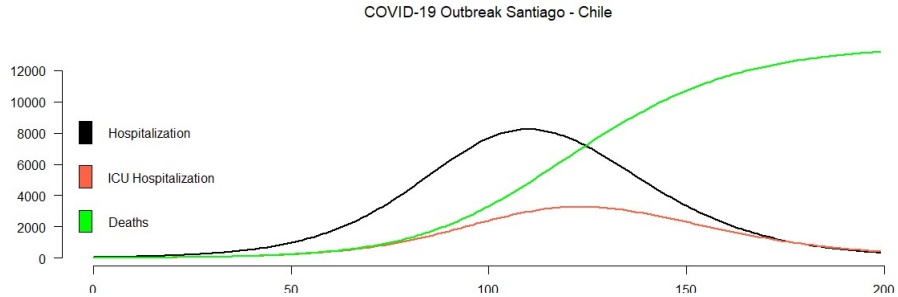

FIGURE 8. Number of non-critic hospitalizations, hospitalizations requiring ICU and deaths due to COVID-19 in Santiago de Chile, from the first day of infection, for $\mathcal{R}_0 = 1.5$.

$\mathcal{R}_0$	$H_{\max}$	$H^c_{\max}$
3	41674	15364
2	21151	8110
1.5	8243	3242

TABLE 8. Results for different values of $\mathcal{R}_0$.

5. FINAL REMARKS

- Since we do not have any reference in Chile about the percentage of infected people that present symptoms, with our model we have simulated different scenarios related to this value.

- We have also simulated scenarios related to different values of the basic reproduction number $\mathcal{R}_0$. In [2] this is interpreted as different mitigation strategies. Indeed, stronger mitigation strategies during time will imply lower levels of $\mathcal{R}_0$. Nevertheless, the interpretation of how to deduce a precise strategy from a value of $\mathcal{R}_0$ is not straightforward. In Report # 1 we present an interpretation of strategies through

changing the values of the contact rates (constant in time). In future reports we will include the effect of temporal strategies, that is, to reduce contact rates only for a given period of time.

- The results obtained with the model introduced in [2] are similar to such obtained with our simpler model (without age structure) and with the model introduced in Report #1.

- The parameters identification described in Section 3 is a very poor and ill-conditioned method. We are working on improving that. It is known (see [4]) that the parameter identification of an outbreak model before the peak can produce large errors in the outputs.

- The type of model we propose allows estimating the magnitude order of maximal demands, but it is not appropriate for deducing an accurate estimation of daily cases.

- Simulations for other cities, countries or regions can be easily implemented. In these moments, we are using data from China, reported in [4], to calibrate and test our model in a dataset more complete than what is available now in Chile.

- Authors of [4] have proposed to run their model for Santiago if daily data about the disease in the city is provided (infected, hospitalized, recovered, etc.).

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References

[1] F. Brauer and C. Castillo-Chávez. *Mathematical models in population biology and epidemiology*, volume 40 of *Texts in Applied Mathematics*. Springer-Verlag, New York, 2001. URL: https://doi-org.usm.idm.oclc.org/10.1007/978-1-4757-3516-1, doi:10.1007/978-1-4757-3516-1.

[2] S. Cauchemez and C. Tran Kiem. Personal communication: Model description for the coronavirus disease 2019 (COVID- 19) considering age classes. Technical report, Mathematical Modelling Of Infectious Diseases, Institut Pasteur, 03 2020.

[3] N. Ferguson, D. Laydon, G. Nedjati-Gilani, N. Imai, K. Ainslie, M. Baguelin, S. Bhatia, Z. Boonyasiri, A.and Cucunubá, G. Cuomo-Dannenburg, et al. Impact of non-pharmaceutical interventions (npis) to reduce covid-19 mortality and healthcare demand. Technical report, Imperial College COVID-19 Response Team, 03 2019.

[4] B. Ivorra, M.R. Ferrández, M. Vela-Pérez, and A.M. Ramos. Mathematical modeling of the spread of the coronavirus disease 2019 (COVID- 19) considering its particular characteristics. The case of China. Technical report, MOMAT, 03 2020. URL: https://doi-org.usm.idm.oclc.org/10.1007/s11538-015-0100-x.

[5] J. R. Koo, A. R. Cook, M. Park, Y. Sun, H. Sun, J. T. Lim, C. Tam, and B. L. Dickens. Interventions to mitigate early spread of sars-cov-2 in singapore: a modelling study. *The Lancet Infectious Diseases*,

2020/03/25 2020. URL: https://doi.org/10.1016/S1473-3099(20)30162-6, doi:10.1016/S1473-3099(20)30162-6.

[6] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, R. Ren, K. Leung, E. Lau, J. Y Wong, et al. Early transmission dynamics in wuhan, china, of novel coronavirus–infected pneumonia. *New England Journal of Medicine*, 2020.

[7] T. Liu, J. Hu, M. Kang, L. Lin, H. Zhong, J. Xiao, G. He, T. Song, Q. Huang, Z. Rong, et al. Transmission dynamics of 2019 novel coronavirus (2019-ncov). *bioRxiv*, 2020.

[8] World Health Organization. Report of the who-china joint mission on coronavirus disease 2019, 03 2020. URL: https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.

[9] R. Verity, L. C. Okell, I. Dorigatti, P. Winskill, C. Whittaker, N. Imai, G. Cuomo-Dannenburg, H. Thompson, P. Walker, H. Fu, et al. Estimates of the severity of covid-19 disease. *medRxiv*, 2020.