Annals of the University of Craiova, Mathematics and Computer Science Series
Volume 49(1), 2022, Pages 75–83, DOI:
ISSN: 1223-6934

Development and simulation of a mathematical model to simulate the phase transmissibility of covid19 in Morocco

Hamza Alaa, Nour Eddine Alaa, and Fatima Aqel

Abstract. In this work we develop a new Reservoir-People (RP) transmission network model to simulate the potential transmission of the COVID-19 virus in the population of Morocco. Our model is original in the sense that it contains parameters that depend on the confinement phases that Morocco has adopted so far. After developing the mathematical model COVID-19-Morocco we define a cost function to minimize with respect to the parameters. We then use genetic algorithms to optimize this functional. The numerical results we obtain confirm that our model is robust and can predict the evolution of the virus in Morocco.

2010 Mathematics Subject Classification. Primary 60J05; Secondary 60J20.
Key words and phrases. Covid-19, mathematical model, basic reproduction number, genetic algorithm, transmissibility, parameters identification.

---

1. Introduction

COVID-19 refers to "Coronavirus Disease 2019", a disease caused by a virus of the Coronaviridae family, SARS-Cov-2. This infectious disease is a zoonotic disease, whose origin is still debated. The virus emerged in December 2019 in the city of Wuhan, Hubei province, China. Within a few months, the virus extended out quickly all over the world, causing a global epidemic (pandemic).

It has become known today that COVID-19 can lead to a wide range of potential complications and can be fatal especially for patients weakened by age or another chronic disease such as Cancer, Diabetes, high blood pressure, arterial hypertension etc... . It has also been observed that direct/indirect contact with a symptomatic or asymptomatic person leads to the transmission of the virus. Also, the average mortality rate for the population, in general, is estimated to be between 1% and 3%.

The fatality of the virus thus comes from its rapid spread. In fact the outbreak led to an enormous economic damage and a high number of hospitalized cases and deaths worldwide. Morocco recorded the first case in March the 2nd 2020, an event after which the moroccan authorities took immediate action to stop an uncontrollable outbreak of the virus. Pasteur Institute of Morocco confirmed that a Moroccan citizen residing in Italy was case number one detected in the country.

The procedures established by the moroccan ministry of health restricted the travel of citizens between cities, and also imposed the wearing of masks in public places. The

---

Received May 11, 2021. Accepted May 23, 2021.

Moroccan government adopted a draft decree-law aimed to establish a state of health emergency in the kingdom, which became effective on March 20th, 2020 at 06:00 pm. Morocco's confinement strategy was a success and effectively aided in the prevention of a catastrophic situation. In fact the number of daily confirmed cases reached a maximum of 6195 recorded on November 12th, 2020 (data dating back to March 15th, 2021).

The necessity of modeling the spread of the virus is thus undeniable. In literature, there are several researches on mathematical modeling of epidemics [6, 8]. In [6, 9], the authors used serial intervals and intrinsic growth rate or ordinary differential equations, whereas in [8], Markov chain Monte Carlo methods were used. However, the confinement phases to determine the parameters have not been taken into account in these published models.

In this study, we developed a new Reservoir-People (RP) transmission network model for simulating the potential transmission of COVID-19 virus in the Moroccan population, while establishing different phases that take into account the different changes in conditions enabling the transmissibility (such as confinement or other measures). A central point in our research is the computation of the basic reproduction (R_0) for each phase. Note that in the case of Morocco the virus was introduced through commercial air and sea travel (what we refer to as the reservoir in our model).

The remainder of our paper is organized as follows: In section two we present the proposed RP transmission network model. In section three, we talk about Genetic Algorithms (GAs) and their use in finding the global optimal parameters by minimizing the cost functional associated with our problem (F_l). In section four, this cost functional was detailed as well as the algorithm that was developed for computing the optimal parameters relative to each phase of the outbreak. The obtained results are presented in section five.

2. Methods

Data source. The COVID-19 data was collected for the modeling study from the daily disclosed information by the Moroccan ministry of health, and is comprised of the number of new daily cases and new death cases as well as the dates of these occurrences.As reported by the Moroccan authorities, the date of onset of the first case was March 2, 2020, and the air, sea, and land borders were closed on March 13, 2020. Epidemic data from March 2, 2020 to March 15, 2021 was collected for our study, and the simulation time step was 1 day. This data can be downloaded at https://github.com/alaanoureddine/coronavirus.git

2.1. The proposed reservoir-people transmission network model.

The first transmission network model of COVID-19 named BHRP was published on bioRxiv on January 19, 2020 [2]. The authors hypothesized that the virus was transmitted between bats and then spread to unknown hosts. Hosts were hunted and sent to the seafood market, which was defined as the reservoir of the virus. Thus, it is at the market that people are exposed to the risk of infection. This model was simplified in [1] into a Reservoir-People (RP) transmission network. The authors assumed that

SARS-COV-2 could be imported into the seafood market in a short period of time. Therefore Bats-Host transmission was ignored see figure 1.

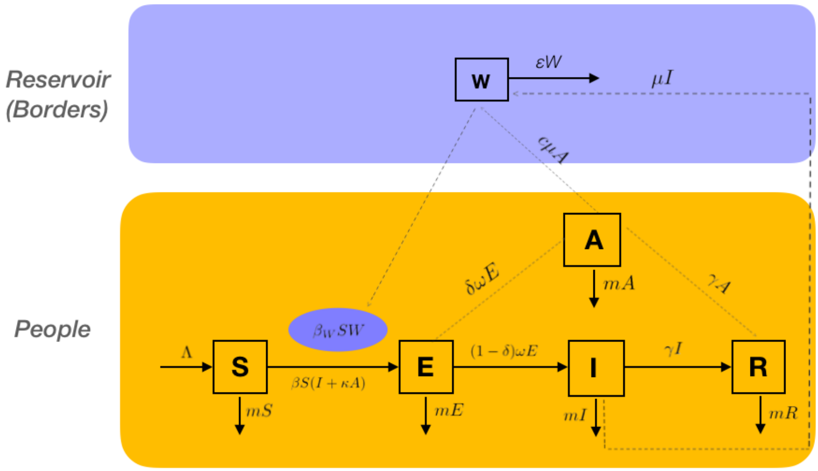

Figure 1. Flowchart of the Reservoir-People transmission network model

Thus their proposed model is given as follows:

$$\left\{\begin{aligned} \frac{dS}{dt} &= \Lambda - mS - \beta S\left(I+\kappa A\right) \\ &\quad - \beta_W SW \\ \frac{dE}{dt} &= -(m+\rho)E + \beta S\left(I+\kappa A\right) \\ &\quad + \beta_W SW \\ \frac{dI}{dt} &= -\left(\gamma+m\right)I + \left(1-\delta\right)\rho E \\ \frac{dA}{dt} &= -\left(\gamma+m\right)A + \delta\rho E \\ \frac{dR}{dt} &= -mR + \gamma I + \gamma A \\ \frac{dW}{dt} &= -\varepsilon W + \mu(I+cA) \end{aligned}\right. \tag{1}$$

Where the SARS-COV-2 in reservoir (the seafood market) was denoted as W. Symptomatic infected persons and asymptomatic infected persons export the virus with the level of μ and $c\mu$ in W repectively. The virus will then leave the W compartment at a rate of εW, where $\frac{1}{\varepsilon}$ is the lifetime of the virus. In this model, people are divided into five compartments: susceptible individuals S, exposed individuals E, infected symptomatic I and asymptomatic A.

The birth and death rates are n and m. N denotes the total number of persons and $\Lambda = n \times N$. The incubation period and latency period of human infection were defined as $\frac{1}{\rho}$.

The infection period of I and A was repectively defined as $\frac{1}{\rho}$ and $\frac{1}{\gamma}$. The proportion of asymptomatic infection was defined as δ. The S will be infected by sufficient contact with W and I, and the transmission rates were defined as β_W and β, respectively. It is also assumed that the transmissibility of A was κ times that of I, where $0 \leq \kappa \leq 1$. In addition, since people and viruses have different dimensions, they therefore have to carry out the following normalization:

$$\begin{aligned} s &= \frac{S}{N}, e = \frac{E}{N}, i = \frac{I}{N}, a = \frac{A}{N}, \\ r &= \frac{R}{N}, \; w = \frac{\varepsilon W}{\mu N}, \; b = \beta N, \; b_w = \frac{\mu \beta_W N}{\varepsilon} \end{aligned} \tag{2}$$

Finally their normalized RP model becomes:

$$\begin{cases} \dfrac{ds}{dt} = n - ms - bs\left(i + \kappa a\right) - b_w sw \\ \dfrac{de}{dt} = -(m+\rho)e + bs\left(i + \kappa a\right) + b_w sw \\ \dfrac{di}{dt} = -\left(\gamma + m\right) i + \left(1 - \delta\right) \rho e \\ \dfrac{da}{dt} = -\left(\gamma + m\right) a + \delta \rho e \\ \dfrac{dr}{dt} = -mr + \gamma i + \gamma a \\ \dfrac{dw}{dt} = -\varepsilon w + \varepsilon(i + ca) \end{cases} \tag{3}$$

In order to use the model for the case of Morocco, the first key difference will be at the level of the Reservoir, in fact in our case the W will represent the SARS-COV-2 brought into the country by means of air and sea travel. And as mentioned before, the country's government imposed several confinement phases, which influences the transmission scheme of the virus. This also needs to be taken into account. For this reason, we will assume that the model parameters $(b, c, b_w, \delta, \kappa, \gamma)$ are functions that vary over time. Therefore our proposed model is as follows:

$$\begin{cases} \dfrac{ds}{dt} = n - ms - b(t)s\left(i + \kappa(t) a\right) - b_w(t) sw \\ \dfrac{de}{dt} = -(m+\rho)e + b(t)s\left(i + \kappa(t) a\right) + b_w(t) sw \\ \dfrac{di}{dt} = -\left(\gamma(t) + m\right) i + \left(1 - \delta(t)\right) \rho e \\ \dfrac{da}{dt} = -\left(\gamma(t) + m\right) a + \delta(t) \rho e \\ \dfrac{dr}{dt} = -mr + \gamma(t) i + \gamma(t) a \\ \dfrac{dw}{dt} = -\varepsilon w + \varepsilon(i + c(t) a) \end{cases} \tag{4}$$

We can get the disease free equilibrium point (DFE) as:

$$(\frac{n}{m}, 0, 0, 0, 0, 0)$$

To know if the virus is spreading in the population and at what speed (doubling time), we calculate the average number of individuals that an infectious person infects while he is contagious. This rate is called the basic reproduction number, and is denoted R_0. If $R_0 < 1$, then the infected individual infects less than one other individual on average, which means that the disease is disappearing from the population. If $R_0 > 1$, then the disease spreads in the population and becomes epidemic. In our proposed model we assume that the parameters are constant in each phase $[T_i^l, T_f^l], l = 1, .., 4$. This will allow us to obtain the basic reproductive number R_0^l in each phase for our proposed model by the next generation matrix approach (see [7], [3]) as follows:

$$\begin{aligned} R_0^l =& b^l \frac{n}{m} \frac{(1-\delta^l)\omega^l}{(\omega^l + m)(\gamma^l + m)} + \kappa^l b^l \frac{n}{m} \frac{\delta^l \omega^l}{(\omega^l + m)(\gamma^l + m)} \\ &+ b_w^l \frac{n}{m} \frac{(1-\delta^l)\omega^l}{(\omega^l + m)(\gamma^l + m)} + b_w^l \frac{n}{m} \frac{c^l \delta^l \omega^l}{(\omega^l + m)(\gamma^l + m)} \end{aligned} \tag{5}$$

3. Background and basic concepts

Genetic Algorithms (GAs) form a class of biology inspired optimization methods derived from the genetic and Darwin's theory of evolution seen in [4] and [5]. They are a global search paradigm based on principles imitating mechanisms of genetics, natural selection, evolution and heredity, including the survival of the fittest individuals and extinction to the worst adapted individuals. The basic concepts of genetic algorithms were first formulated by Holland. However, the mathematical formulation was set later in a global framework and showed a significant improvement as the world of computing knew a considerable amount of development.

Genetic algorithms operate on generic structures called chromosomes. Each chromosome, which is a representation of elements in the solution domain, is associated with a fitness score that evaluates the performance and adequacy of a possible solution. A choice of representation is either binary or real. The evolution of the population of chromosomes is then insured by five components common to all genetic algorithms:

- Population to be generated as a representative sample;
- Fitness function for optimization of a given cost;
- Selection of individuals for reproduction;
- Crossover to produce a generation of offspring;
- Mutation to explore wildly the solution domain.

4. Application and implementation

The data alongside the policy adopted by Morocco show that there are four different phases regarding the evolution of the epidemic. Each one is defined by the measures taken by the Moroccan authorities, as well as the number of registered cases and

describes a specific scheme of outbreak.
These phases are:

- day 1 (first case) to day 150: here although the Moroccan authorities took the necessary measures to stop a disastrous outbreak, global awareness wasn?t established yet.
- Day 151 to day 220: the confinement came to an end in the entire country.
- Day 221 to day 300: during this period the epidemic curve revealed a remarkable upward rise followed by a steady decline.
- Day 301 to day 379 : a curfew was established throughout the national territory to stem the spread of the virus.

Our implementation is about determining the optimal parameters for every phase of the epidemic, through the use of a genetic algorithm. The initial population was generated randomly by using the uniform law in each field which guarantees diversity initially. The size of the population is M.

In each phase $[T_i^l, T_f^l]$, $l = 1,..,4$ and for each individual $K = (b, c, b_w, \delta, \kappa, \gamma)$ of the population, we solve the system (4) to obtain the unique solution (s, e, i, a, r, w) and we associate it with the following cost function F_l (called fitness):

$$F_l(K) = \int_{T_i^l}^{T_f^l} (i(t) - i_{obs}(t))^2 + (a(t) - a_{obs}(t))^2 \tag{6}$$

The goal is to determine the global optimum $K_l^* = (b^*, c^*, b_w^*, \delta^*, \kappa^*, \gamma^*)$ of the functional F_l for each phase $[T_i^l, T_f^l]$.
The genetic operations are carried out as follows:

Selection: We use the roulette-wheel selection. This first operation is done through the computation of the probability p of reintroduction of each individual $K_i = (b^i, c^i, b_w^i, \delta^i, \kappa^i, \gamma^i)$ into the next generation (of size M) based on this individual?s fitness value $F_l(K_i)$:

$$p = \frac{F_l(K_i)}{\displaystyle\sum_{j=1}^{M} F_l(K_j)}$$

We then choose a random number z between 0 and 1, and with respect to the accumulated fitness value (and therefore to the probability p), the first individual with an accumulated normal value larger than z is chosen.

We repeat this operation until enough individuals are selected.

Crossover: We use the barycentric crossover operator. This is carried out by first choosing a random number $d \in [0.25, 0.75]$ and selecting two elements $P_1(j)$ and $P_2(j)$ from each parent vector relative to an index j. These two elements are then combined linearly to generate two children:

$$\begin{aligned} C_1(j) &= dP_1(j) + (1-d)P_2(j) \\ C_2(j) &= (1-d)P_1(j) + dP_2(j) \end{aligned} \tag{7}$$

Note that the crossover operation is subject to a crossover probability which we set equal to 0.7

Mutation: The mutation is then used to maintain the diversity of the population from one generation to the next. This operator is applied to each child according to a probability pr which decreases as the number of the current generation increases: $G = 1, 2, ..., G_{max}$ (therefore decreases with time): $pr = 0.15 + 0.33/G$.

Where G is the generation number, G_{max} is the maximum number of generations.

Algorithm 1 Steps of the used algorithm

```
for $l = 1, .., 4$
for each generation G
Compute the fitness of each individual of the population $P_G$ by means of (6)
Generate a new population of children $C_G$ by applying the operators : selection,
    crossing and mutation.
Gathering of the intermediate population
    $$R_G = P_G \cup C_G$$
Application of the Elitism over $R_G$ to get the new population $P_{G+1}$
$G = G + 1$, incrementation to move to the next generation.
The algorithm stops if $G_{max}$ is reached or if the mean fitness of the population is
    exactly equal to the fitness of the best element.
endfor $G$
endfor $l$
```

5. Numerical algorithm and results

We summarize the steps of implementing Algorithm 1 based on the previous explanation. We applied this algorithm to the identification of the parameters of our model RP 4 for each phase of confinement. The obtained parameters will then be used for computing the relative basic reproduction rate (R_0^l). We set the value (5.2 days) of the incubation period and the latent period in this study, thus, $\rho = 0.1923$. The birth and death rates in the case of Morocco are given respectively by $n = 18.1 * 10^{-3}; m = 6.55 * 10-3$.
The following table summarizes the results obtained:

In Figure 2, we present the comparison between the normalized infected new cases, and those obtained by simulation of our model with the optimal parameters during the whole period of the experiment.

6. Conclusion

We notice that in Phase 1, the virus was in its first stages of propagation, this is reflected by our results as R_0 is greater than 1. The Phase 2 is characterised by the establishment and reinforcement of preventive measures and the speed of spread is decreased this is reflected by the obtained value of $R_0 < 1$. This endorses the efficiency of total confinement. On the other hand, Phase 3 reflects the end of the

TABLE 1. each column represents the phase and the optimal values $(\kappa, c, b, b_w, \delta, \gamma, R_0)$ of our model as well as the value of the reproduction rate R_0.

	Phase 1	Phase 2	Phase 3	Phase 4
κ	0.0554	0.5249	0.7318	0.7002
c	0.2381	0.6898	0.6484	0.3930
b	0.6604	0.2807	0.2295	0.5117
b_w	0.7552	0.6368	0.7218	0.7065
δ	0.43124	0.3519	0.2124	0.5066
γ	0.2699	0.3150	0.1880	0.5575
R_0	1.15348	0.88313	1.61647	0.57907

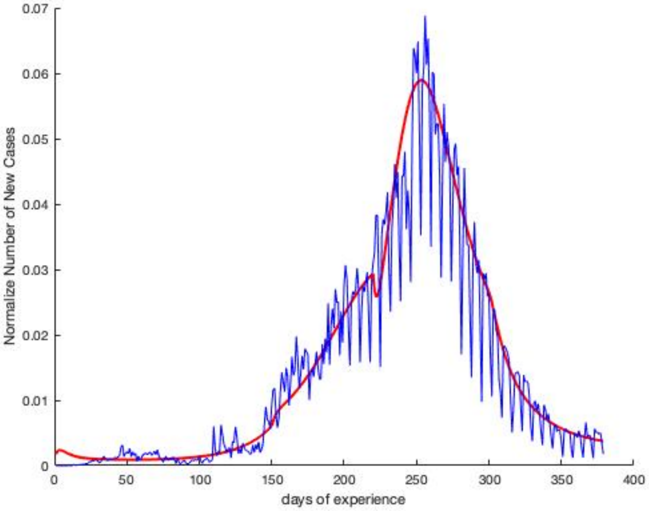

FIGURE 2. The blue curve for the symptomatic and asymptomatic infected cases observed $(i + a)$, and the one in red represents those obtained by simulation of our model with the optimal parameters obtained during the entire period of the experiment

confinement phase simultaneously with national holidays. The spread records show a drastic growth and results show that R_0 is greater than 1. But by the end of this phase the Moroccan authorities rapidly established control over the outbreak. In Phase 4, control was established over the situation as the number of confirmed cases was nearing 0. During this phase vaccination was initiated. This is reflected by the obtained results as $R0 = 0.59707$.

The results show that total confinement helped greatly in reducing the value of basic reproduction.

In this work, we have developed a new mathematical model Reservoir-People (RP) to model the transmission of the coronavirus COVID-19 in Morocco. Our model takes into account the confinement phases that the Moroccan government has put in place to minimize the spread of this pandemic. Based on the recorded data, we succeeded in obtaining the optimal parameters of our model using global minimization based on genetic algorithms. Our approach is very satisfactory and our developed model was able to reproduce the reality of the spread of this pandemic in Morocco. Our numerical algorithm is efficient and robust as shown by the simulations obtained. Our model can therefore give a prediction of the further spread of this pandemic.

References

[1] T. M. Chen, J. Rui, Q.P. Wang, Z.Y. Zhao, J.A. Cui, and L. Yin, A mathematical model for simulating the phase-based transmissibility of a novel coronavirus, In: *Infectious Diseases of Poverty* (2020), **9** 24(2020). DOI: 10.1186/s40249-020-00640-3

[2] T. Chen, J. Rui, Q. Wang, Z. Zhao, J.-A Cui, L. Yin, A mathematical model for simulating the transmission of Wuhan novel Coronavirus, In *bioRxiv* (2020), 1–9.

[3] J.-A. Cui, S. Zhao, S. Guo, Y. Bai, X. Wang, and T. Chen, Global dynamics of an epidemiological model with acute andchronic, *Applied Mathematics Letters* **103** (2020), 106203. DOI: 10.1016/j.aml.2019.106203

[4] J.H. Holland, *Adaptation in natural and artificial systems: an introductory analysis with applications to biology, control, and artificial intelligence*, MIT Press, 1992.

[5] D.E. Goldberg, *Genetic algorithms in search optimization and machine learning*, Addison-Wesley Longman Publishing Co., Boston, MA, United States, 1989.

[6] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, et al., Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia, *N Engl J Med.* **2020** (2020), 1199–1207. DOI: 10.1056/NEJMoa2001316

[7] P. Van Den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemicequilibria for compartmental models of disease transmission, *Mathematical Biosciences* **180** (2002), 29–48. DOI: 10.1016/S0025-5564(02)00108-6

[8] J.T. Wu, K. Leung, and G.M. Leung, Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study, *The Lancet*, **395** (2020), 689–697. DOI: 10.1016/ S0140-6736(20)30260-9

[9] S. Zhao, S.-S. Musa, Q. Lin, J. Ran, G. Yang, W. Wang, Y.-L. Wang, L. Yang, D. Gao, D. He, and M.-H. Wang, Estimating the Unreported Number of Novel Coronavirus (2019-nCoV) Cases in China in the First Half of January 2020: A Data-Driven Modelling Analysis of the Early Outbreak, *Journal of Clinical Medicine* **9** (2020), no. 2, 388. DOI: 10.3390/jcm9020388

(Hamza Alaa) Laboratory LAMAI, Cadi Ayyad University, Marrakesh 40000, Morocco
E-mail address: `hamza.alaa@cde.uca.ma`

(Nour Eddine Alaa) Laboratory LAMAI, Cadi Ayyad University, Marrakesh 40000, Morocco. ORCID ID 0000-0001-8169-8663
E-mail address: `n.alaa@uca.ac.ma`

(Fatima Aqel) Computer, Networks, Mobility and Modeling laboratory (IR2M), Hassan First University of Settat, Settat 26000, Morocco
E-mail address: `fatima.aqel@uhp.ac.ma`