

Model H: Predicting dynamics of hospitalized COVID-19 patients

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The Czech Republic is facing the second wave of COVID-19 epidemic, with the rate of growth in the number of confirmed cases (among) the highest in Europe. This raises concerns about whether our public health system will be able to cope with a potential inflow of patients that would need to be hospitalized or even require an intensive care. The aim of Model H is to predict dynamics of the numbers of actually hospitalized individuals, the actual numbers of patients in a severe state and hence in need of ICU, and the cumulative numbers of deaths due to COVID-19. Model H is a variant of the classic SEIR model. It exploits data from sociological surveys to modulate the presumed numbers of inter-personal contacts and a degree of personal protection, and uses expectations on changes in these numbers for making predictions. Therefore, it is structured by the types of contact and consists of an epidemic layer and a hospital layer.

Epidemic layer The epidemic model is a variant of the classic SEIR model. Due to contacts with infectious individuals, susceptible individuals (S) may become exposed (E), that is, infected but not yet infectious. The exposed individuals then become asymptomatic for the whole course of infection (I_a , with probability $1 - p_S$) or presymptomatic for just a short period of time before becoming symptomatic (I_p , with probability p_S). The I_p individuals later become symptomatic (I_s), reducing their contacts with others by a factor r_C . The I_a individuals eventually recover (R).

Hospital layer A proportion p_H of symptomatic individuals (those with relatively severe symptoms) are hospitalized (H). The remaining proportion $1 - p_H$ of symptomatic individuals (those that have only mild symptoms) are sent home to stay there (I_z) until

recovery. Hospitalized individuals follow two different pathways. After some time spent on a common hospital bed, a proportion p_J of them require intensive care (J). While those that do not need intensive care (H_R) eventually recover, those that do either die (D) with probability p_D or recover with probability $1 - p_D$.

Model equations Considering discrete time, with one time step corresponding to one day, our model consists of the following system of equations:

$$\begin{aligned}
S[t + 1] &= S[t] - \lambda S[t], \\
E[t + 1] &= E[t] + \lambda S[t] - \sigma E[t], \\
I_a[t + 1] &= I_a[t] + (1 - p_S) \sigma E[t] - \gamma_A I_a[t], \\
I_p[t + 1] &= I_p[t] + p_S \sigma E[t] - \xi I_p[t], \\
I_s[t + 1] &= I_s[t] + \xi I_p[t] - \alpha_I I_s[t], \\
H[t + 1] &= H[t] + p_H \alpha_I I_s[t] - \alpha_H H[t], \\
I_z[t + 1] &= I_z[t] + (1 - p_H) \alpha_I I_s[t] - \gamma_Z I_z[t], \\
J[t + 1] &= J[t] + p_J \alpha_H H[t] - \alpha_J J[t], \\
H_R[t + 1] &= H_R[t] + (1 - p_J) \alpha_H H[t] - \gamma_H H_R[t], \\
D[t + 1] &= D[t] + p_D \alpha_J J[t], \\
R[t + 1] &= R[t] + \gamma_H H_R[t] + \gamma_A I_a[t] + \gamma_Z I_z[t] + (1 - p_D) \alpha_J J[t].
\end{aligned} \tag{1}$$

The model parameters σ , ξ , $\alpha_{I/H/J}$, and $\gamma_{A/Z/H}$ represent probabilities at which individuals leave the respective model classes. They are related to the mean duration an individual spends in each such class (Table 1). All model variables are summarized in Table 2.

The force of infection λ in the model (1) sums contributions from all infectious classes, that is, I_a , I_p , I_s , and I_z :

$$\lambda = \beta C \frac{r_\beta I_a[t] + r_p I_p[t] + r_C I_s[t] + r_C I_z[t]}{N[t]}. \tag{2}$$

Here, β is the probability of infection transmission upon (sufficiently close and lengthy) contact between susceptible and infectious individuals, C is the contact rate (the mean number of other individuals an individual has an effective contact with per day), r_β is a factor reducing the infection transmission probability for an a/presymptomatic individual relative to a symptomatic one, r_C is a factor reducing the contact rate of a symptomatic individual relative to an a/presymptomatic one (having symptoms should force an individual to reduce contacts with others, but not completely), and $N[t]$ is the total population size at time t , except dead, those in hospitals and symptomatic that do not move (these latter types of individuals are not expected to encounter susceptible ones). All parameters that need to be specified to run the model are given in Table 3.

Notation	Description	Relationship to delays
σ	Rate of leaving E class	$1 - \exp(-1/d_E)$
ξ	Rate of leaving I_p class	$1 - \exp(-1/d_{I_p})$
α_I	Rate of leaving class I_s	$1 - \exp(-d_{I_s})$
α_H	Rate of leaving class H	$1 - \exp(-1/d_{HJ})$
α_J	Rate of leaving class J	$1 - \exp(-1/d_J)$
γ_A	Rate of leaving class I_a for recovery	$1 - \exp(-1/d_{I_a})$
γ_Z	Rate of leaving class I_z for recovery	$1 - \exp(-1/d_{I_z})$
γ_H	Rate of leaving class H_R for recovery	$1 - \exp(-1/d_{H_R})$

Table 1: Probabilities of leaving particular model classes calculated from average times spent in those classes.

Notation	Description
S	Susceptible individuals
E	Exposed individuals
I_a	Asymptomatic individuals for the whole course of infection
I_p	Presymptomatic individuals before becoming symptomatic
I_s	Symptomatic individuals
I_z	Symptomatic individuals staying at home
H	Hospitalized individuals before ICU (non)admission
H_R	Hospitalized individuals that do not go to ICU
J	Hospitalized individuals on ICU
D	Dead individuals
R	Recovered individuals

Table 2: List of state variables used in the model.

While the above model development is quite straightforward and follows the common practice in composing epidemiological compartmental models, the hard part follows and needs to resolve the following issues.

Initial conditions Our simulation starting date is August 31, 2020, a date around which the second wave presumably begins and also is Monday (sociological data described below are provided for calendar weeks). Whereas initial values of many state variables can be estimated from observed data, some are not available and need to be estimated through model calibration. These are the variables E , I_a , I_p , I_s , and I_z . Calibration procedure we use is described below.

Types of contact The daily number of efficient contacts C is a composed of sum four types of contact: contacts at home, work, school, and in the community. Estimates of

the prepandemic numbers of these contacts are for many countries, including the Czech Republic, provided in Prem et al. (6). The numbers aggregated across all age cohorts considered by Prem et al. (6) are $C_H = 3.19$ (home), $C_W = 1.99$ (work), $C_S = 2.39$ (school), and $C_C = 3.55$ (community). Each of these numbers is weighted by a proportional reduction factor that changes every week, depending on the adopted interventions and in particular on their compliance by people, using sociological data from public opinion polls organized by the PAQ Research agency (www.zivotbehempandemie.cz).

Model calibration Whereas some model parameters can be taken from the literature or estimated from data provided by the Institute of Health Information and Statistics of the Czech Republic (“IHIS CR”); www.uzis.cz, the others, such as the transmission probability β , are uncertain and need to be obtained by model calibration. To estimate this and some other model parameters, listed in Table 3, we used the Approximate Bayesian Computation (ABC), a technique used to estimate parameters of complex Markov models in genomics and other biological disciplines (1, 3), including epidemic modeling (2, 5). As the observed summary statistics we used the actual numbers on ICUs (J), cumulative numbers of deaths (D), and actual numbers of hospitalized ($H + H_R + J$). We compared the simulated summary statistics with the observed ones, using the the sum squares of their distance. To apply the ABC technique, we use the `abc` package in R (4), modified to work with non-normalized summary statistics.

Predictive scenarios To make predictions of dynamics of hospitalized COVID-19 patients beyond the current date, we need to formulate alternative hypotheses on how people will behave in the near future, in terms of proportional reductions of the various types of contact and a degree of obedience of personal protective measures (wearing face masks, using disinfection, etc.).

References

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Parameter	Notation	Value
Transmission probability	β	uniform on [0.01, 0.66]
Proportional reduction of β in a/presymptomatic individuals	r_β	uniform on [0.4, 0.99]
Proportional reduction of the number of contacts C in symptomatic individuals	r_C	uniform on [0.01, 0.5]
Proportion symptomatic	p_S	uniform on [0.5, 0.99]
Proportion hospitalized among symptomatic	p_H	0.055
Proportion on ICU among hospitalized	p_J	normal, mean 0.23, sd 0.1
Proportion dying on ICU	p_D	normal, mean 0.49, sd 0.1
Latent period	d_E	6.31
Time to recovery when asymptomatic	d_{I_a}	9.38
Presymptomatic period	d_{I_p}	3.63
Symptomatic period	d_{I_s}	4.8
Time from hospital to ICU admission	d_{HJ}	1.92
Recovery time when symptomatic at home	d_{I_z}	1.95
Time on ICU	d_J	4.38
Time from ICU non-admission to recovery	d_{JR}	3.03

Table 3: Quantities needed to parameterize Model H. Numbers provided in this table are based on data provided by The Institute of Health Information and Statistics of the Czech Republic (“IHIS CR”); www.uzis.cz; mean values are provided over the period from September 1, 2020 until present. Times are presented in days. The indicated distributions are prior distributions for the calibration procedure, and are based on the literature.