

# A model for the covid-19 epidemic

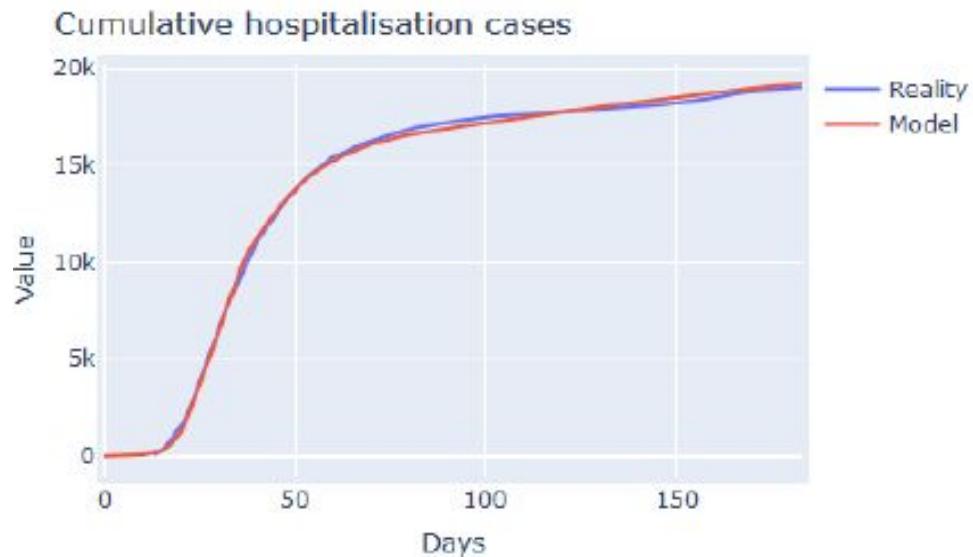
## Abstract

We present here a simple model for the covid-19 epidemic. There is no innovative conceptual idea. However, we think that several models, that have been used recently, are influenced by the scientific literature, whose goal is to develop a theoretical understanding, and an analytic approach. However, we think that for practical purpose, one should probably prefer a model  
-as simple as possible,  
-which, on the contrary, may contain a large number of variables.

A large number of variables is a weakness for a theoretical model, but a strength for a pragmatic representation of the epidemiologic behaviour, and it will allow us to accurately describe the impact of the sickness' properties on the epidemiologic behaviour.

The model could be made more complex in a straightforward way, in order to include factors such as geographic clusters, age clusters, retirement homes, etc. Again our goal is to first study the simplest model, with the least number of parameters.

The model can very well track the number of hospitalizations, with only a little number of parameters. It also allows us to compute a coefficient R which, to our eyes, describes more accurately the growth of the epidemics.



# Model

## Qualitative description

### Variables:

The model describes, at any time  $t$ , the total number of patients having been infected  $k$  days ago, for  $0 \leq k \leq 30$  (we assume that the sickness lasts less than 30 days; this is not conservative, see below). This makes **30 variables**.

$I_k(t)$  := **number of people that, on day  $t$ , have been sick for  $k$  days.**

On top of this, we add 1 variable, which represents the global immunity  **$S(t)$ : the remaining susceptible people at time  $t$** , that is, the number of people that have not yet been infected. **This makes 1 more variable.**

### Dynamics:

- I. We assume that the patients are not infectious during the whole sickness. Rather, there is a window  $[k_{\text{init}}, k_{\text{final}}]$  such that **a patient is infectious between the day  $k_{\text{init}}$  and the day  $k_{\text{final}}$  of his/her sickness**. During this period, in normal conditions (this means, at the very first day (march 1st)), **the patient infects every day a fixed number beta of individuals**.

On top of this, two phenomena have an impact on the progression of the epidemics:

- II. **the global immunity**: if, at time  $t$ , half of the population is immune, the patient will infect twice less people. More generally, the number of individuals that a sick and infectious patient infects is **multiplied by a factor  $(S(t)/N)$** , where  **$S(t)$  is the total number of susceptible people**, and  $N$  is the size of the Belgian population.
- III. Finally, the **impact of public measures** against the virus propagation impacts the infectiousity of each patient. We assume that a set of measures at some time  $t$  is represented by a **multiplicative coefficient  $c$** , which is constant over time and depends on the political decisions (or other exogenous factors).

**Putting this together**, we have the following equation for the number of people that are infected at day  $t$ :

$I_0(t+1) := [\sum_{k_{\text{init}} \leq k \leq k_{\text{final}}} \beta I_k(t)] (S(t)/(N)) c$ .

### Output/identification

In order to identify the model, **we rely on the hospitalizations**. A bit similarly to the infections, we assume that every day, **a fixed proportion gamma of sick people go to the hospital. But this only occurs to patients that are between day  $k_{\gamma_{\text{init}}}$  and  $k_{\gamma_{\text{final}}}$  of their sickness**. We assume that hospitalized people do not infect anybody anymore.

# Mathematical description

## Variables

$S(t)$ : number of susceptible people left in the population at day  $t$ .

$I_k(t)$ : number of people, at day  $t$ , which have been sick for  $k$  days ( $0 \leq k \leq 30$ ).

## Equations

$$\begin{aligned}I_0(t+1) &:= [\text{Sum}_{\{k\_init \leq k \leq k\_final\}} \beta I_k(t)] (S(t)/N) c_t. \\I_{\{k+1\}}(t+1) &= (1 - \gamma_k) I_{\{k\}}(t)^1 \\S(t+1) &= S(t) - I_0(t)\end{aligned}$$

$$\text{hosp}(t) = \sum_{\{k\_gamma\_init \leq k \leq k\_gamma\_final\}} (\gamma_k I_k(t))$$

## Parameters

**$k\_init, k\_final$ :** number of days after which an infected patient becomes infectious (resp. not infectious anymore)

**$k\_gamma\_init, k\_gamma\_final$ :** number of days after which an infected patient becomes susceptible to go to the hospital (resp. not susceptible anymore)

**$\beta$ :** number of people that an infectious patient infects every day in initial conditions

**$c_t$ :** multiplicative coefficient for infectiousity due to public measures (we assume for simplicity that  $c$  is constant per interval:  $c=1$  before confinement of mid-march,  $c_t$  is constant between mid-march and mid-may (heavy confinement), and  $c_t$  is constant between mid may and end of august. A new  $c$  might be needed after end of august, but we did not study that period yet).

**Initial conditions ( $N_0, k_0$ ):** We assume that, on march first, there are  $k_0 N_0$  people infected in the country, homogeneously spread in the  $k_0$  first days of sickness, that is, the state vector at time zero is equal to  $I(0)=(N_0, N_0, \dots, N_0, 0, 0, \dots, 0)$ .

---

<sup>1</sup> The  $(1-\gamma_k)$  factor represents the sick people that leave the system because they enter the hospital. We denote  $\gamma_k := \gamma$  if  $k\_gamma\_init \leq k \leq k\_gamma\_final$ ;  $\gamma_k := 0$  else.

# Results and numerical values of the parameters

We performed an extensive search for the best values of the parameters in order to fit the true observed number of hospitalizations. Even if we do not claim that the obtained values for the parameters are the true physical ones, we manage to explain very well the curve of hospitalizations. **At least, it shows that such values are mathematically plausible. Are they biologically plausible?**

**k\_init=3, k\_final=18:** The patients become infectious on day 3 of their sickness, and stop infecting people on the day 18.

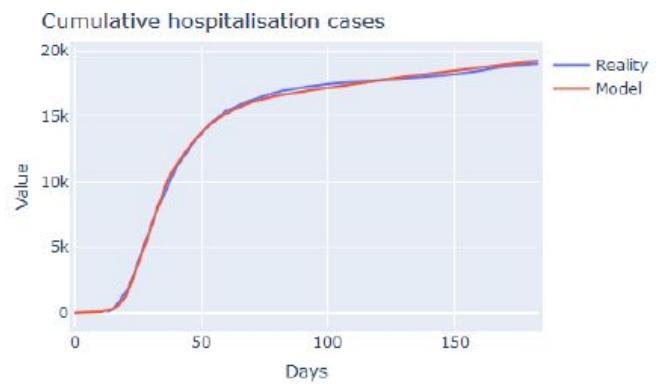
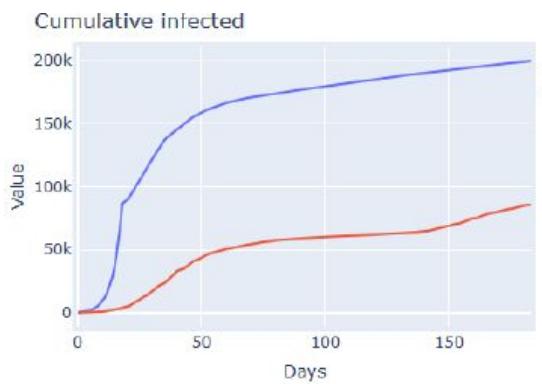
**k\_gamma\_init=4, k\_gamma\_final=21:** Patients are susceptible to go to the hospital between day 4 of their sickness, and day 21 of their sickness.

**beta=0.75:** In normal conditions, infectious patients infect three people every four days (0,75 per day).

**c\_1=0,05; c\_2=0,09:** the strong confinement of mid-march mid-may has divided by 20 the infectiosity of people (multiplied by 0,05). In the summer, the measures were still dividing the infectiosity by a little more than 10 (multiplied by 0,09).

**N0=50, k0=8:** Beginning of march (at day 1 of our model), there was 450 sick people in belgium, equally spread between their day 0 and day 8 of the sickness.

As one can see below, we observe a very good fit of the hospitalization curve. Also, interestingly, the model computes that, by the end of august, roughly 200k people had been infected since the beginning of the epidemics:



## Appendix: online simulation tool

One can try the model with arbitrary parameters at <https://covid-icteam.herokuapp.com/>. There, the model is slightly more complicated, with refined time periods, and refined evolution of the sickness in the patient's body, but the simpler model presented here can be implemented, by selecting several parameters equal to each other. The choice of parameters mentioned above is represented in the screenshot below.

k\_max  N\_days  Initial infected per day (k)

Initial infected vector: position i  
Initial infected vector: position j

5 10 15 20 25 30  
5 10 15 20 25 30

### Infectivity beta parameters:

$\beta_0$    $\beta_1$    $\beta_2$    $\beta_3$    
 $\beta_4$    $\beta_5$    $\beta_6$    $\beta_7$    
k0\_beta0  k1\_beta1  k2\_beta2  k3\_beta3

### Hospitalization parameters:

$\gamma_0$    $\gamma_1$    $\gamma_2$    $\gamma_3$    
 $\gamma_4$    $\gamma_5$    $\gamma_6$    $\gamma_7$    
k0\_gamma  k1\_gamma  k2\_gamma  k3\_gamma   
Value c':  Value c'':  Value c'''  Value c4:  Value c5:

With optimisation by k  Use specified k

**Run model!**