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A compartmental epidemiological model applied to the Covid-19 epidemic

Anne-Flore Baron[2], Olivier Boulant[1], Ivan Panico[2], Nicolas Vayatis[1]

[1] Université Paris-Saclay, ENS Paris-Saclay, CNRS, Centre Borelli, 94235 Cachan, France
[2] onepoint, 29 rue des Sablons, 75116 Paris, France

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Abstract

The objective of this work is to provide a sophisticated but accessible compartmental epidemic model. Our algorithm is highly inspired from the compartmental model developed by Sofonea and al [7]. This model has been used as a reference for several working groups in France during the Covid-19 crisis. Each individual is allocated to a compartment according to her age, her current state with respect to the disease, as well as the length of time she has been in that state. The model then reproduces the mechanisms of transition from one state to another: mathematically, this translates into a system of recurrence relations. It captures how much individuals interact with one another through a parameter that estimates compliance with hygiene measures and lifestyle habits. The present work aims to make the code available and give control to users so that they are able to test the model in total transparency. Focus has been put on reproducibility and explanation of the various parameters. The hard-coded parameters correspond to the data for the Covid-19 epidemic in France.

Source Code

The reviewed source code and documentation for this algorithm are available from the web page of this article[1]. Usage instruction are included in the `readme.md` file of the archive.

Keywords: COVID-19, prediction model, compartmental model, contact factor

[1] http://www.ipol.im/

1 Introduction

In the context of the Covid-19 crisis, epidemics models have been in the spotlight since they have been considered to support government decisions to contain the propagation of the virus. When the first wave of contagion reached Western Europe, the model elaborated by the team of N. Ferguson at Imperial College [8] was foreseen as a realistic model to provide forecasts on the number of casualties depending on a series of parameters (characteristics of the pandemic, sociodemographic data of the population, behavior of citizens, structure of their contact network, etc.). In the early days of the contagion in France, the use of such a model was discarded by the authorities, first because of its complexity, and second, because it required the input of many parameters which were not available with sufficient accuracy at the time. Inspired from another category of epidemic models, merely known as compartmental models, some other propositions emerged in France in order to provide tools for the policy-makers while taking into account the features of the present pandemic. The most discussed propositions were those of three teams: Institut Pasteur ([6]), INSERM ([3]), Université de Montpellier - ETE team ([4], [7]). These three approaches are sophisticated variants of the well-known SIR (Susceptible-Infected-Recovered) or the SEAIR (Susceptible-Exposed-Asymptomatic-Infected-Recovered). However, none of these teams has provided access to open source implementation of the proposed models, therefore reducing the capacity to reproduce the results. In the present work, we propose a reproducible version of an SEAIR model which follows the principles described in [7] with a finer description of compartments and including divisions with respect to age groups and duration of stay in certain compartments.

2 A compartmental model with age and time subdivisions

2.1 A compact view of the model

The model developed in [7] proposes to consider an extension to the plain SEAIR model by adding extra compartments to better account the propagation process of the pandemic at the national or regional level. The compartments introduced in their model are the following:

- S (Susceptible),
- J (Non critical infectious),
- Y (Critical infectious: it designates individuals whose life is threatened by the disease. They will need to be hospitalized at some point.),
- W (Other critical hospitalized patients: it designates critical infectious individuals who will not benefit from a long stay in ICU. They will die either after a short stay in ICU or in another ward.),
- H (Long-stay ICU hospitalized: it designates critical infectious individuals who are admitted to the intensive care unit for a long stay - at least one day. After their long-stay in ICU, they may either die or recover.),
- R (Recovered immunized),
- D (Dead).

Furthermore, all these compartments are subdivided according to age groups. Moreover, compartments J, Y, H and W also include subdivisions according to the length of time the individual has

remained in that state. This subdivision allows to take into account the susceptibility of different age groups to the virus, as well as the time dimension in the evolution of the disease. The model is described schematically in Figure 1.

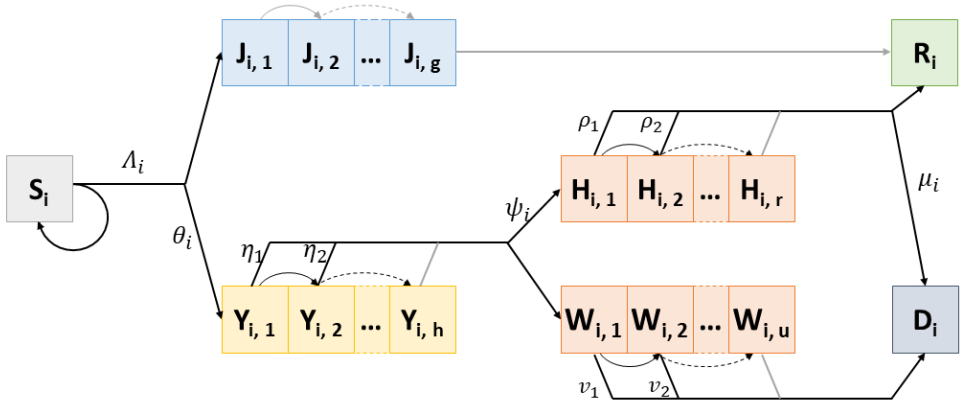


Figure 1: A compact view of the dynamics of the model. S stands for susceptibles, J for non critical infectious, Y for critical infectious, H for people in ICU, W for other critical hospitalized patients, R for recovered, D for deaths. Each compartment is duplicated for each age group, designated by subscript i. Subscripts i, j indicate the age group i and the length of the current state j. Values above arrows indicate the rate of passage from the associated compartments. All these transition probabilities are fixed, except for the force of the infection Λ_i calculated from the density of infected people J+Y among the susceptible population S.

The objective of the present work is to provide a user's guide for this type of compartmentalized model, for which numerous parameters are needed. Estimation of those parameters can be complicated due to the diversity of data made available and their granularity.

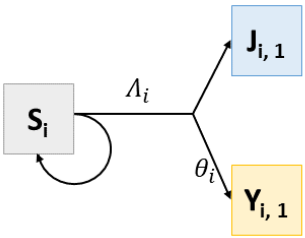
2.2 Key parameters of the epidemic model

2.2.1 Age groups

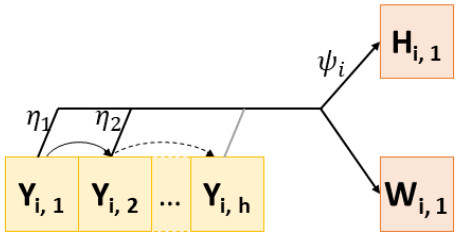
The first parameters to be set are the age groups. The sub-division of the population according to their age enables us to take into account their different sensitivities to the disease and the variability of their exposure to it. Thus, the branching probabilities described below as well as the contact factor will vary according to age groups.

2.2.2 Branching probabilities

These probabilities determine the ratio of individuals at a fork between two possible compartments. Their role is detailed on figure 2 with the corresponding equations. The index i of each variable relates to an arbitrary age group. For each compartment Q, Q' stands for $Q(t+1)$, the daily update of the variable $Q = Q(t)$.



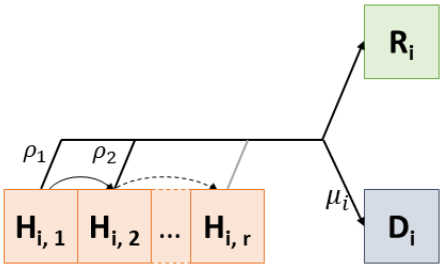
(a) θ_i: proportion of critical infected $Y_{i,1}$ among the $\Lambda_i S_i$ newly infected individuals.



(b) ψ_i: proportion of admissions in ICU $H_{i,1}$ among the $\sum_{k=1}^{h} \eta_k Y_{i,k}$ newly hospitalized critically infected individuals.

$$J'_{i,1} = (1-\theta_i)\Lambda_i S_i$$
$$Y'_{i,1} = \theta_i \Lambda_i S_i$$

$$H'_{i,1} = \psi_i \sum_{k=1}^{h} \eta_k Y_{i,k}$$
$$W'_{i,1} = (1-\psi_i) \sum_{k=1}^{h} \eta_k Y_{i,k}$$



(c) μ_i: proportion of deaths D_i among the $\sum_{k=1}^{r} \rho_k H_{i,k}$ individuals out of ICU.

$$R'_i = R_i + J_{i,g} + (1-\mu_i) \sum_{k=1}^{r} \rho_k H_{i,k}$$
$$D'_i = D_i + \sum_{k=1}^{u} \upsilon_k W_{i,k} + \mu_i \sum_{k=1}^{r} \rho_k H_{i,k}$$

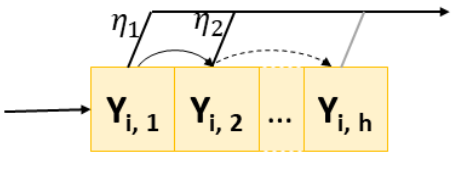
Figure 2: Segments of Figure 1
to illustrate the role of branching probabilities.

- θ_i is the ratio of critical infected Y among all infected individuals $Y+J$, also called critical illness frequency. Its purpose is illustrated in figure 2(a).
- ψ_i is the ratio of individuals H among all hospitalized individuals $H+W$ who are admitted to intensive care for more than one day. ψ_i is also called long-stay ICU admission frequency. Its purpose is illustrated in figure 2(b).
- μ_i is the ratio of dead individuals D among individuals discharged from ICU $D+R$, also called long-stay ICU fatality rate. Its purpose is illustrated in figure 2(c).

These ratios strongly depend on the age groups i. The age groups and these ratios (except μ_i) are computed from other metrics. The proposed values can be found in Table 1.

2.2.3 Interval distributions

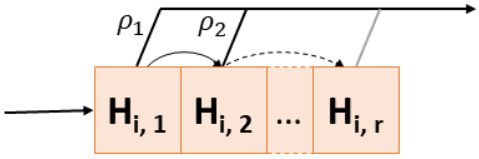
Every day step of the simulation, the states are updated. The interval distributions determine whether an individual transitions to a new state or stays in the same one by moving on to the next time sub-division within this same state. The update method is not the same for all time sub-divided states. Namely :



(a) η_k: Probability for an individual critically infected for k days to be hospitalized.

$\sum_{k=1}^{h} \eta_k Y_{i,k}$ individuals out of Y each day.

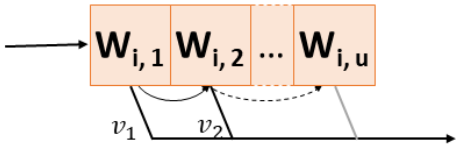
$Y'_{i,k} = (1-\eta_{k-1})Y_{i,k-1} \quad 1 < k \leq h$



(b) ρ_k: Probability for an individual in ICU for k days to leave ICU.

$\sum_{k=1}^{r} \rho_k H_{i,k}$ individuals out of H each day.

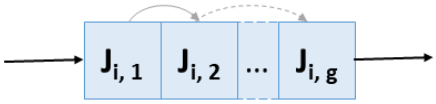
$H'_{i,k} = (1-\rho_{k-1})H_{i,k-1} \quad 1 < k \leq r$



(c) v_k: Probability for a critical individual hospitalized in a non intensive care unit for k days to die.

$\sum_{k=1}^{u} v_k W_{i,k}$ individuals out of W each day.

$W'_{i,k} = (1-v_{k-1})W_{i,k-1} \quad 1 < k \leq u$



(d) Individuals in J stay there for a fixed period of time g. They move deterministically from one time sub-compartment to the next one.

$J_{i,g}$ individuals out of J each day.

$J'_{i,k} = J_{i,k-1} \quad 1 < k \leq g$

Figure 3: Segments of Figure 1
to illustrate the role of interval distributions.

- Individuals in Y, H or W remain in these compartments for variable durations. It is then necessary to determine for each of these compartments, a probability distribution that associates to the current time of the state, the probability of leaving it. This distribution will also determine the maximum duration of each state h, r and u (for Y, H and W respectively). The transitions of Y, H and W time sub-divisions are depicted respectively in figures 3(a), 3(b) and 3(c).
- Individuals in J remain in this state until they are no longer considered contagious. For the sake of simplicity, the average probability of contamination according to the time since infection have been considered: it is the generation time distribution ζ. It results in a fixed duration g of the J-state for all individuals. The transitions of J sub-divisions are depicted in figure 3(d).

For states that do not include time sub-divisions, the update method is simpler:

- The transition probability of S depends on the force of infection Λ_i (definition 1).
- R and D are stable states. Individuals in these states remain in them. This assumes that a recovered individual cannot be re-infected. This remains a daring hypothesis in view of current knowledge of the disease ([1, 9]).

At the end, the only compartments that require interval distributions are Y, H and W.

Definition 1. *The **force of infection** Λ_i is the probability of being infected for a susceptible individual in age group i. This value is calculated from the current state of the population and the transmission parameters.*

2.2.4 Transmission parameters

For the computation of force of infection Λ_i mentioned above, some additional parameters are needed. These are the transmission parameters:

- ζ_k, the generation time distribution (definition 2),
- $\mathcal{R}_0$, the basic reproduction number (definition 3),
- $c_i(t)$, the contact factor (definition 4).

Definition 2. *The **generation time distribution** ζ_k is the distribution of the delay between the onset of the disease in one individual and its transmission to another one.*

Definition 3. *The **basic reproduction number** $\mathcal{R}_0$ used in this model is the number of secondary infections generated by an infected individual during her entire infectious period at the onset of the epidemic. It is then adjusted by the contact factor.*

Definition 4. *The **contact factor** $c_i(t)$ is a a time-dependant behavioral parameter for each age group, which depends mostly on the political measures and the behavior of the population. This parameter will temper the basic reproduction number $\mathcal{R}_0$. The closer the contact factor is to 0, the lower the force of infection. The aim of this parameter is to take into account within the dynamics of the epidemic, the temporal variations in exposure to the virus of the different age groups.*

2.3 System of recurrence relations

The system of recurrence relations corresponding to the model is given below. Identically to previous notations, $Q' = Q(t+1)$ refers to the next daily value of the Q compartment. Figure 1 provides a schematic view of the model for an arbitrary age group i, where the rate from one compartment to another is indicated above the corresponding arrow.

$$
\begin{aligned}
S_i' &= (1-\Lambda_i)S_i \\
J_{i,1}' &= (1-\theta_i)\Lambda_i S_i & J_{i,k}' &= J_{i,k-1} & 1 < k \leq g \\
Y_{i,1}' &= \theta_i \Lambda_i S_i & Y_{i,k}' &= (1-\eta_{k-1})Y_{i,k-1} & 1 < k \leq h \\
H_{i,1}' &= \psi_i \sum_{k=1}^{h} \eta_k Y_{i,k} & H_{i,k}' &= (1-\rho_{k-1})H_{i,k-1} & 1 < k \leq r \\
W_{i,1}' &= (1-\psi_i) \sum_{k=1}^{h} \eta_k Y_{i,k} & W_{i,k}' &= (1-v_{k-1})W_{i,k-1} & 1 < k \leq u \\
R_i' &= R_i + J_{i,g} + (1-\mu_i) \sum_{k=1}^{r} \rho_k H_{i,k} \\
D_i' &= D_i + \sum_{k=1}^{u} v_k W_{i,k} + \mu_i \sum_{k=1}^{r} \rho_k H_{i,k}
\end{aligned}
$$

The force of infection Λ_i is computed for each age group. For a susceptible individual of group i exposed at date t, it corresponds to the daily probability of being infected. To estimate it, we begin by calculating $\bar{I}(t)$, the density of contagious individuals in the non-hospital community, weighted by the degree of social distancing of each group $c_i(t)$ (ranging from a simple barrier gesture to total confinement) as well as the degree of contagiousness corresponding to the time elapsed since the beginning of the infection ζ_k of the individuals.

$$\bar{I}(t) = \sum_i c_i \sum_k \zeta_k (J_{i,k} + Y_{i,k})$$

The force of infection can then be deduced from this:

$$\Lambda_i := \frac{\bar{I}(t)}{\frac{\mathcal{S}_0}{c_i(t)\mathcal{R}_0} + \bar{I}(t)}$$

This system of recurrence relations has an advantage over regular ODEs in the sense that it does not require resolution by integration: next day's reports can be calculated directly from the previous day.

3 Value recommendations for key parameters

In order to run an experiment, some parameters are hard-coded or computed from others:

- age groups,
- branching probabilities.

The user can also select the following parameters:

- ICU fatality rate (used to compute some branching probabilities)
- interval distributions,
- transmission parameters,
- a set of initial conditions.

3.1 Age groups

It is crucial to differentiate between age groups that respond unequally to the disease and are targeted differently by political measures (school closure, remote work...). The choice of age groups should be made in such a way that:

- it is possible to differentiate groups affected by different policy measures,
- data is available to compute the branching probabilities for each group.

The ETE team [7] chose 3 age groups: $0-24$, $25-64$ and $65+$. Then the branching probabilities were computed by extrapolating data from other age groups. To avoid as much as possible extrapolation, we have chosen the most common age groups in the data, that is : $0-19$, $20-29$, $30-39$, $40-49$, $50-59$, $60-69$, $70-79$, $80+$.

3.2 Branching probabilities

We need to find three branching probabilities:

- θ_i: critical illness frequency
- ψ_i: long-stay ICU admission frequency among critically infected individuals
- μ_i: long-stay ICU fatality rate

The long-stay ICU admission frequency among critically infected individuals ψ_i is not a value we can directly find in public data. We compute the three branching probabilities in a similar way as [7], based on four other metrics (estimated for each age group i):

- Infection Fatality Rate (IFR): death probability among all infected individuals
- Proportion of hospitalized patients - critical or not - admitted in ICU u_i
- Death probability among those hospitalized (ICU or not) d_i
- Long-stay ICU fatality rate μ_i

The first three metrics are estimated in [6] and hard-coded in the present work. Values can be found in table 1. For the long-stay ICU fatality rate μ_i, we propose by default values calculated from French public health data [2], but they can be modified in the parameters.

We can then estimate successively:

$$\hat{\psi}_i := \frac{1}{1 - \mu_i + \frac{d_i}{u_i}} \quad \text{and then} \quad \hat{\theta}_i := \frac{IFR_i}{1 - (1 - \mu_i)\hat{\psi}_i}$$

Age group	0-19	20-29	30-39	40-49	50-59	60-69	70-79	80+	**Source**
Fatality rate in ICU μ (%)	5.6	4.4	4.4	6.6	8.6	12.9	21.8	32.7	[2]*
$p(H\|U)$(%)	22.2	11.6	15.9	22.2	27.6	30.8	24.9	5.6	[6]
$p(D\|U)$(%)	0.6	1.1	1.9	3.3	6.5	12.6	21.0	31.6	[6]
Infection Fatality Rate (%)	0.001	0.005	0.02	0.05	0.2	0.7	1.9	8.3	[6]

Table 1: Chosen branching parameters. (*Adapted age groups. Can be modified in the model parameters.)

It can be noted that the ETE team [7] calculates these parameters with similar methods and then calibrates them on the data with a correction factor.

3.3 Interval distributions

In section 2.2, we came to the conclusion that only Y, H and W needed a transition policy. We implemented the distributions suggested by [7].

- Choosing a distribution for the time spent in the state:
  - Weibull distribution, with shape parameters greater than one for the duration of Y. $F_w(x, k, \lambda_w) = 1 - e^{-(x/\lambda_w)^k}$

  - Exponential distributions for the durations of H and W.
    $F_e(x, \lambda_e) = 1 - e^{-\lambda_e x}$

  We note F the chosen cumulative distribution function.

- Truncating the distribution so as to have a finite number of time sub-divisions. The truncation is carried out at the upper-integer-rounded 99%-quantile of the original distribution. Then we have to normalize the new cumulative distribution function obtained.

$$F^*(x) = \frac{F(x)}{F(x_m)} \quad \forall x \in [0, x_m] \quad \text{where} \quad x_m = \underset{x \in \mathbf{N}}{\operatorname{argmin}}\{F(x) \geq 0.99\}$$

- Computing the probability of exiting the state at day k, conditioned by not having exited the state previously.

$$p_k = \frac{F^*(k) - F^*(k-1)}{1 - F^*(k-1)} \quad \text{for } 1 \leq k \leq x_m$$

The choice of the parameters (λ_w, k) of the Weibull's law for the duration of Y and the parameter λ_e for the exponential law for the durations of H and W are left to the user's choice. However, we draw your attention to the role of λ_w and λ_e, which varies from one distribution to another as you can see in the cumulative distribution functions. A Weibull distribution with parameters (λ_w, k=1) is equivalent to an exponential law with parameter $\lambda_e = \frac{1}{\lambda_w}$. All these probabilities are computed in the function *parameters_init*().

3.4 Transmission parameters

Three parameters must be determined to compute the force of infection Λ:

- the basic reproduction number $\mathcal{R}_0$,
- the contact factor c_i,
- the generation time distribution ζ_i.

All these parameters are chosen by the user. The contact factor varies over the course of the epidemic. It can be interesting to specify it from one age group to another, for example to model school closures. For reasons of simplicity, the parameters available in the demo only allow the contact factor to vary over time. The generation time distribution is computed with the same method as interval distribution, using a Weibull distribution with chosen parameters. The only difference is that the probability does not need to be conditioned, since transmitting the virus on day k is not considered to have any impact on the probability of transmission in the following days. F being the cumulative distribution function of the chosen distribution as in the previous sub-section, we obtain:

$$F^*(x) = \frac{F(x)}{F(g)} \quad \forall x \in [0, g] \quad \text{where} \quad g = \underset{x \in \mathbf{N}}{\operatorname{argmin}}\{F(x) \geq 0.99\}$$

$$\zeta_k = F^*(k) - F^*(k-1) \quad \text{for} 1 \leq k \leq g$$

g determines the number of time sub-sections in J. As we can see on figure 3(d), all non critical infected individuals stay in J for g days.

3.5 Initial conditions

Initial conditions should be chosen depending on the country/region. More precisely, we let the user choose:

- N_0: total number of individuals in the population. Please note that nursing homes are not included in this model and then the 730,000 French people in nursing homes should not be included in this initialization. The default values proposed correspond to the French population as on January 1, 2020 according to INSEE data.
- $I_0 = J_0 + Y_0$: number of individuals who were carrying the disease at time 0,
- H_0: number of individuals in ICU at time 0 (and we deduce W_0 from it),
- R_0: number of individuals who recovered from the disease at time 0,
- D_0: number of individuals who died from the disease at time 0,

The initial number of susceptible individuals is then computed by

$$S_0 = N_0 - (J_0 + Y_0 + H_0 + R_0 + D_0).$$

In our code, initialization is done in the function *conditions_category_init*() based on the following rules:

- Individuals in I_0, H_0, R_0 and D_0 are distributed equitably among age groups.
- $J_{0,i} = (1-\theta_i)I_{0,i}$ and $Y_{0,i} = \theta_i I_{0,i}$ are computed from the number of infected individuals in each age group.
- $W_{0,i} = \frac{1-\psi_i}{\psi_i} H_{0,i}$ is deduced from the number of people in ICU.
- All individuals in J, Y, W or H are placed in the first temporal sub-compartment.

For this last point (temporal distribution within a compartment), the choice to put all the individuals in the first box is judicious if the initialization is done at the very beginning of the epidemic. However, to initialize the model in the middle of an outbreak, other methods can be considered:

- Individuals can be distributed equally across all time compartments.
- One can find the geometric sequence with common ratio $\mathcal{R}_0 c_i$ so as to have the right number of people in total.

As the distribution of individuals within the compartments at initialisation has a great impact on the results, it is important to think carefully about the selected approach.

4 Example

In this section, we present the graphical outputs produced by a simulation run. In order to do so, we have to set the parameters introduced by the model and presented above.

4.1 Example parameters

- Simulation parameters
  - Simulation duration: 250
  - Lockdown start date: 57
  - Lockdown contact factor: 0,71
  - Deconfinement start date: 112
  - Deconfinement contact factor: 0,91
- Initial conditions
  - Total infectious at time 0: 1
  - ICU hospitalizations at time 0: 0
  - Recoved at at time 0: 0
  - Deaths at time 0: 0
- Total number of individuals N^0 at time 0: table 2

Age group	0-19	20-29	30-39	40-49	50-59	60-69	70-79	80+	**Source**
N^0 (10^6)	16,08	7,47	8,29	8,59	8,79	8,00	5,70	3,43	INSEE

Table 2: Chosen number of individuals N0 at time 0.

- Transmission parameters
  - Generation time distribution - k: 2,24
  - Generation time distribution - lbd: 5,42
  - Basic reproduction number: 2,5
- Interval distributions
  - Contamination to hospitalization interval distribution - k : 3,6
  - Contamination to hospitalization interval distribution - lbd: 16,1
  - Long stay ICU interval distribution - lbd: 0,06
  - Other critical hospitalized patients interval distribution - lbd: 0,15
- ICU fatality rate (%): table 3

Age group	0-19	20-29	30-39	40-49	50-59	60-69	70-79	80+	**Source**
Fatality rate in ICU μ (%)	5.6	4.4	4.4	6.6	8.6	12.9	21.8	32.7	[2]*

Table 3: Chosen ICU frequencies. (*Adapted age groups.)

4.2 Simulation graphical outputs

All the model parameters have now been chosen. A simulation run then outputs the following figures.

- Figure 4 shows the number of both susceptible (blue) and recovered (orange) individuals over time.
- Figure 5 shows the number of non critical infected individuals over time.
- Figure 6 shows the number of critical infected individuals over time.
- Figure 7 shows the number of critical infected in ICU (blue) or hospitalized outside ICU (orange) over time.
- Figure 8 shows the number of deaths over time.

As can be noticed, these parameters come from different sources ([2], [5], [6] and [7]) and the results obtained are not consistent with reality.

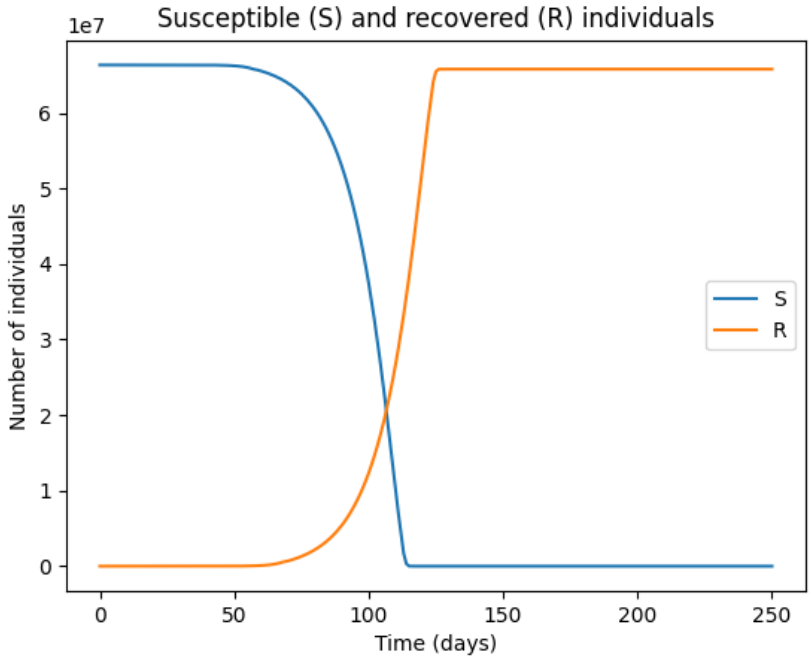


Figure 4: Example response for number of susceptible and recovered individuals.

5 Limitations and comparison with reality

It seems relevant to note some considerations around this model:

- Compartment J has a fixed length, determined by the generation time distribution ζ. We only consider the average contagion period of individuals.
- According to this dynamic, people outside hospitals cannot die: deaths in nursing homes or at home are not included. According to INSERM, 1,362 covid-related deaths at home were recorded in March and April. An estimated 10,560 people died in nursing homes (EHPAD or EMS) in France by September 22, 2020. It should therefore be kept in mind that about half of the deaths in France are not taken into account by the model.

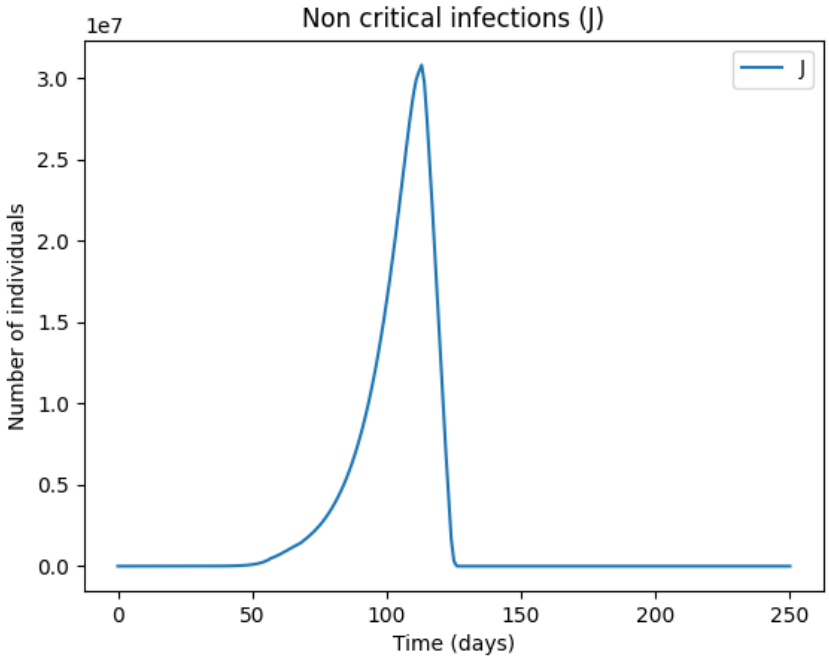


Figure 5: Example response for number of non critical infections.

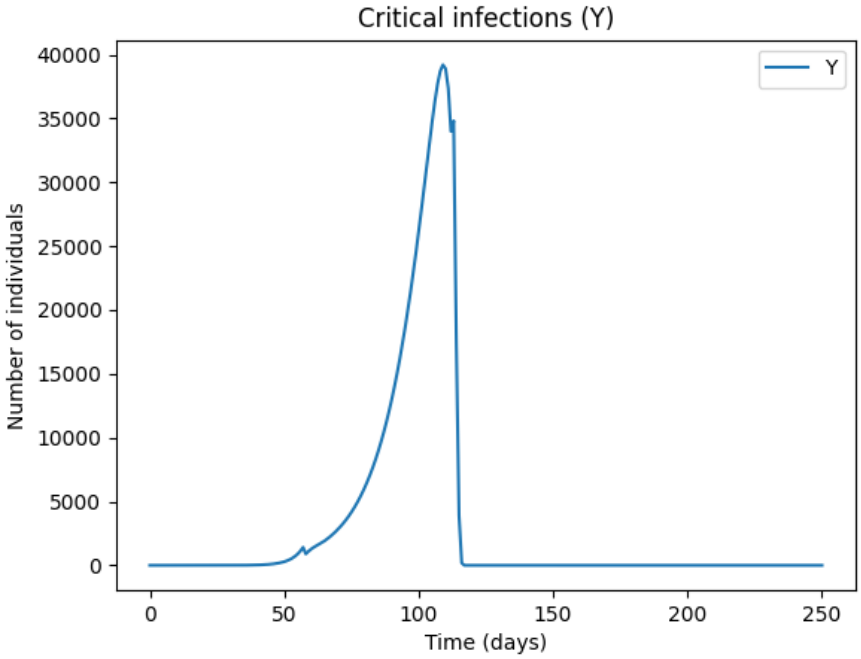


Figure 6: Example response for number of critical infections.

- The temporal sub-division of states raises questions. It probably allows a more accurate modelling of the dynamics of the epidemic. However, it can be noted that this creates several additional difficulties: it multiplies the parameters needed for the model and the initialization of the model is much more complex.

- It is quite interesting to have the H and D compartments because they correspond to metrics

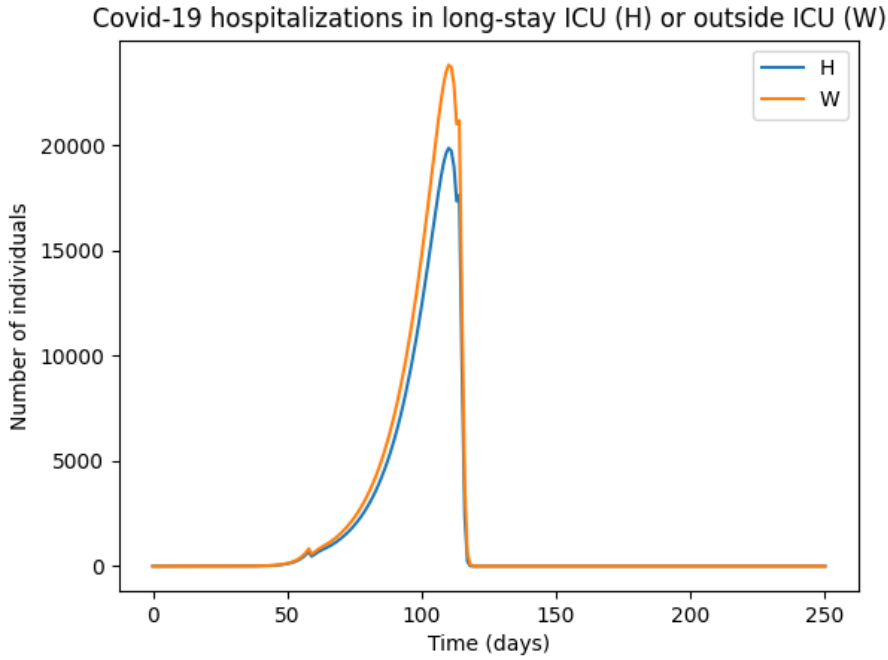


Figure 7: Example response for number of critical individuals hospitalized or in ICU.

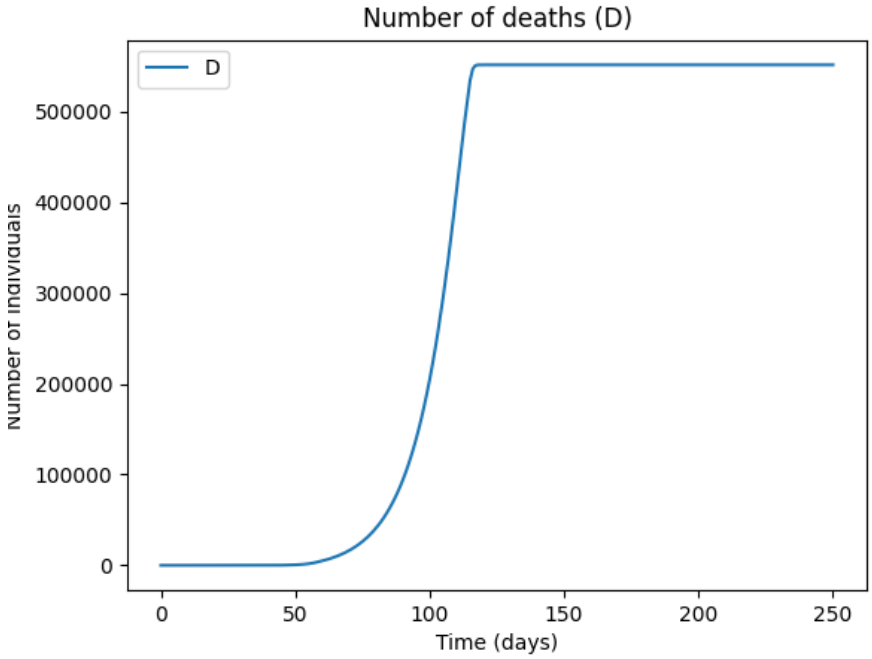


Figure 8: Example response for number of deaths.

that are collected in hospitals. One can wonder about the meaning of W, because out of overload most people who do not go through ICU survive. In this case, would it not be relevant to set a threshold for the calculation of W rather than a ψ frequency? A possible answer is that it includes deaths of people that were less than 1 day in ICU and therefore were not counted.

6 Next steps

Working on a transparent and reproducible version of the model was the building block for the policy and decision maker toolbox. So as to enrich this toolbox, future work based on the current approach may focus on a sensitivity analysis on the parameters using Sobol indices. It would allow stakeholders to make better use of the model outputs depending on what data is available at a precise point in time during the epidemic and how it helps in computing the model parameters.

Future work may also focus on how to specify a method for initializing the model based on publicly available data. This initialization consists of determining the number of individuals in each compartment and sub-compartment at a chosen start date. Given the large number of sub-compartments in the current model, it may be necessary to simplify it.

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