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Research project report

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SIR model and cellular automata for disease propagation

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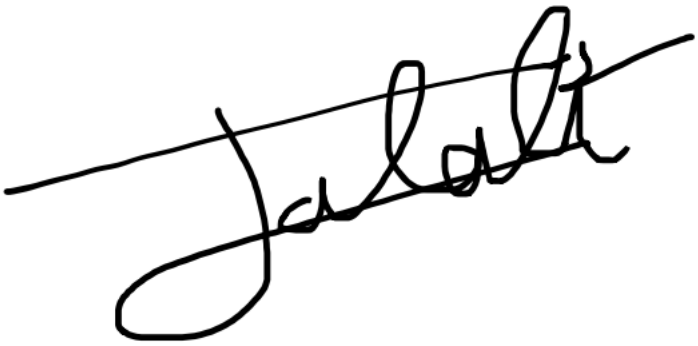

Acknowledgements

This research work was carried out in a particular context. This project intervenes as a substitution of an internship abroad that was cancelled due to the coronavirus health crisis that started at the beginning of the year 2020. Indeed, this one was scheduled from May to July 2020. Period during which the government implemented a containment. A period that was more or less complicated for some people. This is why I would like to thank all the professionals who participated to help get through these complicated moments and especially the medical staff.

I would also thank Laurent Hardouin, my supervisor, for helping me throughout this research work.

Glossary

Cellular automaton: A cellular automaton consists of cells arranged on a grid. Each cell of the grid can be in a state defined by the automaton. This state evolves in time. Indeed, the state of a cell at time t will depend on its state at time t-1, but also on the state of its neighboring cells according to certain transmission rules. At each iteration of time these same rules are applied, creating a new generation of cells. (1)

Infectious disease: An infectious disease is a disease caused by a pathogenic agent (virus, bacteria...) and spread directly or indirectly from a person to another. (2)

Virus: A virus is a micro-organism that infects a host human organism. (3)

Status variable: A status variable is one of a set of variables that are used to describe the mathematical "state" of a dynamic system. (4)

Differential equations: A differential equation of n-order is an equation linking a function to its first n deriveds. (5)

Epidemic: An epidemic is the rapid development and spread of a contagious disease among a large number of people in a particular area. (6)

Pandemic: A pandemic describes the worldwide or continental spread of a disease. (6)

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1 Introduction

1.1 Justification of the topic choice

The world is currently going through a health crisis that will stay in history. The outbreak of the new coronavirus SARS-CoV-2, which appeared between late 2019 and early 2020 in Wuhan, China, has become a pandemic as it has spread throughout the world. The disease caused by this virus, called COVID-19 (COrona VIrus Disease 2019), is a highly infectious disease that can be fatal for some people. In addition, some people are asymptomatic to the disease. These people can become infected, and thus infect other people, without feeling the effects of the disease. The problem with the SARS-CoV-2 virus is that despite all the global clinical efforts, there is no treatment available as of the date of writing this report. (7)

In response to this pandemic, governments have taken steps to limit the spread of the virus. Thus, social distancing measures and even containment measures have been put in place. To take such measures, governments are conducting mathematical simulations to predict the evolution of the epidemic. One of the simple mathematical models used is the SIR model. Therefore, this report will focus on the analysis of the simple SIR model.
This report will also discuss about cellular automata. These provide a more visual representation for the spread of disease.

1.2 Presentation of the issue

The purpose of a mathematical model is to describe real-life situations with variables linked by equations. In this way, predictions can be made to analyse the behaviour of real phenomena.

"Mathematics can be defined as a science in which you never know what you're talking about, or if what you're saying is true."

Bertrand Russell (8) (9)

The SIR model is a very simple simulation model, so it is legitimate to ask if it is true to reality. In other words, can the behaviour of an infectious disease in a population be correctly simulated using the SIR model? This analysis will focus on the SIR model and some modifications that can be made to it. It will also present other compartmentalized simulation models.

2 Latest developments

The SIR model is a basic mathematical model for simulating the spread of an infectious disease. This model is called compartmentalized because the population to which the simulation is applied is divided into three compartments : S for healthy people (who are not infected but susceptible to infection), I for the infected population, R for people who are no longer infected, recovered (cured or dead). This explains the name of the model, SIR model. Each compartment is characterized by a status variable, representing the share of the population present in the block at time t. The status variable is S(t) for healthy persons, I(t) for infected persons and R(t) for recovered persons. In the SIR model two other variables are involved: β a ratio that takes into account contacts between infected and susceptible persons. He also takes into account the probability that the infected person transmits the virus to the healthy person; λ (in days) is the average number of days needed for an individual infected to get better. It is these variables that characterize the epidemic.

Figure 1 : SIR model represented with blocs

The variables can now be linked together by translating the assumptions of the SIR model into equations. These assumptions are essential for the model to work properly but also to keep the model simple.

- The SIR model considers the population has homogeneous. Each individual has the same chances of coming into contact with an infected person and the same chances of recovery.

- As shown in the figure below, a recovered individual can no longer be infected with the disease, he will be considered immune.

- During the simulation the population P remains constant. The model is considered closed.

$$P = S(t) + I(t) + R(t) = Cte$$

- The proportion of newly infected persons (leaving the Susceptible class for the Infected class) is proportional to the number of infected and susceptible persons multiplied by β.

$$S'(t) = -\beta I(t)S(t)$$

- The proportion of people who recover is equal to the ratio between the number of infected people and λ.

$$R'(t) = I(t)/\lambda$$

- From the two previous hypotheses we deduce the differential equation of the number of infected persons

$$I'(t) = \beta I(t)S(t) - \frac{I(t)}{\lambda}$$

In summary, the SIR model is defined by three differential equations:

$$\begin{cases} S'(t) = -\beta I(t)S(t) \\ I'(t) = \beta I(t)S(t) - \dfrac{I(t)}{\lambda} \\ R'(t) = I(t)/\lambda \end{cases}$$

To use this system of differential equations, the initial values must first be determined. Thus, $I(0)$ must be found, which represents the number of people infected at the beginning of the epidemic. $S(0)$ (population susceptible to be infected at the beginning of the epidemic) must also be identified. $R(0) = 0$ is usually taken because no one is immune at the beginning of the epidemic.

The SIR model remains a simple model but useful for understanding the behaviour of the epidemic and thus understanding the decisions made by health authorities in crisis management. To do this, we need to look at the reproduction coefficient: $R_0 = \beta\lambda$. Indeed, if $R_0 > 1$, it means that an infected individual will contaminate more than one person thereafter. The disease will thus cause an epidemic. If $R_0 < 1$, an infected individual will infect less than one person. To reduce R_0, the authorities have two possibilities:

- Decrease β, by implementing social distancing measures, containment or apply barrier gestures.
- Decrease λ, by finding a treatment for the disease for example.

As stated above, the SIR model is a simple mathematical model that contains various defects. Therefore, some modifications can be made to improve the model. (10) (11) (12)

One of the problems with the SIR model is that the disease does not impact the population size. Therefore, mortality caused by the disease can be taken into account. To do this, we need to add a block to the model, a D block for those who die from the disease. This block will therefore involve adding a state variable $D(t)$, the number of people who died from the disease. It is also necessary to characterize the mortality of the disease with the parameter μ, which represents the mortality rate. Thus, an infected person will be able to recover or die from the disease.

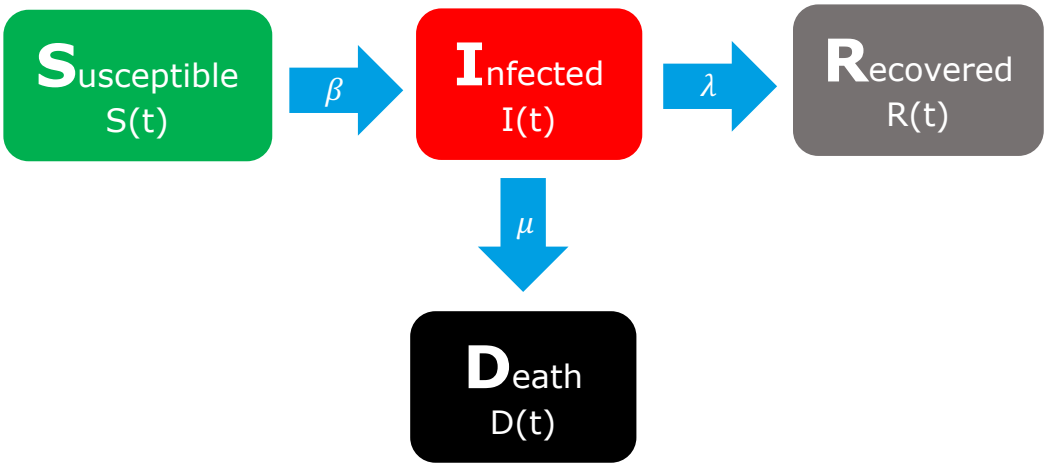


Figure 2 : SIR model represented with blocs, with taking into account the mortality of the disease

This implies a change in the differential system equations but also in the population equation. So, we need to add the number of people who die at each instant t, $\mu I(t)$. (11)

$$\begin{cases} S'(t) = -\beta I(t)S(t) \\ I'(t) = \beta I(t)S(t) - \frac{I(t)}{\lambda} - \mu I(t) \\ R'(t) = I(t)/\lambda \\ D'(t) = \mu I(t) \end{cases} \qquad P(t) = S(t) + I(t) + R(t)$$

Another way to improve the SIR model is to consider a possible treatment for the disease if one exists. As done previously, a block T, with its associated status variable $T(t)$, is added to consider those who are undergoing treatment. This treatment must now be described using three parameters. The first one will characterize the proportion of infected individuals chosen to follow the treatment at each time t, represented by α. The second will be the rate at which a treated individual recover from the disease, a rate noted η. The individual will be considered immune. Finally, the third parameter will be δ. It will represent the factor that reduces the rate of infection for a treated individual. In fact, despite the fact that the person is undergoing treatment, he may still be infected. Furthermore, it is hypothesized that a treated person is also considered susceptible.

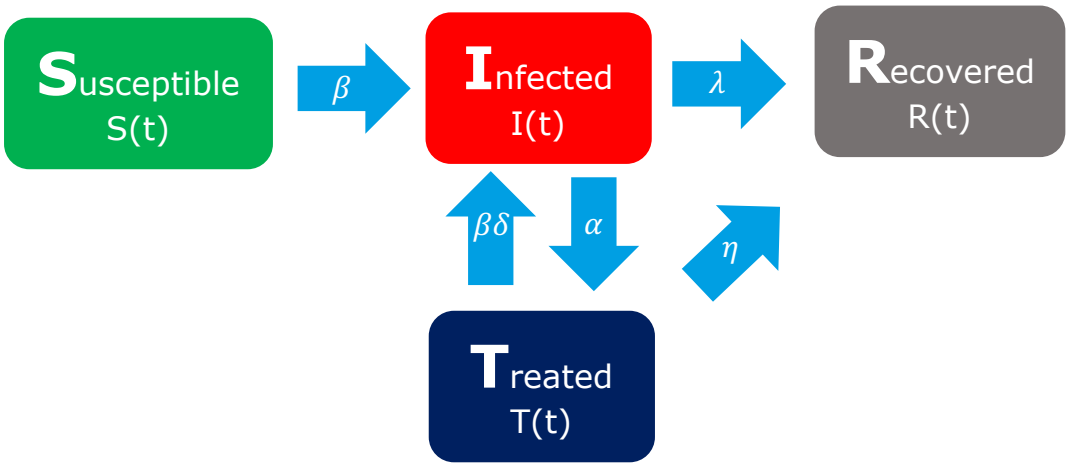


Figure 3 : SIR model represented with blocs, with taking into account a treatment of the disease

As realized previously, we can easily modify the differential equations by taking the different parameters and their role. (13) (14)

$$\begin{cases} S'(t) = -\beta I(t)S(t) - \beta\delta T(t) \\ I'(t) = \beta I(t)S(t) + \beta\delta T(t) - \alpha I(t) - \dfrac{I(t)}{\lambda} \\ T'(t) = \alpha I(t) - \eta T(t) \\ R'(t) = \dfrac{I(t)}{\lambda} + \eta T(t) \end{cases}$$

Another fault of the SIR model is that it does not take into account the incubation period of the disease. For an infectious disease, the incubation period is the time it takes for the disease to develop (15). A healthy individual who catches the virus will therefore only be contagious to other people after this incubation period. In the SIR model, this translates into the fact that a healthy person from block S who comes into contact with an infected person and catches the disease will only be considered infected after the incubation period, which will be represented by τ in the model equations. This variable representing the incubation period is usually in days. This obviously implies changes in the differential system. As a result, the proportion of infected individuals will no longer depend solely on time t but on the time at time $t-\tau$. This gives the following system: (16)

$$\begin{cases} S'(t) = -\beta I(t-\tau)S(t-\tau) \\ I'(t) = \beta I(t-\tau)S(t-\tau) - \dfrac{I(t)}{\lambda} \\ R'(t) = I(t)/\lambda \end{cases}$$

Now that we know how to modify the SIR model, we can improve it by combining the three modifications seen above:

- Consider the mortality of the disease with the parameter μ.
- Take into account the existence of a potential treatment, characterized by the parameters η, α and δ.
- Add the incubation period τ.

It will be assumed that the mortality for treated individuals is decreased with the parameter δ. By combining the block representations, the figure below is obtained:

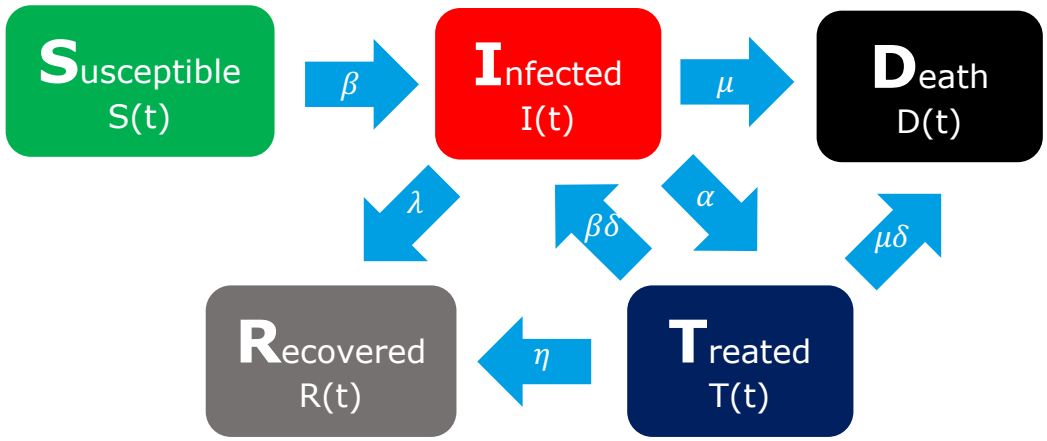


Figure 4 : SIR model represented with blocs, with taking into account the three changes

It is now possible to combine the three systems of differential equations, previously seen for the three changes of the SIR model, into a single system: (11) (13) (14) (16)

$$\begin{cases} S'(t) = -\beta I(t-\tau)S(t-\tau) - \beta\delta T(t) \\ I'(t) = \beta I(t-\tau)S(t-\tau) + \beta\delta T(t) - \alpha I(t) - \dfrac{I(t)}{\lambda} - \mu I(t) \\ T'(t) = \alpha I(t) - \eta T(t) - \mu\delta T(t) \\ R'(t) = \dfrac{I(t)}{\lambda} + \eta T(t) \\ D'(t) = \mu I(t) + \mu\delta T(t) \end{cases}$$

$$P(t) = S(t) + I(t) + T(t) + R(t)$$

Other compartmentalized models are also available. The SEIR model is a more complex model than the SIR model but it is still accessible and easy to use. As its name suggests, in the SIR model the population is divided into four parts. The model retains the S, I and R categories of the SIR model. In addition, there is block E for people who have been in contact with the disease and who have been caught it, but who are not yet contagious to the rest of the healthy population. Block often referred to as "exposed". Another way of taking into account the incubation of the disease but with the difference that the person is not considered to be contagious. Like the SIR model, the SEIR model retains the parameters β and λ and their function. In addition, a new parameter comes into play, α will represent the incubation rate. This mathematical model, different from the SIR model, corrects assumption of the latter. Indeed, this model takes into account the birth rate of the population, noted υ. This new population will be considered healthy, in the susceptible bloc. The model also takes into account mortality not related to disease. So, any person, regardless of his condition (susceptible, exposed, infected or recovered) can be a victim of this mortality. This will depend on the mortality rate of the population noted μ. The population therefore varies over time.

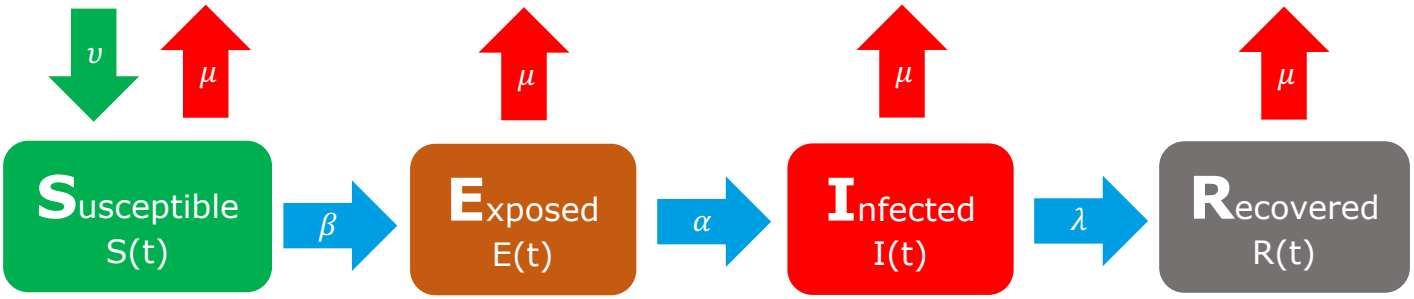


Figure 5 : SEIR model represented with blocs

The system of differential equations can now be taken from the SIR model and modified to include mortality, births and the fourth state variable $E(t)$. $P(t)$ will represent the total population at time t: (17)

$$P(t) = S(t) + E(t) + I(t) + R(t)$$

$$\begin{cases} S'(t) = -\beta I(t)S(t) + \upsilon P(t) - \mu S(t) \\ E'(t) = \beta I(t)S(t) - \alpha E(t) - \mu E(t) \\ I'(t) = \alpha E(t) - \dfrac{I(t)}{\lambda} - \mu I(t) \\ R'(t) = \dfrac{I(t)}{\lambda} - \mu R(t) \end{cases}$$

We can also look at another compartmentalized model, the SEIQR model. The state variables for the different blocks are as follows: $S(t)$ for susceptible people; $E(t)$, the exposed people. These are the individuals who have caught the disease but are asymptotic, have no symptoms, but are still contagious for healthy individuals; $I(t)$ is the variable for infected individuals with symptoms; $Q(t)$ is the variable for individuals placed in quarantine once symptoms have appeared; $R(t)$ is the variable for individuals who have recovered. Concerning the parameters, the model retains the parameters of the SEIR model: β, λ, α, υ and μ. They play the same role in the SEIQR model. The only difference is that only healthy people are considered to reproduce. Other variables are involved in the model: δ for the proportion of individuals placed in quarantine once symptoms appear. κ which represents the proportion of asymptotic individuals who recover. ε for individuals in quarantine who recover.

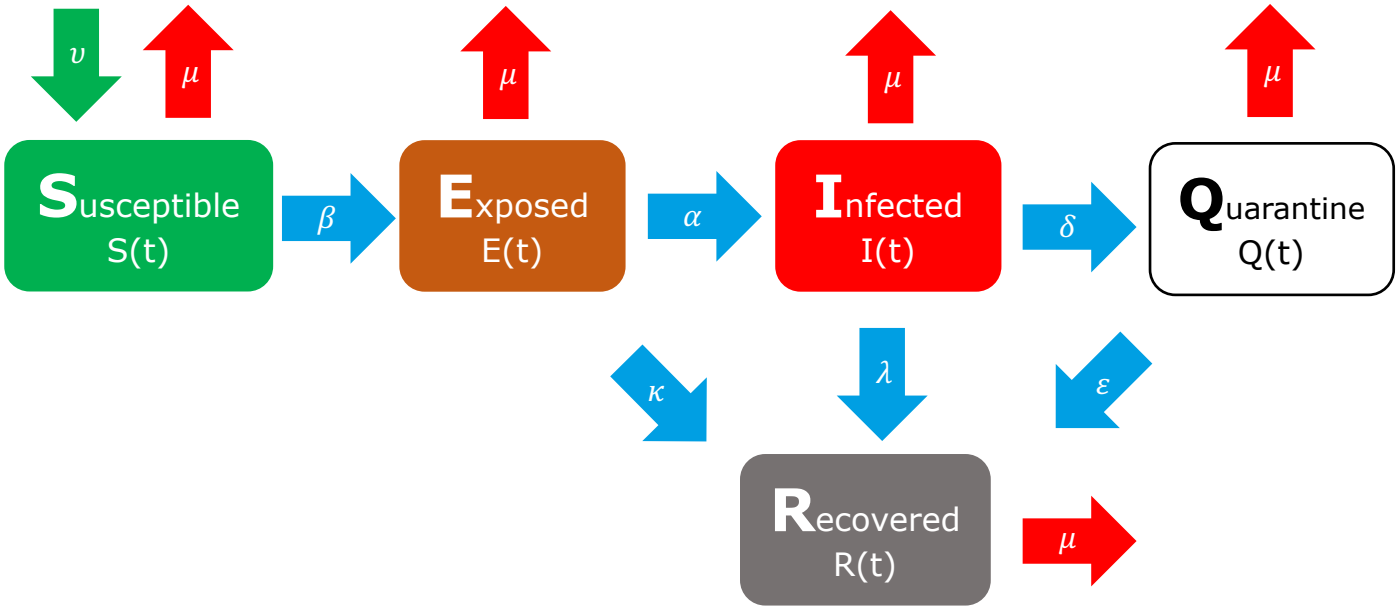


Figure 6 : SEIQR model represented with blocs

For this model the system of differential equations is the following: (18)

$$\begin{cases} S'(t) = \upsilon P(t) - \beta S(t)[I(t) + E(t)] - \mu S(t) \\ E'(t) = \beta S(t)[I(t) + E(t)] - E(t)[\mu + \alpha + \kappa] \\ I'(t) = \alpha E(t) - I(t)[\mu + \delta + \frac{1}{\lambda}] \\ Q'(t) = \delta I(t) - Q(t)[\mu + \varepsilon] \\ R'(t) = \kappa E(t) + \frac{I(t)}{\lambda} + \varepsilon Q(t) - \mu R(t) \end{cases}$$

3.1 Action presentation

The subject of this report being "SIR model and cellular automata for disease propagation", I decided to develop an application simulating the propagation of an infectious disease, at the scale of France, using the SIR model.

The SIR model used is the simple model, with a possible modification, in which the disease is characterized by two or three parameters:

- The probability that an infected individual will transmit the disease when in contact with a healthy person.
- The average number of days for an infected person to recover from the disease.
- It is possible to take in consideration the mortality of the disease with the percentage of chance that an infected person die from the disease.

To give a more graphical aspect to the SIR model, usually represented using graphics, I decided to integrate cellular automata into the simulation. The cellular automaton used to represent the SIR model is a one-dimensional automaton, where the grid represents the map of metropolitan France (without Corsica). Each cell has eight neighbouring cells (adjacent cells and diagonal cells) and can be in three possible states, representing the SIR model states, healthy (susceptible), infected and recovered (and dead if you consider the mortality). The transmission rules of the automaton will be those of the SIR model. If a healthy cell has one or more infected cells in its neighbourhood, then, depending on the probability defined in the SIR model, it will in turn be infected for the number of days also defined in the model. If disease mortality is taken into account, then an infected cell may die.

I also decided to add a part for cellular automata to the application. In this part, we can discover the behaviour of cellular automata presented by Nazim Fatès in his article "A la Découverte des Automates Cellulaires" (19), article summarized in the rest of the report. In this way, the application presents the Game of Life, the Parity Counter and the Majority Rule and I invite you to discover how they work in the previously cited article.

3.2 Implemenatation

To design this application, I decided to develop it in Python language (20), while using the Tkinter interface (21). A graphical interface already seen during Modeling and Simulation courses. The Tkinter interfaces remain simple to use and manipulate, but they are still complete. The application consists of three interfaces. A welcome interface that provides information on how the application works. Using the "Help" button. A second interface for the simulation of the SIR model on the scale of France. An interface for cellular automata. And finally, an interface to discover how to use the two previous ones. This part will only present the graphical aspect of the application. The Python code will be available in appendix.

The home page is very simple. It simply useful to displays the other interfaces.

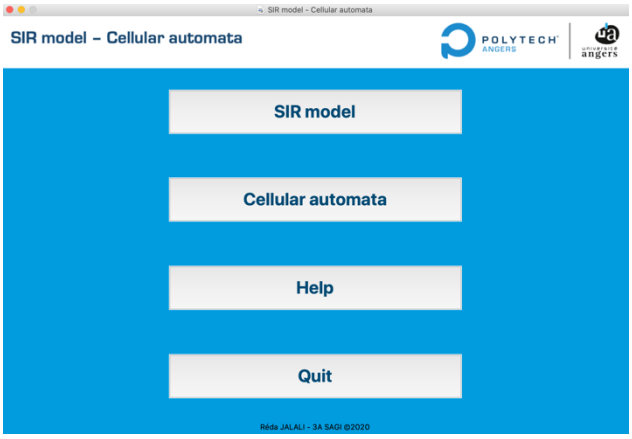


Image 1 : Application homepage

The "Help" section simply explains how to use the "SIR Model" and "Cellular automata" sections.

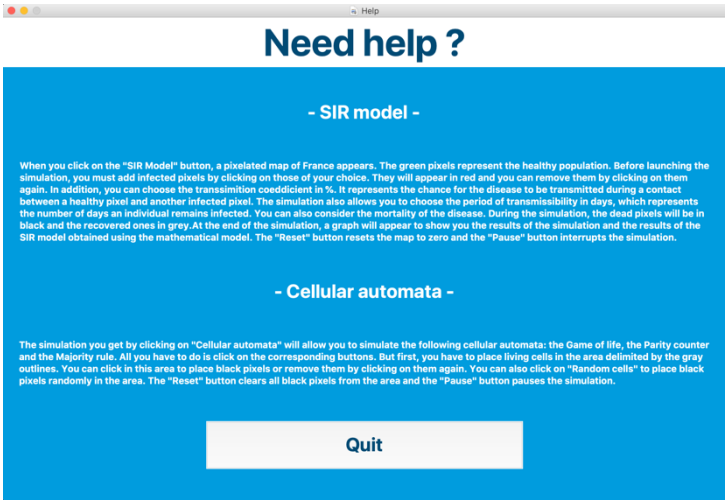


Image 2 : "Help" page of the application

For the SIR model, I designed a pixelated image of the map of metropolitan France (without Corsica). At the beginning of each simulation, green pixels are randomly added to represent the healthy cells of the SIR model. These cells will evolve red (infected), grey (recovered) or black (dead) during the simulation. Coloured cells can move around the map unless they are in a dead state. The changes in cell states will depend on the two or three parameters of the SIR model that can be set using the various "+" and "-" buttons. At the end of each simulation, a graph appears with the curves to summarize the evolution of the simulation and the dotted curves obtained with the SIR model mathematical equations.

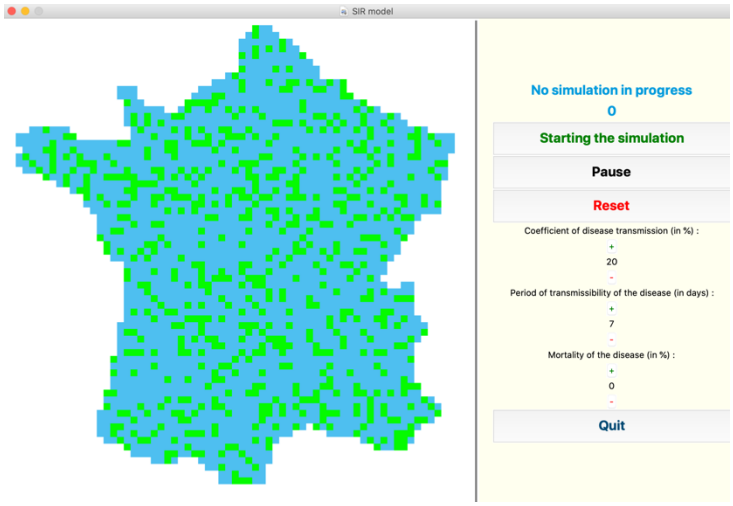


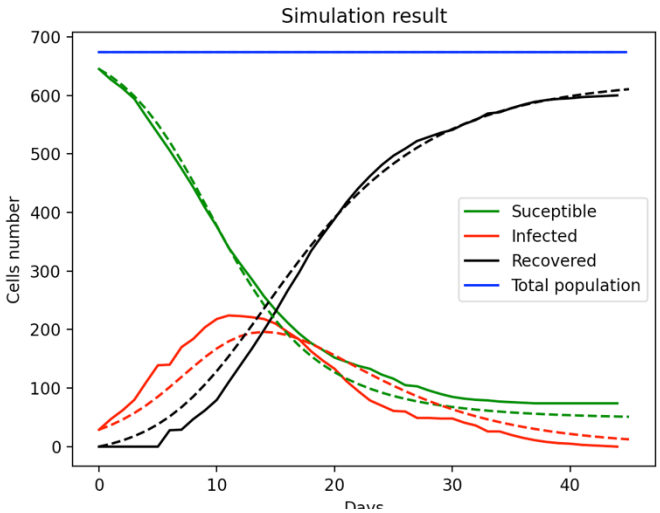
Image 3 : « SIR model» page of the application

To finish the part "Cellular automata" allows to simulate the operation of three cellular automata. I invite you to understand how they work by reading the summary of Nazim Fatès' article dedicated to cellular automata. In this interface you can choose to place the living cells randomly or manually by clicking in the grid represented by the white area.

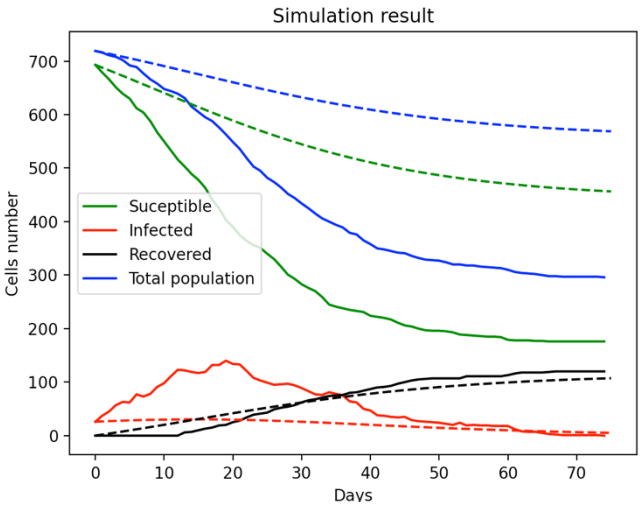
Image 4 : « Cellular automata » page of the application

3.3 Results and discussion

In a first time, simulations of the SIR model make it possible to observe the different behaviours of the SIR model. Notably the peak of the epidemic after several iterations and the disappearance of the disease. After several simulations with different settings for the different parameters of the SIR model, the results of these simulations can be compared with the mathematical results of the SIR model. It can be noted that for some simulations the SIR model can be considered as faithful to the behaviour of the simulation. But for some simulations, the SIR model deviates from the simulation. This can be explained by some unexpected events during the simulation. These events may be that an infected cell does not come into contact with a healthy cell, or that the infected cells die quickly due to the random aspect of mortality.



Graph 2 : Example of a result obtain with a simulation



Graph 1 : Example of a result obtain with a simulation

In a second time, the part dedicated to cellular automata allows us to observe the phenomena described by Nazim Fatès in his article. Indeed, after several simulations of the Game of Life, we observe the phenomena of self-organization, emergence of sliders and unpredictable evolution of the system. This is also the case with the other automata. The phenomena of self-organization appear in the Majority Rule. We can observe the phenomenon of self-reproduction of the Parity Counter by initially and manually placing a figure on the grid and then launching the simulation.

4.1 Summary of article 1

- Title : À la Découverte des Automates Cellulaires (19)
- Authors : Nazim Fatès
- Journal : Interstices
- Publisher : Inria
- Year : 2007

Nazim Fatès is a researcher at INRIA, the French National Institute for Research in Digital Science and Technology. His article, published in April 2007, entitled "A la Découverte des Automates Cellulaires", presents different examples of cellular automata. In his article, Nazim Fatès presents one of the objectives of cellular automata: to make the analogy between the phenomena observed in living beings and the phenomena of machines.

To begin his study, Nazim Fatès explains the origin of cellular automata. In the middle of the 20th century, scientists were looking for correlations between the world of machines and that of living beings. In this way, they tried to describe artificial machines as living beings. Turing proposed a mathematical model of morphogenesis (a set of laws that determine the shape and structure of tissues, organs and organisms, Wikipedia) and Von Neumann a self-reproducing machine. A machine capable of building copies of itself. Later, Nazim Fatès tells us that with the help of the mathematician Marcin Ulman, Von Neumann proposes a mathematical model for his machine, a model that he will end up calling "cellular automaton". His automaton is two-dimensional, and each cell has 29 possible states and 5 neighbouring cells. Nazim Fates also explains that Von Neumann will demonstrate that cellular automata can simulate the operation of any machine or simulate any algorithm (Church's thesis). Unfortunately, we learn that Von Neumann's automaton is too complex to simulate but other models have been proposed.
First, Nazim Fatès presents the Game of Life, a model of cellular automaton. In this automaton, each cell can be in a state of life or death. This state depends on the 8 adjacent neighbouring cells respecting the two following transmission rules: the rule of life says that a cell remains alive if, and only if, 2 or 3 neighbouring cells are alive, otherwise the cell dies, and finally the rule of birth says that a cell becomes alive if 3 neighbouring cells are alive. Nazim Fatès explains that this automaton, simple to program and simulate, was a real

success. After several simulations, three phenomena appeared, phenomena explained by Nazim Fatès. First, the phenomenon of self-organization. Starting from a random initial state, after several simulations a certain organization can be observed. Islets of cells of cells stabilize in the state of life, areas without any living cells appear and other cells keep the random aspect of the automaton. Secondly, we can observe the emergence of sliders, figures composed of several living cells moving diagonally on the grid. More precisely in a sequence of 4 figures, the first one being identical to the last one but shifted by one cell on the grid. Finally, we notice an unpredictable evolution of the system. Nazim Fatès explains that it is impossible, for a given initial configuration, to predict its evolution. It is impossible to find a logic to predict the evolution of the system. Nazim Fatès adds that only a Laplace demon would be able to do so.
In a second step, Nazim Fatès proposes to look at the majority rule. A cellular automaton that remains simple with a rule of transmission: the cell takes the majority state present in its surroundings. Nazim Fatès tells us that with this model we can observe a self-organization of the system. Starting from a random initial situation, the grid stabilizes. Islets of living cells appear and others of dead cells. For Nazim Fatès, concerning the emergence for this system, it is difficult to answer. But in terms of prediction, Nazim Fatès explains that nowadays, we are unable to predict from how many iterations the automaton will stabilize. He also says that certain properties can be proven using static physics.
To finish his article, Nazim Fatès exposes the Parity Counter. Like the previous automaton, it is governed by a single transmission rule: if the number of neighbouring living cells is even, then the cell dies, otherwise it lives. With this transmission rule, Nazim Fatès explains that it is difficult to observe self-organization. Indeed, from a random initial situation, the system remains random. But with this automaton Nazim Fatès presents a new phenomenon. All initial figures are self-reproducing with the only limit the size of the grid. Nazim Fatès specifies that this is demonstrated with mathematical relations. The parity counter keeps the initial state and duplicates it. This explains the absence of self-organization for a random initial state. Iterations are superimpositions of random states.

In conclusion of his article, Nazim Fatès tells us that by imitating the genesis of living organisms we could create machines, electronic or computer systems able to organize themselves autonomously, in the image of the Game of Life and majority rule, or capable of self-replicating like the Parity Counter or Von Neumann's machine.

4.2 Summary of article 2

- Title : SIR Model (10)
- Authors : Robert Geofroy
- Year : 2020

The SIR Model article was published in May 2020 by Robert Geofroy, Professor of Science and Mathematics at the University of the West Indies. His article aims to present the SIR model described by the mathematician Tom Rocks from the University of Oxford. In addition, Robert Geofroy applies this SIR model to the Republic of Trinidad and Tobago for the COVID-19 epidemic. The purpose of this study is to understand the decisions made by the government and health authorities in terms of managing the health crisis. According to Robert Geofroy's study, studying the SIR model helps to understand and determine the number of people infected over time and so to understand the management of the epidemic.

The SIR model was introduced in 1927 by William Kermach, biochemist, and Anderson Mckendrick, physicist and epidemiologist. Robert Geofroy described this model as simple to handle and containing all the characteristics of a pandemic. Before presenting the model, Robert Geofroy gives us the assumptions to be taken into account in the SIR model to facilitate his approach. The population remains constant throughout the simulation, the rate of infected persons is proportional to the number of contacts between infected and susceptible (healthy) persons, the rate of decrease of infected persons is proportional to the number of infected persons, the incubation period is not taken into account and each individual has the same chances of recovering or being infected by the disease.
To begin, Robert Geofroy presents the variables of the model. $S(t)$ for healthy, potentially contaminated people at time t. $I(t)$ for infected persons and $R(t)$ for recovered persons (who are no longer infected, cured or dead). β for the contact coefficient between persons S and I, γ for the recovery coefficient of the disease and finally R_0 which represents the reproduction ratio. In a second step, Robert Geofroy presents the link between the variables based on the model's assumptions. The model is composed of three differential equations:

$$\begin{cases} \mathrm{S}'(\mathrm{t}) = -\beta \mathrm{I}(\mathrm{t})\mathrm{S}(\mathrm{t}) \\ \mathrm{I}'(\mathrm{t}) = \beta \mathrm{I}(\mathrm{t})\mathrm{S}(\mathrm{t}) - \gamma \mathrm{I}(\mathrm{t}) \\ \mathrm{R}'(\mathrm{t}) = \gamma \mathrm{I}(\mathrm{t}) \end{cases}$$

Finally, differential equations mean initial values. So, Robert Geofroy chooses $R(0)$ and $I(0)$ for his example the republic of Trinidad and Tobago. The total

population will be equal to 1 and $I(0) = 1/116$ because on March 13, 2020 116 people were infected in the country. This means that $S(0) = 1 - I(0)$ and $R(0) = 0$. After having seen the basics of the model Robert Geofroy is interested in its behaviour. This SIR model is considered closed because the population remains constant ($d(S + I + R))/dt = 0$). Robert Geofroy adds that at the beginning of the epidemic $I'(t) > 0$ (the number of infected people increases) and we can consider that the epidemic begins its regression when $I'(t) = 0$ (inflection point of $I(t)$), this also represents the peak of the epidemic.
In the continuation of his study, Robert Geofroy explains the purpose of the SIR model.
Firstly, it allows us to determine if the disease will spread. For that Robert Geofroy tells us to observe $R_0 = \beta/\gamma$,, the reproduction coefficient. If $R_0 > 1$ the disease will spread while if $R_0 < 1$ the disease will dissipate. To give an example, Robert Geoffroy say that for COVID-19 $R_0 \approx 2$. Which explains the pandemic.
Secondly Robert Geoffroy explains how to determine the maximum number of people infected, the peak of the epidemic. By manipulating the equations he gets : $I_{max} = I_0 + S_0 - \frac{\gamma}{\beta}\log S_0 - \frac{\gamma}{\beta} + \frac{\gamma}{\beta}\log\frac{\gamma}{\beta}$. In his example, for $R_0 \approx 2$, I_{max}would represent 50% of the population. This is an important number for health authorities because it should not be higher than the capacity of hospitals.
Finally, Robert Geofroy is interested in the total number of people infected by the disease represented by R_{end} which is obtained with the equation $R_{end} = I_0 + S_0 - S_{end}$ where S_{end} is obtained with $S_{end} - \frac{1}{R_0}\ln S_{end} = I_0 + S_0 - \frac{1}{R_0}$. In his example Robert Geofroy explains that R_0 is too big so R_{end} represents a large part of the population. To decrease R_0, you have to decrease the contact coefficient β (containment, social distancing...) or increase γ, (treatment, immunity...).
Finally, Robert Geofroy applies the model to the Republic of Trinidad and Tobago. Using data provided by the government, he performs a numerical analysis to determine the parameters. He obtains $\beta = 1.5$ and $\gamma = 2.16$, which gives $R_0 = 0.69$. So, as Robert Geofroy explained, there will not be an epidemic, which has been the case in the country. Furthermore, in his simulation Robert Geofroy observes a peak after the tenth day of simulation, a peak that he also observes in the government data.

In conclusion, although the SIR model is a simple model with several faults, it allows us to understand the basics of an epidemic and to answer some questions. However, we also learn that there are other more or less complex models such as the SI, SIS, SEIR, or SEIQR models. Unfortunately, no model is perfect, but they are still useful.

4.3 Summary of article 3

- Title : Modified SIR Model Yielding a Logistic Solution (22)
- Authors : Paul A. Reiser
- Year : 2020

Modified SIR Model Yielding a Logistic Solution, written by Paul A. Reiser, was released in June 2020. The author has a background in mathematics and medicine, particularly in infectious diseases. In his article, Paul A. Reiser presents a modified SIR model because the basic model is flawed due to an irrational assumption. Indeed, Paul A. Reiser explains that in the SIR model, the rate of individuals leaving the infected class for the recovered class is proportional to the number of infected individuals. This is why Paul A. Reiser proposes a more logical hypothesis, which is that an individual leaves the infected class after a certain period of time.

To begin his study Paul A. Reiser presents the time variables he will use. Variables of type $t_x$will represent a time and variables of type T_x will represent a time interval with their associated frequency f_x.
In addition, Paul A. Reiser also gives us a reminder of the SIR model. He explains that in this model the population is separated into three categories: $S(t)$ the number of healthy people, $I(t)$ the number of infected people, $R(t)$ the number of recovered people, who are no longer infected. The SIR model is composed of three differential equations:

$$\begin{cases} \mathrm{S}'(\mathrm{t}) = -\mathrm{f_c S(t) I(t)} \\ \mathrm{I}'(\mathrm{t}) = \mathrm{f_c S(t) I(t)} - \mathrm{f_r I(t)} \\ \mathrm{R}'(\mathrm{t}) = \mathrm{f_r I(t)} \end{cases}$$

With $\mathrm{f_c}$ representing the frequency of contact between healthy and infected individuals and $\mathrm{f_r}$ the frequency representing the probability of leaving the infected class for the recovered class.
Paul A. Reiser explained that the problem with the SIR model lies in equation $\mathrm{I}'(\mathrm{t}) = \mathrm{f_c S(t) I(t)} - \mathrm{f_r I(t)}$. Note that a change in the infection rate $\mathrm{f_c S(t) I(t)}$ will increase the number of infected persons $I(t)$, which at the same time implies a change in the rate of recovered persons $\mathrm{f_r I(t)}$. Paul A. Reiser proposes to take into account the time spent in the infected class. He explains that with this hypothesis, an individual remains in the infected class for a time T_r. So, a change at time t in the number of infected persons will lead to a change at time $t + T_r$ in the number of recovered persons. To model this mathematically, Paul A. Reiser uses $n(t) = I(t) + R(t)$, representing the cumulative number of people who have been infected. He easily derives the following equations from this:

$$\begin{cases} S(t) = 1 - n(t) \\ I(t) = n(t) - n(t - T_r) \\ R(t) = n(t - T_r) \end{cases}$$

By maintaining the infection rate as a function of frequency of contact, i.e. $n'(t) = f_c S(t) I(t)$, Paul A. Reiser gets: $n'(t) = f_c[1 - n(t)][n(t - T_r]$. The epidemic is then characterized with the parameters f_c (frequency of contact between individuals) and T_r (incubation period of the virus). Without detailing his reasoning, Paul A. Reiser integrates $n'(t)$ and obtains: $n(t) = n_m + \frac{n_p - n_m}{1 + e^{-f_e(t-th)}}$

He explains that $n_m = n(-\infty)$ is an initial condition (often equal to 0), t_h the time when $n(t)$ knows its inflection point (peak of the epidemic), $n_p = n(\infty)$ and f_e are dependent parameters of f_c and T_r, also called phenomenological parameters. In the continuation of his study Paul A. Reiser expresses the parameters f_e and n_p. In the first step, Paul A. Reiser expresses f_e as a function of f_c and T_r. For this, he observes the limit $\lim_{t \to -\infty} n'(t)$. After several mathematical manipulations Paul A. Reiser deduces the following equation $f_e = \frac{R_m + W(0, -R_m e^{-R_m})}{T_r}$. With $R_m = f_c T_r (1 - n_m) = R_0(1 - n_m)$. R_0 represents the reproduction ratio of the epidemic and $W(i, j)$ the Lambert function. In a second step, Paul A. Reiser is focused on n_p. Following the same reasoning as before and then using his mathematical skills, Paul A. Reiser obtains $n_p = \frac{f_e}{f_c} - n_m$. Paul A. Raiser adds that we can now express the characteristics of the epidemic (f_c, T_r) as function of the phenomenological parameters (f_e, n_p): $f_c = \frac{f_e}{n_p - n_m}$ and $T_r = \frac{1}{f_e} \ln \frac{1 - n_m}{1 - n_p}$.

Finally, Paul A. Reiser proves that his model is correct with mathematical manipulations. He proves that the derivative of $n(t)$ equals the differential equation of the model: $n'(t) = f_c[1 - n(t)][n(t) - n(t - T_r)]$.

In conclusion, we could see that in his article, Paul A. Reiser proposes a more rational solution to the classical SIR model. Thanks to the hypothesis that an individual remains for a certain time in the infected class. With this hypothesis, Paul A. Reiser proposes a new SIR model characterized by the following equations:

$$\begin{cases} S(t) = 1 - n(t) \\ I(t) = n(t) - n(t - T_r) \\ R(t) = n(t - T_r) \end{cases}$$

Where $n(t)$ characterizes the number of cumulative infected and recovered persons at time t governed by the equation $n(t) = n_m + \frac{n_p - n_m}{1 + e^{-f_e(t-th)}}$. Although this model corrects an error in the SIR model, it remains a mathematical model.

5 Conclusion

During the management of a sanitary crisis, as it is currently occurring with COVID-19, health authorities and governments use very complex simulation models using a maximum of parameters characterizing the disease and the population. In addition, by virtue of their powers, they have numerical data on the population, data that are more or less accessible to the general public. This is why simple models, such as the SIR model, exist. It has allowed us to understand how health authorities and governments simulate the spread of infectious disease in order to make decisions to control a possible epidemic. Although the SIR model is a very simple model with assumptions that more or less respect reality, it is still useful to observe the different aspects of an epidemic and how to combat it (barrier measures, treatment, containment...). This simplicity of the SIR model makes it easy to simulate. However, it remains a mathematical model and although it contains the basic characteristics of an epidemic, it is difficult to simulate the reality with this model. There are other more complex simulation models, as we have seen with the compartmentalized SEIR and SEIQR models. The family of compartmentalized system models forms a very large mathematical model family. Although the purpose of a mathematical model is to describe reality with variables and equations, it is difficult to simulate the behaviour of the real world, a world where anything can happen.

From a personal point of view, this work has allowed me to acquire and deepen skills. Indeed, it allowed me to develop my bibliographical research skills by analysing and synthesizing different sources, in particular by summarizing scientific articles. In addition, I was also able to discover how to simulate the spread of a disease with a simulation model that I had never seen before. My eye will take a different look at the management of the COVID-19 disease crisis. Finally, developing a Python application allowed me to deepen my knowledge of this programming language, particularly in terms of Tkinter graphical interfaces.

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7 Appendix

Appendix 1 : Link to download the python files

http://perso-laris.univ-angers.fr/~hardouin/jalali.html

Modèle SIR & Automates cellulaire

pour la propagation de maladie

Un modèle mathématique a pour but de décrire des situations réelles avec des variables reliées par des équations. Le modèle SIR modélise la propagation d'une maladie infectieuse au sein d'une population causant une éventuelle épidémie.

Modèle SIR

Le modèle SIR est dit compartimenté car à chaque instant t, il devise la population en trois catégories :

- Les personnes saines, susceptibles d'être infectées représentées par la variable S(t)
- Les personnes infectées caractérisées par I(t)
- Les personnes rétablies avec R(t), qui ne présentes plus de signe de la maladie, qu'elle soit morte ou guérie.

De plus ce modèle caractérise la maladie avec deux paramètres :

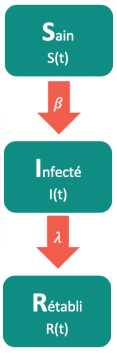
- β le ratio de contact infectieux entre S(t) et I(t)
- λ le nombre de jours moyen pendant lequel un individu I(t) reste infecté

Le modèle SIR est caractérisé par un système de trois équations différentielles :

$$\begin{cases} S'(t) = -\beta I(t)S(t) \\ I'(t) = \beta I(t)S(t) - \dfrac{I(t)}{\lambda} \\ R'(t) = I(t)/\lambda \end{cases}$$

Pendant la simulation la population total P reste constante:

$$P=S(t)+I(t)+R(t)$$



Automates cellulaires

Un automate cellulaire est composé d'une grille de cellules se trouvant dans un état particulier à chaque instant t. L'état d'une cellule à l'instant t+1 dépend de l'état de ses cellules voisines sur la grille et de son état à l'instant t en fonction de règle(s) de transition.

Pourquoi utiliser un automate cellulaire pour simuler la propagation d'une maladie ?

Les simulations mathématiques sont très souvent représentées à l'aide de graphiques. Les automates cellulaires apportent un aspect plus visuel à la simulation. Les cellules le composant représentent les individus et leur état dépend des cellules voisines.

Peut-on correctement simuler le comportement d'une maladie infectieuse, au sein d'une population, à l'aide du modèle SIR ?

Le modèle SIR est considéré comme un modèle de base et très simple. Celui-ci considère des hypothèses ne respectant pas la réalité. Bien qu'il contienne les caractéristiques de base d'une épidémie, avec notamment le ratio de reproduction Ro = βλ, il est difficile de simuler la réalité avec ce modèle. Mais il reste utile pour observer et comprendre les différents aspects d'une épidémie. Il est possible d'apporter des modifications au modèle SIR pour l'améliorer et corriger ses hypothèses irrationnelles. Il existe également d'autres modèles de simulation plus complexe.

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Réda JALALI - 3A SAGI

Août 2020

Appendix 3 : Choice of topic

NOM Prénom : **JALALI Réda**

Département : **SAGI (3A-TD2)**

Sujet (cocher l'option retenue) :

☒ ***Option 1 :***

→ Proposition du sujet : **Modèle SIR (modèle de systèmes compartimentés) et automates cellulaires pour la propagation de maladie**

- 3 sources bibliographiques dont au moins 1 article scientifique pour justifier le choix du sujet :
  - https://interstices.info/modeliser-la-propagation-dune-epidemie/
  - http://automatecellulaire.altervista.org/documents/TPE%20-%20Automates%20Cellulaires.pdf
  - https://fr.wikipedia.org/wiki/Modèles_compartimentaux_en_épidémiologie

❑ ***Option 2 :***

→ Proposition du sujet : **Création de modèle 3D photo-réaliste en utilisant la photogrammétrie**

- 3 sources bibliographiques dont au moins 1 article scientifique pour justifier le choix du sujet :
  - https://fr.wikipedia.org/wiki/Photogrammétrie
  - https://www.sciencedirect.com/topics/earth-and-planetary-sciences/photogrammetry
  - https://www.youtube.com/watch?v=POQj3BlH7gc

❑ ***Option 3 :***

→ Proposition du sujet : **L'informatique durable**

- 3 sources bibliographiques dont au moins 1 article scientifique pour justifier le choix du sujet :
  - https://fr.wikipedia.org/wiki/Informatique_durable
  - https://www.wwf.fr/sites/default/files/doc-2018-10/20181003_etude_wegreenit_démarche_green_it_entreprises_francaises_WWF-min.pdf
  - https://www.lemondeinformatique.fr/publi_info/lire-les-bases-de-donnees-automanagees-une-innovation-majeure-pour-les-entreprises-389.html

Appendix 4 : List of bibliographical sources consulted

NOM Prénom : **JALALI Réda**

Département : **SAGI (3A-TD2)**

Liste des sources bibliographiques consultées (au moins 3 types de sources différentes) :

Type de source*	Titre	Auteurs	Année	Lien internet**	Intérêt***
Article scientifique	Modéliser la propagation d'une épidémie	F. Rechenmann	2011	https://interstices.info/modeliser-la-propagation-dune-epidemie/	++
E-book	Mathematics for Life Science and Medicine	Y. Takeuchi Y. Iwasa K. Sato	2007	http://bu.univ-angers.fr/rechercher/description?notice=001039848&champ=tout&recherche=modele+sir&start=&end=	++
Article scientifique	SIR Model	R. Geofroy	2020	https://www.researchgate.net/publication/341726299_SIR_Model	+++ (1)
Vidéos x3	Oxford Mathematician explains SIR Disease Model for COVID-19 (Coronavirus)	T. Crawford	2020	https://www.youtube.com/watch?v=NKMHhm2Zbkw&list=PLMCRxGutHqfmBoC2YyFradH8NqpvbovMt&index=2	++
Article scientifique	Modified SIR Model Yielding a Logistic Solution	P. Reiser	2020	https://www.researchgate.net/publication/341851268_Modified_SIR_Model_Yielding_a_Logistic_Solution	+++ (2)
Article scientifique	A la découverte des automates cellulaires	N. Fatès	2007	https://interstices.info/a-la-decouverte-des-automates-cellulaires/	+++ (3)
Mémoire	Les automates cellulaires : vers une nouvelle épistémologie ?	N. Fatès	2001		+

* Peut être : article scientifique, rapport, site internet, livre, film, reportage, etc.
** Le cas échéant
*** Il est possible de mettre une note type --/-/+/++

Résumé des 3 sources les plus intéressantes parmi les articles scientifiques :

- Source 1 : ***SIR Model*** **de R. Geofroy est un article au l'auteur présente les bases du modèle de simulation. Ainsi on découvre les variables, les équations et l'utilité du modèle SIR. Dans son étude, R. Geofroy applique un modèle de simulation SIR à la population de Trinité-et-Tobago pour l'épidémie du corona virus.**

- Source 2 : **Dans cet article l'auteur, P. Reiser, propose une solution à l'un des problèmes du modèle SIR. En effet dans celui-ci, le taux de personnes rétablies est proportionnel aux personnes infectées ce qui, dans le cas d'un changement de taux d'infection implique un changement du taux des personnes rétablies. En contrepartie, l'auteur établit l'hypothèse qu'un individu passe de la case « Infecté » à la case « Rétabli » après un intervalle de temps, ce qui change les équations du modèle.**

- Source 3 : ***A la découverte des automates cellulaires*** **est, comme son titre l'indique, un article présentant l'origine des automates cellulaires. On y découvre le Jeu de la vie, un modèle mettant en œuvre l'auto-organisation, l'émergence et l'évolution imprévisible. De plus, on peut également découvrir d'autres modèles d'automates cellulaires comme le Compteur de parité et la Règle de majorité.**

Appendix 5 : Definition of an issue

NOM Prénom : **JALALI Réda**

Département : **SAGI (3A-TD2)**

Formulation d'une problématique en lien avec le sujet de recherche :

- **Peut-on simuler correctement l'évolution d'une maladie infectieuse à l'aide du modèle SIR ?**

Axes de réponses à la problématique :

- **Modèle SIR**
- **Modification du système SIR**
- **Autres modèles de simulation**

Abstract

This report is based on the abstracts of three scientific papers on the **SIR model** and **cellular automata** for **disease propagation**.
This research work presents an analysis of the SIR model to understand how it works. As the SIR model is a simple **mathematical model** with several flaws, the report also presents **modifications** that can be made to the basic SIR model.
In addition to the SIR model, this report also provides a brief presentation of other compartmentalized simulation models. These include the **SEIR and SEIQR models**.
This report also presents an **application** to **simulate** the spread of an infectious disease by combining the principle of cellular automata and the SIR model. The application also simulates some popular cellular automata.

Keywords : SIR model, cellular automata, disease propagation, mathematical model, modifications, SEIR and SEIQR models, application, simulate

Résumé

Ce rapport s'appuie sur les résumés de trois articles scientifiques portant sur le **modèle SIR** et les **automates cellulaires** pour la propagation de maladie.
Ce travail de recherche présente une analyse du modèle SIR qui permet de comprendre son fonctionnement. Le modèle SIR étant un **modèle mathématique** simple avec plusieurs défauts, le rapport présente également des **modifications** que l'on peut apporter au modèle SIR basique.
En plus du modèle SIR, ce compte rendu propose également une présentation rapide d'autres **modèles compartimentés** de simulation. On retrouve ainsi les **modèles SEIR et SEIQR**.
Ce rapport présente également une **application** qui permet de **simuler** la propagation d'une maladie infectieuse en combinant le principe des automates cellulaire et du modèle SIR. L'application permet également de simuler certains automates cellulaires populaires.

Mots-clé : modèle SIR, automates cellulaire, modèles mathématiques, modifications, modèles compartimentés, modèles SEIR et SEIQR, application, simuler