PandemicAnalytics

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Chapter 1

Motivation

In the midst of the COVID19 pandemic, which changed the world order as we know it, we can quickly get overwhelmed. With all the news, numbers and new measures taken by different governments, it's hard to get a clear understanding of the situation and to distinguish the truth.

One can wonder if these measures can really help slow down the spread? If so at which rates do they have to be implemented to be effective? How do different measures add up ?

As students, we consider that the LauzHack is a great opportunity to put into practice concepts we learnt so far towards a good cause.To do so we are using mathematical models: in fact, they can give quite precise ideas of the situation and allow us to make relevant predictions.

Due to the lack of data on the current pandemic: we study general epidemics and try to analyse their spread. We allow the visitors to choose different values for parameters through an interactive platform. The different options will give a better interpretation on how different values lead to different spread rates and thus how strategies like confinement to different rates and social distancing for instance affect.

Chapter 2

Theoretical Aspects

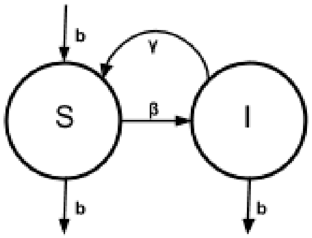
2.1 Two mix density R_0

We consider the two mix density SIR developed in the semester project [1]. In a n population with n_H local scale, we consider the case of μ_G the expected value of the number of infections in a global scale and μ_i the expected value of the number of infections in the i^{th} local scale, $i \in \{0, \cdots, n_H - 1\}$.

Those parameter allows us to compute $x_{n,i}$ the expected value at the n^{th} global step and j^{th} local step (steps represent spacial data and not temporal data, for more information consulte [1]). In addition we also compute x_n the expected value of the number of infection at step $n \in \mathbb{N}$. We shall use those expected values to compute the R_0 parameter.

2.2 Continuous SIS Model without immunity

Note that in this simulation, a person that has recovered develops no immunity and thus can be recontaminated a second time. This approach can be helpful in case there are mutations of the virus. The cure rate is the proportion of people that comes back to a healthy state after having been infected. We use the average duration of infection to compute.



This wonderfull schema comes from [1].

We use the continuous SIS Model defined in [1]:

$$\left\{ \begin{array}{rcl} S' & = & -\frac{\beta}{N}SI + (b+\gamma)I, \\ I' & = & -\frac{\beta}{N}SI - (b+\gamma)I, \end{array} \right.$$

Where $b \in \mathbb{R}_+$ is the birth/death rate, $\gamma > 0$ the cure rate, $\beta > 0$ the contact rate and N the population number. Furthermore, $I(t)$ describes the evolution of the number of the infected people over time and $S(t)$ represents the numbers of healthy people.
We denote the initials conditions $I_0 = I(t_0)$ and $S_0 = S(t_0)$ and consider that N the population number is constant, thus for any time $N = I(t) + S(t)$.

The solution for $I(t)$ is given by :

$$\left\{ \begin{array}{rcl} I(t) & = & I_0 \qquad \text{If } I_0 = \frac{c}{\beta}N, \\ I(t) & = & \frac{I_0}{1+\beta\frac{I_0}{N}t} \qquad \text{If } I_0 \neq \frac{c}{\beta}N \text{ and } c = 0, \\ I(t) & = & \frac{c}{\frac{\beta}{N} - (\frac{\beta}{N} - \frac{c}{I_0})e^{-ct}} \qquad \text{If } I_0 \neq \frac{c}{\beta}N \text{ and } c \neq 0. \end{array} \right.$$

Where $c = \beta - (b - \gamma)$ and $t \in \mathbb{R}_+$.

2.3 Continuous SIR Model

We use the continuous SIR Model presented in [2] defined by :

$$\left\{ \begin{array}{rcl} x' & = & -\frac{bxy}{x+y}, \\ y' & = & \frac{bxy}{x+y} - cy, \\ z' & = & cy. \end{array} \right.$$

Where $b \in \mathbb{R}_+$ is the average number of individual a given individual encounters in a time unit and $c \in \mathbb{R}_+$ the rate at which the population leaves the infected class (death or recovery). The initial conditions are denoted $x_0 = x(t_0)$,$y_0 = x(t_0)$, $z_0 = z(t_0) = 0$.
We obtain, using the method describe in [2], the following solution assuming $b \neq c$:

$$\left\{ \begin{array}{rcl} x(t) & = & x_0(1+\kappa)^{\frac{b}{b-c}}(1+\kappa e^{(b-c)(t-t_0)})^{-\frac{b}{b-c}}, \\ y(t) & = & y_0(1+\kappa)^{\frac{b}{b-c}}(1+\kappa e^{(b-c)(t-t_0)})^{-\frac{b}{b-c}}e^{(b-c)(t-t_0)}, \\ z(t) & = & x_0 + y_0 - (x_0+y_0)^{\frac{b}{b-c}}(x_0 + y_0 e^{(b-c)(t-t_0)})^{-\frac{c}{b-c}}. \end{array} \right.$$

We shall plot dynamically the solutions depending on the parameters to highlight the impact of b, c on the x, y, z.

Chapter 3

Implementation

3.1 Two mix density R_0 (MATLAB)

Given how societies are organised, it can be clever to divide the population into smaller communities. Indeed, we all have a group of people we meet more frequently, be it family, coworkers or just a local community. In the case of a pandemic, this will mean that when there's an infected person in a small group, it is more likely that people in the same group will be infected with higher chances.

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We therefore studied this aspect to generate an R_0 defined as the basic reproductive ratio that takes this distribution into account.

To do so, we consider different global and local mean values of the number of people infected per person. These considerations allow us to visualise the consequences of different levels of confinement on the evolution of the pandemic: by taking a smaller global expectation, we model a situation of higher degree confinement.

We implemented situations with three levels of confinement local low and moderate and high. The total population is set to 1,000,000 people and communities of equal size with 100 people. The results are implemented on Matlab and we used the output excel files to create the graphs. The interactivity on the compare page, does not not actually do a live simulation it reads into the right part of the excel file.

3.2 SIS model (MATLAB)

The population considered is now divided into two groups: the infected and the healthy people. We are trying to track the evolution of the number of people in each group over time. This problem can be described in terms of a system of differential equations that admits a unique solution to fixed initial conditions.

Note that in this simulation, a person that has recovered develops no immunity and thus can be recontaminated a second time. This approach can be helpful in case there are mutations of the virus. The cure rate is the proportion of people that comes back to a healthy state after having been infected. We use the average duration of infection to compute it.

The values of both infected and healthy people always stabilise over time towards a fixed value depending on the value in R_0 computed by the two mix density method described above. Naturally, the stabilisation value depends on the total number of populations (proof can be found in [1]).

To generate the data, we looped over time the solution equations and stopped when we reached the stabilisation values. This generates a $2 \times n$ array where n is the total number of loops and where the first and second columns represent respectively the number of healthy and infected people.

3.3 SIR model (MATLAB)

This time we choose the SIR model which is more complex because it takes into consideration more parameters and hence generates numbers closer to reality. Now, in addition to dividing the population into healthy and contaminated people, we also study the number of people that leave the infected state, either they developed an immunity or are dead.

Note that in this simulation, we do not consider the possibility of being infected a second time after healing contrary to the SIS model.

With the cure rate, we get a system of differential equations which will be in terms of the average number of individual meetings and the rate at which the population leaves the infected state (death or recovery). Then, we loop on the explicit solution equations cited above until we reach a limit value: in this case once R reaches N. We get a $3 \times n$ array with n being the number of generations of the spread where the three columns represent respectively the number of healthy, contaminated and recovered people.

3.4 Website (HTML5/CSS3)

We decided to share with anyone our experiment using a website.

The website is divided in three major parts. First we have a single view tab introducing the simulation models used. Here we give an overview of how each model works and list the parameters taken into account.
Then, there is a second tab dedicated to comparing results under different models. The visitor will have the possibility to change the value of parameters and see their influence on the graph, making our platform interactive. To guarantee a better comparison, we will put two graphs side by side. Both can be changed from parameters.
Finally we also have a preselected comparison tab where we chose for each model two graphs with predetermined parameters. Here we give a more in depth explanation of the two processes and how the different parameters have affected the final graph.

Bibliography

[1] Hugo Falconet et Antoine Jego. Modéliser la propagation d'une épidémie. Juin 2015.

[2] Delfim F.M. Torres Martin Bohner, Sabrina Streipert. *Nonlinear Analysis: Hybrid Systems*, December 2018.