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Behavior simulation of the SRAS-Cov-2 pandemic in Niger

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Abstract

The coronavirus (covid-19) is a viral pandemic that has affected the whole world. In the case of covid-19, it has started to be significantly propagated in China. Then it has evolved to Europe, Asia, the United States of America and Africa. In Niger, the first case was diagnosed on March 19, 2020, more precisely in Niamey. On the date of April 9, 2020, the city has 342 cases of infected among which 11 have already died and 28 have been cured. In order to prevent a disaster like the European countries, we are interested in the question. Thus, this document presents a model simulating the evolution of the pandemic in Niger. The main objective is to have an idea about the number of people infected and those who died in the worst (no preventive measure), medium and best case.

Keywords: Covid-19, Model, Simulation

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1. Introduction

Coronaviruses is a family composed of a large number of viruses. The latter can cause a wide variety of diseases in humans, ranging from the common cold to SARS (Severe Acute Respiratory Syndrome) and possibly digestive disorders such as gastroenteritis. It is a particular strain never identified in humans until the 1960s. The incubation time is evaluated between 3 and 5 days in the majority of cases, but can last in extreme cases of 12 and 14 days [1, 2, 3]. The epidemic started in the city of Wuhan, China in late December 2019 and quickly spread around the world [4].

More than 1,288,000 cases, throughout the world, have already been confirmed, including more than 70,000 deaths [5]. Meanwhile in Niger, there are 342 cases. The city of Niamey, the capital of the country, is the one that recorded the first official case on March 19, 2020 and currently has more than 330 cases including 11 deaths [6].

The pandemic in question continues to keep the whole world in a worrying situation when we look at the number, not least important, of dead per day in Spain (more than 700), in France (more than 1000), in Italy (more than 700) and in the United States of America (more than 1400). We are interested in the question to simulate and predict the behavior of the pandemic in Niger. This, like the researchers who have already published results along the same lines [7, 8].

This document is structured as follows: in the second section, we present some methods on which other researchers have based themselves to simulate the behavior of a contagious disease in general. Section three presents the model we have designed. In this section, we will explain the method that we have adapted in our approach. In the fourth section, we present the results which we will discuss. We end this document with a conclusion.

2. Method

To design a Simulation Model, several methods are used depending on the areas and the nature of the problem that we want to model. Some researchers use PDEs (partial differential equations). This is the case for the references [9, 10, 11, 12]. In [9], the authors discuss the analysis of local and global stability of a modified age-structured model for the dynamics of non-vertical transmission of hepatitis B. In [10], the authors present a numerical simulation model and the resolution of a problem of optimal control of surface water pollution. The article [11] deals with modeling and numerical simulation of the sand dunes formation (on the effect of the wind). The article [12] studies an age-structured model of tuberculosis.

In IT, other tools are used. We can cite, among others, cellular automata [13, 15], multiagent programming [14, 16, 17], etc. The article [13] deals with modeling based on cellular automata, analysis and control of distributed systems usually described by PDEs.

These were also used for multi-scale modeling of biological systems (for example in [15]). Multi-agent systems have been used to:

- evaluation of control strategies endemic communicable animal diseases across a small agricultural region [14];
- designing a spatial distribution model of epidemics [16];
- the design of a meta-model called AOC (Agents-Organisations-Comportements in French), which is expressed by a formal ontology and serves as a conceptual framework for a platform for simulating complex spatial systems, compatible with the problems of the widest one geographic dynamics [17];
- etc.

In our case, we use a state machine to represent the behavior of the coronavirus (Covid-19) pandemic. The following section presents the state machine in question and how it works.

3. Designed model

3.1 Presentation

The state machine is presented in figure 1. The states are:

- S: represents the group of susceptible;
- I: represents the group of undeclared infected (unknown) persons;
- I_t: represents the group of infected persons declared (therefore in treatment);
- M: represents the group of people died due to the pandemic;
- Q: represents the group of people in quarantine (therefore who have been in contact with the people of group I).

The transitions are:

- φ_i: it is the probability that a susceptible person will be infected;
- φ_{t1}: it is the probability that an infected person will be declared;
- φ_{q1}: it's the probability that a susceptible person will be quarantined (therefore in contact with an infected and declared person);
- φ_{t2}: is the probability that a person in quarantine become infected;
- φ_{m1}: it is the probability that an unreported infected person will die from the coronavirus;
- φ_{m2}: it is the probability that an infected person in treatment dies of the coronavirus;
- φ_{m3}: it is the probability that a quarantined person will die from the coronavirus;
- φ_{s1}: it is the probability that an infected and undeclared person will recover (therefore becomes susceptible again);
- φ_{s2}: it is the probability that an infected person in treatment will recover (therefore becomes susceptible again);
- φ_{s3}: it's the probability that a quarantined person will recover (therefore becomes susceptible again);

- φ_{cr}: it is the population growth rate of Niger for 2020 [18].

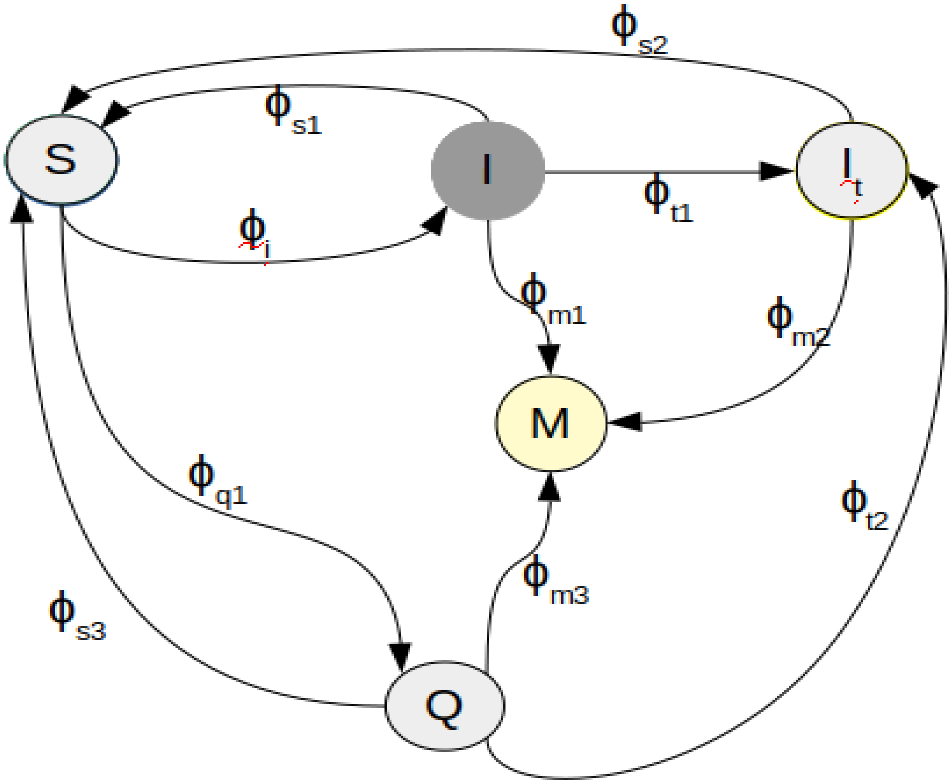

Figure 1: The state machine

3.2 How it works

The state machine operates in three phases:

- an initialization phase for groups (S, I, I_t, Q, M) and parameters (φ);
- a phase of recursive calculation of $S_{i+1}, I_{i+1}, I_{ti+1}, Q_{i+1}, M_{i+1}$ values based on $S_i, I_i, I_{ti}, Q_i, M_i$, so the evolution on the number of days;
- and a stop phase which is checked at each iteration during the second phase.

At the initialization phase, we have:

- P = 22442948. This is the total number of inhabitants in Niger [18].
- φ_{q1} =2.5. It should be noted that if $\varphi_{q1} = 0$, it is not necessary to model the system because there is no possible contamination.
- $\varphi_{t1} = 0.4$
- $\varphi_{t2} = 0.2$
- $\varphi_{m1} = 0.006$
- φ_{m2} : varies from 0.01 (best case) to 0.2 (worst case)
- $\varphi_{m3} = 0.001$

- $\varphi_{s1} = 0.4$
- φ_{s2} : varies from 0.17 (worst case) to 0.3 (best case)
- $\varphi_{s3} = 0.4$
- $\varphi_i = 0.005$
- $\varphi_{cr} = 0.039$
- $S = P$
- $I = I_0$ (I_0 is the number of people infected and undeclared initially)
- $I_t = I\varphi_{t1}$
- $I = I - I_t$ (updating the value of I)
- $Q = I\varphi_{q1}$ (φ_{q1} is not yet defined, is involved in the worst, medium and best case)
- $S = S - I - I_t - Q$
- $M = 0$

In the recursive calculation phase, we first update the groups I, I_t, Q and S with respect to the population growth rate:

- $I_i = I_i + I_i\varphi_{cr}$
- $I_{ti} = I_{ti} + I_{ti}\varphi_{cr}$
- $Q_i = Q_i + Q_i\varphi_{cr}$
- $S_i = S_i + S_i\varphi_{cr}$

Then, we proceed to a conditioned update of the groups I, I_t and Q compared to the average number of days for an infected person to heal (10 days):

- $I_i = I_i - I_i\varphi_{s1}$
- $I_{ti} = I_{ti} - I_{ti}\varphi_{s1}$
- $Q_i = Q_i - Q_i\varphi_{s1}$

Finally, we update for the groups I, I_t and Q compared to the remaining parameters:

- $I_{i+1} = I_i + S_i\varphi_i - I_i\varphi_{t1} - I_i\varphi_{m1}$
- $I_{ti+1} = I_{ti} + I_i\varphi_{t1} + Q_i\varphi_{t2} - I_{ti}\varphi_{m2}$
- $Q_{i+1} = Q_i + I_i\varphi_{q1} - Q_i\varphi_{t2} - Q_i\varphi_{m3}$
- $M_{i+1} = I_i\varphi_{m1} + I_{ti}\varphi_{m2} + Q_i\varphi_{m3}$
- $S_{i+1} = S_i - I_{i+1} - I_{ti+1} - Q_{i+1}$

The conditions of the iteration stop are:

- $j = Nb_j$, Nb_j is the maximum number of iterations set in the execution of the algorithm;
- $I_t = 0$

  ⇨ $I_t + I\varphi_{t1} + Q\varphi_{t2} - I_t\varphi_{s2} = 0$

  ⇨ $I\varphi_{t1} + Q\varphi_{t2} = 0$

  Or $\varphi_{t1} > 0$ and $\varphi_{t2} > 0$

  Therefore $I = 0$ and $Q = 0$

  Hence the main stop condition is $I_t = 0$.

4. Results and discussions

The figure 2 shows, in general and in the worst case:

- the evolution of the number of infected people in medical treatment (in blue);
- the evolution of the number of infected and undeclared (therefore undiagnosed) people (in green);
- the evolution of the number of infected (undeclared or treated) people who died from the coronavirus (in red).

At this level (in the worst case), we have:

- $\varphi_{m2} = 0.2$
- $\varphi_{s2} = 0.17$

In the programming, we have introduced counters to calculate the total number of infected persons in treatment, the total number of undeclared infected persons and the total number of those who died from the disease. Figure 2 shows that these numbers are respectively 221,662, 134,865, and 8,201. The difference between the numbers means that the curves are less explicit when they are represented in the same frame. For this, we have represented them in different reference points according to the evolution of the number of days (see figures 3, 4 and 5).

The figure 3 shows that, in the worst case, the number of infected people in treatment can exceed 2,000 per day, at the national level, during peak periods (figures figure 3 and 4). It should be noted that an infected and healed person can still be re-infected a second, a third, etc. times and this is due to the fact that there is no immunity to the virus. The number of deaths per day, meanwhile, could reach 115 people (see figure 5).

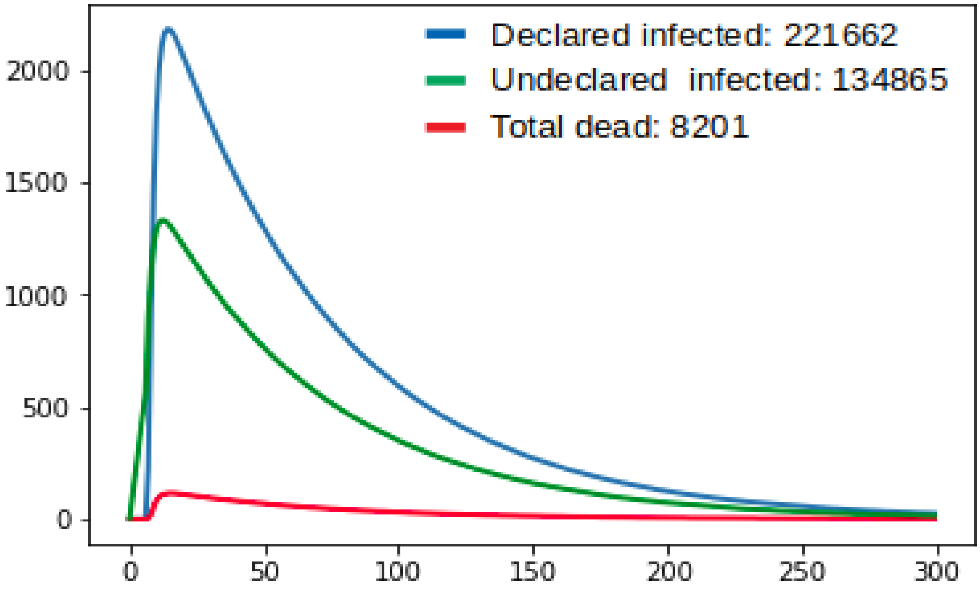

Figure 2: Curves of infected people and dead people in the worst case

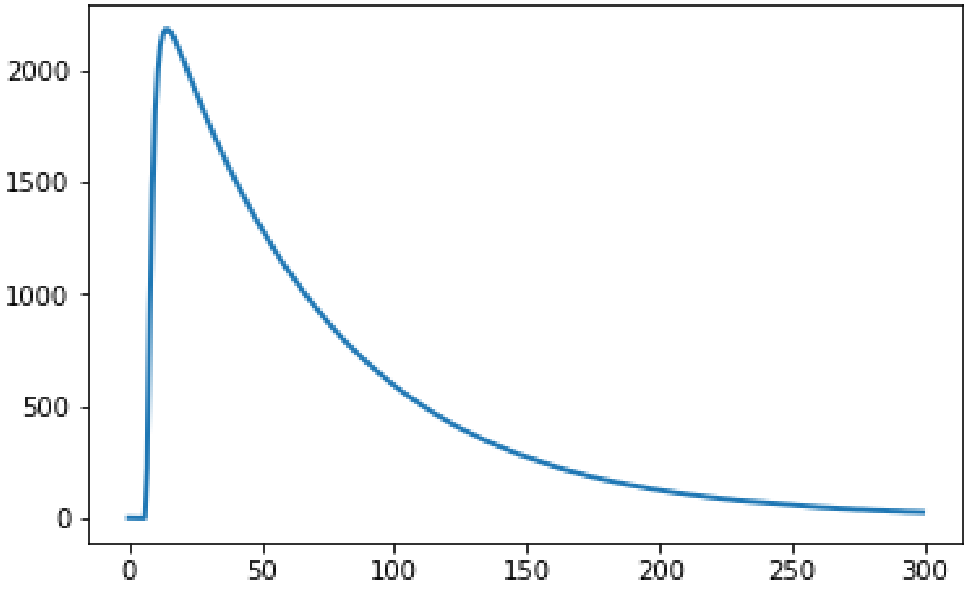

Figure 3: Curve of infected people in treatment in the worst case

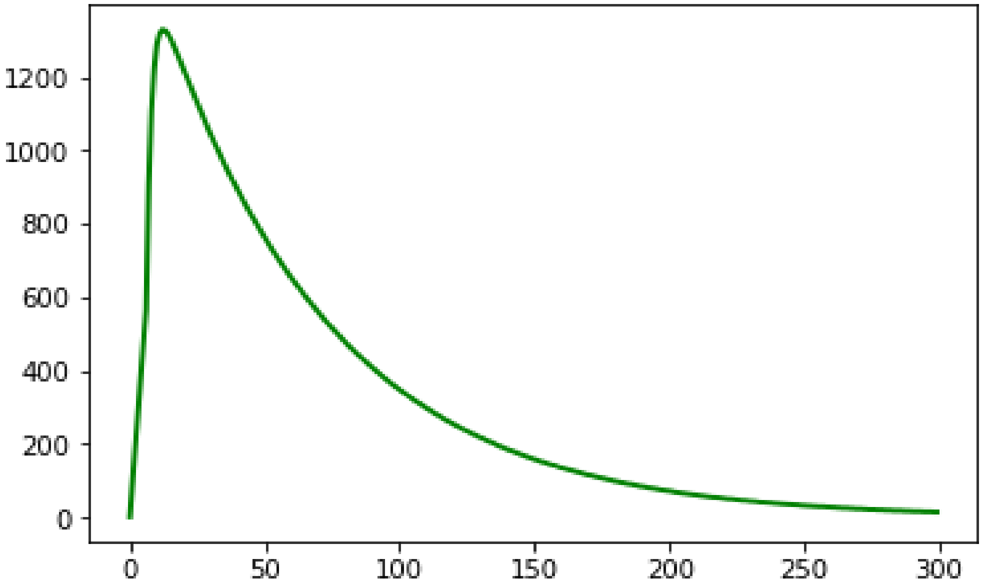

Figure 4: Curve of undeclared infected persons in the worst case

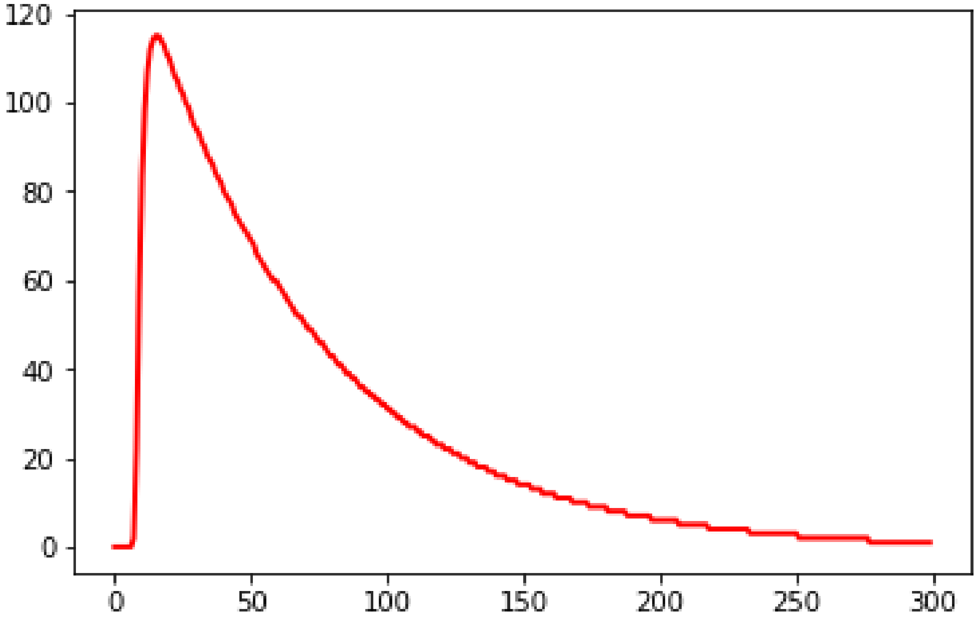

Figure 5: Curve of infected people who died in the worst case

The figures 6, 7, 8 and 9 give the results in the middle case.

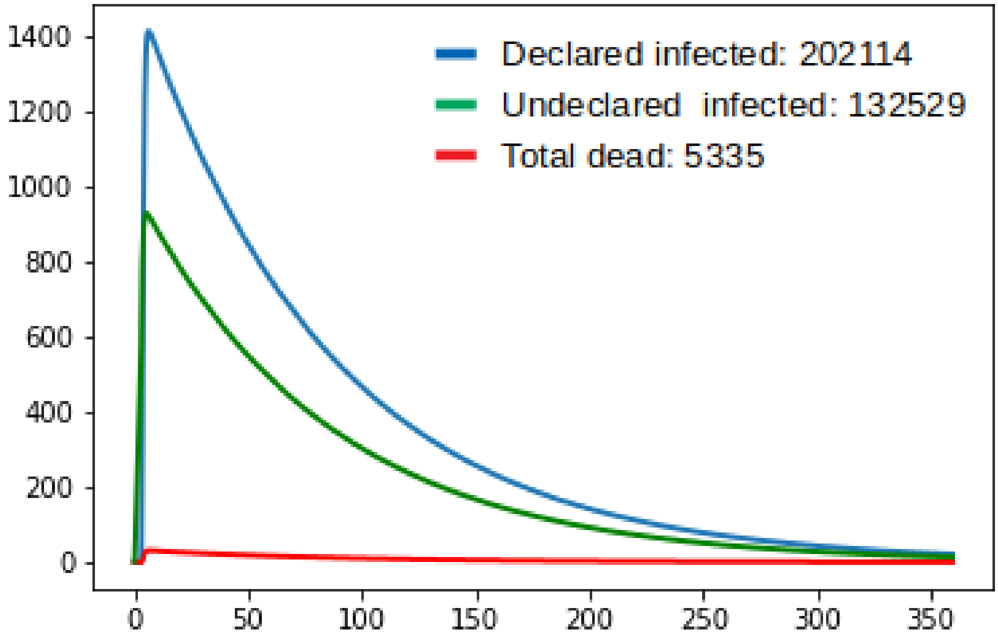

Figure 6: Curves of infected people and dead people in the middle case

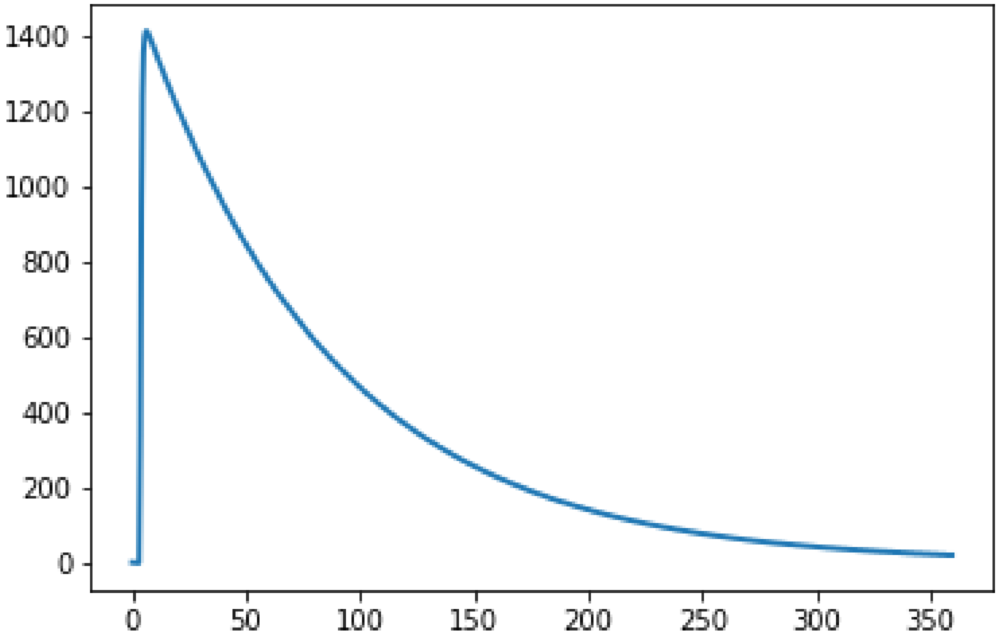

Figure 7: Curve of infected people in treatment in the middle case

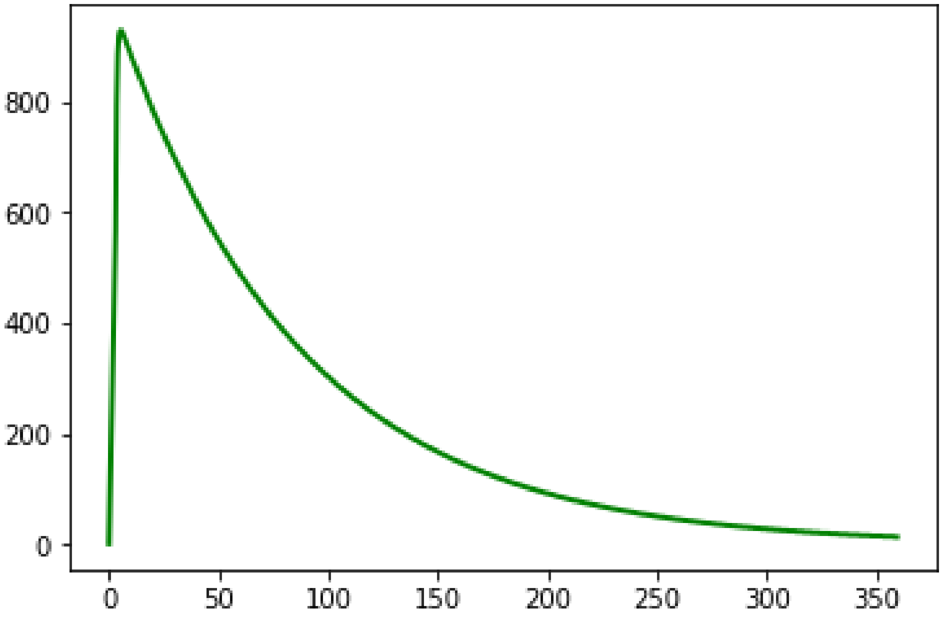

Figure 8: Curve of undeclared infected persons in the middle case

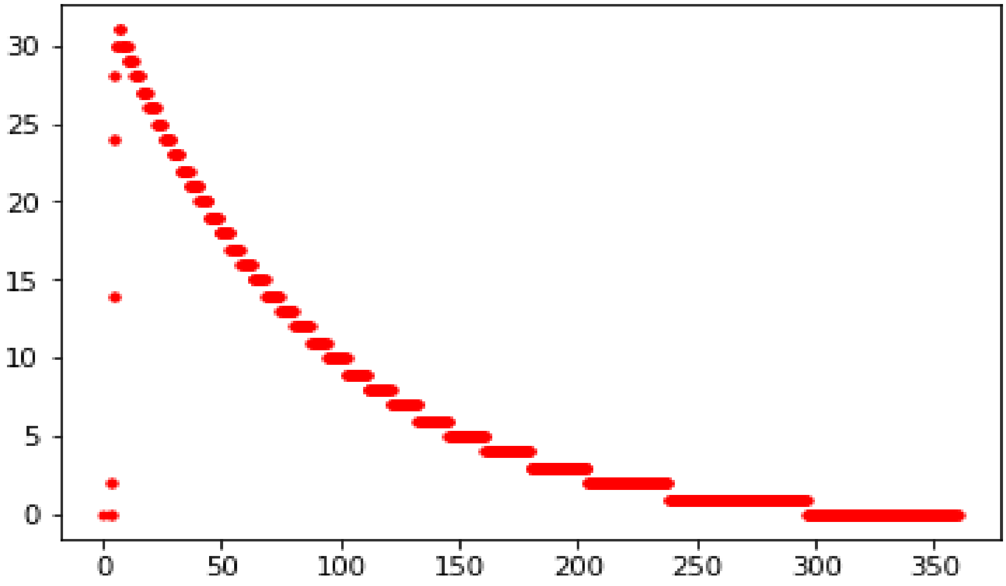

Figure 9: Curve of infected people who died in the middle case

The figures 10, 11, 12 and 13 give the results in the best case. We have a total of 204,791 people who could be infected (and 1200 per day during peak periods) for a period of 350 days, including 2,339 dead (14 per day during peak periods) for a period of 220 days.

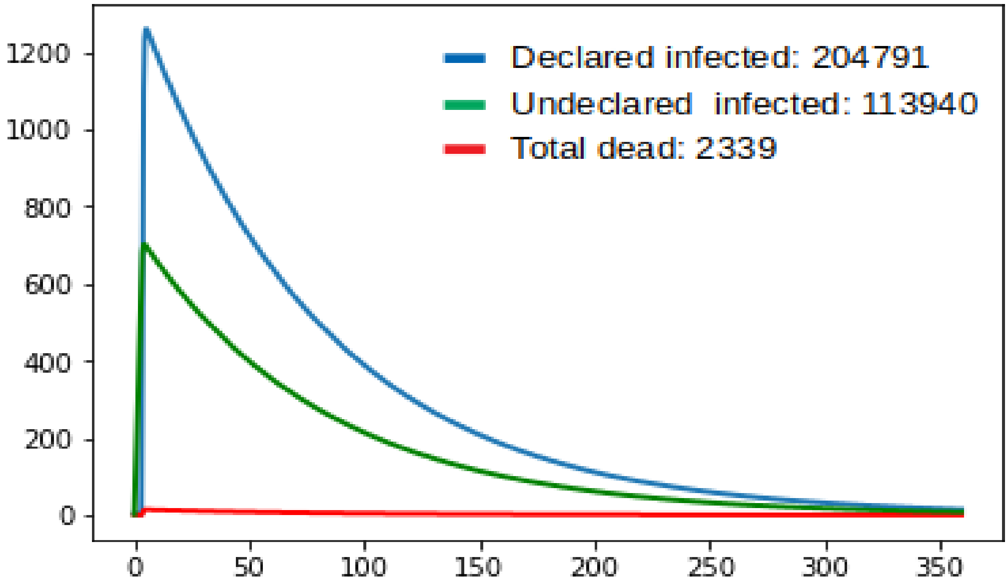

Figure 10: Curves of infected people and dead people in the best case

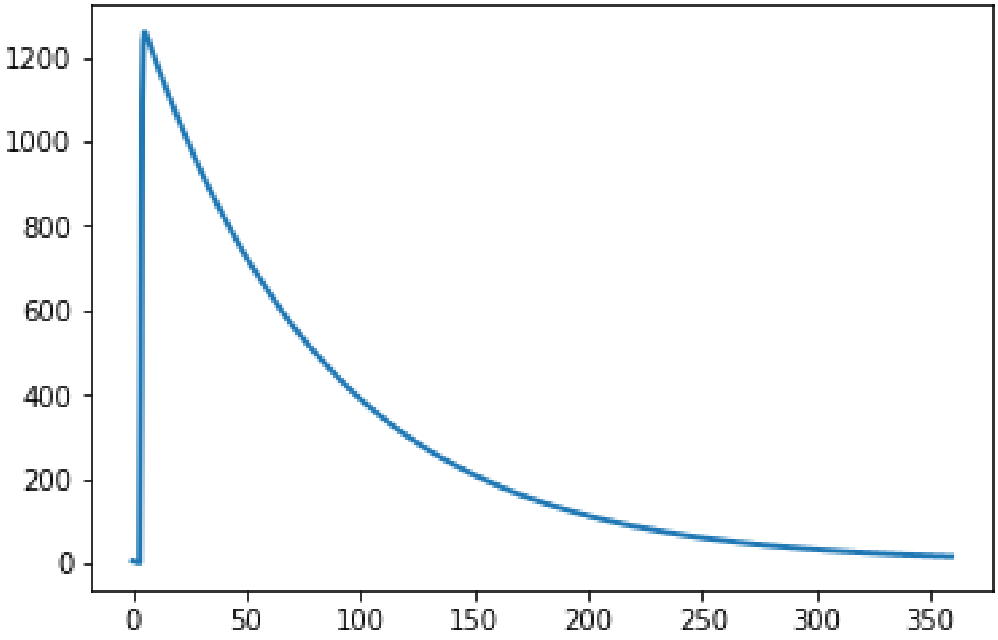

Figure 11: Curve of infected people in treatment in the best case

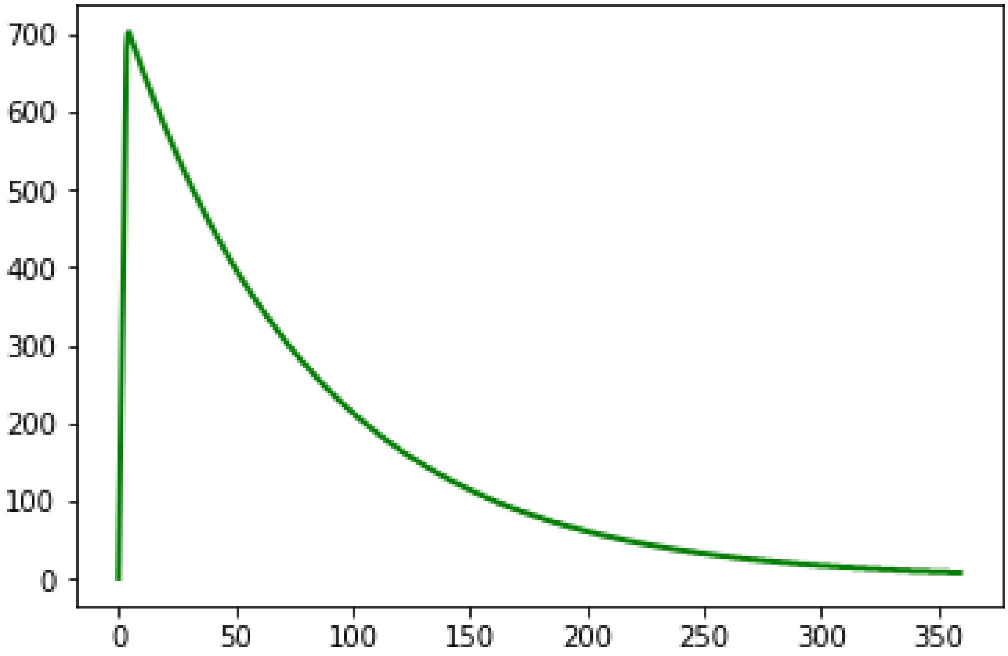

Figure 12: Curve of undeclared infected persons in the best case

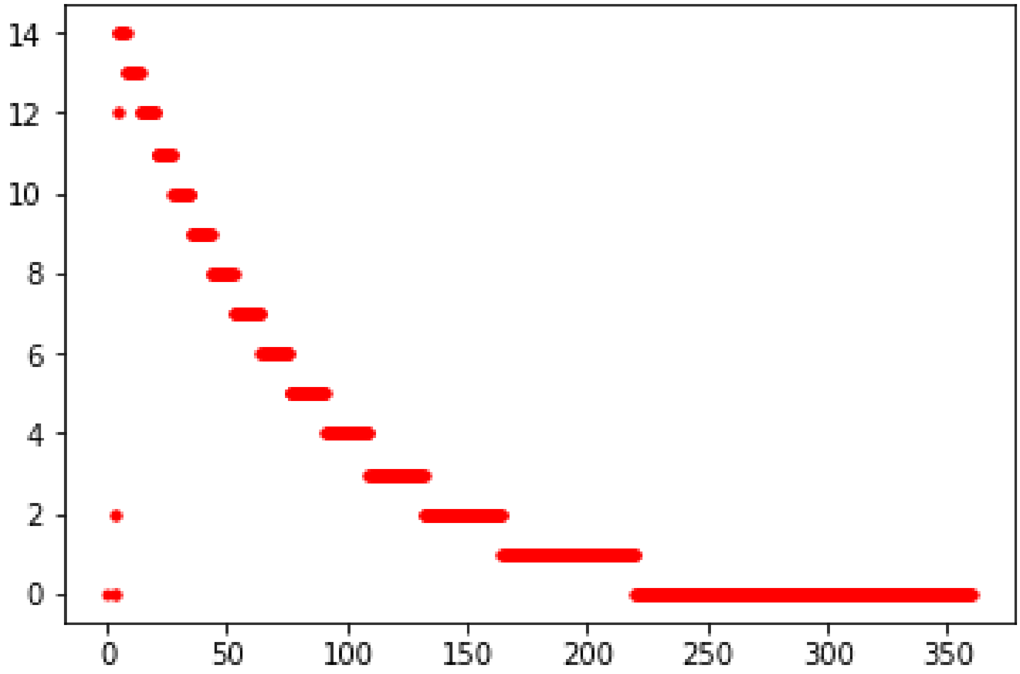

Figure 13: Curve of infected people who died in the best case

5. Conclusion

In this document, we have presented a simulation of the behavior of the coronavirus pandemic (covid-19) in Niger. This simulation takes into account, in all cases (worst, medium and best) of the border closure. The results, even in the best case, are alarming (more than 2,000 dead for a period of 220 days). This must challenge all Nigeriens (authority and citizen) in the sense of clearly defining the disease prevention measures and ensuring that they are strictly observed. This could make us strive towards a zero contamination rate ($\varphi_{q1}=0$) and therefore further cushion the curves as well as the duration of the pandemic.

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