Initiative Model antiCOVID-19 for the Czech Republic

MODEL B

A Technical Description

April 2020

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Model B

Here we describe a mathematical model we have developed to (1) reproduce the actual state of COVID-19 epidemic in the Czech Republic, accounting for all hitherto implemented interventions, (2) predict the future course of the epidemic given the actual interventions, and (3) assess how weakening or exiting some of the actually implemented interventions may affect the future course of epidemic. Our primary aim is to help public health authorities in designing efficient strategies of intervention relaxation and hence societal recovery to its normal state of functioning. Our model is structured by age, space, and type of inter-individual contacts, thus allowing one to compare relative efficiency of a number of realistic interventions, including the actually implemented ones. It contains a core epidemic layer, hospital layer, quarantine layer, and an observation layer directly linked to data reported by the public health authorities. Minimization of a distance between outputs of the observation layer and the reported data is a basis of the model calibration procedure. We first describe unstructured versions of all model layers; their extensions to age (and contacts) and space, then follow.

Epidemic layer

Our core epidemic model is a variant of the classic SEIR model, extended for two groups of asymptomatic individuals, individuals that stay asymptomatic for the whole course of infection and individuals that stay asymptomatic only for a short period of time before becoming symptomatic.

Following contacts with infectious individuals, susceptible individuals (S) may become exposed (E), that is, infected but not yet infectious (the process of infection transmission is described below). The exposed individuals then become asymptomatic for either the whole course of infection (I_n, with probability p_S) or for just a short period of time before becoming symptomatic (I_a, with probability $1 - p_S$). The I_a individuals then become symptomatic (I_s). Both the I_n and I_s individuals may recover (R) or die.

Since deaths attributed to COVID-19 do not happen outside hospitals in the Czech Republic, we consider deaths only in the hospital layer described below. However, deaths outside hospitals may be an important player for countries such as Italy or Spain, heavily impacted by the novel coronavirus. Some researchers speculate that a proportion of the population may be immunized against COVID-19, so a transition from the exposed class E to the recovery class R may be possible. Likewise, we do not consider this transition in the current model version, but we note that it may become important when an epidemic of the same of a similar virus variant appears in the future.

The epidemic layer thus consists of the following system of six equations:

$$\begin{aligned}
S[t+1] &= S[t] - \lambda\, S[t] - L[t]/p_S \\
E[t+1] &= E[t] + \lambda\, S[t] - \sigma\, E[t] + L[t]/p_S \\
I_a[t+1] &= I_a[t] + p_S\, \sigma\, E[t] - \xi\, I_a[t] \\
I_n[t+1] &= I_n[t] + (1-p_S)\, \sigma\, E[t] - \gamma_n\, I_n[t] \\
I_s[t+1] &= I_s[t] + \xi\, I_a[t] - \gamma_s\, I_s[t] \\
R[t+1] &= R[t] + \gamma_s\, I_s[t] + \gamma_n\, I_n[t]
\end{aligned} \tag{1}$$

The hitherto unexplained variable $L[t]$ accounts for the imported cases of COVID-19 from abroad, mostly from Italy and Austria, at the initial phase of the epidemic. A list of all such confirmed (symptomatic) imported cases is available at `https://onemocneni-aktualne.mzcr.cz/api/v1/covid-19`. Nonetheless, we do not introduce such imported cases as symptomatic. Rather, we assume they came earlier as exposed, and introduce them eight days before they were actually detected as positive (approximate delay between exposition and confirmation). Moreover, to account for the likely situation that some of the imported cases might have remained undetected as being asymptomatic for the whole course of infection, we divide the number of known imported cased by p_S, the probability of exposed individuals eventually becoming symptomatic.

The force of infection λ in model (1) sums contributions from all infectious classes I_n, I_a and I_s:

$$\lambda = \beta\, \chi\, \frac{r_\beta\, I_n[t] + r_\beta\, I_a[t] + r_C\, I_s[t]}{N[t]} \tag{2}$$

Here, β is the probability of infection transmission upon contact between susceptible and infectious individuals, χ is the contact rate between individuals in the population (the mean number of other individuals an individual has a contact with per day), r_β is a factor of reduction of the infection transmission probability for an asymptomatic individual relative to the symptomatic one, r_C is a factor of reduction of the contact rate of a symptomatic individual relative to the other ones (which hopefully reduces contact rate with others), and $N[t]$ is the total population size at time t.

Hospital layer

A proportion p_T of symptomatic individuals decide to undertake testing for the presence of the novel coronavirus. Testing (both sampling and processing) takes time that may vary during the course of epidemic; the I_s individuals are always tested positive. If symptoms are relatively severe, the I_s individuals are sent to a hospital and placed on a common bed (H_L, with probability p_H); those that have only mild symptoms are sent home to stay isolated (I_Z, with probability $1-p_H$). A fraction $1-p_T$ of the I_s individuals (those with very mild symptoms) decide not to undertake testing and stay at home (I_H) until

recovery. Both I_Z and I_H individuals eventually recover. The H_L individuals may recover, die (D) or, if they get worse, obtain an oxygen mask (H_K). The oxygenated individuals may recover, die or, if they get even worse, end up on lung ventilators (H_V). Some H_L individuals may even go straight to lung ventilators. Finally, the ventilated individuals either recover or die.

Again, we do not assume dying outside hospitals (that is, when in I_Z or I_H). Also, we do not consider going to a hospital later if initially isolated at home (that is, from I_Z or I_H). In general, the model should also consider any existing upper bounds on the hospital capacities (common beds, oxygen masks and lung ventilators). However, in contrast to Italy where the actual requirements exceeded such upper bounds, this is (so far) not the case in the Czech Republic. Therefore, we do not consider any such upper bounds here. Exceeding such upper bounds would certainly cause many deaths of patients staying at home that would otherwise be hospitalized.

The system of 12 equations comprising both epidemic and hospital layers is now:

$$
\begin{aligned}
S[t+1] &= S[t] - \lambda\, S[t] - L[t]/p_S \\
E[t+1] &= E[t] + \lambda\, S[t] - \sigma\, E[t] + L[t]/p_S \\
I_a[t+1] &= I_a[t] + p_S\, \sigma\, E[t] - \xi\, I_a[t] \\
I_n[t+1] &= I_n[t] + (1-p_S)\, \sigma\, E[t] - \gamma_n\, I_n[t] \\
I_s[t+1] &= I_s[t] + \xi\, I_a[t] - \eta\, I_s[t] - \gamma_s\, I_s[t] \\
I_H[t+1] &= I_H[t] + (1-p_T)\, \eta\, I_s[t] - \gamma_s\, I_H[t] \\
I_Z[t+1] &= I_Z[t] + p_T\, (1-p_H)\, \eta\, I_s[t] - \gamma_s\, I_Z[t] \\
H_L[t+1] &= H_L[t] + p_T\, p_H\, \eta\, I_s[t] - \gamma_l\, H_L[t] \\
H_K[t+1] &= H_K[t] + p_K\, \gamma_l\, H_L[t] - \gamma_k\, H_K[t] \\
H_V[t+1] &= H_V[t] + p_{VL}\, \gamma_l\, H_L[t] + p_V\, \gamma_k\, H_K[t] - \gamma_v\, H_V[t] \\
D[t+1] &= D[t] + p_{DL}\, \gamma_l\, H_L[t] + p_{DK}\, \gamma_k\, H_K[t] + p_{DV}\, \gamma_v\, H_V[t] \\
R[t+1] &= R[t] + (1-p_K-p_{VL}-p_{DL})\, \gamma_l\, H_L[t] + (1-p_V-p_{DK})\, \gamma_k\, H_K[t] + \\
&\quad + (1-p_{DV})\, \gamma_v\, H_V[t] + \gamma_s\, I_Z[t] + \gamma_s\, I_H[t] + \gamma_s\, I_s[t] + \gamma_n\, I_n[t]
\end{aligned}
\tag{3}
$$

The force of infection λ in model (3) needs to account also for the I_H individuals that may not strictly obey home isolation rules:

$$
\lambda = \beta\, \chi\, \frac{r_\beta\, I_n[t] + r_\beta\, I_a[t] + r_C\, I_s[t] + r_C\, I_H[t]}{N[t]} \tag{4}
$$

Now, $N[t]$ is the total population size at time t *except those that have already died.*

Quarantine layer

Currently, quarantine is ordered to anyone that has potentially had a contact with a positively tested individual. Hence, for any newly positively tested individual (that is, an individual entering classes I_Z or H_L), we use the overall contact matrix to calculate the number of contacts (s)he might have within one day. Since contacts are sought for over a period of several days into the past, but at the same time sets of persons encountered over any two subsequent days may overlap (likely I meet my neighbour more frequently than someone in a more distant grocery store), we multiply the number of contacts for one day by an ad hoc scaling factor (currently set to 1.5). We then use multinomial distribution to distribute these encounters into the quarantine classes Q_S, Q_E, Q_{Ia}, Q_{In} (and at the same time subtract them from classes S, E, I_a, I_n), with probabilities (in the respective age classes) $(1-w)S/N$, $(wS+E)/N$, I_a/N, I_n/N, where $N = S+E+I_a+I_n+R$. The weight w accounts for the fact that the infection can be transmitted upon such contact, so that the distribution of states among contacts may be biased towards E in comparison with the distribution of states in the general population; we current use $w = \beta$ and denote the respective total numbers of individuals going to quarantine due to a contact with a positively tested individual at time t as $nq_S[t]$, $nq_E[t]$, $nq_{Ia}[t]$, and $nq_{In}[t]$.

Adding the quarantine classes requires modification of the force of infection:

$$\lambda = \beta\,\chi\,\frac{r_\beta\,I_n[t] + r_\beta\,I_a[t] + r_C\,I_s[t] + r_C\,I_H[t] + r_{CQ}\,Q_{In}[t] + r_{CQ}\,Q_{Ia}[t]}{N[t]} \tag{5}$$

The quarantined exposed individuals then pass the class Q_{In} when asymptomatic for the whole course of infection or the class Q_{Ia} when symptomatic. Since symptomatic, from Q_{Ia} the individuals go to I_s. The quarantined susceptible individuals may become quarantined exposed by meeting an infectious individuals, yet their the force of infection is reduced by a factor r_{CQ}.

Denoting by α the rate at which individuals sent to quarantine as S (hence to class Q_S) return to the class S if not infected in the meantime (in which case they would go to Q_E),

the complete set of 16 state variable equations is thus:

$$
\begin{aligned}
S[t+1] &= S[t] - \lambda\, S[t] + \alpha\, Q_S[t] - L[t]/p_S[t] - nq_S[t] \\
E[t+1] &= E[t] + \lambda\, S[t] - \sigma\, E[t] + L[t]/p_S[t] - nq_E[t] \\
I_a[t+1] &= I_a[t] + p_S\, \sigma\, E[t] - \xi\, I_a[t] - nq_{Ia}[t] \\
I_n[t+1] &= I_n[t] + (1-p_S)\, \sigma\, E[t] - \gamma_n\, I_n[t] - nq_{In}[t] \\
I_s[t+1] &= I_s[t] + \xi\, I_a[t] + \xi\, Q_{Ia}[t] - \eta\, I_s[t] - \gamma_s\, I_s[t] \\
I_H[t+1] &= I_H[t] + (1-p_T)\, \eta\, I_s[t] - \gamma_s\, I_H[t] \\
I_Z[t+1] &= I_Z[t] + p_T\, (1-p_H)\, \eta\, I_s[t] - \gamma_s\, I_Z[t] \\
H_L[t+1] &= H_L[t] + p_T\, p_H\, \eta\, I_s[t] - \gamma_l\, H_L[t] \\
H_K[t+1] &= H_K[t] + p_K\, \gamma_l\, H_L[t] - \gamma_k\, H_K[t] \\
H_V[t+1] &= H_V[t] + p_{VL}\, \gamma_l\, H_L[t] + p_V\, \gamma_k\, H_K[t] - \gamma_v\, H_V[t] \\
D[t+1] &= D[t] + p_{DL}\, \gamma_l\, H_L[t] + p_{DK}\, \gamma_k\, H_K[t] + p_{DV}\, \gamma_v\, H_V[t] \\
R[t+1] &= R[t] + (1-p_K-p_{VL}-p_{DL})\, \gamma_l\, H_L[t] + (1-p_V-p_{DK})\, \gamma_k\, H_K[t] + \\
&\quad + (1-p_{DV})\, \gamma_v\, H_V[t] + \gamma_s\, I_Z[t] + \gamma_s\, I_H[t] + \gamma_s\, I_s[t] + \gamma_n\, I_n[t] + \gamma_n\, Q_{In}[t] \\
Q_S[t+1] &= Q_S[t] - r_{CQ}\, \lambda\, Q_S[t] - \alpha\, Q_S[t] + nq_S[t] \\
Q_E[t+1] &= Q_E[t] + r_{CQ}\, \lambda\, Q_S[t] - \sigma\, Q_E[t] + nq_E[t] \\
Q_{Ia}[t+1] &= Q_{Ia}[t] + p_S\, \sigma\, Q_E[t] - \xi\, Q_{Ia}[t] + nq_{Ia}[t] \\
Q_{In}[t+1] &= Q_{In}[t] + (1-p_S)\, \sigma\, Q_E[t] - \gamma_n\, Q_{In}[t] + nq_{In}[t]
\end{aligned}
\tag{6}
$$

All state variables are summarized in Table 1.

Observation layer

In addition to 16 state variables, we consider also several tracing variables that correspond to cumulative variables or variables related to them. These include the cumulative number of infectious individuals (T_i), the cumulative number of symptomatic individuals (T_s), the actual number of positively tested individuals to be reported (B), the cumulative number of reported positively tested individuals (C), and the number of reported recovered individuals (U). The corresponding equations for these tracing variables are as follows:

$$
\begin{aligned}
T_i[t+1] &= T_i[t] + \sigma\, E[t] + \sigma\, Q_E[t] \\
T_s[t+1] &= T_s[t] + \xi\, Ia[t] + \xi\, Q_{Ia}[t] \\
B[t+1] &= B[t] + p_T\, \eta\, I_s[t] + \tau[t]\, (I_a[t] + I_n[t]) - \kappa[t]\, B[t] \\
C[t+1] &= C[t] + \kappa[t]\, B[t] \\
U[t+1] &= U[t] + (1-p_K-p_{VL}-p_{DL})\, \gamma_l\, H_L[t] + (1-p_V-p_{DK})\, \gamma_k\, H_K[t] + \\
&\quad + (1-p_{DV})\, \gamma_v\, H_V[t] + \gamma_s\, I_Z[t]
\end{aligned}
\tag{7}
$$

Here, κ is the publication rate and τ is a time-varying rate of testing in the general

population (currently set to 0, so actually having no effect). All tracing variables are summarized in Table 1.

Age structure

As the novel coronavirus is known to have different virulence in children, adults and seniors, we distinguish three age classes: 0-19 years (children), 20-64 years (adults), and 65+ years (seniors). These classes interact via the force of infection, since all age classes contribute to the force of infection of any susceptible individual of any age class; both β and χ are thus actually matrices of type 3×3, referred to below as transmission matrix and contact matrix, respectively. Once infected, individuals of each age class go through the system independently of individuals of the other age classes. Equations for the state variables E to R of model (6) are thus mirrored for each age class, as well as equations for all tracing variables. Many model parameters are age-specific and thus actually vectors composed of three elements, each corresponding to one age class. Also, since age is specified for each imported case, we can easily assign it to the appropriate age class. Finally, since we know age class of each positively tested case as well as the numbers of contacts with people from individual age classes, the numbers of quarantined individuals are also calculated for each age class.

Space structure

The Czech Republic is geographically divided into well-defined 206 counties. For each county, the population size and its distribution into the three age classes is known. Moreover, a 206×206 mobility matrix is specified that gives daily mobility patterns of individuals between all pairs of counties (numbers of individuals travelling per day from one county to another). Due to lack of age-specific data, this matrix is identical for all three age classes. The actual movement of individuals between counties is modelled using multinomial distribution to place a given number of travellers leaving one county into the other ones. Only individuals from classes S, E, I_a, I_n, and R can travel in our current model version, unless interventions are implemented to limit their movemet, too (see below). So, in each time step corresponding to one day, the age-structured extension of model (6) is first run (independently) in each county, followed by application of the mobility matrix to the updated county populations. Regarding the imported cases in the initial phase of epidemic, we have information about the region each case comes from, so we assign a random county from the corresponding region for each such case.

Data description

The mobility matrix is a 206×206 matrix that describes daily mobility patterns of individuals between all pairs of counties (numbers of individuals travelling daily from one county to another), currently assumed the same for each age class (because of lack of age-specific data). The matrix is constructed by averaging mobility patterns obtained from telecommunication companies across two weeks. Two such matrices are used, one representing normal state using data from January 2020, and the other representing intervention state using data from second half of March 2020.

The parameter χ in model (6) becomes a 3×3 contact matrix that describes the mean number of other individuals of an age class any individual of an age class has a contact with per day. Prem et al. (2017) published this matrix for 152 countries, including the Czech Republic. Moreover, they calculated it as a sum of four specific contact matrices describing numbers of contacts at home, school, work, and other types of contacts. We exploit this division when defining impacts of various realistic intervention strategies.

Data on the course of epidemic in the Czech Republic are taken from the Johns Hopkins University cumulative data repository at `https://github.com/CSSEGISandData/COVID-19/tree/master/csse_covid_19_data/csse_covid_19_time_series`.

Model calibration

Values of several model parameters are quite uncertain, of which the transmissibility matrix, the probability p_S of becoming symptomatic after a short asymptomatic period, and the probability p_T of not undertaking testing despite becoming symptomatic are among the most important. The transmission matrix is a 3×3 matrix that describes the probability of infection transmission upon contact between an individual of an age class with an individual of an age class. In any epidemiological model, this is the least accessible parameter from the perspective of easily setting it up. We assume all nine elements of this matrix are identical and denoted as β. The main motivation for keeping it as a 3×3 matrix is that various intervations may impact various of its elements differently.

These and also some other uncertain model parameters are estimated by fitting the tracing variable C to the time series on the reported cumulative numbers of confirmed cases and the variable D to the time series on the reported numbers of dead cases. We use the Approximate Bayesian Computation (ABC) with rejection sampling algorithm based on Euclidean distance to perform the fit. The fitting is performed across 1000 runs of the model with uncertain parameter values generated from their prior distributions, and posterior values of those parameters are selected based on 0.005 tolerance (i.e. five best realizations out of 1000 are selected). The specific parameter values from these five realizations are used for visual inspection of model uncertainty. The very best realization is then used for

exploring the exit scenarios discussed above.

The list of uncertain parameters estimated by the ABC is given in Table 6, together with their corresponding prior distributions. This table also shows the parameter values for the five best realizations out of 1000 runs within this statistical procedure.

Interventions

Several interventions are tested for their effect on the course of epidemic in the Czech Republic. We summarize the options here. We start with interventions that are actually (as on April 15, 2020) in operation in the Czech Republic:

Closing schools This happend on March 11, 2020. Here we exploit the fact that the contact matrix is divided into four matrices that add up to form the total one: contacts at home, school, work, and other types of contacts. We thus assume that the school contact matrix is reduced by a factor $r_{C\,\mathrm{School}}$ to nearly zero. Since some parents then decided to place their kids with grandparents, to continue going to work, we assume this also somewhat increased elements [1,3] and [3,1] of the home contact matrix, by a factor $r_{C\,\mathrm{Home1}}$.

Contact limitations This intervention, set by the government on March 16, 2020, and setting travel restrictions, avoiding unnecessary contacts and closing many shops and all restaurants, is modelled as a decrease in the matrix of other contacts by a factor $r_{C\,\mathrm{Other}}$. The geographic mobility is limited by using the intervention mobility matrix instead of the normal one. Following contact limitation, many employers allowed, recommended or even ordered many workers to stay at home, on home office or vacation. Also, many parents were forced to stay home with their small kids, as well as many people due to closing many shops and all restaurants. This generally resulted in a decrease in the work contact matrix by a factor $r_{C\,\mathrm{Work}}$ but in an accompanying increase in the home contact matrix by a factor $r_{C\,\mathrm{Home2}}$.

Protection This measure includes wide use of desinfection, wearing face masks on public, and keeping inter-individual distance of more than 2 metres on public. This measure was widely activated on March 18, 2020, and since then we assume that all elements of the transmission matrix are reduced by a given factor $r_{\beta\,\mathrm{Protection}}$.

We include all these interventions in the model to describe the actual package of interventions, and use the time series of the cumulative number of confirmed cases and the number of dead individuals to estimate the (relatively) unknown parameters (see the section on model calibration below). The intervention parameters and their values roughly corresponding to the actual state are given in Table 5.

With this baseline scenario of continuing lockdown set up, we apply several modifications to it. In particular, since the current measures impact the economy of the Czech Republic as well as mental health of their inhabitants, the government aims at weakening or even exiting some of the interventions. We model several plausible strategies that are discussed in this respect.

School closure mitigation We assume opening schools since May 15, 2015. Thus, we set $r_{C\,\mathrm{School}}$ and $r_{C\,\mathrm{Home1}}$ to 1. We also assume that protection measures cannot be fully kept, especially with younger children, and we thus increase $r_{\beta\,\mathrm{Protection}}$ for children from 0.2 to 0.6. The other values in Table 5 are kept unchanged.

Removing all interventions, except for seniors We switch all interventions off since June 1, 2020, leaving contact limitations and protection only for people of age 65 and more. This means keeping the intervention mobility matrix for elderly, keeping the reduction in the third row and third column of the contact matrix by a factor s_C (0.2), and keeping the reduction in the third column (unlike contact reduction, transmission reduction is not symmetric) of the transmissibility matrix by a factor s_β (0.2). Actually, it means keeping these factors at values applied for everyone in the full lockdown.

References

[1] Ferguson et al. (2020) Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. Available at

`www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf`.

[2] Di Domenico et al. (2020) Expected impact of lockdown in Île-de-France and possible exit strategies.

Available at `www.epicx-lab.com/uploads/9/6/9/4/9694133/inserm-covid-19_report_lockdown_idf-20200412.pdf`.

Notation	Description
S	Susceptible individuals
E	Exposed individuals
I_n	Asymptomatic individuals for the whole course of infection
I_a	Asymptomatic individuals before becoming symptomatic
I_s	Symptomatic individuals
I_Z	Positively tested individuals isolated at home
I_H	Symptomatic individuals that avoided testing and are at home
H_L	Positively tested individuals hospitalized at a common bed
H_K	Hospitalized individuals on oxygen
H_V	Hospitalized individuals on ventilator
R	Recovered individuals
D	Dead individuals
L	Number of importation cases at the beginning of epidemic
Q_S	Quarantined susceptible individuals
Q_E	Quarantined exposed individuals
Q_{In}	Quarantined asymptomatic individuals for the whole course of infection
Q_{Ia}	Quarantined asymptomatic individuals before becoming symptomatic
T_i	Cumulative number of infectious individuals
T_s	Cumulative number of symptomatic individuals
B	Positively tested individuals to be reported
C	Cumulative number of reported positively tested individuals
U	Number of reported recovered individuals

Table 1: List of state and tracing variables used in the model.

Data description	Children	Adults	Seniors	Notation	Reference
Duration of exposed period	5.1	5.1	5.1	d_E	[1]
Duration of permanent asymptomatic period	14	14	14	d_N	WHO, 7 in [1]
Duration of asymptomatic period before symptoms	1	1	1	d_A	0.5 in [1]
Duration of recovery period when home	14	14	14	d_S	WHO, 6.5 in [1]
Duration of period between symptoms and test results	3	3	3	d_T	variable
Duration of recovery period when on hospital bed	21	21	21	d_L	WHO (up to 6 weeks)
Duration of recovery period when on oxygen	28	28	28	d_K	WHO (up to 6 weeks)
Duration of recovery period when on lung ventilator	35	35	35	d_V	WHO (up to 6 weeks)
Duration of quarantine period	14	14	14	d_Q	Governmental policy
Duration of publication of test results	1	1	1	d_P	variable

Table 2: List of epidemiological data (part 1) – numbers in days.

Data description	Children	Adults	Seniors	Notation	Reference
Probability of an individual becoming symptomatic	0.5	0.5	0.5	p_S	subject to calibration
Probability of becoming hospitalized	0.01	0.15	0.25	p_H	[2]
Probability of showing self to system	0.8	0.8	0.8	p_T	subject to calibration
Proportion of hospitalized on bed going to oxygen	0.05	0.08	0.57	p_K	[1]
Proportion of hospitalized on bed going to ventilator	0.05	0.05	0.05	p_{VL}	ad hoc
Proportion of hospitalized on oxygen going to ventilator	0.4	0.4	0.4	p_V	ad hoc
Proportion of hospitalized on bed that die	0.001	0.055	0.39	p_{DL}	[2], subject to calibration
Proportion of hospitalized on oxygen that die	0.01	0.13	0.45	p_{DK}	[2], subject to calibration
Proportion of hospitalized on ventilator that die	0.01	0.13	0.45	p_{DV}	[2]
Proportional infectivity reduction in asymptomatic individuals	0.5	0.5	0.5	r_β	[2]
Proportional contact reduction in symptomatic individuals	0.5	0.5	0.5	r_C	ad hoc
Proportional contact reduction in quarantined individuals	0.2	0.2	0.2	r_{CQ}	ad hoc

Table 3: List of epidemiological data (part 2).

Notation	Description	Relationship to data
σ	Rate of leaving E class	$1-\exp(-d_E)$
ξ	Rate of leaving I_a class	$1-\exp(-d_A)$
γ_n	Rate of recovery from I_n	$1-\exp(-d_N)$
γ_s	Rate of recovery from I_s, I_Z, I_H	$1-\exp(-d_S)$
γ_l	Rate of recovery from H_L	$1-\exp(-d_L)$
γ_k	Rate of recovery from H_K	$1-\exp(-d_K)$
γ_v	Rate of recovery from H_V	$1-\exp(-d_V)$
α	Rate of leaving QS to S	$1-\exp(-d_Q)$
η	Rate of passing testing	$1-\exp(-d_T)$
κ	Test results publication rate	$1-\exp(-d_P)$

Table 4: List of model parameters.

Parameter	Value
$r_{C\,\mathrm{School}}$	0.01
$r_{C\,\mathrm{Home1}}$	1.2
$r_{\beta\,\mathrm{Protection}}$	0.2
$r_{C\,\mathrm{Other}}$	0.2
$r_{C\,\mathrm{Work}}$	0.5
$r_{C\,\mathrm{Home2}}$	1.2

Table 5: List of intervention parameters and their values roughly corresponding to the actual state.

Parameter	Prior distribution	1st	2nd	3rd	4th	5th
β	Uniform between 0.1 and 0.9	0.39	0.36	0.39	0.4	0.37
d_S	Discrete values 6, 8, 10, 12, 14, 16	8	12	10	6	12
p_S	Discrete values 0.1, 0.3, 0.5, 0.7, 0.9	0.1	0.5	0.9	0.1	0.7
p_T	Discrete values 0.5, 0.7, 0.9	0.5	0.5	0.5	0.7	0.7
p_{DL} adults	Uniform between 0.02, 0.4	0.17	0.27	0.26	0.16	0.28
p_{DL} seniors	Uniform between p_{DL} adults and 0.4	0.36	0.28	0.39	0.25	0.32
p_{DK} adults	Uniform between 0.02 and 0.5	0.04	0.094	0.17	0.15	0.49
p_{DK} seniors	Uniform between p_{DK} adults and 0.5	0.33	0.47	0.22	0.27	0.49

Table 6: List of parameters fitted by the ABC, together with their prior distributions.