Supplementary Material - Percolation across households in mechanistic models of non-pharmaceutical interventions in SARS-CoV-2 disease dynamics

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I. Introduction

This model framework was first introduced in Aguas et al. (1). The code is available at https://github.com/francocarol/covid_perc. In Section II we introduce our modifications for the CoMo model structure (1) to account for particularities in the Brazilian health system. Nevertheless, modifications to better reflect other localities should be easily included in the model. Section II-A describes the equations, along with the explanation and sources of the parameters used. Section II-B describes how non-pharmaceutical interventions work in the model. Section II-D thoroughly describes our modifications to model hospital burden in Brazil. Section II-C lists the interventions used in the main paper. Finally, Section III shows the procedure used to fit the model to data.

II. Model structure

A. Model equations

The model consists in an expanded SEIR model to account for asymptomatic individuals and detailed structure of the Brazilian health system. We write such epidemiological dynamics as

$$
\begin{aligned}
\frac{d\mathbf{S}}{dt} &= -\lambda\mathbf{S} + \omega\mathbf{R} + \bar{\mathbf{Ag}}\cdot\mathbf{S} + \mu_b - \mu_d\mathbf{S}\\
\frac{d\mathbf{E}}{dt} &= \lambda\mathbf{S} - \gamma\mathbf{E} + \bar{\mathbf{Ag}}\cdot\mathbf{E} - \mu_d\mathbf{E}\\
\frac{d\mathbf{A}}{dt} &= \gamma(1-P_{clin})(1-IHR)\mathbf{E} - \nu_i\mathbf{A} + \bar{\mathbf{Ag}}\cdot\mathbf{A} - \mu_d\mathbf{A}\\
\frac{d\mathbf{I}}{dt} &= \gamma P_{clin}(1-P_{selfis})(1-IHR)\mathbf{E} - \nu_i\mathbf{I} + \bar{\mathbf{Ag}}\cdot\mathbf{I} - \mu_d\mathbf{I}\\
\frac{d\mathbf{X}}{dt} &= \gamma P_{selfis}P_{clin}(1-IHR)\mathbf{E} - \nu_i\mathbf{X} + \bar{\mathbf{Ag}}\cdot\mathbf{X} - \mu_d\mathbf{X}\\
\frac{d\mathbf{H}}{dt} &= \gamma IHR(1-P_{icu})(1-H_c)\mathbf{E} - \nu_s\mathbf{H} + \bar{\mathbf{Ag}}\cdot\mathbf{H} - \mu_d\mathbf{H}\\
\frac{d\mathbf{HC}}{dt} &= \gamma IHR(1-P_{icu})H_c\mathbf{E} - \nu_{sc}\mathbf{HC} + \bar{\mathbf{Ag}}\cdot\mathbf{HC} - \mu_d\mathbf{HC}\\
\frac{d\mathbf{ICU}}{dt} &= \gamma IHRP_{icu}(1-ICU_c)\mathbf{E} - \nu_{icu}\mathbf{ICU} + \bar{\mathbf{Ag}}\cdot\mathbf{ICU} - \mu_d\mathbf{ICU}\\
\frac{d\mathbf{ICUH}}{dt} &= \gamma IHR\ P_{icu}ICU_c(1-ICU\ H_c)\mathbf{E} - \nu_{icuh}\mathbf{ICUH} + \bar{\mathbf{Ag}}\cdot\mathbf{ICUH} - \mu_d\mathbf{ICUH}\\
\frac{d\mathbf{ICUC}}{dt} &= \gamma IHR\ P_{icu}ICU_cICU\ H_c\mathbf{E} - \nu_{icuc}\mathbf{ICUC} + \bar{\mathbf{Ag}}\cdot\mathbf{ICUC} - \mu_d\mathbf{ICUC}\\
\frac{d\mathbf{R}}{dt} &= \nu_i\mathbf{A} - \omega\mathbf{R} + \nu_i\mathbf{X} + \nu_i\mathbf{I} + \bar{\mathbf{Ag}}\cdot\mathbf{R} - \mu_d\mathbf{R} + \nu_s(1-P_dIHFR_h)\mathbf{H}\\
&\quad + \nu_{icu}(1-P_{dicu}IHFR_{icu})\mathbf{ICU} + \nu_{icuc}(1-P_{dicuc}IHFR_{icu})\mathbf{ICUC}\\
&\quad + \nu_{sc}(1-P_{dhc}IHFR_h)\mathbf{HC} + \nu_{icuh}(1-P_{dicuh}IHFR_{icu})\mathbf{ICUH}
\end{aligned}
$$

and, to represent the report dynamics, we also write the cumulative cases and deaths, respectively, as:

$$
\begin{aligned}
\frac{d\mathbf{C}}{dt} &= r\gamma(1-IHR)(1-P_{clin})\mathbf{E} + r_c\gamma(1-IHR)P_{clin}\mathbf{E} + r_h\gamma IHR\mathbf{E}\\
\frac{d\mathbf{D}}{dt} &= \nu_sP_{dh}IHFR_h\mathbf{H} + \nu_{sc}P_{dhc}IHFR_h\mathbf{HC} + \nu_{icu}P_{dicu}IHFR_{icu}\mathbf{ICU} + \nu_{icuc}P_{dicuc}IHFR_{icu}\mathbf{ICUC}\\
&\quad + \nu_{icuh}P_{dicuh}IHFR_{icu}\mathbf{ICUH} + \mu_d(\mathbf{H}+\mathbf{HC}+\mathbf{ICU}+\mathbf{ICUC}+\mathbf{ICUH}+\mathbf{I}+\mathbf{X})
\end{aligned}
\tag{1}
$$

where each of the dynamic variables (corresponding to the compartments shown in Table I) is further subdivided in $D = 19$ 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 $\bar{Ag}$ (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

$$\hat{\mu_d} = \mathrm{diag}(\mu_{d1}, \mu_{d2}, ..., \mu_{dD}) = \mathrm{diag}(\vec{\mu_d}). \tag{2}$$

Note that, in the system of equations presented above, we suppress the hat or bold notation from all diagonal matrices to avoid an overloaded notation, but we choose to keep all dynamic variables in bold as a reminder that each of them actually represents a vector of dimension $D = 19$. Hence, the dimension of the ordinary differential equation system that needs to be solved is $D \cdot 11$, where 11 is the number of compartments in the system. A description of each parameter from the model is available at table II.

B. Contact matrices and the force of infection

The model has over 300 equations, but the main mechanisms regarding infection and NPI effects are encoded in its force of infection, λ, which is describe in this subsection. Basically, a Susceptible individual

Code	Equations	Description
S	$\mathbf{S}$	Susceptible population
E	$\mathbf{E}$	Infected and presymptomatic population
I	$\mathbf{A}$	Infected population, asymptomatic and not isolated
CL	$\mathbf{I}$	Infected population, mildly symptomatic and not isolated
X	$\mathbf{X}$	Infected population, mildly symptomatic and self-isolated at home
H	$\mathbf{H}$	Infected population, hospitalized in simple bed.
HC	$\mathbf{HC}$	Infected population that require hospital treatment but but are denied, due to healthcare system overload
ICU	$\mathbf{ICU}$	Infected population, hospitalised in Intensive Care Units (ICU).
ICUH	$\mathbf{ICUH}$	Infected population that require ICU but are hospitalised in simple beds, due to unavailability in ICU beds.
ICUC	$\mathbf{ICUC}$	Infected population that require ICU but are denied both an ICU or hospital simple bed, due to healthcare system overload.
R	$\mathbf{R}$	Recovered population
C	$\mathbf{C}$	Cumulative reported cases
CM	$\mathbf{D}$	Cumulative reported deaths

TABLE I: List of model variables definitions and notations both for the equations and the R code.

in the n-th age class, written as S_n, can have contact with any of the infected groups of all age classes, so we would have

$$\frac{dS_n}{dt} \propto -S_n \sum_j c_{n,j}(a_j^A A_j + a_j^E E_j + a_j^I I_j + ...) \tag{3}$$

where $c_{n,j}$ measures the contact strength between people of n-th and j-th age classes, forming the contact matrix $\hat{c}$, of dimension $D \times D$. The $a_j^A, a_j^E, a_j^I, ...$ measures how infectious these different model compartments are. For example, asymptomatic people, $\mathbf{A}$, may be more infectious than the symptomatic ones, $\mathbf{I}$, since they may not be isolating themselves, given they are unaware of their infectious state. The NPIs are considered as modifications on both $\hat{c}$, reducing contacts between people, and also on the different $a_j^A, a_j^I, ..$, accounting for behavioural aspects, such as increased hand hygiene.

Given the definitions above, we are finally able to breakdown the general structure of $\hat{c}$. It is mainly composed of 4 matrices, $\hat{c}_{home}$ - which measures the amount of contacts of people at home, $\hat{c}_{work}$ - for contacts at work, $\hat{c}_{school}$ - for contacts at school and $\hat{c}_{other}$ - for other kinds of human interactions, such as going to restaurants, movies and churches. Therefore, in absence of any NPIs, the resultant contacts matrix would be simply

$$\hat{c} = \hat{c}_{home} + \hat{c}_{work} + \hat{c}_{school} + \hat{c}_{other} \tag{4}$$

But as NPIs are inserted, the contact matrix is modified. Suppose the simple case of home-office policies, that is, people should work at home for a period of $work_{dur}$ weeks. A fraction $work_{cov}$ of the population is able to adhere to such policies, and they have an effectiveness $work_{eff}$ in reducing this kind of contact, then we have that the contact matrix becomes

$$\hat{c} = (1 - f_{perc})\hat{c}_{home} + (1 - work_{cov} work_{eff} \theta_{work}(t))\hat{c}_{work} + \hat{c}_{school} + \hat{c}_{other} \tag{5}$$

Here, f_{perc} is as defined as in section 2.2 of the main paper, whilst $\theta_{work}(t)$ is a function that measures if either home office policies are being applied or not, and is usually a step function, being 1 during the period $work_{dur}$, defined by starting and finishing dates of such policies, and 0 out of said period. We could apply this same mathematical form for other interventions, such as school closing, commerce and restaurants functioning in reduced periods or not functioning at all, and many other NPIs we have seen being tried out in order to contain virus spread. We would get

Code	Equation	Description	Value	Source
lam	λ	force of infection	Variable	Eq. (16)
mort	μ_d	natural mortality ($days^{-1}$)	Age dependent	IBGE (9)
ageing	$\overline{\mathbf{Ag}}$	speed of population ageing ($days^{-1}$)	-	-
birth	μ_b	birth rate ($days^{-1}$)	-	IBGE (10)
gamma	γ	Inverse of incubation period ($days^{-1}$)	$1/5.8$	Wei et al. (18)
ihr	IHR	Infection hospitalisation rate	Age dependent	Salje et al. (13)
omega	ω	Rate of which recovered people become susceptible again ($days^{-1}$)	0	Assumed
rho	ρ	Relative infectiousness of presymptomatic individuals	0.105	Wei et al. (17)
rhos	ρ_s	Relative infectiousness of hospitalised individuals (reduced due to hospitalisation)	0.10	Assumed
pclin	P_{clin}	Proportion of symptomatic individuals	0.30 (0-19) 0.56 (20-59) 0.69 (60+)	SMSSP Sun et al. (15) Sun et al. (15)
selfis	P_{selfis}	Proportion of symptomatic individuals who self-isolate	Variable	Section II-B
prob_icu	P_{icu}	Proportion of hospitalised individuals who need ICU beds	Age dependent	SIVEP (6)
critH	H_c	Proportion of hospitalised individuals who have not received attendance	Variable	Section II-D
critICU	ICU_c	Proportion of hospitalised individuals who need ICU beds and have not received one	Variable	Section II-D
critICUH	ICU_h	Proportion of hospitalised individuals who need ICU beds and have not received one and also not have received simple beds	Variable	Section II-D
nui	ν_i	Recovery rate of mild symptomatic/asymptomatic individuals ($days^{-1}$)	1/9	Cevik et al. (4)
nus	ν_s	Recovery/death rate of hospitalised individuals ($days^{-1}$)	1/8.3	SIVEP (6)
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	SIVEP (6)
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[,3]	$IHFR_{icu}$	In hospital fatality rate (ICU required)	Age dependent	Portella et al. (12)
ifr[,4]	$IHFR_h$	In hospital fatality rate (common bed)	Age dependent	Portella et al. (12)
pdeath_h	P_d	Maximum probability of death for a hospitalised infection requiring common bed	45.9	SIVEP (6)
pdeath_icu	P_{dicu}	Maximum probability of death for a hospitalised infection requiring ICU	69	SIVEP (6)
pdeath_hc	P_{dhc}	Maximum probability of death for a hospitalised infection requiring common bed but not receiving attendance	80	Assumed
pdeath_icuh	P_{dicuh}	Maximum probability of death for a hospitalised infection requiring ICU but receiving common bed attendance	97	Assumed
pdeath_icuc	P_{dicuc}	Maximum probability of death for a hospitalised infection requiring ICU but not receiving attendance	99	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
give	q	Threshold of occupancy for loss of health system efficiency	0.65	Assumed

TABLE II: 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).

$$\begin{aligned}\hat{c} &= (1-f_{perc})\hat{c}_{home} + \\ &\quad (1-work_{cov}work_{eff}\theta_{work}(t))\hat{c}_{work} + \\ &\quad (1-school_{cov}school_{eff}\theta_{school}(t))\hat{c}_{school} + \\ &\quad (1-dist_{cov}dist_{eff}\theta_{dist}(t))\hat{c}_{other}\end{aligned} \tag{6}$$

With this final form of contact matrix we can add yet another possible NPI, cocooning the elderly. That means they are more isolated and protected, since they are one of the most vulnerable to COVID-19 death. When cocooning is applied, the contacts of people above a certain age, let's say age_{cocoon}, are reduced by $cocoon_{cov}cocoon_{eff}$, implying that $\hat{c}$ values from the $D^\dagger$ (the index from which cocooning starts) to D lines and rows must be reduced. If we recall that in our model we have 19 age classes defined from 0-4 to 90+, we would have, for instance, $D^\dagger = 13$ if cocooning is applied for people over 65 years old, since this threshold would correspond to the 13th class index. Defining the proportional reduction of contacts between the elderly as $\eta = 1 - cocoon_{cov}cocoon_{eff}\theta_{cocoon}(t)$ we write

$$\hat{g}_{D^\dagger}(\eta) = \mathrm{diag}(\vec{1}_{D^\dagger}, \eta\vec{1}_{D-D^\dagger}) \tag{7}$$

and with it, make the final contacts matrix

$$\overline{c} = \hat{g}_{D^\dagger}(\eta)\hat{c}\hat{g}_{D^\dagger}(\eta) \tag{8}$$

Note that

$$\hat{g}_{D^\dagger}(\eta)\hat{c}\hat{g}_{D^\dagger}(\eta) = \begin{bmatrix} c_{1,1} & c_{1,2} & \cdots & c_{1,D^\dagger-1} & \eta c_{1,D^\dagger} & \cdots & \eta c_{1,D} \\ c_{2,1} & c_{2,2} & \cdots & c_{1,D^\dagger-1} & \eta c_{1,D^\dagger} & \cdots & \eta c_{1,D} \\ \vdots & \vdots & \ddots & & \vdots & & \vdots \\ \vdots & \vdots & & \ddots & \vdots & & \vdots \\ \eta c_{D^\dagger,1} & \eta c_{D^\dagger,2} & \cdots & \eta c_{D^\dagger,D^\dagger-1} & \eta^2 c_{D^\dagger,D^\dagger} & \cdots & \eta^2 c_{D^\dagger,D} \\ \vdots & \vdots & & \vdots & \vdots & \ddots & \vdots \\ \eta c_{D,1} & \eta c_{D,2} & \cdots & \eta c_{D,D^\dagger-1} & \eta^2 c_{D,D^\dagger} & \cdots & \eta^2 c_{D,D} \end{bmatrix} \tag{9}$$

so the elderly are more isolated among themselves, since $\eta < 1 \implies \eta^2 < \eta$, whilst still having reduced contacts with the other age classes.

C. Non-pharmaceutical interventions

In all three model versions, we have implemented different NPI that affected the age-dependent contact rates encoded by the setting-specific contact matrices. Here we describe each of the seven NPI implemented in our model, followed by the resultant formulation of the system's force of infection (λ).

- *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

$$P_{selfis} = selfis_{cov}(t)selfis_{eff}\theta_{selfis}(t) \tag{10}$$

- *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:

$$dist(t) = dist_{cov}(t) dist_{eff} \theta_{dist}(t); \tag{11}$$

- *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 effectiveness $(mask_{eff})$, where

$$mask(t) = mask_{cov}(t) mask_{eff} \theta_{mask}(t); \tag{12}$$

- *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:

$$work(t) = work_{cov}(t) work_{eff} \theta_{work}(t); \tag{13}$$

- *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 reduction of contacts in school upon school closure $(school_{eff})$, where:

$$school(t) = school_{cov}(t) school_{eff} \theta_{school}(t); \tag{14}$$

  Note that in the main text, $school_{cov}$ is also referred as PCS (potential contacts in school).
- *Cocoon elderly*: 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 reduction of contacts with older adults in all settings as a results of cocooning older adults $(cocoon_{eff})$.
- *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:

$$imports = (1 - travel_{eff}) mean\_imports \tag{15}$$

  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.

Taking into account that Self-Isolated $(\mathbf{X})$ individuals are only able to infect through home and "other" matrices, we can wrap everything in a force of infection given by:

$$\begin{aligned} \lambda = {} & (1 - mask(t)) p \overline{c} [\rho \mathbf{E} + \mathbf{A} + \mathbf{I} + imports + \rho_s (\mathbf{H} + \mathbf{ICU} + \mathbf{ICUH})] / P \\ & + (1 - mask(t)) p (\overline{c}_{home} + \overline{c}_{other}) (\mathbf{X} + \mathbf{HC} + \mathbf{ICUC}) / P \end{aligned} \tag{16}$$

A thorough description of the NPI related parameters can be found in Tables III and IV. All definitions are valid across all three model versions, although all adherence values are increased by 30% (not surpassing 1) in the model with 30% more NPI adherence. Hence, we include an additional table with the parameter values used in the model with stronger interventions (Table V). Figure 1 shows coverages $(NPI_{cov}\theta_{NPI}(t))$, efficiencies (NPI_{eff}) and their corresponding product $NPI_{cov}NPI_{eff}\theta_{NPI}(t)$ over time (valid for the standard and percolation model versions).

Code	Equation	Description	Value	Source
mask_cov	$mask_{cov}$	Adherence to mask usage	See Table IV	(8; 14; 16)
mask_eff	$mask_{eff}$	Estimated reduction of contact due to mask use	0.85	Chu et al. (5)
selfis_cov	$selfis_{cov}$	Adherence to self-isolation	See Table IV	(8; 14; 16)
selfis_eff	$selfis_{eff}$	Estimated reduction of contact due to self-isolation if symptomatic	0.80	Assumed
dist_cov	$dist_{cov}$	Adherence to social distancing in community level	See Table IV	(8; 14; 16)
dist_eff	$dist_{eff}$	Reduction of contacts in the community among those adhering to social distancing	0.95	Assumed
work_cov	$work_{cov}$	Adherence to work from home policies	See Table IV	(8; 14; 16)
work_eff	$work_{eff}$	Reduction of contacts at work among those adhering to work from home policies	0.95	Assumed
school_cov	$school_{cov}$	Adherence to online (not in-person) school activities	See Table IV	(8; 14; 16)
school_eff	$school_{eff}$	Reduction of contacts in school upon school closure	1.00	Assumed
cocoon_cov	$cocoon_{cov}$	Adherence to cocooning of older adults	See Table IV	(8; 14; 16)
cocoon_eff	$cocoon_{eff}$	Reduction of contacts with older adults in all settings as a result of cocooning older adults	0.95	Assumed
travel_eff	$travel_{eff}$	Effectiveness of travel interruption policies	See Table IV	Assumed
mean_imports	$mean\_imports$	Mean number of infected individuals that travel to the study site	0.2	Assumed

TABLE III: Brief description of intervention parameters, together with values (if not time-dependent) and sources. In the case of time-dependent parameters, we supply additional tables with dates of interventions for the models standard and percolation (Table IV) and standard +30% NPIs (Table V).

Parameter	Start date	End date	Value
$selfis_{cov}$	2020-03-24	2020-08-31	0.70
$dist_{cov}$	2020-03-18	2020-05-31	0.70
$dist_{cov}$	2020-06-01	2020-06-30	0.59
$dist_{cov}$	2020-07-01	2020-08-31	0.45
$school_{cov}$	2020-03-21	2020-08-31	0.95
$mask_{cov}$	2020-03-19	2020-05-31	0.20
$mask_{cov}$	2020-06-01	2020-06-30	0.35
$mask_{cov}$	2020-07-01	2020-08-31	0.42
$work_{cov}$	2020-03-16	2020-05-31	0.60
$work_{cov}$	2020-06-01	2020-06-30	0.48
$work_{cov}$	2020-07-01	2020-08-31	0.36
$cocoon_{cov}$	2020-03-14	2020-05-31	0.10
$cocoon_{cov}$	2020-06-01	2020-06-30	0.40
$cocoon_{cov}$	2020-07-01	2020-07-31	0.50
$cocoon_{cov}$	2020-08-01	2020-08-31	0.60
$travel_{eff}$	2020-02-19	2020-03-18	0.00
$travel_{eff}$	2020-03-19	2020-08-31	0.70

TABLE IV: Values of time-dependent interventions used for model fitting in the case of Standard and Percolation model. The patterns observed in (8; 14; 16) were used as qualitative proxies for intervention coverage values.

D. Hospital burden

We slightly change the way hospital burden is added to the model from Aguas et al. (1). We assume that, if the occupation of beds is under some threshold value the health system infrastructure is able to handle correctly any new entrance to the hospital. After this threshold q, some of the patients might not find the needed support due to hospital overload, until full capacity, where patients are not accepted anymore. This is modelled by the following function:

Parameter	Start date	End date	Value
$selfis_{cov}$	2020-03-24	2020-08-31	0.910
$dist_{cov}$	2020-03-18	2020-05-31	0.910
$dist_{cov}$	2020-06-01	2020-06-30	0.767
$dist_{cov}$	2020-07-01	2020-08-31	0.585
$school_{cov}$	2020-03-21	2020-08-31	1.000
$mask_{cov}$	2020-03-19	2020-05-31	0.258
$mask_{cov}$	2020-06-01	2020-06-30	0.458
$mask_{cov}$	2020-07-01	2020-08-31	0.552
$work_{cov}$	2020-03-16	2020-05-31	0.780
$work_{cov}$	2020-06-01	2020-06-30	0.624
$work_{cov}$	2020-07-01	2020-08-31	0.468
$cocoon_{cov}$	2020-03-14	2020-05-31	0.130
$cocoon_{cov}$	2020-06-01	2020-06-30	0.520
$cocoon_{cov}$	2020-07-01	2020-07-31	0.650
$cocoon_{cov}$	2020-08-01	2020-08-31	0.780
$mean\_imports$	2020-02-19	2020-08-31	0.140
$travel_{eff}$	2020-02-19	2020-03-18	0.000
$travel_{eff}$	2020-03-19	2020-08-31	0.700

TABLE V: Values of time dependent interventions used for model fitting with stronger interventions (Standard model + 30% NPIs). Here we created an hypothetical intervention scenario with adherence 30% higher than the ones described in Table IV.

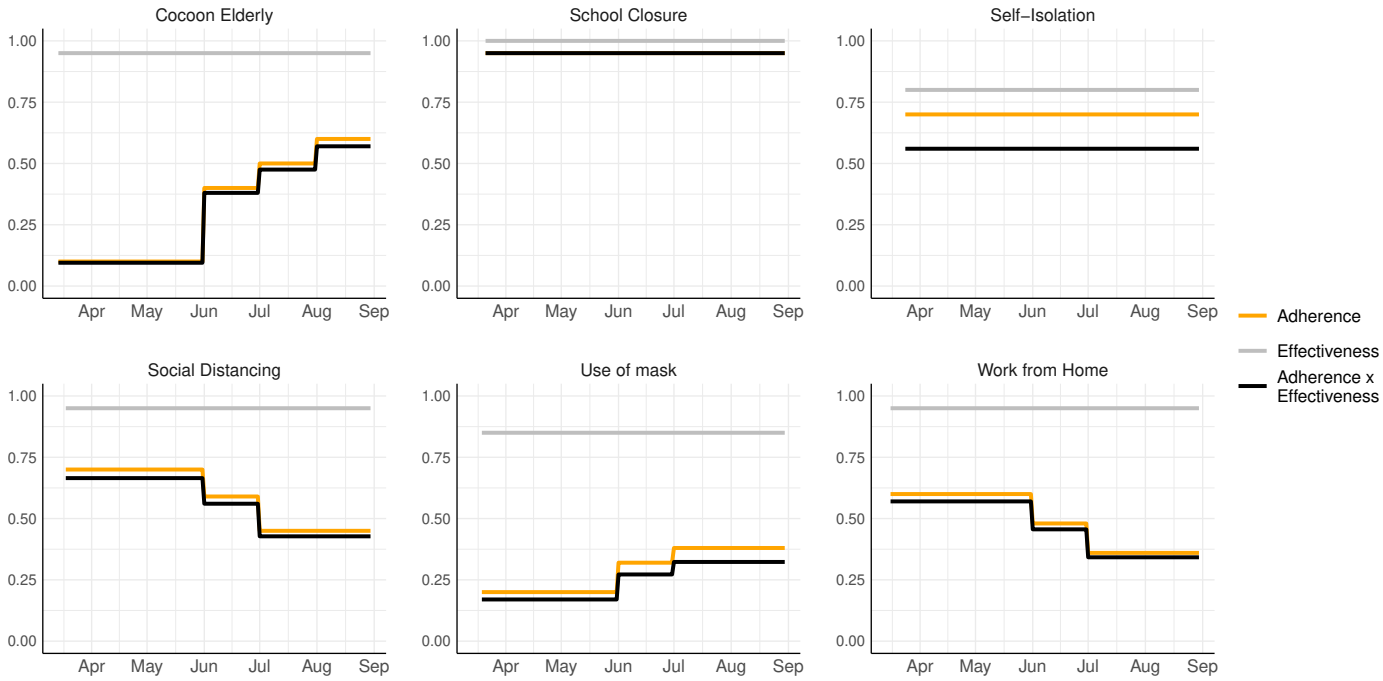

Fig. 1: Diagram of adherence, efficiency (estimated reduction of contact due to each NPI) and their product over time ($NPI_{cov}NPI_{eff}\theta_{work}(t)$), for each of the non-pharmaceutical interventions considered both in the standard model and the model with percolation. The diagrams for the model with 30% more NPI adherence are similar, only with 30% higher values for adherence and the product.

$$f(x) = \begin{cases} 0, & \text{if } x < q, \\ 1 - (x(b - ax) + c), & \text{if } q \leq x \leq 1 \\ 1, & \text{if } x > 1 \end{cases} \tag{17}$$

Where x is the ratio between number of patients and available beds and a, b, c are computed in a way to ensure continuity of the function and its first derivative:

$$a = \frac{1}{q(q-1) + (q^2 - 1)}$$
$$b = 2aq$$
$$c = a - b$$

We have then ICU_c being computed using $\mathbf{ICU}/\#$ ICU beds, H_c computed using $(\mathbf{ICUH} + \mathbf{H})/\#$ common beds (as $\mathbf{ICUH}$ uses common beds). Finally, to model priority of common beds to ICU needing individuals compared to $\mathbf{H}$ we simply assume that $ICU_h = H_c^2$, since these values are between 0 and 1, therefore $ICU_h \leq H_c$. The figure 2 shows these values assuming that $q = 0.65$.

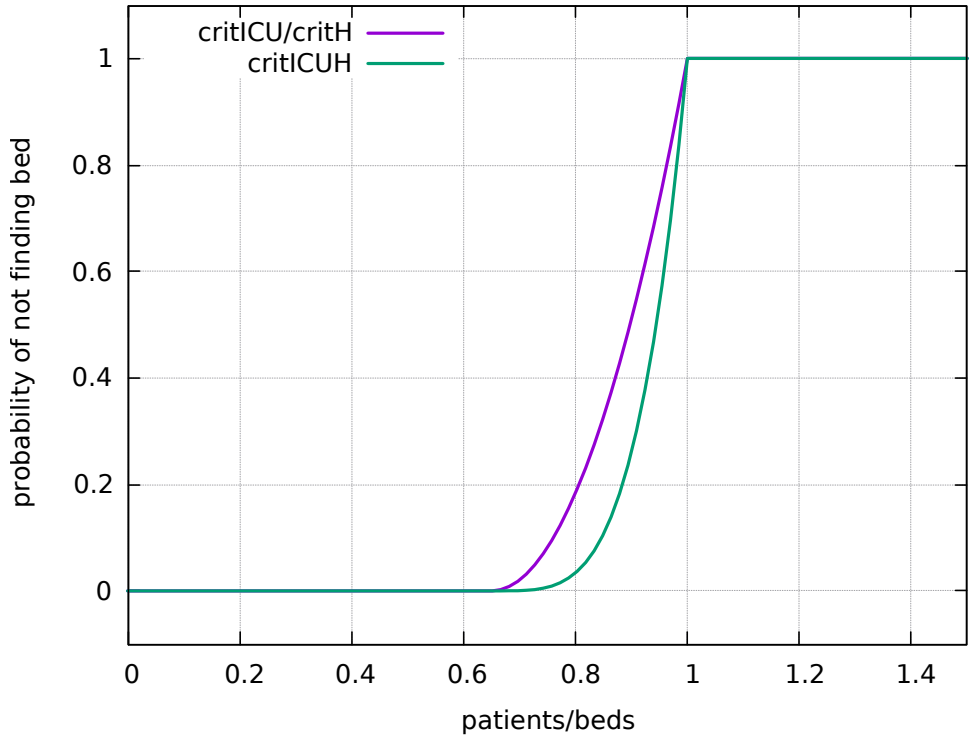

Fig. 2: Probability of not finding a bed as function of the current occupancy. $q = 0.65$.

E. Basic Reproduction Number

To calculate the Basic Reproduction Number (R_0) through the Next Generation Matrix (NGM) Method (2, Chapter 6) we need to redefine the model as a system of differential equations subdivided into two groups: the infected one, $\mathbf{y} = (\mathbf{E}, \mathbf{A}, \mathbf{I}, \mathbf{X}, \mathbf{H}, \mathbf{HC}, \mathbf{ICU}, \mathbf{ICUH}, \mathbf{ICUC})^T$, and the non-infected one, $\mathbf{z} = (\mathbf{S}, \mathbf{R}, \mathbf{D})^T$. We can then write the system as

$$\dot{\mathbf{y}} = F(\mathbf{y}, \mathbf{z}) - G(\mathbf{y}, \mathbf{z}) \tag{18}$$
$$\dot{\mathbf{z}} = J(\mathbf{y}, \mathbf{z}), \tag{19}$$

where F stands for the transition of Susceptible individuals, $\mathbf{S}$, into infected ones, $\mathbf{y}$, whilst G accounts for transitions within infected classes, from exposed to all other classes in $\mathbf{y}$, as well as recoveries and deceases. The function J accounts for the counterparts of these same effects into the $\mathbf{z}$ equations. Then, to calculate R_0, we linearize the system around disease free equilibrium, where $\mathbf{y} \approx \mathbf{0}$ and $\mathbf{z} \approx (\mathbf{P}(t = 0), \mathbf{0}, \mathbf{0})^T$, where $\mathbf{P}(t)$ is the population age distribution at time t. That way, the $\mathbf{y}$ equation becomes

$$\dot{\mathbf{y}} = (\hat{F} - \hat{G})\mathbf{y} \ , \tag{20}$$

where $\hat{F}$ and $\hat{G}$ are the linearized matrices that come from the functions F and G, respectively. Noticing that the only entrance of new infected comes from the λS terms in the exposed classes, $\mathbf{E}$. That way, only the first D lines/rows of $\hat{F}$ are not null. That way, defining

$$\hat{\sigma} = \text{diag}(\mathbf{S}) \ \bar{c} \ \text{diag}(\mathbf{P}(t=0))^{-1} \tag{21}$$

and

$$\hat{\sigma}_{ho} = \text{diag}(\mathbf{S}) \ (\bar{c}_{home} + \bar{c}_{other}) \ \text{diag}(\mathbf{P}(t=0))^{-1} \tag{22}$$

allow us to write

$$\hat{F} = (1 - hand(t))p \begin{bmatrix} \rho\hat{\sigma} & \hat{\sigma} & \hat{\sigma} & \hat{\sigma}_{ho} & \rho_s\sigma & \hat{\sigma}_{ho} & \rho_s\sigma & \rho_s\sigma & \hat{\sigma}_{ho} \\ & & & & \mathbb{0}_{8D,9D} & & & & \end{bmatrix} \tag{23}$$

The matrix $\hat{G}$ will have its first D columns as terms of exposed, $\mathbf{E}$, becoming the other infected compartments considered, that is, $(\mathbf{A}, \mathbf{I}, \mathbf{X}, \mathbf{H}, \mathbf{HC}, \mathbf{ICU}, \mathbf{ICUH}, \mathbf{ICUC})$. It's diagonal blocks are terms of recovery, decease and ageing effects. For the sake of simplifying notation, let $\hat{\phi}_j = \nu_j - \bar{A}g + \mu_d$, for $j = i, \ s, \ sc, \ icu, \ icuh, \ icuc$, so that the full form of $\hat{G}$ can be given by

$$\hat{G} = \begin{bmatrix} \gamma - \bar{A}g + \mu_d & \mathbb{0} & & \dots & & \mathbb{0} \\ -(1 - P_{clin})(1 - IHR)\gamma & \hat{\phi}_i & & & & \\ -P_{clin}(1 - P_{selfis})(1 - IHR)\gamma & \mathbb{0} & \hat{\phi}_i & & & \\ -P_{clin}P_{selfis}(1 - IHR)\gamma & & \hat{\phi}_i & \ddots & & \vdots \\ -IHR(1 - P_{icu})(1 - H_c)\gamma & & & \hat{\phi}_s & & \\ -IHR(1 - P_{icu})H_c\gamma & \vdots & & \ddots & \hat{\phi}_{sc} & \\ -IHR \ P_{icu}(1 - ICU_c)\gamma & & & & & \hat{\phi}_{icu} \\ -IHR \ P_{icu}ICU_c(1 - ICUH_c)\gamma & & & & & \hat{\phi}_{icuh} \\ -IHR \ P_{icu}ICU_cICUH_c\gamma & \mathbb{0} & & \dots & & \mathbb{0} \end{bmatrix} \begin{matrix} & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & & \\ & & & & \mathbb{0} & \hat{\phi}_{icuc} \end{matrix} \tag{24}$$

Finally, we can define the NGM as in chapter 6 of Allen et al. (2), $\hat{M}_{NGM} = \hat{F}\hat{G}^{-1}$. With that, R_0 is defined as the spectral radius of $\hat{M}_{NGM}$, which in the simplest cases is just its dominant eigenvalue, here calculated with rARPACK R package.

III. Model Fitting

To fit the model onto epidemiological data, we have used time series from Severe Acute Respiratory Infection (SARI) hospitalisations and deaths in São Paulo between 15 March and 31 August 2020. The data were retrieved the from the Brazilian Government database on SARI cases and deaths (SIVEP-Gripe, 31/05/2021 (6)). In Brazil, SARI cases notification is compulsory (leading to high reporting rates) and SARS-CoV-2 suspected and confirmed severe cases are included as a SARI category. As we have consistently monitored both SRAG and confirmed SARS-CoV-2 time-series, it was clear that SARS-CoV-2 cases comprised the great majority of SARI notifications since the beginning of 2020 and they were more reliable, since SARS-CoV-2 tests were scarce and testing protocols were inconsistent throughout the first few months of the pandemic in Brazil (11).

Hence, we assume that SARI cases are a better approximation to the number of SARS-CoV-2, rather than only cases recorded as confirmed by laboratory tests. Also, note that we used data on severe cases and,

therefore, hospitalised. Hence, we are fitting SARI cases to the sum over all hospitalised compartments of the model.

We specifically chose to use weekly time series for new cases and new deaths to avoid carrying past information into current values, as could happen if we used time series of cumulative data.

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 (7).

In order 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. The resulting residual (R) is, therefore:

$$R = \frac{\sum(C_{model} - C_{observed})}{\sum C_{observed}} + \frac{\sum(D_{model} - D_{observed})}{\sum D_{observed}} \tag{25}$$

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

To perform this kind of non-linear optimisation, we need to input the algorithm with a series of initial guesses. We tested a wide range of $startdate$ values (from $2020-10-01$ 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 (3), 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:

$$L_t = N \ln\left(\frac{1}{N}\sum_{i=1}^{N} R_{i,t}^2,\right) \tag{26}$$

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

$$P_t = \frac{exp(-L_t + min(\{L_t\}))}{\sum_t exp(-L_t + min(\{L_t\}))}. \tag{27}$$

Finally, maximising the probability (equivalent to minimising the negative log-likelihood), we find sets of best fitted parameters for each of the model versions considered (See Table VI).

We selected the model that was best supported by the data trough the Akaike Information Criteria (AIC):

$$AIC_i = 2NLL_{min} + 2n_{par} \tag{28}$$

where NLL_{min} is the minimum negative log-likelihood obtained from fitting each model, and n_{par} is the number of fitted parameters (two free parameters for the standard models and four for the model with percolation).

The AIC estimates the loss of information in data of each model, and thus the model with the lowest AIC is the best supported by the data. To compare the models we thus use ΔAIC:

$$\Delta AIC_i = AIC_i - AIC_{min} \tag{29}$$

where AIC_{min} is the minimum over all AIC values obtained.

The resultant AIC and ΔAIC obtained for each model version can be found in Table 1, in the main paper.

Model	Parameter	Mean	SD	Quantile 2.5%	Quantile 50%	Quantile 97.5%
Percolation	startdate	2020-01-30	-	2020-01-30	2020-01-30	2020-01-30
Percolation	p	0.0461	0.0002	0.0461	0.0461	0.0462
Percolation	T_{perc}	0.516	0.003	0.513	0.516	0.520
Percolation	h_{steep}	4.83	0.02	4.81	4.83	4.84
Standard	startdate	2020-01-15	-	2020-01-15	2020-01-15	2020-01-15
Standard	p	0.0294	≈ 0	0.0294	0.0294	0.0294
Standard + 30% NPIs	startdate	2020-01-30	-	2020-01-30	2020-01-30	2020-02-01
Standard + 30% NPIs	p	0.0402	0.0003	0.0401	0.0401	0.0411

TABLE VI: List of parameters values for the three models with mean, standard deviation (SD), and 2.5th, 50th and 97.5th percentiles.

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