Computer aided simulations and performance evaluations - Lab 4

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1 Introduction

The aim of this laboratory is to study the epidemic evolution trough the SIR model in numerical and simulative (agent-based model) approach. The SIR model is based on the following assumptions:

- The probability of being is contact with other individuals is equal for all the population;
- "Tele-transport" mobility model;
- The population is fixed;
- There are only three category of individuals: S = Susceptible, I = Infected, R = Removed;
- If an infected is removed, it will no longer be susceptible;
- In case of contact between susceptible and infected, the infection happens always.

Although these assumptions are restrictive, studies confirm that the SIR model is pretty accurate even in reality. The input parameters that make the models comparable are shared, and those are:

- The population, N, fixed at 10000 individuals;
- β i.e. the rate of contact per individual fixed at 0.2 day^{-1};
- The infection period fixed at 14 days, leading to the recovery rate $\gamma = 1/14$ day^{-1};
- The time period under analysis, 365 days.

In order to start the epidemic is required to insert manually the first infected, then at day 0:

$$S(0) = N - 1; I(0) = 1; R(0) = 0;$$

and the choice for the end of the epidemic adopted is: **the epidemic is over when the number of infected individuals is zero.**

2 Numerical SIR model

The numerical SIR model is solved trough three differential equations that regulate the evolution of the categories over time:

$$\frac{\partial S(t)}{\partial t} = -\frac{\beta}{N} S(t) I(t) \tag{1}$$

$$\frac{\partial I(t)}{\partial t} = \frac{\beta}{N} S(t) I(t) - \gamma I(t) \tag{2}$$

$$\frac{\partial R(t)}{\partial t} = \gamma I(t) \tag{3}$$

The coefficients β and γ are kept here deterministic, so the confidence intervals are not required and a single run is enough to get coherent results.
The simulation outputs is displayed below:

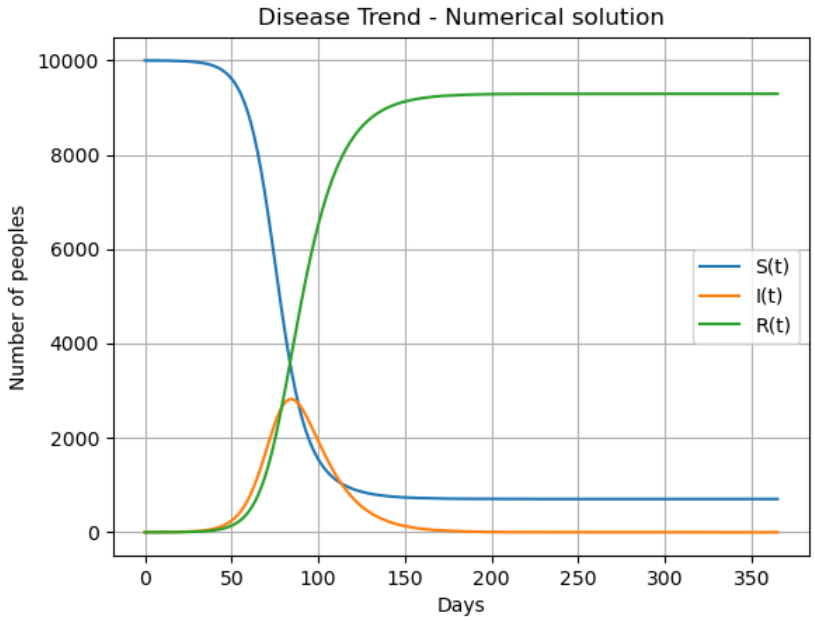


Figure 1: Epidemic evolution solved numerically trough the SIR model.

The epidemic ends after 243 days reaching a peak of 2822 infected individuals at day 84.
To get the R_0 i.e., the average number of secondary infections made by the first infected measured at day 0, is sufficient to multiply the coefficient β by the period of infection, getting $R_0 = 0.2 \cdot 14 = 2.8$.

3 Simulative SIR model

The simulative SIR model is made through the so-called *agent-based model*, where each individuals is modeled as an agent (coded "digital twin") that can interact with other agent around the world.
Differently from the numerical approach here the formulation isn't deterministic, so as additional input parameters we have:

- The confidence level, set to 95%;
- The seed, for replicability;
- The number of runs equal to 10.

The outputs parameters are the same of the numerical approach, i.e. the evolution of S(t), I(t) and R(t) with the addition of R_t, really hard to compute analytically, but feasible trough simulation. Instead of single value, here the output is intended as mean value with its own confidence interval of level 95%.
The data structures used for the simulation are:

- *Numpy* boolean arrays for susceptible, infected and removed. The first initialized to one and the latters to 0, in order to easily compute the total number of individuals belonging to a specific category;
- Python lists for keeping track the evolution of S(t), I(t), R(t) and R_t throughout the year;
- A Python dictionary with key the index of the individual and with value an instance of the class `Person` which contains for each individuals all the status information, such as if it is infected; how many days remain to recover; the number of infected individuals etc.

The simulation engine consists in nested loops, where the outermost is through the days while the inner trough the infected individuals, that meeting other people according to a Poisson distribution with $\lambda = \beta$ can infect them if susceptible. This experiment launched for 10 (2 of them removed since degenerative) runs produces the following results:

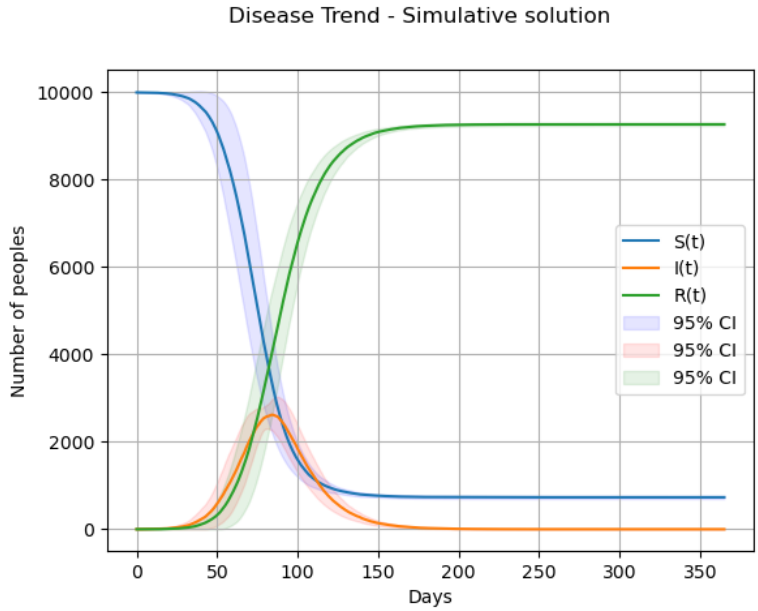


Figure 2: Epidemic evolution solved trough simulation adopting the SIR model. 8 runs for a 95% CI.

The epidemic ends in 240.00 days reaching a peak of 2957.62 infected individuals at day 80.75 (mean values). As we can the analytical solutions fit the boundaries of the confidence intervals, giving credibility to the model.

As said before, is easy here to get statistics about the R_t index (Figure 3), that as expected is maximum in the first 20 days while it goes to 0 as the days go by. Interesting to notice is that there is a decreasing elbow close to day 50, where also the susceptible curve starts to fall. The inflection point in the R_t curve is perfectly overlapped with the one in the susceptible curve, i.e. the less susceptible individuals there are in the population, the less an individual causes secondary infections. Of course when there aren't infected in the population the R_t is equal to 0.

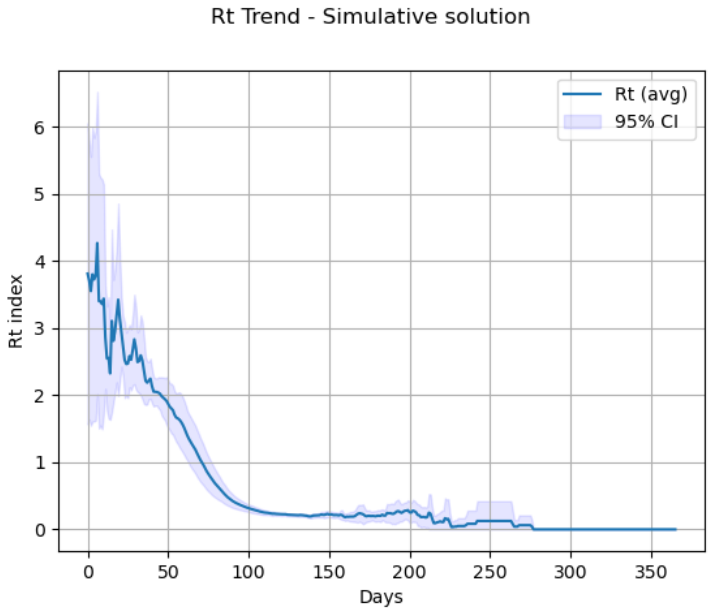


Figure 3: R_t index evolution through 365 days. 95% CI in 8 runs.

4 Extensions of SIR model

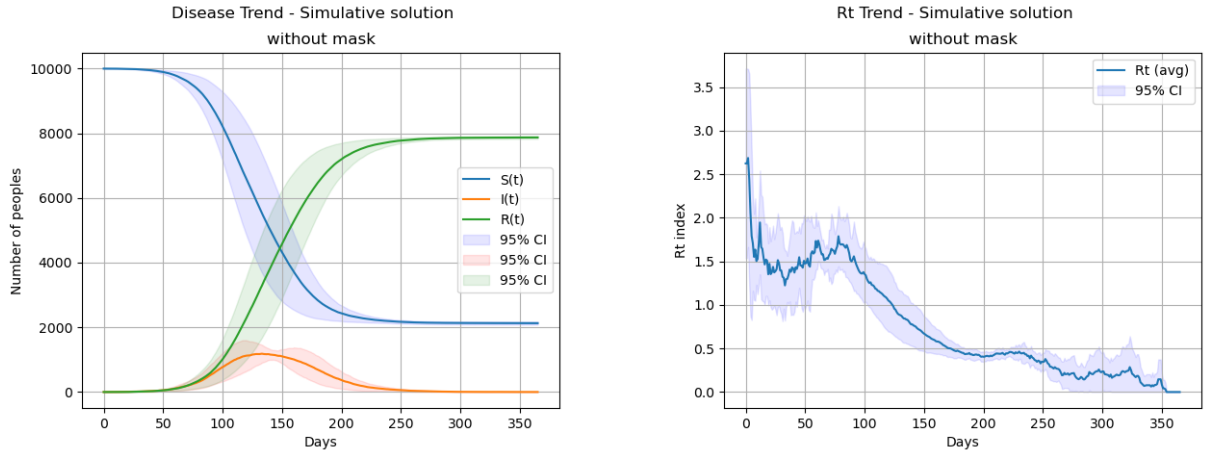
The extensions proposed for this laboratory are:

1. The probability of infect a susceptible individual when met is < 1;
2. Once recovered and after a period of immunity, an individual return in state susceptible (SIRS model);
3. The introduction of a lockdown period.

The input parameters are exactly the same as before, except for the number of runs increased to 15 since degenerative runs were more frequent. The extensions are introduced progressively, meaning that the extension 3 encloses also extension 1 and 2.

4.1 Probability of infecting < 1

According to the study available here, the choice adopted for the probability of infection is $P(infection) = 0.7$ without wearing the surgical mask, whereas without it $P(infection\_with\_mask) = 0.2$.
Assuming all the population wears the surgical mask ($p = 0.2$), in this setting there is not enough time to spread the infection; the simulator produces only degenerative runs without any meaningful result, so it has been discarded.
Instead, keeping $P(infection) = 0.7$ there is a relaxation effect: all the curves reach their own peak later and the peak is less accentuated. The epidemic duration increases due to the previous considerations (Figure 4) and the R_t decreases slowly.

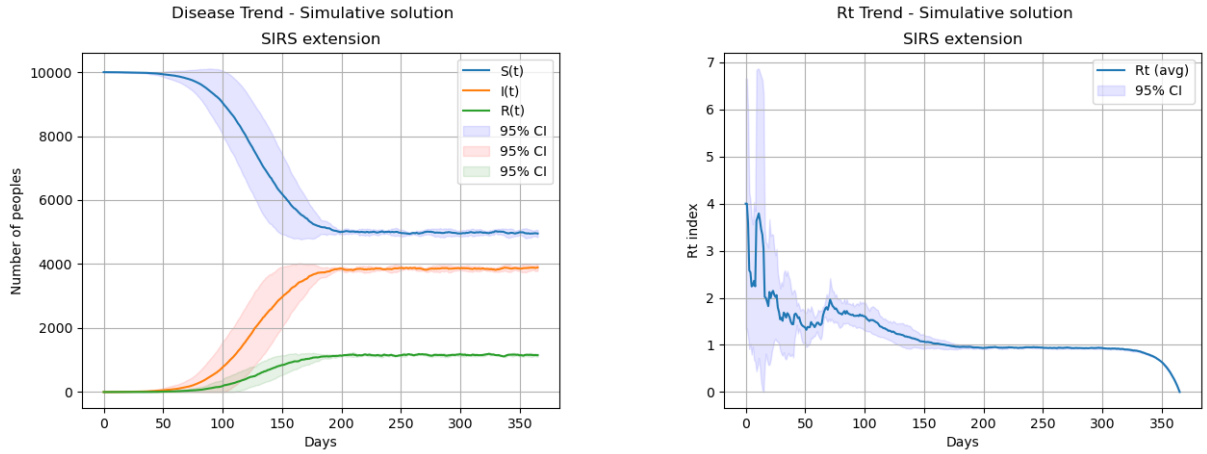


(a) *Epidemic trends* (b) R_t *trend*

Figure 4: Outputs of the first extension. *Right*: the SIR curves; *left*: the R_t trend. 95% CI in 15 runs (7 degenerative)

4.2 SIRS model

In the SIRS model once an infected individual gets recovery, it becomes again susceptible after a period on post-infection immunity, the choice here is that the period follows a Uniform distribution $U(0, 10)$.
What happens is that after a transition phase, all the curves become steady since there is always a mutual switch of status between susceptible, infected and recovered individuals, because the epidemic spread is faster that the recovery time.



(a) *Epidemic trends* (b) R_t *trend*

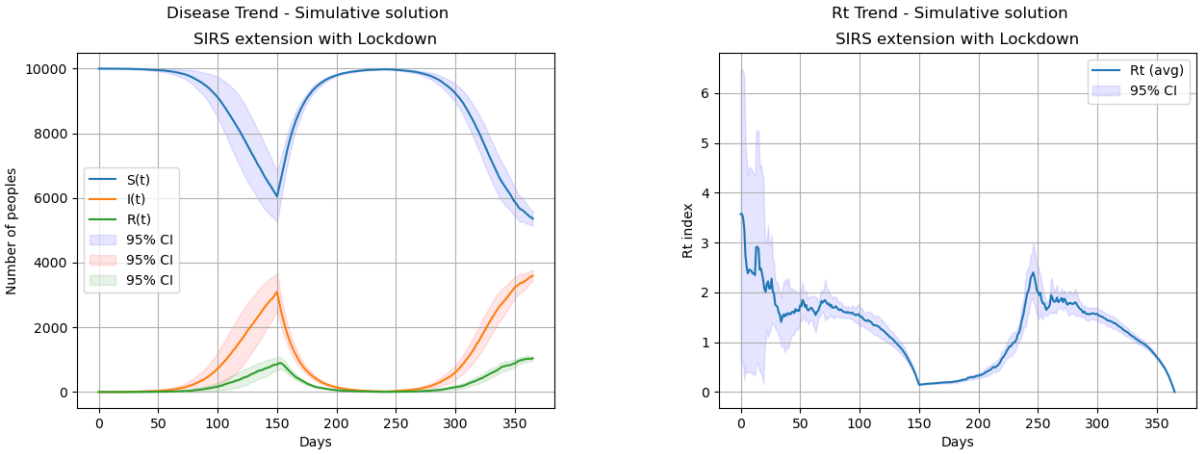
Figure 5: Outputs of SIRS extension. *Right*: the SIR curves; *left*: the R_t trend. 95% CI in 15 runs (9 degenerative)

Also here the R_t is strictly related to the susceptible curve, mimicking the latter's behaviour (the tail of R_t

is meaningless since the termination is induced by the end of the year, not of the infection).

4.3 Lockdown

In the previous extension we saw that the infection spreading is faster than the epidemic recovery, then in order to mitigate the curves, here a lockdown period is introduced with the assumption that during this period the coefficient β is reduced by factor 10, precisely $\beta_{lock} = 0.02\ days^{-1}$. The lockdown period chosen to contain the epidemic is from day 150 to day 240.



(a) *Epidemic trends*

(b) R_t *trend*

Figure 6: Outputs of SIRS extension. *Right*: the SIR curves; *left*: the R_t trend. 95% CI in 15 runs (9 degenerative)

Looking at the charts in Figure 6, the lockdown contribute is clear, it reduces the epidemic bringing the infections close to zero but still in not enough to terminate it; this is much clearer looking at the R_t chart that remains always greater than zero. To resume in the following table are reported all the extensions' results:

Extension	Infection Peak	Day of Peak	Infection duration
None	2957.62	80.75	240.00
1	1575.75	134.87	322.37
2	3998.66	292.16	365*
3	3597.00	364.71	365*

Table 1: Summary of the result. Mean values in 15 runs (7 discarded since degenerative). Values with * means that are bounded to the 365 days of simulation.