

# Lab7 - Epidemic processes

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**Assignment** The goal of Lab L7 is to define and simulate simple strategies to control an epidemic (SIR) process through non-pharmaceutical interventions (I.e. by introducing mobility restrictions).

Consider a homogeneous population of 50M individuals. Fix  $R(0)=4$  and  $\gamma=1/14$  days (recovering rate). Assume that 10% (6%) of the infected individuals needs to be Hospitalized (H) (undergo Intensive Treatments (IT).)

Fix the fatality rate of the epidemic to 3%. H/IT places are limited (10k/50k). Design some non-pharmaceutical intervention strategy that avoids H/IT overloads, and limits the number of death in 1 year to 100K. To design your strategy you can use a mean-field SIR model.

Then, once you have defined your strategy simulate both the stochastic SIR and its mean field. Are there significant differences, why? What happens if you scale down your population  $N$  to 10k (of course you have to scale down also other parameters, such as H and IT places)?

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## 1 Random elements, inputs and main assumptions

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### 1.1 Introduction

the SIR model represents one way to simulate an epidemic process, such as the COVID-19. In such a scenario, the population of the initial individuals is, basically, divided into 3 groups: the Susceptible people (i.e., the people exposed to the infection but not infected, yet), the Infected people (i.e., the people who transmit the virus) and the Recovered people (i.e., the ones who are healed from the infection or that are already dead, but that, in any case, are not susceptible anymore). This process is defined by a Markov chain and its evolution is given by the rate of the generation of the Infected people: this event happens when a Susceptible individual gets in contact with an Infected one. Moreover, the dynamism of this model depends on some parameters, such as the infection rate  $\lambda$ , the recovery rate  $\gamma$ , the hospitalization rate  $h$ . All of these features are modeled and simulated in the code provided, in addition to the further explanation given in this report. In conclusion of the work, it is also introduced non-pharmaceutical restrictions in order to limit hospitalized cases and deaths.

### 1.2 Stochastic elements

To simulate such an epidemic process, just a few stochastic elements must be considered. Firstly, randomness is introduced when I compute the number of new recovered people or the number of new dead people. This is a needed passage since, when I calculate the people that need to be Hospitalized, this number is added to the previous number of Hospitalized people and it is subtracted from the number of Infected people.

Given that, I considered the Hospitalized people as *severe* cases of infection, so that, when a portion of the Infected people gets Recovered, some of them must come from the Hospitalized group and some others form the *non-severe* Infected group. This mechanism introduces some variability in the computation of the number of Susceptible, Infected and Recovered timestamp by timestamp. To be clear, an example of this trick is given in the Figure 1. As explained in the code, I check if subtracting the random fraction of people is feasible: to do this I exploit the following pseudo-algorithm:

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**Algorithm 1** Trick for avoiding negative numbers when computing fractions

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Compute the n of new R people *new\_R*

Randomly select fraction *frac*

**if** removing *frac* from H and (1-*frac*) from I > 0 **then**  
    A *frac* of new\_R is removed from I

    The remaining 1-*frac* is removed from H

**end**

**if** one of the differences is < 0 **then**

    Check which of them is < 0

**if**  $H - (frac * new\_R) < 0$  **then**

        Remove as many people as possible from R

        Remove the remaining people from I

**end**

**if**  $I - ((1-frac) * new\_R) < 0$  **then**

        Remove as many people as possible from I

        Remove the remaining people from H

**end**

**end**

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A seed is introduced for reproducibility purposes.

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new_R = round(gamma * (I + H)) # compute the number of Recovered people -> Note: both H and I are taken because when I store new_H, I remove them from I
R = R + new_R
frac = round(random.uniform(0, 1), 1) # compute a random fraction of people in order to simulate that some people in hospital is healed/dead (i.e., Recovered)
# and some other 'non-Hospitalized' infected people is healed/dead (i.e., Recovered) people
if (H - round(frac * new_R)) > 0 and (I - round((1 - frac) * new_R)) > 0: # if removing a fraction of people from H and from I does not produce negative result
    I = I - round((1 - frac) * new_R) # a fraction of deaths is taken from the infected people
    H = H - round(frac * new_R) # the other fraction is removed from the Hospitalized people
else: # if one of the 2 differences produces negative result
    if (H - round(frac * new_R)) < 0: # in the case in which removing a fraction of Recovered people form H gives negative result,
        H = H - H # remove as much recovered people from H and ...
        I = I + (H - round(frac * new_R)) # ... remove the remaining number of recovered people from I
    elif (I - round((1 - frac) * new_R)) < 0: # in the case in which removing a fraction of Recovered people form I gives negative result,
        I = I - I # remove as much recovered people from I and ...
        H = H + (I - round((1 - frac) * new_R)) # ... remove the remaining number of recovered people from H
    # Note: there is a '+' because (I - round((1 - frac) * new_R)) is negative, so H (>0) + (I - round((1 - frac) * new_R)) (<0) means doing 'H minus a quantity'

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Figure 1: Example of the trick used for introducing randomness

Variable name	Input variable	Values
Number of individuals in the population	N	50M; 10K
Hospitalized rate	h	0.1; 0.06
Maximum number of available hospital beds	H max ( $H_{max}$ )	100K; 50K; 200
Maximum number of allowed deaths	D max ( $D_{max}$ )	100K; 200
Recovery rate	gamma	1/14
Fatality rate	f	0.03
Avg number of infections per individual	R.0 ( $R_0$ )	4
Common death rate	mu ( $\mu$ )	0.00001

Table 1: Input parameters and their values

### 1.3 Input parameters

For what concerns the input parameters, I assume to set the variables shown in Table 1. Note that if there is more than 1 value for a given variable, it means that it would be used in different situations with different values. Indeed, for the purposes of the simulation, N, h, H\_max and D\_max are varied to evaluate different system's behaviors under the following conditions:

- case 1** N = 50M, h = 0.1, H\_max = 100k, D\_max = 100k;
- case 2** N = 50M, h = 0.06, H\_max = 100k, D\_max = 100k;
- case 3** N = 50M, h = 0.1, H\_max = 50k, D\_max = 50k;
- case 4** N = 10k, h = 0.1, H\_max = 200, D\_max = 200.

In addition to these parameters, I initialized the following variables: the contact rate  $\lambda$  is initially set to 0.0, the strengths of the restrictions  $\rho$  to 1.0 - in order to be non-influent at the first stage of the spread of the virus -, the number of initial Infected people is just 1 and the Recovered people is, obviously, 0. From that preamble, I compute the starting value of Susceptible people S by applying the formula

$$S = N - I - R.$$

### 1.4 Main assumptions

For this work, some assumptions were needed and they will be listed and explained in this section. Proceeding

in order of appearance in the code, firstly, I assumed that the simulations lasts for 1 year (i.e., 365 days), but day 1 shows a different behavior with respect to the other days: the reason stands in the fact that, at the first stage, there are no Recovered people and no restriction, yet. Furthermore, the average number of people that get infected by a Susceptible individual  $R_t$  and the infection rate  $\lambda$  are computed at this point. Regarding  $R_t$ , I assumed that  $R_t$  is equal to  $R_0 = 4$  for all the simulation time and  $\lambda$  is computed by following the [Wikipedia](#) - and other paper's - approach, by using the formula

$$\lambda = R_t * (\gamma + \mu).$$

Once the simulation started (i.e., from the second day on), I assumed that the parameters  $\lambda$ ,  $\gamma$  and  $\rho$  change based on some quasi-realistic conditions. For what concerns  $\rho$  I assumed that:

- If** there are a few people Infected compared with the entire population (i.e.,  $I/N \geq 0.1$ ), then no restriction is applied and, so,  $\rho$  remains set, as at the beginning, to 1.0;
- If** there are a not-too-much people Infected compared with the entire population (i.e.,  $I/N \leq 0.3$ ), then some low restrictions are applied and, so,  $\rho$  is set to 0.8;
- If** there are an almost-high people Infected compared with the entire population (i.e.,  $I/N \leq 0.5$ ), then the restrictions are increased and, so,  $\rho$  is set to 0.1;

If more than half of the population is infected (i.e.,  $I/N \geq 0.5$ ) or the hospital beds are almost full or both, then the restrictions are increased and, so,  $\rho$  is set to 0.002;

If the number of deaths has almost reached the limit (D\_max), then the restrictions are increased as much as possible and, so,  $\rho$  is set to 0.00001.

Note that lower is  $\rho$  higher is the restriction, since it would be multiplied by a positive quantity (i.e., Infected people I).

Another control is done regarding  $\lambda$ : if the number of Hospitalized people (added with the new Hospitalized ones new\_H) is more than the available hospital beds, the new\_H people (i.e., severe cases) are not isolated in the hospital and, so, their transmissivity rate is higher than the others'. For this reason, since they are still among the other people, I assumed that the contact rate would be increased by a factor given by the ratio between the new\_H people and the Infected ones: this ratio is exactly equal to  $h$ , so  $\lambda$  is updated by using  $\lambda = \lambda + (h * \lambda)$ . Otherwise, if there are enough available beds in the hospital, severe cases are isolated, so the transmissivity would be lowered and  $\lambda$  would

be decremented by the factor  $h$ .

Concerning  $\gamma$ , if there are enough available beds in the hospital, as said before, severe cases are isolated, so the recovery rate  $\gamma$  is decreased by a very low number (i.e., the death rate  $\mu$ ). For this reason, under this condition,  $\gamma = \gamma - \mu$ . Differently, if the number of Infected people is zero,  $\gamma$  is restored to its initial setting 1/14. Finally, I handled the case in which the Susceptible people S are computed as  $\leq 0$ : in this situation, all the susceptible people are infected, so I remove as much as possible people from S and take the remaining infected people (the non-taken ones from S) from I. To clarify this point, as stated in the code, if you take, for example,  $N = 5000$ ,  $I = 1705$  and  $R = 3418$ , then  $S = N - I - R = 5000 - 1705 - 3418 = -123$ . So, if I remove as much Susceptible as possible, S goes to 0 and the remaining 123 people that should be theoretically infected are not taken. Therefore, you compute  $I + S = 1705 + (-123) = 1582$  so that  $S = 5000 - 1582 - 3418 = 0$ .

The following considerations and analyses are done under these assumptions to compute day by day number of new Infected, Recovered, Hospitalized or Dead people.

## 2 Output metrics, data structures and further analyses

### 2.1 Data structures

The data structures are very simple and they consist in lists for containing the results. Moreover, a predefined function *odeint()* is used for resolving the differential equations of the main field.

### 2.2 Output metrics and analyses

As assigned, the lists of S, I and R people are displayed and compared with the deterministic mean field. As noticeable, the curves of the graph are correctly shown, even if they are not precise compared with the deterministic results. Note that the first plot showing the SIR model curves is focused on the first 77 days, which represents the first two months in which, realistically speaking, a virus such as COVID-19 had the biggest spread. This choice was made to evaluate better the results.

However, the plot on the top of the Figure 2 demonstrates that the number of Susceptible people is correctly having a rapid decrease in the first days, since there were not any restrictions, yet. Then, after applying them, the curve decreases slowly and, finally, it reaches a horizontal asymptote of around 2 millions. Instead, the number of Infected people has a rapid increase in the first days and a slow decrease during the rest of the year until it reaches 0. Finally, the Recovered people's curve slowly reaches a stable point under the 3 millions. Generally, all the curves

depict the correct trend, even if they are lying on the expected ones. Figure 2 also shows the Hospitalized, the Dead and the  $\lambda$  curves. From these plots, we can clearly say that the constraint about the number of available beds in the hospitals is respected, while the limit for the deaths, unfortunately, is not. However, the value of the deaths is taken lower than 1 million. Finally, the plot regarding the lambda rate shows an increasing trend and suddenly a decreasing one.

It is also presented in Figure 3 the case in which the number of individuals is 10k. In such a situation, also other parameters are scaled down to fit better with the context. It shows a similar but smoother trend as before regarding the S, I and R curves. The difference with the simulation with a population of 50M people stands in the fact that here there is no timestamp in which the number of Recovered people is higher than the number of Susceptible ones.

Also, the hospital beds' limit is respected. On the contrary, the deaths reached a value a little bit higher than 1200. Lastly, the plot on the bottom of Figure 3 shows perfectly the trend of the infection rate  $\lambda$ , which is always kept under 0.7. In particular, it presents a higher spread in the first 2 weeks, then, after applying restrictions, it slowly decreases until it reaches a very low value from the second month on. This plot depicts realistically the COVID-19 trend and its behavior.

For clearer evaluations, please refer to the code provided.

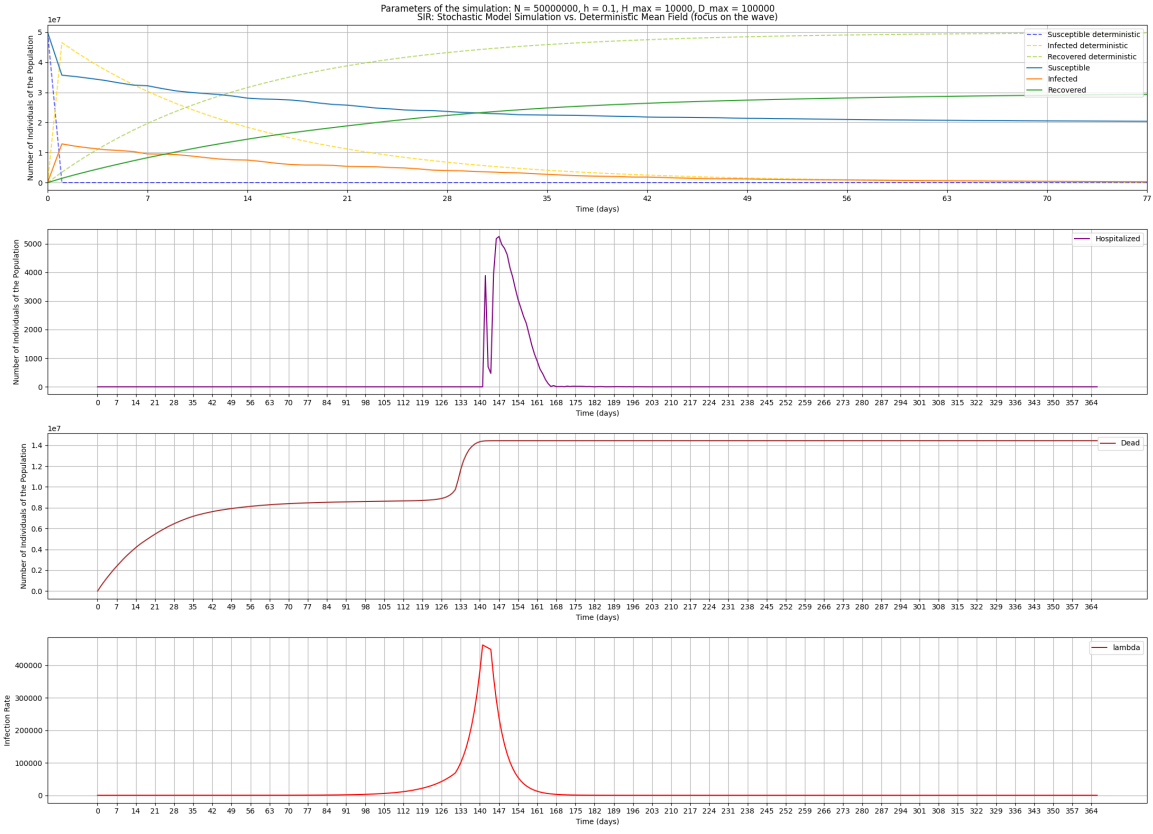


Figure 2: Simulation with  $N = 50M$ ,  $h = 0.1$ ,  $H_{\max} = 10k$  and  $D_{\max} = 100k$

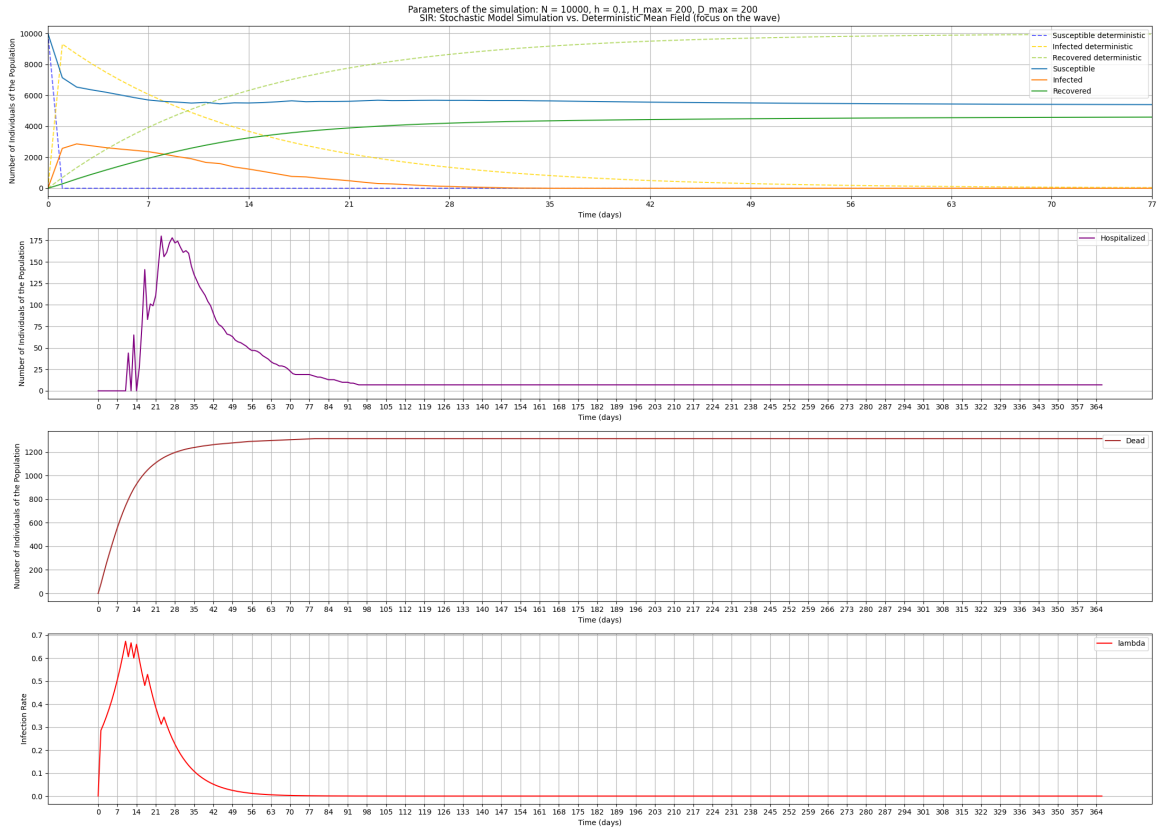


Figure 3: Simulation with  $N = 10k$ ,  $h = 0.1$ ,  $H_{\max} = 200$  and  $D_{\max} = 200$