Supplementary Material - Modeling the impact of school reopening and contact tracing strategies on Covid-19 dynamics in different epidemiologic settings in Brazil

Marcelo Eduardo Borges[1], Leonardo Souto Ferreira[1,2], Silas Poloni[1,2], Angela Maria Bagattini[3], Caroline Franco[1,2,4], Michelle Quarti Machado da Rosa[3], Lorena Mendes Simon[5], Suzy Alves Camey[6], Ricardo de Souza Kuchenbecker[7], Paulo Inácio Prado[1,8], José Alexandre Felizola Diniz Filho[1,5], Roberto André Kraenkel[1,2], Renato Mendes Coutinho[1,9], and Cristiana Maria Toscano[3]

[1] *Observatório Covid-19 BR*
[2] *Instituto de Física Teórica, Universidade Estadual Paulista, São Paulo, SP, Brazil*
[3] *Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brazil*
[4] *Big Data Institute, Li Ka Shing Centre for Health Information and Discovery, Nuffield Department of Medicine, University of Oxford, Oxford, UK*
[5] *Instituto de Ciências Biológicas, Universidade Federal de Goiás, Goiânia, GO, Brazil*
[6] *Instituto de Matemática e Estatística, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil*
[7] *Graduate Program in Epidemiology, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil*
[8] *Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil*
[9] *Centro de Matemática, Computação e Cognição - Universidade Federal do ABC, Santo André, Brazil*

List of Tables

List of Figures

1 Introduction

This model framework was first introduced in Águas et al.[1] and modified to account for brazilian hospital structure and percolation effects in Franco et al.[2]. The code is available at https://github.com/covid19br/school_reopening_manuscript. In Section 2 we introduce our modifications in the Brazilian model structure[2] to account for contact tracing strategies. Section 2.1 describes the equations, along with the explanation and sources of the parameters used. Section 2.2 describes how the force of infection for quarantined and non-quarantined work in the model. Section 2.5 thoroughly describes our contact tracing model. Section 3 lists the interventions used in the main paper. Finally, Section 4 shows the procedure used to fit the model to data and Section 5 describes our approach to sensitivity analysis.

2 Model structure

2.1 Model equations

The model consists of an expanded age-structured SEIR model to account for asymptomatic individuals, a detailed structure of the Brazilian health system, transmission in different settings, and non-pharmaceutical interventions, including contact tracing strategies. The model was simulated by solving its deterministic differential equations and implemented in R with the package *deSolve* Soetaert, Petzoldt, Setzer [3]. We write

$$
\begin{aligned}
\frac{d\mathbf{S}}{dt} &= -\lambda\mathbf{S} + \omega\mathbf{R} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{S} + \mu_b - \mu_d\mathbf{S} - (Q_{in} + Q_{in,2})\mathbf{S} + Q_d\mathbf{QS} \\
\frac{d\mathbf{E}}{dt} &= \lambda\mathbf{S} - \gamma\mathbf{E} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{E} - \mu_d\mathbf{E} - (Q_{in} + Q_{in,2})\mathbf{E} + Q_d\mathbf{QE} \\
\frac{d\mathbf{A}}{dt} &= \gamma(1-P_{clin})(1-\sigma)\mathbf{E} - \nu_i\mathbf{A} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{A} - \mu_d\mathbf{A} - (Q_{in} + Q_{in,2})\mathbf{A} + Q_d\mathbf{QI} \\
\frac{d\mathbf{I}}{dt} &= (1-Q_{cov}T_I)\gamma P_{clin}(1-P_{selfis})(1-\sigma)\mathbf{E} - \nu_i\mathbf{I} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{I} - \mu_d\mathbf{I} + Q_d\mathbf{QC} \\
\frac{d\mathbf{X}}{dt} &= \gamma P_{selfis}P_{clin}(1-\sigma)\mathbf{E} - \nu_i\mathbf{X} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{X} - \mu_d\mathbf{X} \\
\hline
\frac{d\mathbf{H}}{dt} &= \gamma\sigma(1-P_{icu})(1-\phi_H)(\mathbf{E}+\mathbf{QE}) - \nu_s\mathbf{H} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{H} - \mu_d\mathbf{H} \\
\frac{d\mathbf{HC}}{dt} &= \gamma\sigma(1-P_{icu})\phi_H(\mathbf{E}+\mathbf{QE}) - \nu_{sc}\mathbf{HC} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{HC} - \mu_d\mathbf{HC} \\
\frac{d\mathbf{ICU}}{dt} &= \gamma\sigma P_{icu}(1-\phi_c)(\mathbf{E}+\mathbf{QE}) - \nu_{icu}\mathbf{ICU} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{ICU} - \mu_d\mathbf{ICU} \\
\frac{d\mathbf{ICUH}}{dt} &= \gamma\sigma P_{icu}\phi_c(1-\phi_{cH})(\mathbf{E}+\mathbf{QE}) - \nu_{icuh}\mathbf{ICUH} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{ICUH} - \mu_d\mathbf{ICUH} \\
\frac{d\mathbf{ICUC}}{dt} &= \gamma\sigma P_{icu}\phi_c\phi_{cH}(\mathbf{E}+\mathbf{QE}) - \nu_{icuc}\mathbf{ICUC} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{ICUC} - \mu_d\mathbf{ICUC} \\
\hline
\frac{d\mathbf{R}}{dt} &= \nu_i\mathbf{A} - \omega\mathbf{R} + \nu_i\mathbf{X} + \nu_i\mathbf{I} + \mathbb{A}_{\mathbb{G}}\cdot\mathbf{R} - \mu_d\mathbf{R} + \nu_s(1-P_d\mu_H)\mathbf{H} - (Q_{in}+Q_{in,2})\mathbf{R} + Q_d\mathbf{QR} \\
&\quad + \nu_{icu}(1-P_{dicu}\mu_H)\mathbf{ICU} + \nu_{icuc}(1-P_{dicuc}\mu_H)\mathbf{ICUC} + \nu_{sc}(1-P_{dhc}\mu_H)\mathbf{HC} \\
&\quad + \nu_{icuh}(1-P_{dicuh}\mu_H)\mathbf{ICUH}
\end{aligned}
$$

$$
\begin{aligned}
\frac{d\mathbf{QS}}{dt} &= -\lambda_q \mathbf{QS} + \omega \mathbf{QR} + \mathbb{A}_{\mathbb{G}} \cdot \mathbf{QS} - \mu_d \mathbf{QS} + (Q_{in} + Q_{in,2})\mathbf{S} - Q_d \mathbf{QS} \\
\frac{d\mathbf{QE}}{dt} &= \lambda_q \mathbf{QS} - \gamma \mathbf{QE} + \mathbb{A}_{\mathbb{G}} \cdot \mathbf{QE} - \mu_d \mathbf{QE} + (Q_{in} + Q_{in,2})\mathbf{E} - Q_d \mathbf{QE} \\
\frac{d\mathbf{QI}}{dt} &= \gamma(1 - P_{clin})(1-\sigma)\mathbf{QE} - \nu_i \mathbf{QI} + \mathbb{A}_{\mathbb{G}} \cdot \mathbf{QI} - \mu_d \mathbf{A} + (Q_{in} + Q_{in,2})\mathbf{A} - Q_d \mathbf{QI} \\
\frac{d\mathbf{QR}}{dt} &= \nu_i(\mathbf{QI} + \mathbf{QC}) + \mathbb{A}_{\mathbb{G}} \cdot \mathbf{QR} - \omega \mathbf{QR} + (Q_{in} + Q_{in,2})\mathbf{R} - Q_d \mathbf{QR} \\
\frac{d\mathbf{QC}}{dt} &= Q_{cov} T_I \gamma P_{clin}(1 - P_{selfis})(1-\sigma)\mathbf{E} + \gamma P_{clin}(1-\sigma)\mathbf{QE} \\
&\quad - \nu_i \mathbf{I} + \mathbb{A}_{\mathbb{G}} \cdot \mathbf{I} - \mu_d \mathbf{I} - Q_d \mathbf{QC}
\end{aligned}
$$

$$
\begin{aligned}
\frac{d\mathbf{C}}{dt} &= r\gamma(1-\sigma)(1-P_{clin})(\mathbf{E} + \mathbf{QE}) + r_c \gamma(1-\sigma)P_{clin}(\mathbf{E} + \mathbf{QE}) + r_h \gamma \sigma(\mathbf{E} + \mathbf{QE}) \\
\frac{d\mathbf{CM}}{dt} &= \nu_s P_{dh} \mu_H \mathbf{H} + \nu_{sc} P_{dhc} \mu_H \mathbf{HC} + \nu_{icu} P_{dicu} \mu_H \mathbf{ICU} + \nu_{icuc} P_{dicuc} \mu_H \mathbf{ICUC} \\
&\quad + \nu_{icuh} P_{dicuh} \mu_H \mathbf{ICUH} + \mu_d(\mathbf{H} + \mathbf{HC} + \mathbf{ICU} + \mathbf{ICUC} + \mathbf{ICUH} + \mathbf{I} + \mathbf{X}) \\
\frac{d\mathbf{CMC}}{dt} &= \nu_{sc} P_{dhc} \mu_H \mathbf{HC} + \nu_{icuc} P_{dicuc} \mu_H \mathbf{ICUC} \\
&\quad + \nu_{icuh} P_{dicuh} \mu_H \mathbf{ICUH} + \mu_d(\mathbf{HC} + \mathbf{ICUC})
\end{aligned}
$$

where each of the dynamic variables (corresponding to the compartments shown in Table 1) is further subdivided in 19 age classes consisting of 5 years age bins (0-4,5-9, up to 90+). Thereby, each of the parameters written in the model, aside from $\mathbb{A}_{\mathbb{G}}$ (ageing matrix), should be thought of as diagonal matrices containing parameter values corresponding to each age class. Take, as an example, the natural mortality rate, given by

$$\hat{\mu}_d = \mathrm{diag}(\mu_{d1}, \mu_{d2}, ..., \mu_{dD}) = \mathrm{diag}(\vec{\mu}_d).$$

Note that, in the system of equations presented above, we drop the hats/bolds from all diagonal matrices to avoid an overloaded notation, but keep them in all variables. Thus, each of them actually represents $D = 19$ different ODEs, and therefore the number of equations is D multiplied by the number of compartments. A description of each parameter from the model is available at table 2.

Finally, $\mathbb{A}_{\mathbb{G}}$ implements ageing of the population, and it is defined as a 19×19 matrix given by:

$$
\mathbb{A}_{\mathbb{G}} = \frac{1}{1826.25} \begin{pmatrix}
-1 & 0 & 0 & 0 & \dots & 0 & 0 & 0 \\
1 & -1 & 0 & 0 & \dots & 0 & 0 & 0 \\
0 & 1 & -1 & 0 & \dots & 0 & 0 & 0 \\
\vdots & & & & \ddots & & \vdots & \\
0 & 0 & 0 & 0 & & 1 & -1 & 0 \\
0 & 0 & 0 & 0 & \dots & 0 & 1 & 0
\end{pmatrix} \tag{1}
$$

where the denominator accounts for the time to transition between age bins in a 5-year division in units of days.

2.2 Force of infection

Our model assumes two different forces of infection, one for the non-quarantined individuals λ and other for quarantined individuals λ_q. Non-quarantined individuals can be infected by non-quarantined infected individuals in four locations: school, work, home, and in the community. They can also be infected by interacting with quarantined familiars in the "home" setting, and quarantined individuals in other households through the "community" matrix setting. The later considers that transmission by occasional contacts with quarantined individuals in their households may occur, such as in food delivery contexts, for instance. Assuming that $\hat{c}$ is the total contact matrix with percolation effect and non-pharmaceutical interventions described in Franco et al.[2], and $\hat{c}_i$ being the other matrices with the "cocooning of older adults" intervention, with $i = \{\text{home, school, work, community}\}$, we have:

$$
\begin{aligned}
\lambda = & (1 - mask(t))p\hat{c}(\rho\mathbf{E} + \mathbf{A} + \mathbf{I} + imports + \rho_s(\mathbf{H} + \mathbf{ICU} + \mathbf{ICUH}))/\mathbf{N} \\
& + (1 - mask(t))p(1 - f_{perc})\hat{c}_{home}(\rho\mathbf{QE} + \mathbf{QI} + \mathbf{QC} + \mathbf{X} + \mathbf{HC} + \mathbf{ICUC})/\mathbf{N} \\
& + (1 - mask(t))p(1 - Q_{eff,com})\hat{c}_{com}(\rho\mathbf{QE} + \mathbf{QI} + \mathbf{QC} + \mathbf{X} + \mathbf{HC} + \mathbf{ICUC})/\mathbf{N}
\end{aligned} \tag{2}
$$

where $Q_{eff,com}$ is a parameter of reduction in mean contacts between quarantined and non-quarantined by the "community" contact matrix, *imports* is the value of new imported cases added by day (see Section 3 for details), $\mathbf{N}$ is the population size per age group, and f_{perc} and $mask(t)$ are the percolation effect and the usage of mask intervention, respectively, described in Franco et al.[2].

Similarly, a quarantined susceptible individual can be infected by an infected person inside the household, or be infected by interacting through the "community" contact matrix, as follows:

$$\begin{aligned}\lambda_q &= (1 - mask(t))p(1 - f_{perc})\hat{c}_{home}(\rho\mathbf{QE} + \mathbf{QI} + \mathbf{QC} + \mathbf{X} + \mathbf{HC} + \mathbf{ICUC})/\mathbf{N} \\ &+ (1 - mask(t))p(1 - Q_{eff,com})\hat{c}_{com}(\rho\mathbf{E} + \mathbf{A} + \mathbf{I} + imports + \rho_s(\mathbf{H} + \mathbf{ICU} + \mathbf{ICUH}))/\mathbf{N}\end{aligned} \tag{3}$$

2.3 Computing the birth rate

To compute the birth rate, we consider that half of the population is females. With this, we compute the birth rate per female per age b_j using the data described in Table 5. Therefore our birth rate is given by:

$$\mu_b(t) = (\mu_{b,0-4}(t), 0, \ldots, 0) = \left(\sum_{j=0-4}^{85+} b_j \frac{N_j(t)}{2}, 0, \ldots, 0\right) \tag{4}$$

2.4 Computing the probability of dying when unattended

To be able to simulate an age-varying risk of death when an individual does not receive proper health assistance, we do the following: First, we consider the age-stratified risk of dying when the individuals are properly assisted. We then renormalize this vector $\hat{v}$ by the highest value P (pdeath_h and pdeath_icu, for common bed and ICU, respectively). Thus, the age with the highest risk will have a value of 1. Naturally, we can recover the probability of dying when attended simply by doing $P\hat{v}$. To consider the risk of dying when not receiving attendance, we multiply $\hat{v}$ by the highest risk of dying in each case (pdeath_hc if not receiving common bed if needed, pdeath_icuh if needing ICU bed, but receiving a common one and pdeath_icuc if needing ICU bed, but not receiving any attendance). This will naturally be age-stratified, as $\hat{v}$ is. The actual values of the maximum probability of dying are given in Table 4.

2.5 Contact tracing

In our definition, individuals quarantined by contact tracing are the ones that were quarantined not by direct testing, but being detected as contacts of tested (and infected) individuals. We use the contact matrices from [4] as a proxy for the contact network of each infected individual, while still assuming a well-mixed model. To implement the contact tracing strategy, we assume that individuals from compartments **S**, **E**, **A**, **I**, **HC**, **ICUH**, **ICUC**, and **R** can be transferred to their respective "quarantined" compartments where their remain isolated, thus, decreasing the chance of infecting other individuals. Isolation occurs after being positively diagnosed as infected by testing, and quarantining occurs when you are traced as a contact of a positively diagnosed individual. For simplicity, we refer to all individuals isolated by the contact tracing strategy as "quarantined". Our model supports two ways of testing, one fixing the probabilities PT_i for each compartment or supplying a number of tests applied per day n_t. While the implementation of the first case is trivial, for the second one, we first calculate the entrance rate F_i from the exposed (quarantined and non-quarantined) compartment to the compartment studied (for example, $F_H = \gamma IHR(1-P_{icu})(1-H_c)(\mathbf{E}+\mathbf{QE})$), with i following the given sequence of priority $i = \{\mathbf{ICU, ICUH, H, ICUC, HC, X+CL}\}$ (here assuming that non-symptomatic individuals are not tested in first place). The index ℓ represents the age group. This gives us the daily number of new cases in each compartment. Then, the probability of testing the compartment j (that follows the same sequence of i) is given by:

$$\begin{aligned}x &= \frac{n_t - \sum_\ell \sum_i^{j-1} F_{i\ell}}{\sum_\ell F_{j\ell} + 1} \\ PT_j &= \begin{cases} 0, & \text{if } x < 0 \\ 1, & \text{if } x > 1 \\ x, & \text{otherwise.}\end{cases}\end{aligned} \tag{5}$$

where we add 1 to the denominator to avoid division by zero. The term $n_t - \sum_i^{j-1} F_i$ calculates the number of tests that are available to be used in compartment j after being used in higher priority compartments. The ratio between the number of tests available and the number of new daily cases in the j compartment then gives the probability of a new case being detected by testing, assuming a completely random testing strategy within the population (but still assuming a priority rule to allocate the tests). Of course, if there are more tests available than needed, the probability will be 1, and if there are no tests left, it will be zero.

Consider again the entrance rate F_i, but this time only considering non-quarantined exposed individuals. Then, the entrance rate from a compartment to the corresponding quarantined one is given by:

$$\mathbf{Q}_{in} = \frac{Q_{cov}\tau_w}{P-Q}\left(\sum_k E_k \hat{c}_k\right)\sum_j PT_j F_j \tag{6}$$

where Q_{cov} is the adherence to quarantine, τ_w is the time window of traced contacts, $P-Q$ is the total (alive) population discounted for the already quarantined individuals, and E_k is the estimated reduction of contacts due to the contact tracing in each k contact matrix (ie. home, work, school, or community; for the results concerning this paper, the only non-zero reduction of contacts is the one related to school contacts). Notice that the entrance rates are age-stratified, thus the entrance rate to quarantine is also stratified.

Finally, if there are still tests available, they are applied to asymptomatic, exposed, recovered, and susceptible individuals who were identified as contacts of already tested individuals:

$$\begin{aligned} x &= \frac{n_{t,2}}{1+\sum_\ell Q_{in,\ell}(\mathbf{S}_\ell + \mathbf{E}_\ell + \mathbf{A}_\ell + \mathbf{R}_\ell)} \\ PT_{sec} &= \begin{cases} 0, & \text{if } x < 0 \\ 1, & \text{if } x > 1 \\ x, & \text{otherwise.} \end{cases} \end{aligned} \tag{7}$$

where we add 1 to the fraction to avoid division by zero, $n_{t,2} = n_t - \sum_{i,\ell} F_{i,\ell} > 0$ is the number of remaining tests. The ratio between the number of tests available per day and the number of new quarantined individuals per day then gives us the probability of a new case being detected by testing, assuming a completely random testing strategy within the population. Notice that $PT_E = PT_A$ (which we call PT_{sec} since we do not distinguish between them, and $PT_S = PT_R = 0$ as we assume there are no false positives. Once again, these probabilities have to remain between 0 and 1.

Then the rate of quarantining of second-order contacts is given by:

$$\mathbf{Q}_{in,2} = \frac{Q_{cov}\tau_w}{P-Q}\left(\sum_k E_k \hat{c}_k\right) PT_{sec}\mathbf{Q}_{in}(\mathbf{E}+\mathbf{A}) \tag{8}$$

Table 6 shows the contact tracing parameters assumed for this study:

3 List of interventions

Here we describe the interventions used as input of the model, reproducing (with permission) Franco et al.[2]. Tables 7, 8 and 9 comprises all interventions used in the fitting of the model. Figures 1, 2 and 3 show the timeline of these interventions.

- *Self-Isolation*: Symptomatic individuals that do not require hospitalization voluntarily isolate themselves during the time of infection and reduce the chance of infecting others. The beginning and end period of this intervention is defined by $\theta_{selfis}(t)$ and represents the days t when the population adheres to this behavior. The impact of this NPI depends on its adherence to self-isolation $selfis_{cov}$ and estimated reduction in contacts by self-isolation $selfis_{eff}$ values, where

$$P_{selfis} = selfis_{cov}(t) selfis_{eff}\theta_{selfis}(t) \tag{9}$$

- *Social Distancing*: the population avoids or reduces contacts in the community setting ($\hat{c}_{com}$). This intervention comprises reduction of contacts on churches, markets, social events and gatherings, shopping activities, gyms, and others. The beginning and end period of this intervention is defined by $\theta_{dist}(t)$. The impact of this NPI depends on its adherence to social distancing at community level ($dist_{cov}$) and reduction of contacts in the community among those adhering to social distancing ($dist_{eff}$) values, where:

$$dist(t) = dist_{cov}(t) dist_{eff}\theta_{dist}(t); \tag{10}$$

- *Use of masks*: This intervention comprises individual protection measures, given by the adoption of mask usage. The beginning and end period of this intervention is defined by $\theta_{mask}(t)$. The impact of this NPI depends on its adherence to mask usage ($mask_{cov}$) and the proportion in the reduction of contacts ($mask_{eff}$), where

$$mask(t) = mask_{cov}(t) mask_{eff}\theta_{mask}(t); \tag{11}$$

- *Work from home*: This intervention reduces contacts in the work environment ($\hat{c}_{work}$) as workers perform their activities from their home. The beginning and end period of this intervention is defined by $\theta_{work}(t)$. The impact of this NPI depends on the adherence to home-office ($work_{cov}$) and reduction of contacts at work among those adhering to home-office ($work_{eff}$), where:

$$work(t) = work_{cov}(t) work_{eff} \theta_{work}(t); \tag{12}$$

- *School closure*: This intervention reduces the contacts in the school setting ($\hat{c}_{school}$) due to limitation of in-school activities or school closures. The beginning and end period of this intervention is defined by $\theta_{school}(t)$. The effectiveness of this NPI depends on the adherence to online (not in-person) school activities ($school_{cov}$) and the estimated reduction of contacts in school upon school closure ($school_{eff}$), where:

$$school(t) = school_{cov}(t) school_{eff} \theta_{school}(t); \tag{13}$$

  Note that in the main text, $school_{cov}$ is also referred as PCS (potential contacts in school).

- *cocooning of older adults*: This intervention reduces the contacts to a proportion of the older adult population, given a minimum age $D^{\dagger}$. The beginning and end period of this intervention is defined by $\theta_{cocoon}(t)$.The effectiveness of this NPI depends on the adherence to cocooning of older adults ($cocoon_{cov}$) and the estimated reduction of contacts with older adults in all settings as a results of cocooning older adults ($cocoon_{eff}$). Additional details of this implementation is described in Franco et al.[2].

- *Travel ban*: This intervention models the interruption of travel flow from outside the city and the isolation of cases coming from outside, which reduces or eliminate import cases. This intervention is given by:

$$imports = (1 - travel_{eff}) mean\_imports \tag{14}$$

  where ($mean\_imports$) is the mean value of imported cases, $travel_{eff}$ the effectiveness of this intervention, and $imports$ the number of new cases that are added to the population per day.

4 Model Fitting

To fit the model onto epidemiological data, we used consolidated time series from Severe Acute Respiratory Infection (SARI) hospitalisations and deaths in São Paulo, Goiânia and Porto Alegre from the SIVEP-Gripe database[5] between the dates described in table 10.

In Brazil, SARI case notification is compulsory (leading to high reporting rates) and SARS-CoV-2 is included as a SARI category. Due to the lack of extensive testing, we assume that using only SARS-CoV-2 confirmed cases would lead to an underestimation of the actual number of cases. Hence, we assume that SARI cases are a better approximation to the number of SARS-CoV-2, rather than only cases confirmed by PCR tests. Since SIVEP-Gripe reports only severe cases that require hospitalisation, we fit SARI cases to the sum over all hospitalised compartments of the model.

Following Franco et al.[2], we chose to use weekly time series for new cases and new deaths to avoid carrying past information into future values, which occurs when using time series of cumulative data.

Based on data from SIVEP[5], we were able to estimate the COVID-19 In-Hospital Fatality Rate (IHFR) and Intensive Care mortality rate (ICMR) for each city (Table 3). Other local parameters are described in Table 4, and local demographic rates per age group in Table 5.

Our model included four free parameters: p, $startdate$, T_{perc}, and h_{steep}. The parameter p indicates the probability of transmission per contact, and $startdate$ is the date of onset of the pandemic, that is, the introduction of the first infected individual. The last two parameters are related to the assumption of a non-linear effect of reducing transmission when increasing social distancing measures in households, following the implementation by [2]. Based on a phenomenological approach, after a critical threshold of adherence to social distancing, the underlying network of transmission composed of a fully connected cluster collapses and breaks down into multiple smaller clusters. As a consequence, the probability of infection decreases drastically after this point. Thus, T_{perc} indicates this threshold, which represents the value of adherence to the social distancing intervention that results in the percolation effect. The parameter h_{steep}, in turn, indicates the steepness of the effect caused by the percolation: while values closer to zero indicate a more linear relationship between the intervention adherence and the reduction of contacts, higher values indicate a steeper change in the reduction of contacts after the percolation effect.

To perform a nonlinear least squares fitting of the free parameters (p, T_{perc}, h_{steep}, $startdate$) to the data, we used the Levenberg-Marquardt algorithm implemented in the minpack.lm R package[6].

To fit both new cases (C) and new deaths (D), we had to account for residuals in different scales. One way to do that was by normalising each of the variables in respect to their total sum. Therefore, the resulting residual (R) is given by:

$$R = \frac{\sum(C_{model} - C_{observed})}{\sum C_{observed}} + \frac{\sum(D_{model} - D_{observed})}{\sum D_{observed}} \tag{15}$$

The algorithm minimises the square of this quantity, while evaluating the respective negative log-likelihood and minimising it.

To perform the non-linear optimisation, the algorithm requires a series of initial guesses. We tested a wide range of *startdate* values (from $2020-01-01$ to $2020-02-24$) and for each one we ran the fitting algorithm using several reasonable initial guesses for the other free parameters. Hence, this method gives us fitted p, T_{perc} and h_{steep} for each *startdate* considered.

With the goal to find a probability distribution for the fitted parameters[7], we selected the run which returned the lowest residual for each *startdate*, with its respective (p, T_{perc}, h_{steep}) set. We then computed the negative log-likelihood for each start date, L_t:

$$L_t = N \ln\left(\frac{1}{N}\sum_{i=1}^{N} R_{i,t}^2,\right) \tag{16}$$

from which we can derive the probability for each *startdate*, given by

$$P_t = \frac{exp(-L_t + min(\{L_t\}))}{\sum_t exp(-L_t + min(\{L_t\}))}. \tag{17}$$

Finally, maximising the probability (which is equivalent to minimising the negative log-likelihood), we find sets of best fitted parameters for each of the cities considered (See Table 11)

5 Sensitivity analysis

For the sensitivity analysis, we evaluated how changes in a parameter of interest can qualitatively and quantitatively alter the simulation results for the different scenarios evaluated for the reopening of schools. We set each parameter of interest to be fitted together with the main parameters, sampling uniformly the initial conditions in the range described in 12 and choosing the best fit as result (see tables 13, 14 and 15). Each parameter was fit independently of the others. Since the adherence to the NPI varies in time, the parameter with "cov" were varied by a scaling factor, maintaining the variation in time.

We then compared the final difference in the incidence of cases and deaths in relation to a baseline scenario without school reopening. The simulations were repeated for the different school reopening values (PCS) and compared with the original simulation (see main text).

References

1. Aguas R, White L, Hupert N, et al. Modelling the COVID-19 pandemic in context: an international participatory approach. BMJ Global Health 2020; 5. Ed. by, Ariana P, et al. DOI: 10.1136/bmjgh-2020-003126. eprint: https://gh.bmj.com/content/5/12/e003126.full.pdf. Available from: https://gh.bmj.com/content/5/12/e003126
2. Franco C, Ferreira LS, Sudbrack V, et al. Percolation across households in mechanistic models of non-pharmaceutical interventions in SARS-CoV-2 disease dynamics. Epidemics 2022 Jun; 39:100551. DOI: 10.1016/j.epidem.2022.100551. Available from: https://doi.org/10.1016%2Fj.epidem.2022.100551
3. Soetaert K, Petzoldt T, Setzer RW. Solving Differential Equations in R: Package deSolve. Journal of Statistical Software 2010; 33:1–25. DOI: 10.18637/jss.v033.i09
4. Prem K, Zandvoort Kv, Klepac P, et al. Projecting contact matrices in 177 geographical regions: an update and comparison with empirical data for the COVID-19 era. PLoS computational biology 2021; 17:e1009098
5. Datasus. SRAG 2020 - Banco de Dados de Síndrome Respiratória Aguda Grave - incluindo dados da COVID-19. 2020. Available from: https://opendatasus.saude.gov.br/dataset/bd-srag-2020 [Accessed on: 2021 May 26]
6. Elzhov TV, Mullen KM, Spiess AN, Bolker B. minpack.lm: R Interface to the Levenberg-Marquardt Nonlinear Least-Squares Algorithm Found in MINPACK, Plus Support for Bounds. R package version 1.2-1. 2016. Available from: https://CRAN.R-project.org/package=minpack.lm

7. Burnham KP, Anderson DR. Model Selection and multi-model inference: A practical information-theoretic approach. Springer New York, 2013
8. IBGE. Tábuas completas de mortalidade. 2019. Available from: https://www.ibge.gov.br/estatisticas/sociais/populacao/9126-tabuas-completas-de-mortalidade.html?=&t=resultados [Accessed on: 2021 Apr 28]
9. IBGE. Pesquisas Estatísticas do Registro Civil - Tabela 2679 - Nascidos vivos, por ano de nascimento, idade da mãe na ocasião do parto, sexo e lugar do registro. 2021. Available from: https://sidra.ibge.gov.br/tabela/2679 [Accessed on: 2021 Apr 28]
10. Wei Y, Wei L, Liu Y, et al. A systematic review and meta-analysis reveals long and dispersive incubation period of COVID-19. 2020 Jun. DOI: 10.1101/2020.06.20.20134387. Available from: https://doi.org/10.1101/2020.06.20.20134387
11. Salje H, Kiem CT, Lefrancq N, et al. Estimating the burden of SARS-CoV-2 in France. Science 2020 May; 369:208–11. DOI: 10.1126/science.abc3517. Available from: https://doi.org/10.1126/science.abc3517
12. SMSSP. Inquérito sorológico para Sars-Cov-2: Prevalência da infecção em escolares das redes públicas e privada da cidade de São Paulo. http://www.capital.sp.gov.br/arquivos/pdf/2021/coletiva_saude_14-01.pdf. [Online; accessed 31-January-2021]. 2021
13. Sun WW, Ling F, Pan JR, et al. Epidemiological characteristics of COVID-19 family clustering in Zhejiang Province. Chinese journal of preventive medicine 2020; 54:625–9. DOI: 10.3760/cma.j.cn112150-20200227-00199
14. Cevik M, Tate M, Lloyd O, Maraolo AE, Schafers J, Ho A. SARS-CoV-2, SARS-CoV-1 and MERS-CoV viral load dynamics, duration of viral shedding and infectiousness – a living systematic review and meta-analysis. 2020 Jul. DOI: 10.1101/2020.07.25.20162107. Available from: https://doi.org/10.1101/2020.07.25.20162107
15. Portella TP, Mortara SR, Lopes R, et al. Temporal and geographical variation of COVID-19 in-hospital fatality rate in Brazil. 2021 Feb. DOI: 10.1101/2021.02.19.21251949. Available from: https://doi.org/10.1101/2021.02.19.21251949
16. IBGE. Projeções da população. 2021. Available from: https://www.ibge.gov.br/estatisticas/sociais/populacao/9109-projecao-da-populacao.html [Accessed on: 2021 Oct 1]

code and equations	description
S	Susceptible population
E	Infected and presymptomatic population
A	Infected population, asymptomatic and not isolated
I	Infected population, mildly symptomatic and not isolated
X	Infected population, mildly symptomatic and self-isolated at home
H	Infected population, hospitalized in simple bed.
HC	Infected population that require hospital treatment but but are denied, due to healthcare system overload
ICU	Infected population, hospitalised in Intensive Care Units (ICU).
ICUH	Infected population that require ICU but are hospitalised in simple beds, due to unavailability in ICU beds.
ICUC	Infected population that require ICU but are denied both an ICU or hospital simple bed, due to healthcare system overload.
R	Recovered population
QS	Susceptible population in quarantine
QE	Infected population in incubation period in quarantine
QI	Infected asymptomatic population in quarantine
QR	Recovered population in quarantine
QC	Mildly symptomatic population in quarantine
C	Cumulative reported cases
$\mathbf{C_M}$	Cumulative death cases
$\mathbf{C_{MC}}$	Cumulative death cases of critical patients, i.e., those who hospitalization was denied.

Table 1: List of model variables in equations on supplementary material and in the code. Variables written in the main text may be different for readability, here, we stick to the nomenclature used throughout the code to help reproducibility.

Code	Equation	Description	Value	Source
lam	λ	force of infection	Variable	Eq. (2)
mort	μ_d	natural mortality ($days^{-1}$)	See table 5	[8]
ageing	$\mathbb{A}_G$	speed of population ageing ($days^{-1}$)	-	Eq. (1)
birth	μ_b	birth rate ($days^{-1}$)	See table 5	[9]
gamma	γ	Inverse average of incubation period ($days^{-1}$)	1/5.8	[10]
ihr	σ	Infection hospitalisation rate	See Table 3	[11]
omega	ω	Rate of which recovered people become susceptible again ($days^{-1}$)	0	Assumed
rho	ρ	Relative infectiousness of incubation phase	0.105	[10]
rhos	ρ_s	Relative percentage of regular daily contacts when hospitalized	0.10	Assumed
pclin	P_{clin}	Probability upon infection of developing clinical symptoms by age groups	0.305 (0-19) 0.560 (20-59) 0.690 (60+)	[12] [13] [13]
selfis	P_{selfis}	Proportion of symptomatic individuals who self-isolate	Variable	[2] (SM)
prob_icu	P_{icu}	Proportion of hospitalised individuals who need ICU beds	See Table 3	[5]
critH	ϕ_H	Proportion of hospitalised individuals who have not received attendance	See Source	[2] (SM)
critICU	ϕ_c	Proportion of hospitalised individuals who need ICU beds and have not received one	See Source	[2] (SM)
critICUH	ϕ_{cH}	Proportion of hospitalised individuals who need ICU beds and have not received one and also not have received simple beds	See Source	[2] (SM)
nui	ν_i	Recovery rate of mild symptomatic/asymptomatic individuals ($days^{-1}$)	1/9	[14]
nus	ν_s	Recovery/death rate of hospitalised individuals ($days^{-1}$)	1/8.3	[5]
nusc	ν_{sc}	Recovery/death rate of hospitalised individuals who have not received attendance ($days^{-1}$)	1/11	Assumed
nu_icu	ν_{icu}	Recovery/death rate of hospitalised individuals in ICU beds ($days^{-1}$)	1/14.7	[5]
nu_icuh	ν_{icuh}	Recovery/death rate of hospitalised individuals who need ICU beds but received simple beds ($days^{-1}$)	1/11	Assumed
nu_icuc	ν_{icuc}	Recovery/death rate of hospitalised individuals who need ICU beds and have not received attendance ($days^{-1}$)	1/11	Assumed
ifr	μ_H	In hospital fatality rate	See Table 3	[15]
pdeath_h	P_d	Maximum probability of death for a hospitalised infection requiring common bed	See Table 4	[5]
pdeath_icu	P_{dicu}	Maximum probability of death for a hospitalised infection requiring ICU	See Table 4	[5]
pdeath_hc	P_{dhc}	Maximum probability of death for a hospitalised infection requiring common bed but not receiving attendance	See Table 4	Assumed
pdeath_icuh	P_{dicuh}	Maximum probability of death for a hospitalised infection requiring ICU but receiving common bed attendance	See Table 4	Assumed
pdeath_icuc	P_{dicuc}	Maximum probability of death for a hospitalised infection requiring ICU but not receiving attendance	See Table 4	Assumed
report	r	Report rate of asymptomatic cases	0.00	Assumed
reportc	r_c	Report rate of symptomatic cases	0.01	Assumed
reporth	r_h	Report rate of hospitalized cases	0.95	Assumed

Table 2: List of model parameters in equations on supplementary material and in the code. These variables are restricted to epidemiological variables (not the NPI-related ones).

Age group	Goiânia-GO		Porto Alegre-RS		São Paulo-SP		prob_icu	σ^1
	ICMR	IHFR	ICMR	IHFR	ICMR	IHFR		
0-4	0.29	0.034	0.26	0.028	0.14	0.014	0.45	0.1
5-9	0.29	0.034	0.26	0.028	0.14	0.014	0.45	0.1
10-14	0.29	0.034	0.26	0.028	0.14	0.014	0.52	0.1
15-19	0.29	0.034	0.26	0.028	0.14	0.014	0.52	0.1
20-24	0.29	0.034	0.26	0.028	0.14	0.014	0.25	0.5
25-29	0.29	0.034	0.26	0.028	0.14	0.014	0.25	0.5
30-34	0.25	0.036	0.21	0.013	0.2	0.028	0.32	1.1
35-39	0.25	0.036	0.21	0.013	0.2	0.028	0.32	1.1
40-44	0.36	0.049	0.25	0.031	0.24	0.045	0.34	1.4
45-49	0.36	0.049	0.25	0.031	0.24	0.045	0.34	1.4
50-54	0.42	0.075	0.35	0.05	0.36	0.087	0.40	2.9
55-59	0.42	0.075	0.35	0.05	0.36	0.087	0.40	2.9
60-64	0.59	0.166	0.56	0.109	0.52	0.162	0.48	5.8
65-69	0.59	0.166	0.56	0.109	0.52	0.162	0.48	5.8
70-74	0.69	0.194	0.71	0.262	0.62	0.248	0.54	9.3
75-79	0.69	0.194	0.71	0.262	0.62	0.248	0.54	9.3
80-84	0.76	0.295	0.82	0.498	0.69	0.459	0.47	26.2
85-89	0.76	0.295	0.82	0.498	0.69	0.459	0.47	26.2
90 +	0.76	0.295	0.82	0.498	0.69	0.459	0.47	26.2

Table 3: National COVID-19 infection-hospitalization rate (IHR), and COVID-19 In-Hospital Fatality Rate (IHFR) and Intensive Care mortality rate (ICMR) in the 3 study sites, by age sub-groups. Brazil, 2020. σ: IHR
[1] Source:[11]

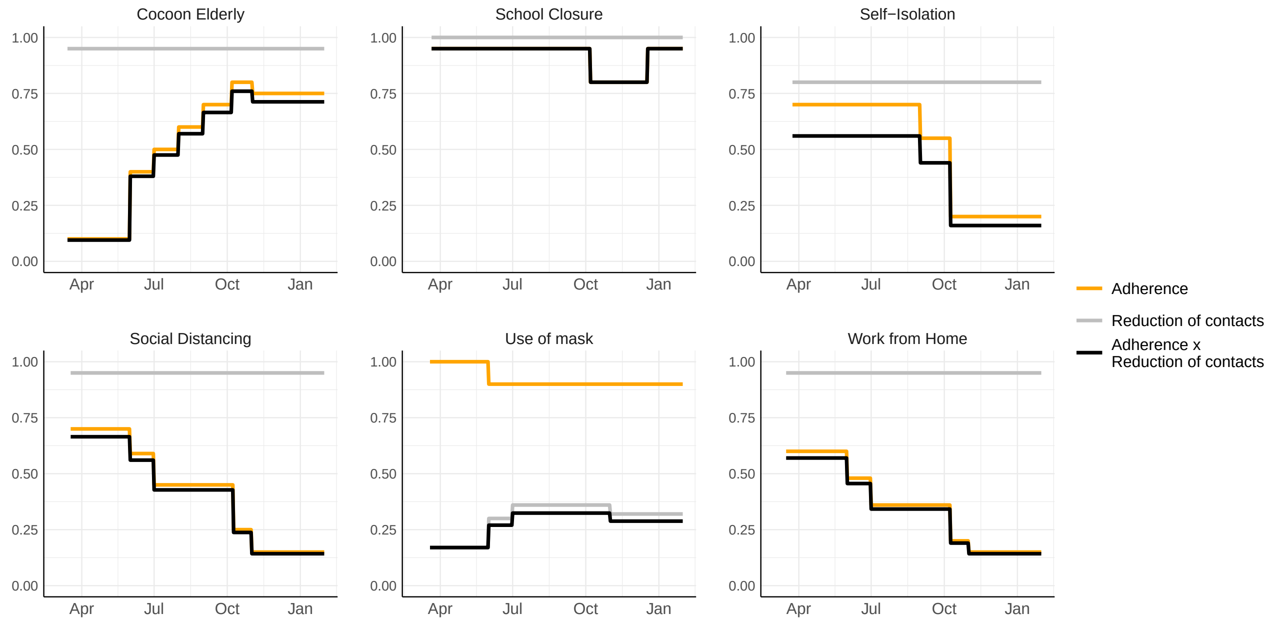

Figure 1: Diagram of adherence, reduction of contacts and their product for each of the considered non-pharmaceutical interventions considered in the model for São Paulo, SP.

Parameter	Description	Parameter by site Goiânia GO	 Porto Alegre RS	 São Paulo SP	Source
pdeath_h	Probability of death hospitalized infection requiring common bed	0.295	0.498	0.459	[5]
pdeath_icu	Probability of death hospitalized infection requiring ICU	0.76	0.82	0.69	[5]
pdeath_hc	Probability of death hospitalized infection requiring common bed but not receiving attendance	0.80	0.80	0.80	Assumed
pdeath_icuh	Probability of death in hospitalized infection requiring ICU but receiving common bed attendance	0.97	0.97	0.97	Assumed
pdeath_icuc	Probability of death hospitalized infection requiring ICU	0.99	0.99	0.99	Assumed
nus	Duration of hospitalized infection	7.6	9.5	8.3	[5]
nu_icu	Duration of ICU infection	13.2	21.7	14.7	[5]
beds_available	Number common bed	191	1096	3000	Health's Secretary by site
icu_beds available	Number ICU bed	189	866	5000	Health's Secretary by site
age_distribution	Population by age groups				[16]
	0-4	84000	88650	768844	
	5-9	87000	84793	803328	
	10-14	111000	76285	682355	
	15-19	108000	106686	750345	
	20-24	123000	92060	898803	
	25-29	115000	109641	881006	
	30-34	122000	117420	983082	
	35-39	131000	121941	1027565	
	40-44	117000	105631	955037	
	45-49	104000	89660	833183	
	50-54	99000	87781	754688	
	55-59	94000	92668	678138	
	60-64	79000	83814	594097	
	65-69	53000	68434	468480	
	70-74	35000	50621	340908	
	75-79	25000	34142	198407	
	80-84	10334	16670	131116	
	85-89	10334	16670	72103	
	90 +	10334	16670	48038	

Table 4: Model Parameter Values used for analysis of COVID-19 school reopening scenarios in Goiânia, Porto Alegre and São Paulo, 2020

Age groups	Population[1]	Mortality rate deaths/1000 live births[2]	Age groups	Live births[3]
0-4 years	14789473	1445		
5-9 years	14540682	118		
10-14 years	15153816	143	10-14 years	8853
15-19 years	16392753	485	15-19 years	201857
20-24 years	17285630	702	20-24 years	345734
25-29 years	17062512	726	25-29 years	335131
30-34 years	17295219	816	30-34 years	295965
35-39 years	16675605	989	35-39 years	177131
40-44 years	14916472	1315	40-44 years	42099
45-49 years	13288554	1874	45-49 years	2437
50-54 years	12302879	2648	50 + years	226
55-59 years	10769470	3667		
60-64 years	8831107	5016		
65-69 years	6855834	6968		
70-74 years	4964070	9617		
75-79 years	3387785	12497		
80-84 years	2201850	50974		
85-89 years	1171537	50974		
90 + years	737781	50974		

Table 5: Demographic data used to calculate the birth and mortality rate in Brazil, 2020.
[1] Source:[16]
[2] Source:[8]
[3] Source:[9]

Parameter	Description	Valu
n_t	Number of tests available at time t	Vari
$n_{t,2}$	Number of tests available at time t for second order testing	Vari
PT_i	Probability of case of compartment i being detected	Vari
Q_{cov}	Level of compliance to the contact tracing strategy	1
τ_w	Time window of the contact tracing strategy	2 da
E_{home}	Estimated reduction of contacts due to the strategy in tracing contacts from "home" environment	0
E_{school}	Estimated reduction of contacts due to the strategy in tracing contacts from "school" environment	1
E_{work}	Estimated reduction of contacts due to the strategy in tracing contacts from "work" environment	0
E_{com}	Estimated reduction of contacts due to the strategy in tracing contacts from "community" environment	0

Table 6: List of model parameters in equations on supplementary material and in the code. These variables are restricted to epidemiological variables (not the NPI-related ones).

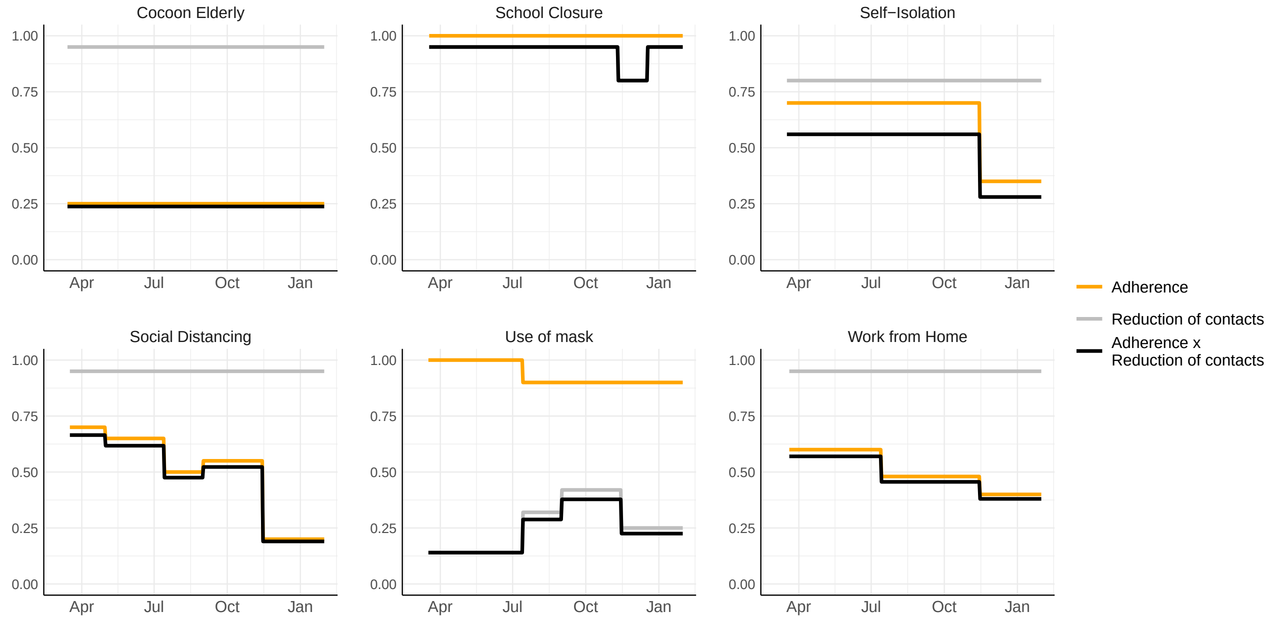

Figure 2: Diagram of adherence, reduction of contacts and their product for each of the considered non-pharmaceutical interventions considered in the model for Goiânia, GO.

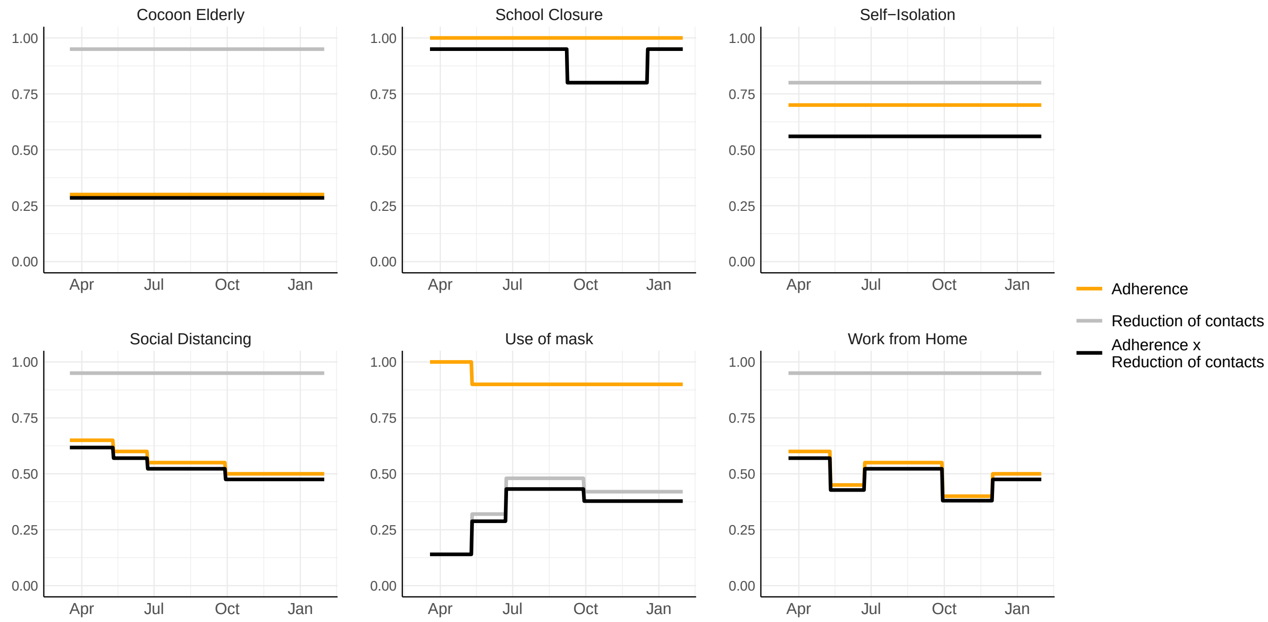

Figure 3: Diagram of adherence, reduction of contacts and their product for each of the considered non-pharmaceutical interventions considered in the model for Porto Alegre, RS.

Self Isolation			
Start date	End date	Adherence	Reduction of Contacts
2020-03-24	2020-08-31	0.70	0.80
2020-09-01	2020-10-08	0.55	0.80
2020-10-09	2021-03-01	0.20	0.80
Social Distancing			
Start date	End date	Adherence	Reduction of Contacts
2020-03-18	2020-05-31	0.70	0.95
2020-06-01	2020-06-30	0.59	0.95
2020-07-01	2020-10-08	0.45	0.95
2020-10-09	2020-10-31	0.25	0.95
2020-11-01	2020-03-01	0.15	0.95
School Closure			
Start date	End date	Adherence	Reduction of Contacts
2020-03-21	2020-10-06	0.95	1.00
2020-10-07	2020-12-17	0.80	1.00
2020-12-18	2021-03-01	0.95	1.00
Use of Mask			
Start date	End date	Adherence	Reduction of Contacts
2020-03-19	2020-05-31	0.20	0.85
2020-06-01	2020-06-30	0.35	0.85
2020-07-01	2020-10-31	0.42	0.85
2020-11-01	2020-03-01	0.37	0.85
Work from Home			
Start date	End date	Adherence	Reduction of Contacts
2020-03-16	2020-05-31	0.60	0.95
2020-06-01	2020-06-30	0.48	0.95
2020-07-01	2020-10-08	0.36	0.95
2020-10-09	2020-10-31	0.20	0.95
2020-11-01	2021-03-01	0.15	0.95
cocooning of older adults			
Start date	End date	Adherence	Reduction of Contacts
2020-03-14	2020-05-31	0.10	0.95
2020-06-01	2020-06-30	0.40	0.95
2020-07-01	2020-07-31	0.50	0.95
2020-08-01	2020-08-31	0.60	0.95
2020-09-01	2020-10-06	0.70	0.95
2020-10-07	2020-11-01	0.80	0.95
2020-11-02	2021-03-01	0.75	0.95
Travel Ban			
Start date	End date	Mean imports	Reduction of Contacts
2020-02-19	2020-03-18	0.20	0.0
2020-03-19	2021-03-01	0.20	0.70

Table 7: List of interventions used for model fitting in the case of São Paulo, SP.

Self Isolation			
Start date	End date	Adherence	Reduction of Contacts
2020-03-17	2020-11-14	0.70	0.80
2020-11-15	2020-03-01	0.35	0.80
Social Distancing			
Start date	End date	Adherence	Reduction of Contacts
2020-03-17	2020-04-30	0.70	0.95
2020-05-01	2020-07-13	0.65	0.95
2020-07-14	2020-08-31	0.50	0.95
2020-09-01	2020-11-14	0.55	0.95
2020-11-15	2020-03-01	0.20	0.95
School Closure			
Start date	End date	Adherence	Reduction of Contacts
2020-03-18	2020-11-10	0.95	1.00
2020-11-11	2020-12-17	0.80	1.00
2020-12-18	2021-01-31	0.95	1.00
2021-02-01	2021-03-01	0.30	1.00
Use of Mask			
Start date	End date	Adherence	Reduction of Contacts
2020-03-17	2020-07-13	0.16	0.85
2020-07-14	2020-08-31	0.38	0.85
2020-09-01	2020-11-14	0.49	0.85
2020-11-15	2021-03-01	0.29	0.85
Work from Home			
Start date	End date	Adherence	Reduction of Contacts
2020-03-20	2020-07-13	0.60	0.95
2020-07-14	2020-11-14	0.48	0.95
2020-11-15	2021-03-01	0.40	0.95
cocooning of older adults			
Start date	End date	Adherence	Reduction of Contacts
2020-03-14	2021-03-01	0.25	0.95
Travel Ban			
Start date	End date	Mean imports	Reduction of Contacts
2020-02-19	2020-03-18	0.20	0.0
2020-03-19	2021-03-01	0.20	0.70

Table 8: List of interventions used for model fitting in the case of Goiânia, GO.

Self Isolation			
Start date	End date	Adherence	Reduction of Contacts
2020-03-19	2020-12-18	0.70	0.80
Social Distancing			
Start date	End date	Adherence	Reduction of Contacts
2020-03-17	2020-05-10	0.65	0.95
2020-05-11	2020-06-22	0.60	0.95
2020-06-23	2020-09-28	0.55	0.95
2020-09-29	2020-12-18	0.50	0.95
School Closure			
Start date	End date	Adherence	Reduction of Contacts
2020-03-19	2020-09-07	0.95	1.00
2020-09-08	2020-12-17	0.80	1.00
2020-12-18	2021-12-18	0.95	1.00
Use of Mask			
Start date	End date	Adherence	Reduction of Contacts
2020-03-19	2020-05-10	0.16	0.85
2020-05-11	2020-06-22	0.38	0.85
2020-06-23	2020-09-28	0.57	0.85
2020-09-29	2020-12-18	0.49	0.85
Work from Home			
Start date	End date	Adherence	Reduction of Contacts
2020-03-19	2020-05-10	0.60	0.95
2020-05-11	2020-06-22	0.45	0.95
2020-06-23	2020-09-28	0.55	0.95
2020-09-29	2020-11-30	0.40	0.95
2020-12-01	2020-12-18	0.50	0.95
cocooning of older adults			
Start date	End date	Adherence	Reduction of Contacts
2020-03-14	2020-12-18	0.30	0.95
Travel Ban			
Start date	End date	Mean imports	Reduction of Contacts
2020-02-19	2020-03-18	0.20	0.0
2020-03-19	2021-03-01	0.20	0.70

Table 9: List of interventions used for model fitting in the case of Porto Alegre, RS.

City	Start date	End date
São Paulo	2020-03-22	2020-12-18
Goiânia	2020-03-22	2021-03-05
Porto Alegre	2020-03-22	2020-12-18

Table 10: Time interval of new hospitalizations from SIVEP-Gripe that were fitted for each city.

City	Parameter	Estimate	Std. Error	t value	$Pr(>\|t\|)$
São Paulo	p	0.04184	0.00010	397.8866	7.318e-155
	T_{perc}	0.55151	0.00152	362.8879	4.578e-151
	h_{steep}	4.58545	0.02065	222.0186	8.082e-131
	startdate	2020-01-26			
Porto Alegre	p	0.04565	0.00019	239.8034	1.701e-107
	T_{perc}	0.48442	0.34299	1.4123	0.16209
	h_{steep}	0.00243	0.00062	3.8858	0.00022
	startdate	2020-02-18			
Goiânia	p	0.02890	5.5e-05	523.3179	3.664e-166
	T_{perc}	0.72814	0.00307	237.4351	1.389e-133
	h_{steep}	15.0106	0.05038	297.9735	6.097e-143
	startdate	2020-01-27			

Table 11: Best fit results for each of the cities studied.

	rho	rhos	pclin young	hand eff	hand cov	selfis eff	selfis cov	dist cov	work cov	cocoon cov
Min	0	1	0.3	0.5	0.4	0.5	0.5	0.5	0.5	0.5
Max	88	100	0.7	0.99	1.25	0.99	1.25	1.25	1.25	1.25

Table 12: Range of variation of each parameter for the sensitivity analysis.

startdate	p	P_{thresh}	P_{steep}	SA parameter	Best fit value	Original value	Residual	Neg loglik
2020-01-26	0.0417	0.55	4.49	-	-	-	0.00208	-798.33
2020-01-26	0.0372	0.60	4.64	rho	16.38	10.50	0.00324	-1011.15
2020-01-26	0.0416	0.58	4.7	rhos	10.15	10.0	0.00412	-987.58
2020-01-26	0.0413	0.58	4.62	pclin young	0.56	0.305	0.00284	-1023.88
2020-01-26	0.0414	0.58	4.63	mask eff	0.94	0.85	0.00313	-1014.5
2020-01-26	0.0416	0.57	4.74	self eff	0.84	0.80	0.00295	-1020.17
2020-01-26	0.041	0.60	4.63	selfis cov	1.17	1.0	0.00278	-1026.02
2020-01-26	0.042	0.61	4.58	dist cov	1.10	1.0	0.00297	-1019.73
2020-01-26	0.0417	0.53	4.67	work cov	0.93	1.0	0.00302	-1017.97
2020-01-26	0.0414	0.57	4.84	cocoon cov	1.11	1.0	0.00377	-996.1

Table 13: Sensitivity analysis of the fitting for São Paulo, SP.

startdate	p	P_{thresh}	P_{steep}	SA parameter	Best fit value	Original value	Residual	Neg loglik
2020-02-18	0.0453	0.50	0	-	-	-	0.00277	-776.77
2020-02-18	0.0455	0.50	0	rho	10.78	10.50	0.00278	-776.44
2020-02-18	0.0455	0.49	0	rhos	10.14	10.0	0.00265	-779.98
2020-02-18	0.0455	0.50	0.01	pclin young	0.3	0.305	0.00266	-779.91
2020-02-18	0.0451	0.20	0.05	mask eff	0.81	0.85	0.00233	-789.71
2020-02-18	0.0432	0.51	0.02	self eff	0.53	0.80	0.00220	-794.24
2020-02-18	0.0446	0.49	0.05	selfis cov	0.87	1.0	0.00229	-791.05
2020-02-18	0.0448	0.50	0	dist cov	0.94	1.0	0.00257	-782.36
2020-02-18	0.0409	0.49	1.31	work cov	0.52	1.0	0.00228	-791.52
2020-02-18	0.0451	0.50	0	cocoon cov	0.83	1.0	0.00256	-782.59

Table 14: Sensitivity analysis of the fitting for Porto Alegre, RS.

startdate	p	P_{thresh}	P_{steep}	SA parameter	Best fit value	Original value	Residual	Neg loglik
2020-01-27	0.0287	0.73	15.0	-	-	-	0.00224	-1012.19
2020-01-27	0.0299	0.70	22.92	rho	9.21	10.50	0.00280	-1025.46
2020-01-27	0.0299	0.71	15.07	rhos	6.56	10.0	0.00280	-1025.24
2020-01-27	0.0293	0.73	15.00	pclin young	0.590	0.305	0.00291	-1021.66
2020-01-27	0.0294	0.71	15.11	mask eff	0.87	0.85	0.00309	-1015.6
2020-01-27	0.0303	0.71	14.38	self eff	0.91	0.80	0.00288	-1022.57
2020-01-27	0.0293	0.72	14.5	selfis cov	0.99	1.0	0.00284	-1024.16
2020-01-27	0.0294	0.74	14.85	dist cov	1.03	1.0	0.00281	-1024.89
2020-01-27	0.0291	0.71	14.92	work cov	0.94	1.0	0.00282	-1024.65
2020-01-27	0.0296	0.71	14.96	cocoon cov	0.82	1.0	0.00255	-1034.54

Table 15: Sensitivity analysis of the fitting for Goiânia, GO.