SISDH: A model based on SMAs and SIRs for the simulation of the evolution of COVID-19 in Cameroon

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January 5, 2021

Abstract We present in this work the modeling the spreading of the new variant COVID-19 in Cameroon using Multi Agent System and the epidemiological system modeling SIR [5](Susceptible, Infected, Recovered). The aim of this work is to respond to the problem of modelling the evolution of epidemics with a high transmission rate like COVID-19 in order to get more insights for decision making to slow down the spread. Our solution is outlined in two parts : the former concerned the application of SIR model and the later concerned the tailoring of the former by using Multi Agent System. Multi-agent systems[1] are used to model SIR model entities, including residents of a given region. The experiment carried out show that the merging of these two concepts is very useful for decision-making for example : **The wearing of the mask**.

1 Introduction

An agent can be defined as a computer system located in an environment capable of perceiving this environment by sensors and acting on this environment by actuators [7]. A Multi-Agent System (MAS) is a network of agents or a set made up of several agents. These agents together can interact to solve problems that are beyond the capabilities of any individual agent. For example, a group of humans can be considered as a multi-agent system where the agent is the human. It is possible to simulate the evolution of an epidemic using multi-agent systems[7]. Two main models are currently widely used to simulate the evolution of the COVID-19 pandemic: **SIR (Susceptible Infected Recovered)** [5] and **SIS (Susceptible Infected Susceptible)** [4].

The SIR model gives 3 possible states of an entity in the population [8, 2]:

- **Susceptible** which defines that it is likely to have the virus
- **Infected** which describes the state of a person infected with the virus
- **Recovered** which states that the person is cured.

The problem with this model in the case of COVID-19 is that it does not take into account some very important aspects such as **the fact that a healed patient may be re-infected**, which is not yet proven by researchers on the disease [6]. Moreover, this model does not highlight the **mortality and critically of the patient** aspect in the description of the states; however, these remain very determining factors for a more real study of the evolution of COVID-19.

The **SIS** model [4], in other way, takes into account two states of an individual: **Susceptible** and **Infected**. Indeed, person in the population is already **Susceptible** to have the virus; then if he has it, he becomes **infected**. Then he either gets cured and becomes **Susceptible** again or he dies. From this description of the model we can see that it is very unrepresentative of the reality of what the COVID 19 complex epidemic is. In fact, this model does not already take into account the mortality aspect, we do not have a formal means of monitoring the mortality of infected individuals in our system, so this model does not take into account the healing and critically aspect of the patient, which undoubtedly has an impact on evolution.

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In addition, it can be observed that for COVID 19, other aspects should be taken into consideration, such as **the wearing or not of a mask**, **the probability of becoming infected** when one has already been infected and then cured. All this leads us to asking ourselves, **what is the most appropriate model to represent the evolution of COVID 19 taking into account all its aspects and of course who is adapting to Cameroon?**.

2 Methodology

We present in this section the construction of the model **SISDH**. (Susceptible, Infected, Severe, Died, Healed) that we suggest. SISDH is inspired by the SIR model where it adds two states (Died, Healed) and simulates the evolution of a human agent within a society made up of other human beings.

2.1 Description of the Human Agent

The properties and methods of the human agent derive from the capacities that a real human possesses in society and which influence its state in the face of disease (Covid-19).
Ses propriétés sont:

- **age**: integer determining the agent's age.
- **wear_mask**: boolean variable describing whether or not an agent wears the mask.
- **state**: describes the state of and agent.
- **infection_time**: the time elapsed since the last infection of an agent.
- **severe_time**: time elapsed since the last critical infection of an agent
- **healed_time**: time elapsed since the healing of an agent

- **recovery_severe_time**: time elapsed since the healing from severe infection

The methods used are described as follows:

- **move()** which allows the agent to move to a neighbouring area randomly and according to the probability of movement.

- **status()** which allows the user to check his current status (infected, cured...). This method also calculates the time since infection (if infected), since recovery, since severe infection... and according to this and its different properties, the calculation of the probabilities of passage from one state to another is carried out.

- **contact()** which is a method in which it comes into contact and infects other agents with a certain probability depending on several parameters such as the wearing of a mask and its current state.

2.2 Model Description

The model constitutes the environment in which the different agents will run as well as the global parameters of the agent systems. This environment has been inspired by our society in order to model as accurately as possible the different movements within a population and to observe the consequences in relation to the disease. Characteristic features of the society include the size of the population, the fact that part of the population wears masks and part does not, the fact that population movements are generally more centred on certain places (markets, schools, places of worship, etc.), the fact that when one is infected or seriously infected (hospitalised) the probability of dying or recovering varies with the passage of time, and the probability of moving also varies (a hospitalised person does not move as much as a healthy person). The properties for representing these features of society in the model are described as follows :

- **population**: the number of agent in the simulation

- **steps**: the duration in days of simulation

- **width, height** the size of environment boundaries

- **ptrans**:the probability that an infected person will transmit the disease when in contact with another agent when not wearing a mask

- **ptrans_mask**: the probability of an infected person transmitting the disease when wearing a mask.

- **proba_wear_mask, proba_move** which represent respectively the probabilities for an agent to wear the mask and to move around

- **initial_outbreak_size** initial number of infected

- **age_old** which defines the age at which a staff member is considered old.

- **age, agesd** which represent the average and standard deviation of the age of the population.

- **nb_places** which represent the number of locations (randomly distributed) where agents are more likely to move.

- **recovery_young_days** which represents the average number of days a young person heals

- **recovery_young_sd** which represents the standard deviation of the number of days a young person has been healed.

- similar parameters corresponding to the elderly.

There are also various parameters for modelling state transitions. These parameters depend on the age of the agent and the time spent (in days) since he is in his current state. This is done in order to get closer to reality, which translates into the fact that a human being has a greater or lesser chance of being infected, passing to a critical state, healing or dying depending on his age and the time he has spent in his current state. Figure 1 below shows the state-transition diagram of an agent:

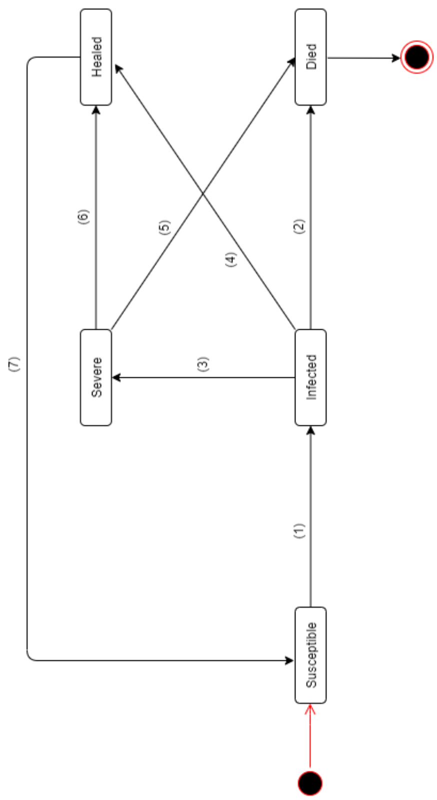

Figure 1: Transition State Diagram

t represents the length of time the agent has been in the given state, age represents his or her age and nbPer the number of infected persons with whom he or she has been in contact in one day.

(1) proba > ContactWithInfected(nbPersons)
(2) proba > InfectedToDeath(t, age)
(3) proba > InfectedToSevere(t, age)
(4) proba > InfectedToHealed(t, age)
(5) proba > SevereToDied(t, age)
(6) proba > SevereToHealed(t, age)
(7) t > immunityTimeAfterHealed
(8) proba > SevereToSusceptible(t, age)

Table 1: Conditions of transition of the agent from one state to another

The model therefore simulates the behaviour of the different agents during **"steps"** days and each evening (of the simulation), the different agents carry out an assessment in order to know their state.

3 Experiments

We will launch the environment with parameters allowing us to simulate the agents in a situation of confinement or release of the population. We will study a population of 30,000 agents with an average age of 30 and distributed in an environment with a size of 400×400, with the duration of observation extending over 365 "steps".
It is worth noting that the various parameters used in this experiment are estimated and not real and are intended to study the relevance of the model according to certain given scenarios.

3.1 Release of the population

Here we test the case where no barrier measures are complied with. We will assume that 1% of the population is initially infected and observe the evolution of the agents' status during 365 "steps". The explicit description of the parameters is given below.

3.1.1 Values of the parameters

Afterwards testing, we obtain the following results:

population = 30000
recovery_young_days = 14
steps = 365
recovery_young_sd = 7
width = 400
recovery_old_days = 21
height = 400
recovery_old_sd = 7
ptrans = 0,2
recovery_severe_young_days = 7
ptrans_mask = 0.03
recovery_severe_young_sd = 3
age_mean = 30
age_sd = 20
age_old = 50
initial_outbreak_size = 300
nb_places = 20
proba_go_to_places = 0,2
proba_wear_mask = 0,1
proba_move = 0,6

Table 2: Parameters of the Experiment

The configurations used to model the transition state are described as follows:

- infectedToDeath(t) = $0,008$
- SeverelyInfectedToDeath(t, age) =

$$\begin{cases} age < 50 \\ : \begin{cases} t < 10 : 0,004 \times (t+1) \\ t \geq 10 : 0,05 \end{cases} \\ \\ age \geq 50 \\ : \begin{cases} t < 9 : 0,02 \times (t+1) \\ t \geq 9 : 0,02 \end{cases} \end{cases}$$

- InfectedToSevere(t, age) = $\begin{cases} age < 50 : 0,01 \\ age \geq 50 : 0,2 \end{cases}$
- HealedToSusceptible(t) = $0,0003$

3.1.2 Results

We obtained the following results:

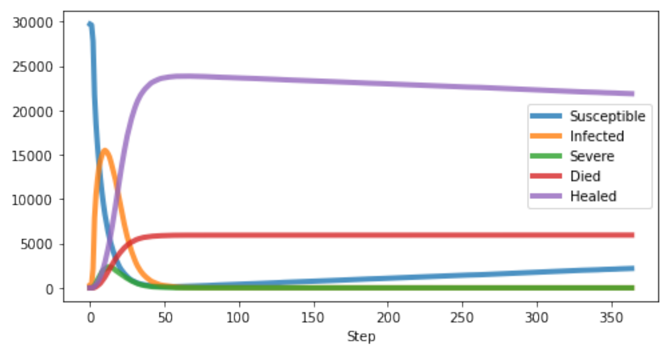

Figure 2: State agent evolution

This graph shows that in a fairly young population with a consistent number of infected people and unapplied containment and distancing rules, the number of infected people increases rapidly after about 20 days with a small number of severely infected people (corresponding to the number of elderly people) then falls rapidly while the number of deaths increases.

P_m, P_T et $\%m$ represent respectively the number of deceased persons in a given category, the total number of persons in that category and the mortality

Category	P_m/P_T	$\%m$
Older persons	$3427/4798$	$71,42\%$
Younger persons	$2518/25202$	$9,99\%$
Whole population	$5945/30000$	$19,82\%$

Table 3: death statistics

rate within that category.

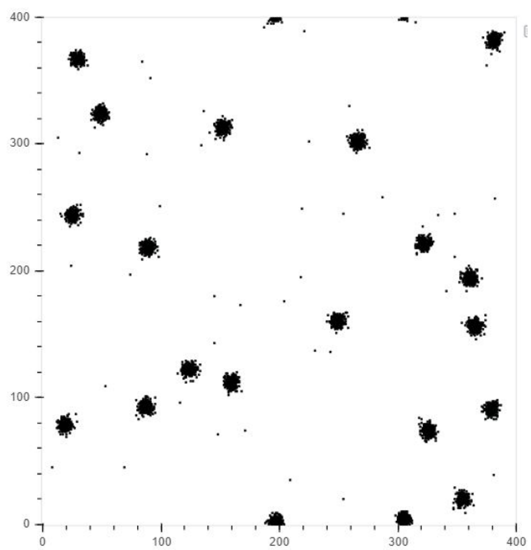

Figure 3: Distribution of the agent in the environment

The following graph shows the repartition of the agents in the environment at the end of the simulation. A higher density can be seen in the public places mentioned. It can therefore be seen that the authorisation to travel in public places has an influence on the number of infected people.

3.2 Mandatory lockdown of the population

We test whether barrier measures as well as containment are imposed on the population.

3.2.1 Parameter values

The above parameters remain unchanged except for :

- proba_wear_mask = 0,9
- proba_move = 0,04
- proba_go_to_places = 0,004
- steps = 365

We note that the fact that the probabilities are not certain or zero just results from the fact that there is always a small proportion of the population that is recalcitrant to the law.

3.2.2 Results

The obtained results are described as follows

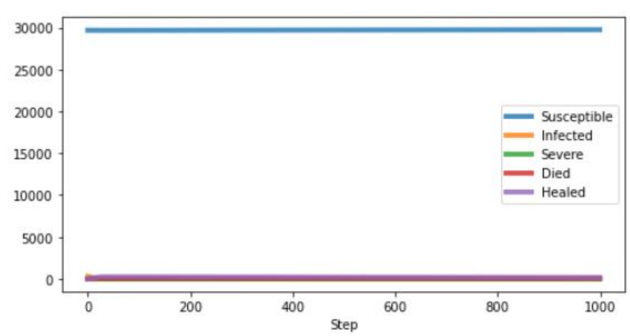

Figure 4: Evolution of the state of the agents

où P_m, P_T et $\%m$ représentent respectivement le nombres de personnes décédées d'une catégorie

Category	P_m/P_T	$\%m$
Older Persons	$32/4723$	$0,68\%$
Younger Persons	$35/25277$	$0,14\%$
Whole population	$67/30000$	$0,22\%$

Table 4: death statistics

donnée, le nombre total de personnes de cette catégorie et le taux de mortalité au sein de cette catégorie.

This curve and table show that for a fairly young population respecting the containment rules, the pandemic remains under control throughout the observation and the mortality rate is generally very low.

4 Discussion

Based on the various experiments that have been carried out, it appears that the behaviour of the COVID 19 epidemic differs from one scenario to another.

- If one decides to implement very strict measures, one observes that the epidemic does not evolve (see Figure 4). The population is virtually unaffected by the epidemic and there are hardly any deaths or people in severe condition. This corresponds approximately to the expected outcome of containment.

- If, on the other hand, one decides to do nothing, one can observe a large peak of infected people in the first few days, before decreasing again and stabilising. This may mean, for example, that the population that was previously infected is immunised (or it becomes more difficult for them to take the virus). Similarly, mortality peaks at about the same time as infections, before stabilising. It stabilises at a relatively high level due to the probability of death (which may depend on age) and the fact that the infections are fairly stable but continue their course. This corresponds a priori to the expected result for this scenario where the population is fairly free but retains a fairly high capacity for healing and resistance (the case of the population of Cameroon).

What can be pointed out here is that these two scenarios allow us to have a certain vision on what the consequences of their application may be. For example, the solution **no particular action(normal behaviour)** can easily lead to a saturation of hospitals in the case of an increase in severe cases of the disease. This can lead to a loss of control over the evolution of the virus. On the other hand, this consideration allows business (economic aspects of the country) to continue "quite" normally, so that Cameroon will not find itself faced with major financial worries, even though hospital saturation could be the cause of many expenses.
On the other hand, if one takes into account a **total containment**, one has a priori control over the evolution of the virus. On the other hand, this confinement can be quite considerable for the Cameroonian state, which will then see the economy suspended or at least very slowed down, which can be to its great disadvantage.

What can be said is to find a healthier solution that takes the advantages of the two previous methods and significantly reduces their respective drawbacks. Hence the solution of **measures barriers** which therefore makes it possible to reduce the population's capacity for infection while allowing the economy to run its course at a healthier pace. This solution is still very challenging in the sense that it will require discipline both from the population but also from the Cameroonian authorities to ensure that they are respected for the good of all.

5 Conclusion

At the end of this article, the modelling of the evolution of COVID 19 in Cameroon using multi-agent systems was discussed. We used the **SISDH** model to model the epidemic after highlighting other propagation models such as **SIR** and **SIS**. The result is that this model provides a closer and more detailed representation of the reality, allowing for a better evolution of the COVID 19. However, for future research, it would be good if we could have real data (infected, healed, dead) corresponding to a locality in Cameroon, thus allowing a deeper appreciation of the effectiveness of our model. Also, the ability to have parameters (probability of passing from one state to another) validated by doctors would be of great help in this research work. In addition, it would also be interesting to be able to use **GIS (Geographic Information Systems** [3] by which one can highlight points of contamination at different levels in cities (markets, schools, bourgeois neighbourhoods for example) and thus be able to experiment with evolution by taking into account these important aspects for the spread of the COVID 19 epidemic.

Conclusion

References

[1] Jacques Ferber. "Les systemes multi-agents : un aperçu general". In: *Technique Et Science Informatiques - TSI* 16 (Jan. 1997), pp. 79–1012.

[2] Joel C. Miller István Z. Kiss and Péter L. Simon. *Mathematics of Epidemics on Networks*. Springer, 2017.

[3] Jean-Louis Kerouanton. *Pour l'utilisation des SIG (systèmes d'information géographique) en histoire des techniques : entre documentation et analyse spatiale*. URL: https://doi.org/10.4000/dht.299. (accessed: 2009).

[4] Maoxing Liu, Gergely Röst, and Gabriella Vas. "SIS model on homogeneous networks with threshold type delayed contact reduction". In: *Computers Mathematics with Applications* 66.9 (2013). BioMath 2012, pp. 1534–1546. ISSN: 0898-1221. DOI: https://doi.org/10.1016/j.camwa.2013.02.009. URL: http://www.sciencedirect.com/science/article/pii/S0898122113001016.

[5] R.Ross. "The SIR model and the Foundations of Public Health". In: *Semantic Scholar* ().

[6] Joel R Sevinksy Richard L Tillet. "Genomic evidence for reinfection with SARS-CoV-2: a case study". In: *THE LANCET* (110 2020).

[7] Stuart Russel and Peter Novig. *Artificial Intelligence A Modern Approach*. Prince Hall, 1995.

[8] David Smith and Lang Moore. "The SIR Model for Spread of Disease - The Differential Equation Model". In: *MAA Publications* ().