Methods in Computational Neuroscience
Modeling Epidemics: SI and SIS Models

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The purpose of this first exercise is to provide a quick overview of the mathematical models that we will implement during the course. In this initial exercise, we will cover the most elementary concepts, assuming only a basic knowledge of Python (specifically, NumPy and Matplotlib). The tasks include implementing loop structures, plotting results in graphs, and, finally, being able to provide scientifically rigorous comments on them. **The maximum length for this report is 6 pages. Additional pages will not be corrected.** Shorter reports are encouraged as long as they are complete.

1. The simplest model: no treatment... The SI model

Let us consider the spread of a virus in a population: what we are interested in is the spread of the epidemic, and to do this we will use the SI model in this first section (Figure 1). This model consists of dividing the population into 'compartments'.

In the simplest model (SI) we have two compartments:

- S (Susceptible): Individuals who are susceptible to the disease but have not been infected.

- I (Infected): Individuals who are currently infected and can spread the disease.

We will assume that the total number of people in the population is N and remains constant, while S and I vary over time, so at each instant t we have $S_t + I_t = N$.
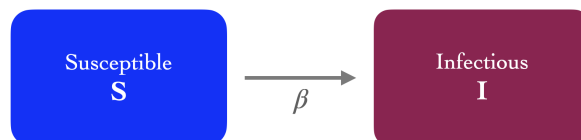

Figure 1: The SI model.

Let us assume that the virus is contagious and that the number of infected increases over time: the number of new cases on day t, which we denote by I_t, will be equal to the number of infected on the previous day, I_{t-1}, plus an amount that is proportional to itself (the more infected at time $t-1$, the more new cases). We denote growth by βI_{t-1}, which depends on the contagiousness of the virus, expressed by the *transmission parameter* β.

Let us therefore try to model the epidemic through the following map:

$$I_t = I_{t-1} + \beta I_{t-1} \tag{1.1}$$

1.1 Model the infection. Assume that in a population of 100 individuals, the initial number of infected patients is $I_0 = 3$ and that the contagiousness parameter is $\beta = 0.02$. Model the epidemic over a course of one year and plot the results in a graph. What is happening? How many days are required for the entire population to be infected? Show it in the plot. [Hint: Create an array I of length nDays. Set the first element to I_0. Simulate the population using a for loop.]

1.2 Vary the parameters. Now try to vary the model parameters. Evaluate how the initial number of infected patients, the infection rate, and the first day of infection influence the evolution of the infection, plotting the results, and motivating them. (Recall to use realistic values: I_0 is the initial number of positive patients and cannot be negative...)

1.3 Plot the S and I curve together. In the same graph as in 1.1, plot the evolution of the number of healthy individuals. Is the model we have just implemented realistic? Why? [Hint: Recall that the total number of individuals remains constant equal to N.]

One way to make the evolution of an epidemic more realistic is to consider the following fact: the number of new cases each day is not uncontrolled, but it is proportional to the probability of getting in contact with healthy individuals. This probability can be modeled by the term $\frac{S}{N}$. We correct the previous model by taking this observation into account:

$$I_t = I_{t-1} + \frac{\beta}{N} I_{t-1} S_{t-1} \tag{1.2}$$

1.4 What has changed? Using the same parameters as in exercise 1.1, simulate the evolution of the epidemic over **2 years** (plot both I and S in the same graph) and comment on the results and differences with the previous case. On which day is the number of infected people equal to the number of susceptible people?

1.5 Change the parameters. What happens with different values of β? Can you identify different regimes? What happens for different initial conditions ($I0$)? Compare the results with the previous simplified model.
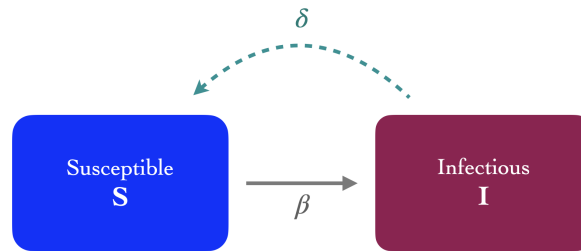
Figure 2: The SIS model.

2. Adding a treatment: the SIS model

The results of the SI model do not seem very encouraging, but it is clear that the model is too simplified with respect to real epidemics, since the dynamics of the model only allow for the transition from compartment S to compartment I.

In reality, individuals can also recover (fortunately!), returning to the S compartment. Therefore, a slightly more sophisticated model is given by the scheme $S \to I \to S$ (Figure 2).

Of course, in this SIS model, the equations become more complex to account for the transition $I \to S$, from infected to susceptible. In particular, each day we subtract an amount of infected proportional to a *recovery rate* γ:

$$I_t = I_{t-1} + \frac{\beta}{N} I_{t-1} S_{t-1} - \gamma I_{t-1}. \tag{2.3}$$

Here, the term γI_{t-1} accounts for the individuals who have recovered and returned to the susceptible compartment.

2.1 Simulate the curves S and I. Set $\gamma = 0.006$ and simulate the pandemics over 2 years. What has changed from the previous scenario (1.4)? Increase and decrease γ to 0.009 and 0.001, respectively, and observe the changes.

2.2 Vary $\frac{\beta}{\gamma}$ and observe the S curve. Study how the S curve varies as the ratio $\sigma = \beta/\gamma$ varies. In particular, try with values of $\sigma <, =, > 1$, find the stationary value and and explain why the behavior of the curve changes [Hint: Remember that the parameters β and γ have a meaning...].

2.3 [Extra points] Provide a mathematical explanation of the results. Use the mathematical tools familiar to you to explain both the problem and the results obtained so far (for both exercises). This can be done in a separate section or progressively integrated while explaining the previous points. (This includes solving the equation and comparing it with simulations, finding stationary points, studying the slope as the parameters vary, ...)
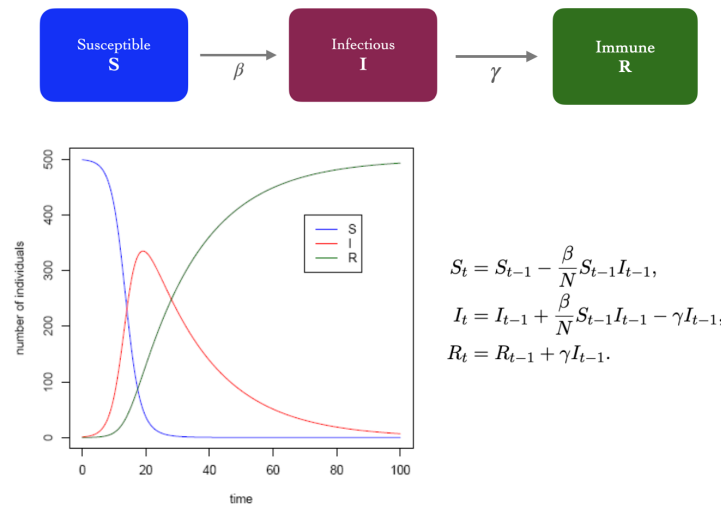
The equations shown in the figure:

$$S_t = S_{t-1} - \frac{\beta}{N} S_{t-1} I_{t-1},$$

$$I_t = I_{t-1} + \frac{\beta}{N} S_{t-1} I_{t-1} - \gamma I_{t-1},$$

$$R_t = R_{t-1} + \gamma I_{t-1}.$$

Figure 3: The SIR model.

3. Final remarks on mathematical models in epidemiology

The models proposed above are a simplification of what actually happens. More complex models, such as the SIR model, also take immunity into account: once recovered, individuals can transit to a third compartment, R=immunity (Figure 3). Other more complex models take into account the possibility of death and new births, so the value of the population N is no longer constant.

To learn more about epidemiological models:
• A simple and accessible text that offers an introduction to the mathematics of infectious diseases is Li's recent book: *An Introduction to Mathematical Modeling of Infectious Diseases* Springer, 2018.
• At a more advanced level, see the Hethcote's mathematical treatment: *The Mathematics of Infectious Diseases* SIAM Review, 42 (2000), 599-653 https://www.maths.usyd.edu.au/u/marym/populations/hethcote.pdf.
• In this video, an in-depth look at the mathematical modeling of epidemics, and references to the case of the recent Covid19 pandemic: https://youtu.be/Kas0tIxDvrg?si=QlLvN3lubmOYLUoP.