Predictive Modelling of the COVID - 19 Epidemic in Cameroon with Innovative Models

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Abstract The mathematical model was recently used for COVID-19 in Wuhan, the Chinese city where the disease first broke out. It helped to outline the interventions needed to reduce the number of people at risk of catching the virus. The SEIR models were also used to predict interventions during the 2009 influenza pandemic in the US. In this project we will develop new models that are able to capture more features that the previous ones. Based on the official data modeling, this research work will study the Corona Virus Disease 2019 (COVID-19) propagation dynamics in Cameroon. The error between the model and the official data curve will be estimated. At the same time, it will realize the forward prediction of the epidemic situation, and the relevant analysis will help Cameroon to make important decisions on the epidemic evolution over time.

Keywords: Covid 19 modelling, SIR, SSIR, SEIR, SSEIR, model loss, model selection,reproduction number, stability analysis.

1 Introduction

Modelling disease propagation is of key importance in epidemiology. In Cameroon, 8681 confirmed cases and 208 deaths of people who tested positive for Covid 19 were registered as of 13 June 2020. Predictive mathematical models for epidemics [15–18] are fundamental to understand the course of the epidemic and to plan effective control strategies. The commonly used model is the SIR model for human-to-human transmission, which describes the flow of individuals through three mutually exclusive stages of infection: susceptible, infected and recovered [18,19]. It is generally agreed that more complex models can accurately capture the dynamic spread of specific epidemics. For the COVID-19 pandemic, several models have been developed. [19] extended a SEIR (susceptible, exposed, infected, recovered) model considering risk perception and the cumulative number of cases,[20] proposed a discrete-time SIR model including dead individuals, [21] developed a control-oriented SIR model that stresses the effects of delays and compares the outcomes of different containment policies [22] and [1,2] used transmission dynamics to estimate the clinical severity of COVID-19. Stochastic transmission models have also been considered [24-30]. However stochastic modelling of the state variable have not yet been developed. Here, we propose new approaches to epidemiological model for the COVID-19 epidemic using data from Cameroon and extend the classical SIR model. Ending the global COVID-19/SARS-CoV-2 pandemic requires implementation of multiple population-wide strategies, including social distancing, testing and contact tracing. (see [15-16] for example). These models will predict the course of the epidemic and help to plan an effective control strategy. The stochastic SIR considers at most three stages of infection: susceptible (S), infected (I), recovered (R) collectively termed as SIR with some noise adjustment terms whereas The stochastic SEIR model considers at most four stages of infection: susceptible (S), exposed (E), infected (I), recovered (R) collectively termed as SEIR with some noise adjustments. Our innovative models discriminate between infected individuals depending on whether they have been diagnosed and on the severity of their symptoms implemented in the stochastic part of the models. The distinction between susceptible and infected individuals is important because the former are typically isolated and hence

less likely to spread the infection[2-4]. We compare simulation results with real data on the COVID-19 epidemic in Cameroon, and we model possible scenarios of implementation of countermeasures. We should mention that there are some interesting mathematical models in the litterature that try to describe the dynamic of the evolution of the covid-19. Three main models can be used to validate the outbreak of the disease. Those models are the SIR, SIRD and SEIR. This is because the Covid-10 is caused by a new virus and generating a world wide emergency situation. The main goal of our paper is to develop new mathematical models well adapted to Covid-19 taking into account the specific caracteristics of the disease [6-10]. Such model should be able to consider different scenarios such as the number of infected people and the number of deaths in the country. They need to be complex enough to capture the most important effects but also simple enough to allow a good identification of the parameters using the data from the government (MINSANTE) and WHO on this pandemic. We propose both deterministic and stochastic models because both models have some advantages such as computational cost, parameter calibration, the use of the theory of differential equations for suitable analysis and the interpretation of the model. Also some authors believe that deterministic models should be the first tool to be used when modelling a new problem with limited data but other authors believe that stochastic models might have some limitations for novel analysis when it is difficult to find the density function or the probability distribution of the model and difficult to analyse as its requires more data for the calibration. Our paper is organized as follows: In section two, we present the old and new mathematical models; in section three we develop the algorithm for optimizing the parameters of the models; in section four we discuss our results; in section five we present the limitations of our results ;we end this work in section six with a conclusion and recommendations

2   Mathematical Models

2.1   Deterministic SIR MODEL

Figure 1. Deterministic SIR

The SIR dynamic system consists of three ordinary differential equations, describing the evolution of the population in each stage over time

$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{I(t)}{N} S(t) \\ \frac{dI(t)}{dt} = \beta \frac{I(t)}{N} S(t) - \lambda I(t) \\ \frac{dR(t)}{dt} = \lambda I(t) \end{cases} \tag{1}$$

where $\mathbf{S(t)}$ is the number of susceptible people, $\mathbf{I(t)}$ is the number of infected people and $\mathbf{R(t)}$ is the number of recovered people.

We should notice that $S_0 = S(0)$.

This system is non-linear, however it is possible to derive its analytic solution in implicit form. Other numerical tools include Monte Carlo methods, such as the Gillespie algorithm.Firstly note that from:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{2}$$

It follows that: $S(t) + I(t) + R(t) = constant = N$

Reproductive Ratio $R_0 = \frac{\beta}{\lambda}$ Let R_0 denote the reproductive ratio. The reproductive ratio is the fundamental parameter governing disease dynamics in our model. Thus we have the following results.

1. $R_0 < 1$ physically interpreted to mean that each person gets the disease will infect less than one person before recovering or dying, so the disease will peter out and eradication is $\frac{dI}{dt} < 0$
2. $R_0 > 1$ physically interpreted to mean that each person who gets the disease will infect more than one person, so the epidemic will spread in the host population $\frac{dI}{dt} > 0$

We examine the dynamics of the Covid 19 under high transmission rate and high recovery rate. We examine the dynamics of the Covid 19 under low transmission rate with high recovery rate. We have simulated both the existing model as well as our modified model. We have selected some initial values for the numerical experiments and obtained the results.

Theorem 1 The disease-free equilibrium of the model is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$. We mention that the basic reproduction number, given in the model equation, can also be derived by the next generation matrix analysis. To study the global asymptotic stability of the DFE, one common approach is to construct an appropriate Lyapunov function. We have found, however, that it is simpler to apply the following result introduced by [17]

Lemma 1 Consider a model system written in the form

$$\begin{cases} \frac{dX_1}{dt} = F(X_1, X_2) \\ \frac{dX_2}{dt} = G(X_1, X_2) \\ G(X_1, 0) = 0 \end{cases} \tag{3}$$

where $X_1 \in \mathbb{R}$ m denotes (its components) the number of uninfected individuals and $X_2 \in \mathbb{R}$ denotes (its components) the number of infected individuals including latent, infectious, etc; $X_0 = (X_1, 0)$ denotes the disease-free equilibrium of the system. Also assume the conditions (H_1) and (H_2) below:

$$(H_1): \textbf{ for } \frac{dX_1}{dt} = F(X_1, 0), \ X_1 \textbf{ is globally asymptotically stable}$$
$$(H2): G(X_1, X_2) = AX_2 - G(X_1, X_2),$$
$$G(X_1, X_2) \geq 0 \textbf{ for } (X_1, X_2) \in \Omega$$

where the Jacobian $A = \partial G X_1 \partial X_2 (X_1, 0)$ is an $M - matrix$ (the off diagonal elements of A are nonnegative) and Ω is the region where the model makes biological sense. Then the DFE $X_0 = (X_1 1, 0)$ is globally asymptotically stable provided that $R_0 < 1$.

Theorem 2 The disease-free equilibrium of the model is globally asymptotic stable if $R_0 < 1$.
Proof   We only need to show that the conditions (H_1) and (H_2) hold when $R_0 < 1$. In our system of equations, $X_1 = (S, R), X_2 = (I, 0)$, and $X_1 = (N, 0)$. We note that the system $dX_1 dt = F(X_1, 0)$ is linear and its solution can be easily found as $R(t) = R(0) \exp{(-bt)}$ and $S(t) = N - N - S(0) \exp{(-bt)}$ Clearly, $R(t) \to 0$ and $S(t) \to N$ as $t \to \infty$, regardless of the values of $R(0)$ and $S(0)$. Thus $X_1 1 = (N, 0)$ is globally asymptotically stable. $\square$

Theorem 3 In the disease-free-equilibrium(DFE) of the model (N,0,0) and Equilibrium (EE) one can show that, independently from biologically meaningful initial conditions.

$$(S(0), E(0), I(0), R(0)) \in \{(S, E, I, R) \in [0, N]^4 : S \geq 0, E \geq 0, I \geq 0, R \geq 0, S + E + I + R = N\}$$

it holds that
$$R_0 \leq 1 \implies \lim_{t \to +\infty} (S(t), E(t), I(t), R(t)) = DFE = (N, 0, 0, 0),$$
$$R_0 > 1, I(0) > 0 \implies \lim_{t \to +\infty} (S(t), E(t), I(t), R(t)) = EE$$

Proof   The detailed proofs can be found in [12-22]. $\square$

Deriving the Exact analytical solutions of the SIR model In 2005,[24] derived an exact analytical solution to the SIR model. In the case without vital dynamics setup, for $S(u) = S(t), R(u) = R(t)$

$$
\begin{cases}
S(u) = S(0)u \\
I(u) = N - R(u) - S(u) \\
R(u) = R(0) - \rho \ln u
\end{cases}
\tag{4}
$$

for $t = \frac{N}{\beta} \int_u^1 \frac{du*}{u*I(u*)}, \rho = \frac{\gamma N}{\beta}$, with initial conditions

$$
(S(1), I(1), R(1)) = (S(0), N - R(0) - S(0), R(0)), \qquad u_T < u < 1,
$$

By dividing the first differential equation by the third, separating the variables and integrating we get:

$$
S(t) = S(0)e^{-R_0 \frac{R(t)-R(0)}{N}}
$$

An equivalent analytcal solution found by [16] yields

$$
\begin{cases}
S(t) = S(0)e^{-\xi(t)} \\
I(t) = N - S(t) - R(t) \\
R(t) = R(0) + \rho\xi(t) \\
\xi(t) = \frac{\beta}{N} \int_0^t I(t*)dt*
\end{cases}
\tag{5}
$$

Here $\xi(t)$ can be interpreted as the expected number of transmissions an individual has received by time t. The two solutions are related by $e^{-\xi(t)=u}$. Effectively the same result can be found in the original work by [18]. These solutions may be easily understood by noting that all of the terms on the right-hand sides of the original differential equations are proportional to t.

Results The output of deterministic SIR with $S_0 = 10000, 20000, 40000$ and 100000 is presented in Figure 2, Figure 3, Figure 4, Figure 5 respectively:
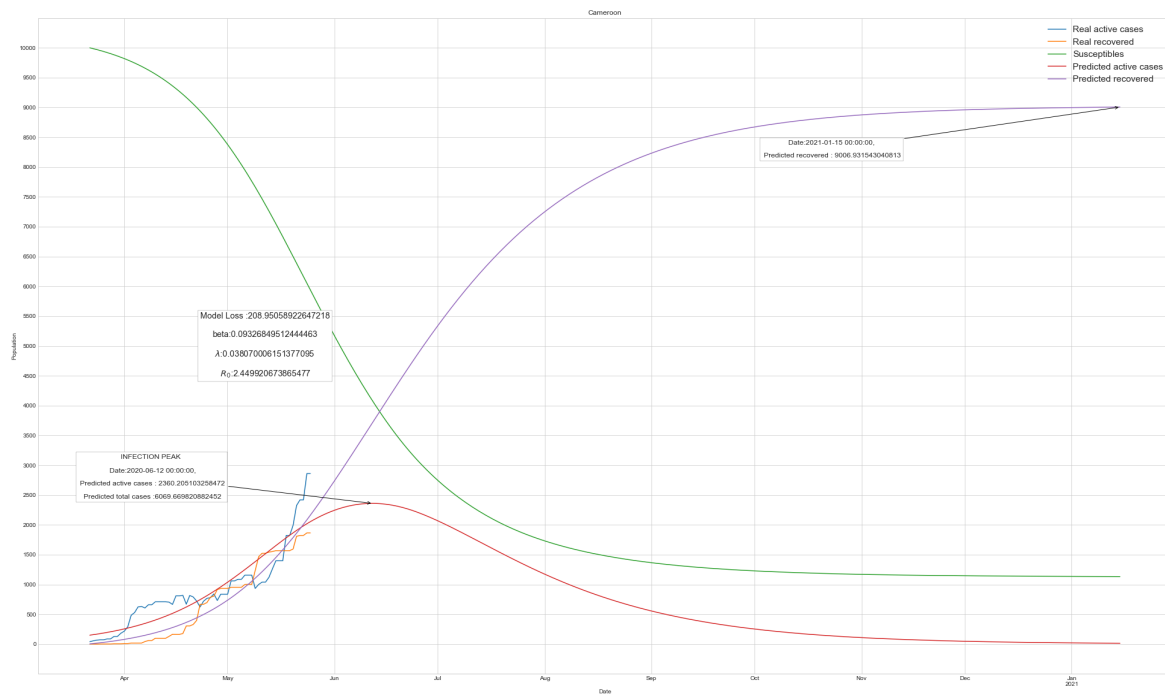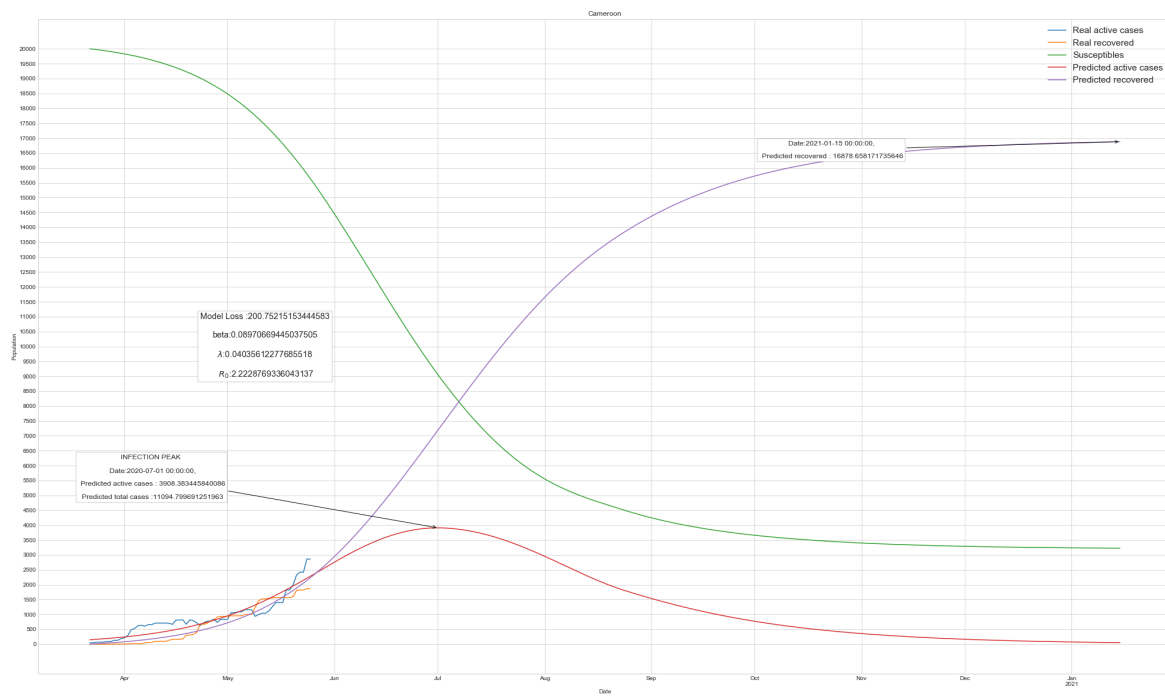
Figure 2. DETERMINISTIC SIR S_0=10000

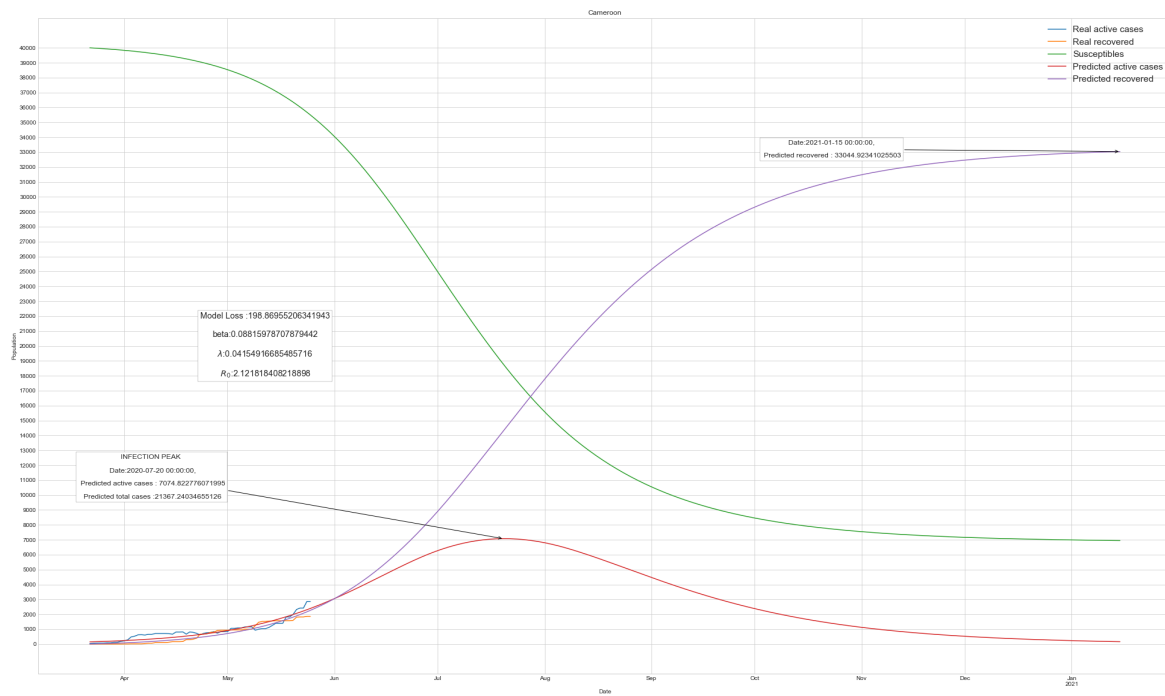**Figure 3.** DETERMINISTIC SIR S_0=20000
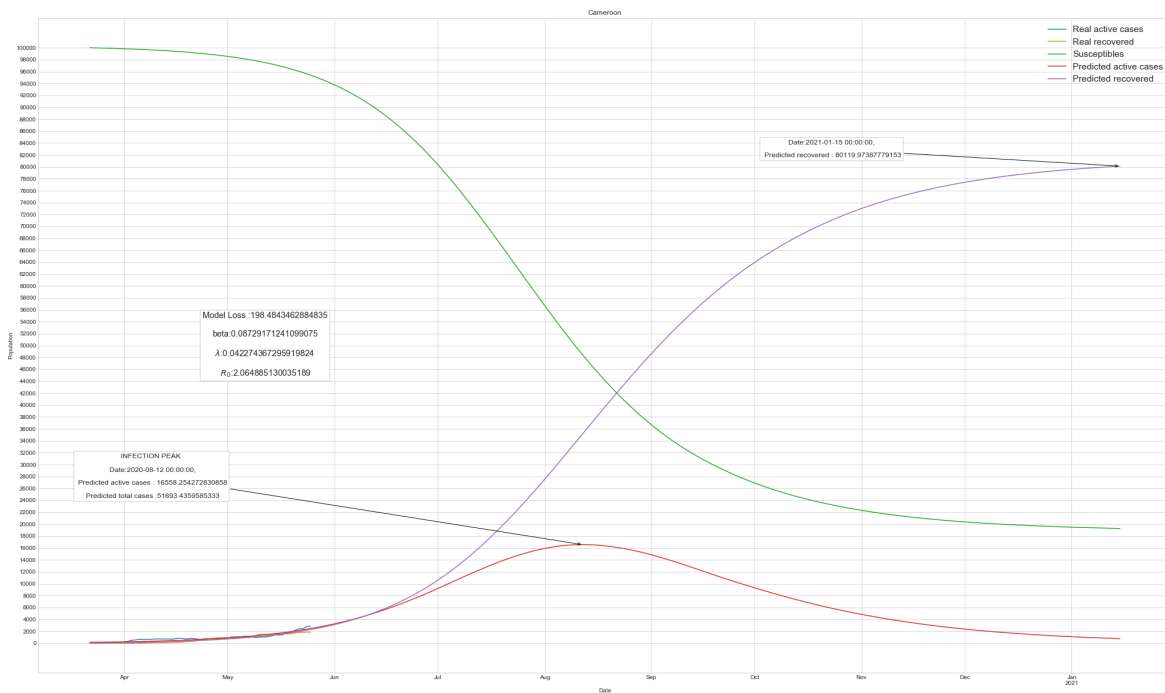
Figure 4. DETERMINISTIC SIR S_0=40000

Figure 5. DETERMINISTIC SIR S_0=100000

The parameters of the model defined as β and λ denote respectively the transmission rate (the probability of disease transmission in a single contact multiplied by the average number of contacts per person) and λ is the recovered rate (the probability of recovered individuals multiplied by the average number of contacts per person). Typically, β is larger than λ in the case of Covid 19 assuming that people tend to avoid contacts with subjects showing symptoms, even though diagnosis has not been made yet). The above parameters can be modified by social-distancing measures, closing schools, remote working, lockdown and so on.

A summary of the main findings, limitations and implications of the model for policymakers is shown in Table 1

Table 1. DETERMINISTIC SIR SUMMARY

S_0	Infection peak [Total cases]	Peak date	Model loss	R_0	Parameters (β, γ)
10000	2360 [6069]	12/06/2020	208.95	2.44	(0.093,0.038)
20000	3908 [11094]	01/07/2020	200.75	2.22	(0.089,0.040)
30000	5488 [16177]	12/07/2020	199.32	2.154	(0.088,0.041)
40000	7074 [21367]	20/07/2020	198.86	2.121	(0.088,0.004)
100000	15182.82 [47457]	10/08/2020	136.134	2.15	(0.091,0.042)

- $S_0 = S(0)$ is the initial value of the state variable S(t) (Susceptible)
- Infection peak is the maximum value of the state variable I(t) representing the exact number of infected person at a given time
- Total cases is the sum of all the infection cases which appeared since the epidemic beginning
- Peak is the date on which Infected peak happens

2.2 Stochastic SIR Model
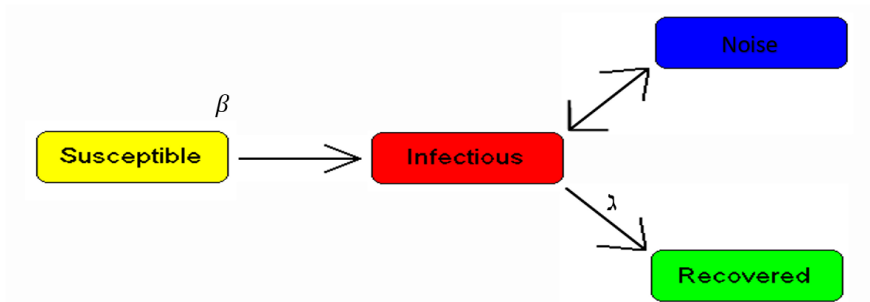
Figure 6. Stochastic SIR

The stochastic SIR model denoted SSIR is an extension of the usual SIR model by adding the noise component in the equation. The noise component stands for all minor impredictible events that might intervent in the dynamic over time. The model is given by:

$$
\begin{cases}
\frac{dS(t)}{dt} = -\beta \frac{I(t)}{N} S(t) + B_1(t) \\
\frac{dI(t)}{dt} = \beta \frac{I(t)}{N} S(t) + \lambda I(t) + B_2(t) \\
\frac{dR(t)}{dt} = \lambda I(t) + B_3(t)
\end{cases}
\tag{6}
$$

with $\{B_1 \sim \mathcal{N}(0, \sigma_1), B_2 \sim \mathcal{N}(0, \sigma_2), B_3 \sim \mathcal{N}(0, \sigma_3)\}$. The output of stochastic SIR with $S_0 = 10000$, 20000, 40000 and 100000 is presented in Figure 7, Figure 8, Figure 9 , Figure 10 respectively.
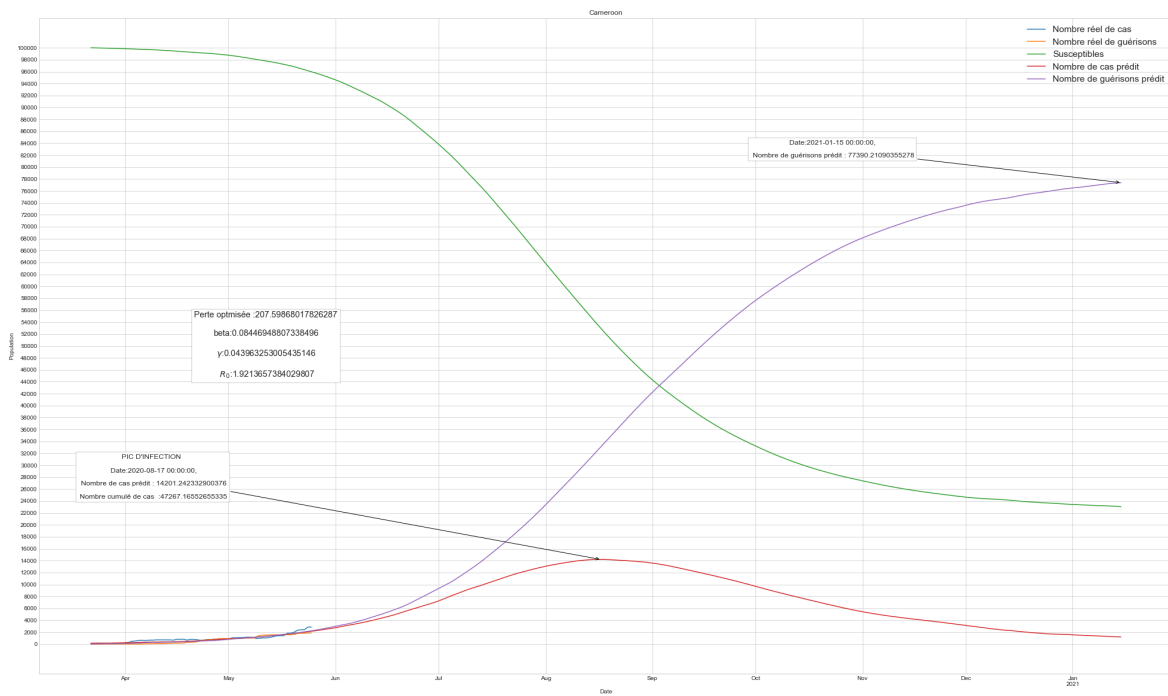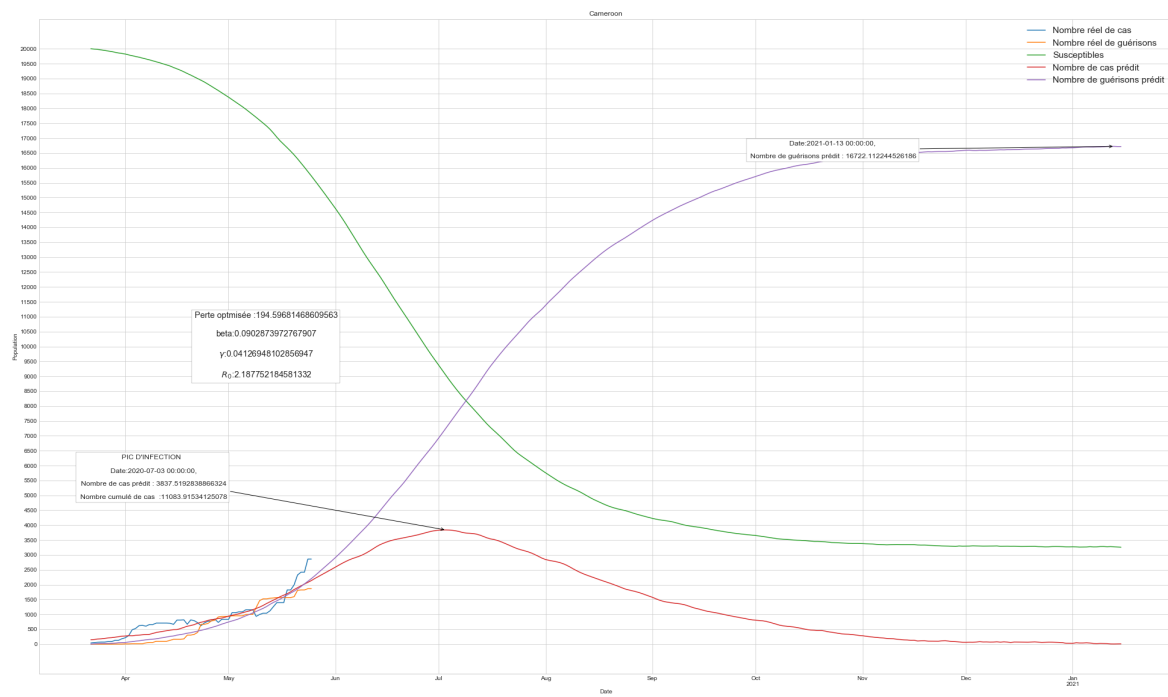
Figure 7. STOCHASTIC SIR S_0=100000

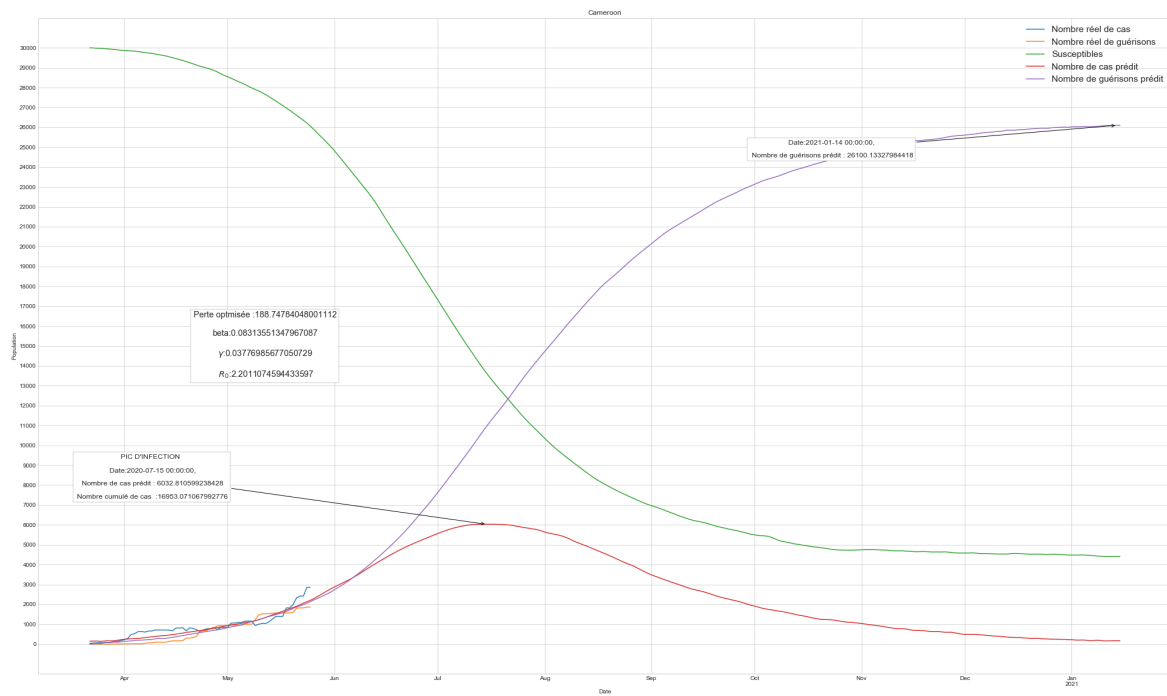**Figure 8.** STOCHASTIC SIR S_0=20000
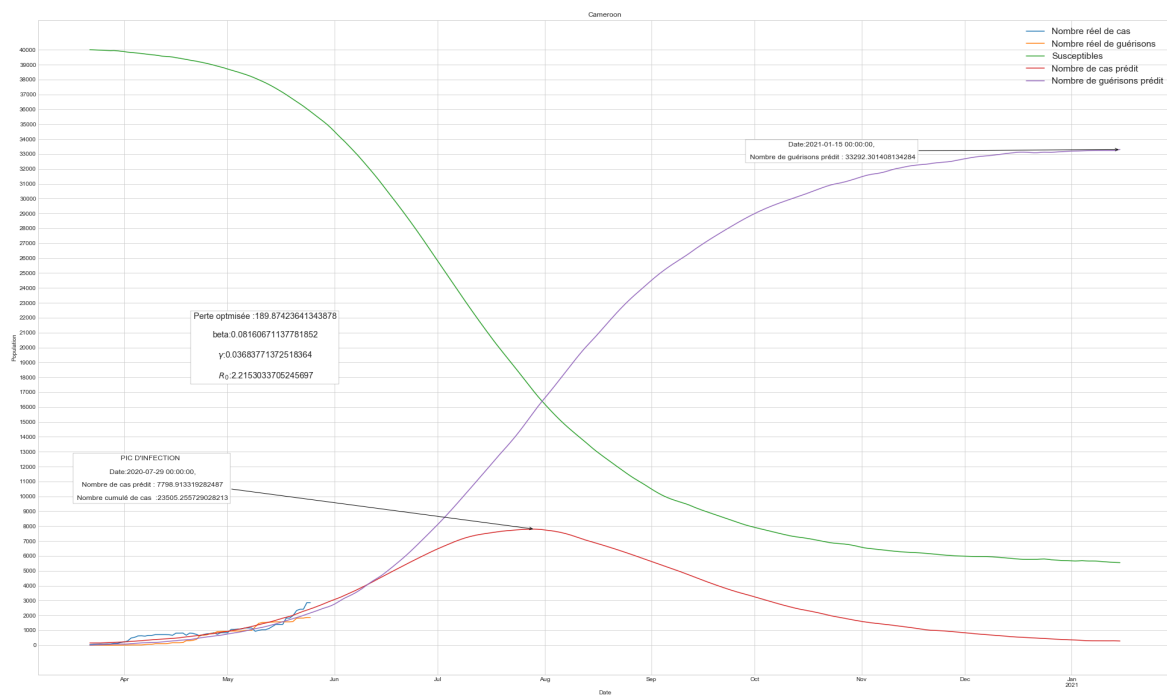
Figure 9. STOCHASTIC SIR S_0=30000

**Figure 10.** STOCHASTIC SIR S_0=40000

A summary of the main findings, limitations and implications of the model with the date from Cameroon is shown in Table 2

Table 2. STOCHASTIC SIR SUMMARY

S_0	Noise	Infection peak [Total cases]	Peak date	Model loss	R_0	Parameters (β, λ)
10000	N(0,5),N(0,10), N(0,10)	2364 [6136]	08/06/2020	214.69	2.326	(0.097,0.042)
20000	N(0,5),N(0,10), N(0,5)	3837 [11083]	03/07/2020	194.60	2.18	(0.090,0.041)
30000	N(0,10),N(0,10), N(0,10)	4684 [15187]	07/07/2020	226.92	1.95	(0.10, 0.052)
40000	N(0,10),N(0,5), N(0,10)	7798 [21367]	29/07/2020	189.874	2.21	(0.081,0.0036)
100000	N(0,10),N(0,10), N(0,10)	14201 [47267]	17/08/2020	207.5986	1.92	(0.0814,0.0044)

- S_0 is the initial value of the state variable S (Susceptibles)
- Noise is the description of the noise distribution added to the model. $N(0, 10)$ refers to the Gaussian law with
- Infection peak is the maximum value of the state variable I representing the exact number of infected person at a given time.
- Total cases is the sum of all the infection cases which appeared since the epidemic beginning
- Peak is the date on which Infected peak happens

2.3 Deterministic SEIR Model
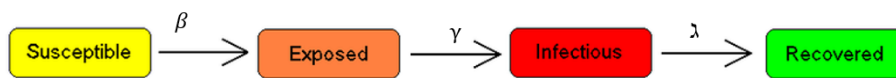
Figure 11. Deterministic SEIR

The deterministic SEIR adds the evolved (E) state variable into the usual SIR model. The equation is as follows:

$$
\begin{cases}
\frac{dS(t)}{dt} = -\beta \frac{I(t)}{N} S(t) \\
\frac{dE(t)}{dt} = \beta \frac{I(t)}{N} S(t) - \gamma E(t) \\
\frac{dI(t)}{dt} = \gamma E(t) - \lambda I(t) \\
\frac{dR(t)}{dt} = \lambda I(t)
\end{cases}
\tag{7}
$$

The output of deterministic SEIR with $S_0 = 10000, 20000, 40000$ and 100000 is presented in Figure 12, Figure 13, Figure 14 and Figure 15.
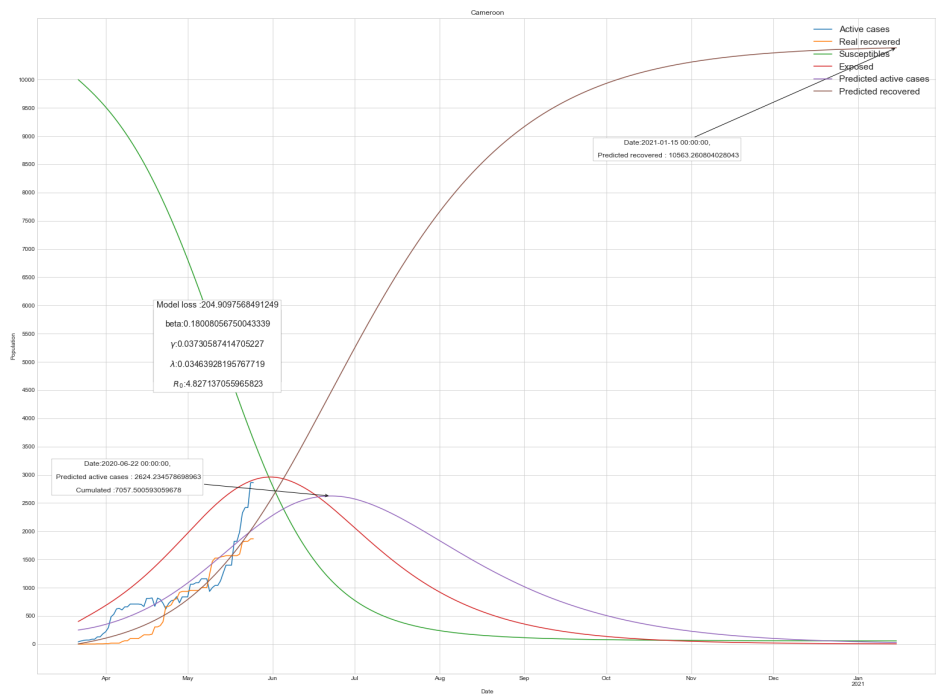
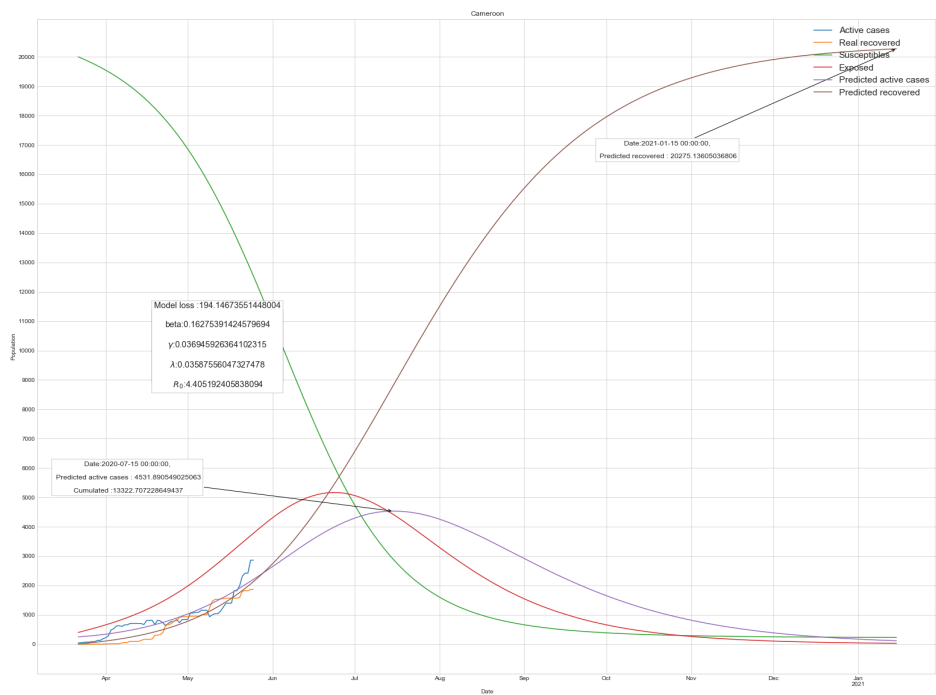**Figure 12.** DETERMINISTIC SEIR S_0=10000

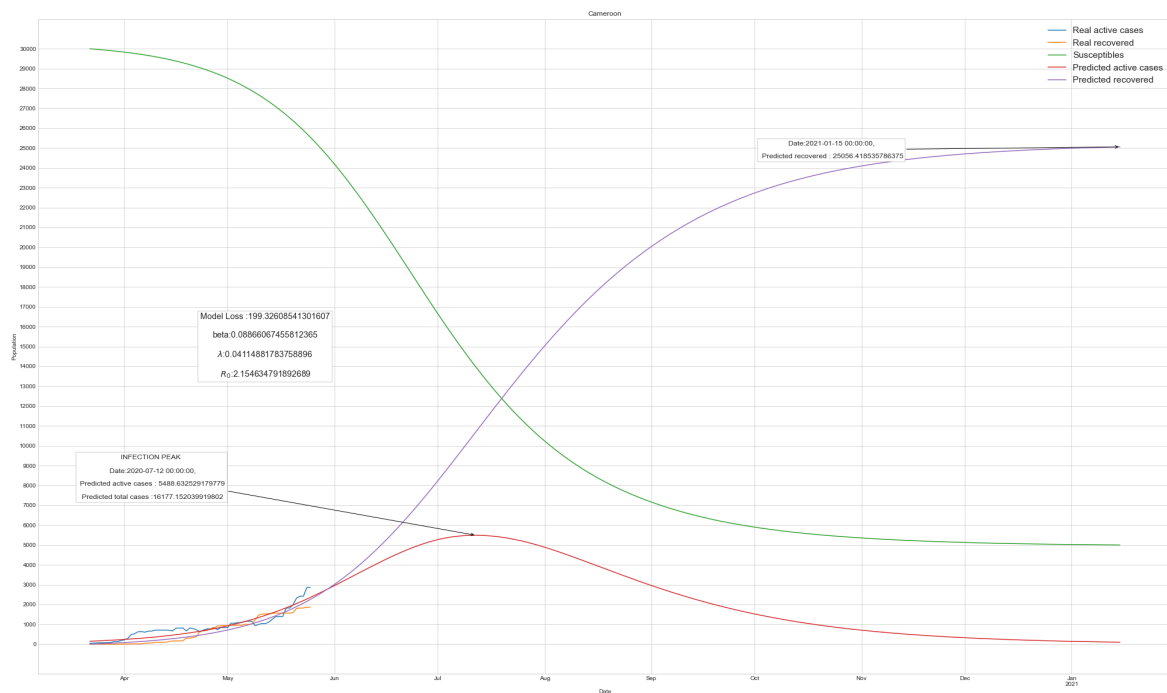**Figure 13.** DETERMINISTIC SEIR S_0=20000
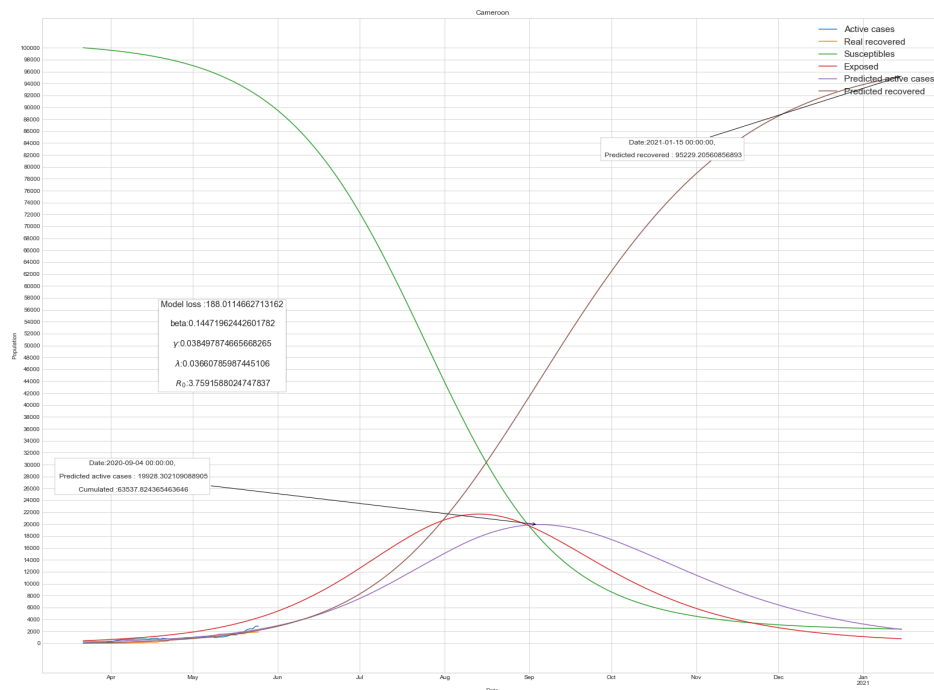
Figure 14. DETERMINISTIC SEIR S_0=40000

Figure 15. DETERMINISTIC SEIR S_0=100000

A summary of the main findings, limitations and implications of the model for policymakers is shown in Table 3

Table 3. DETERMINISTIC SEIR SUMMARY

S_0	Infection peak (Total cases)	Peak date	Model loss	R_0	Parameters(β, γ, δ)
10000	2576 [6952]	22/06/2020	206.00	6.44	(0.200,0.031,0.0344)
20000	4483 [13359]	18/07/2020	195.60	4.210	(0.15268,0.036,0.034)
30000	6364.44 [19653,73]	01/08/2020	191.97	4.14	(0.149,0.035,0.035)
40000	7798 [21367]	11/08/2020	190.47	4.11	(0.146,0.035,0.0351
100000	19537 [63224]	09/09/2020	188.268	3.84	(0.139,0.036,0.0356)

2.4 Stochastic SEIR Model

The stochastic SEIR is a novel extension of the existing SEIR model. It is denoted SSEIR. We present two versions of the SSEIR models. A model with homogeneous and heterogeneous noise is explained in details.

$$\begin{cases} \frac{dS(t)}{dt} = -\beta \frac{I(t)}{N} S(t) + B_1(t) \\ \frac{dE(t)}{dt} = \beta \frac{I(t)}{N} S(t) - \gamma E(t) + B_2(t) \\ \frac{dI(t)}{dt} = \gamma E(t) - \lambda I(t) + B_3(t) \\ \frac{dR(t)}{dt} = \lambda I(t) + B_4(t) \end{cases} \tag{8}$$

with $\{B_1 \sim \mathcal{N}(0, \sigma_1), B_2 \sim \mathcal{N}(0, \sigma_2), B_3 \sim \mathcal{N}(0, \sigma_3), B_4 \sim \mathcal{N}(0, \sigma_4)\}$.

The output of Stochastic SEIR with $S_0 = 10000, 20000, 40000$ and 100000 is presented in Figure 16, Figure 17, Figure 18 and Figure 19.
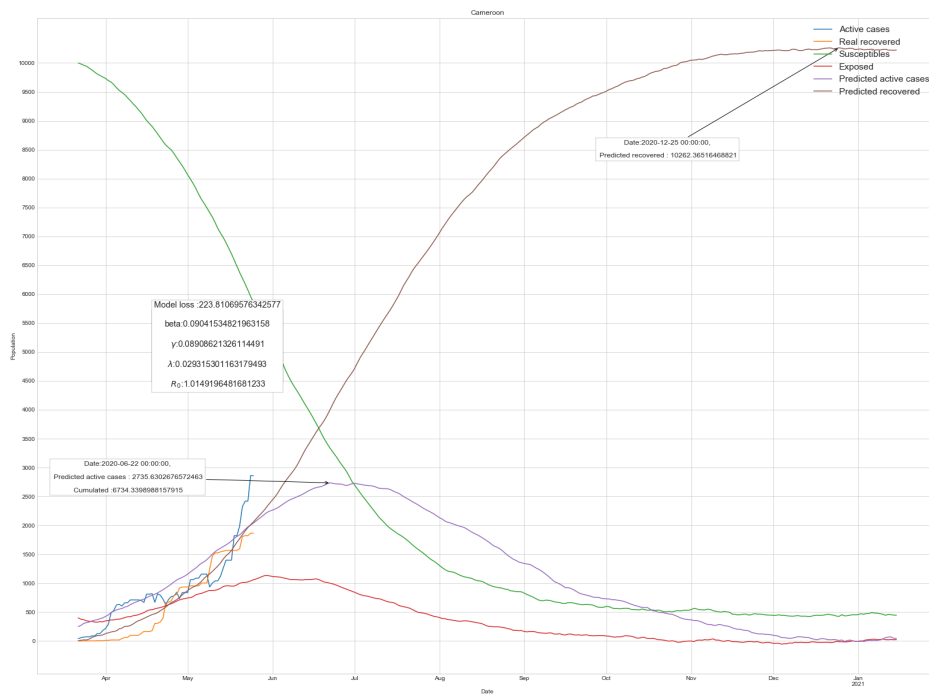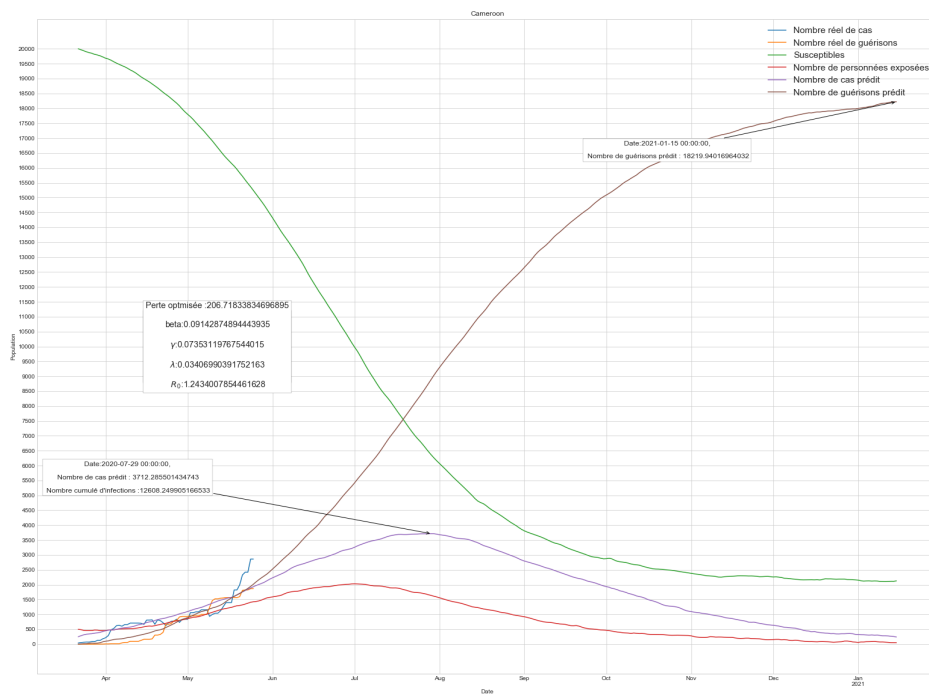
Figure 16. STOCHASTIC SEIR $S_0=10000$

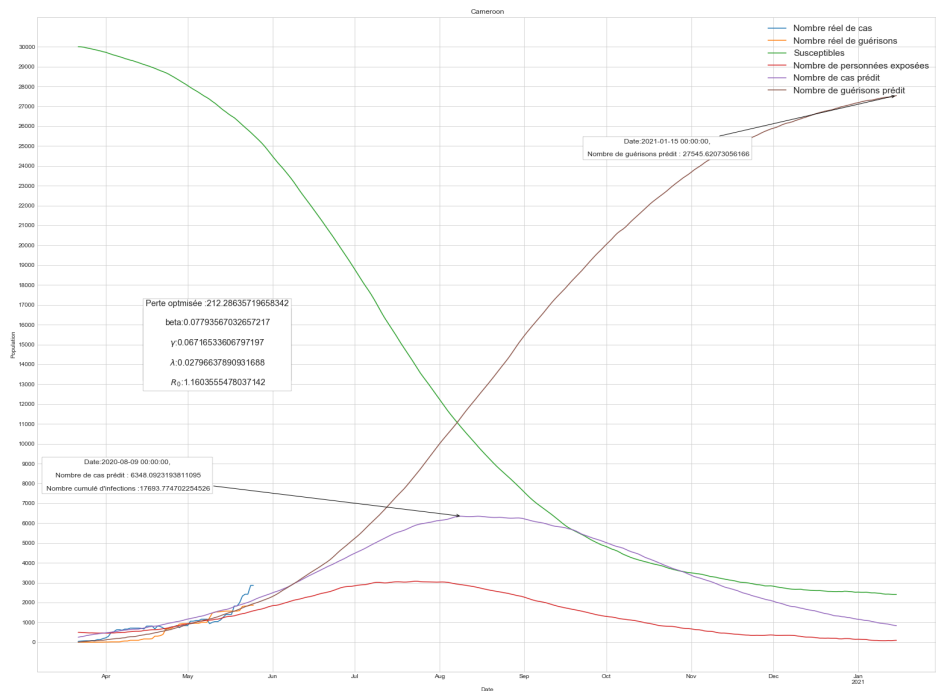**Figure 17.** STOCHASTIC SEIR $S_0=20000$
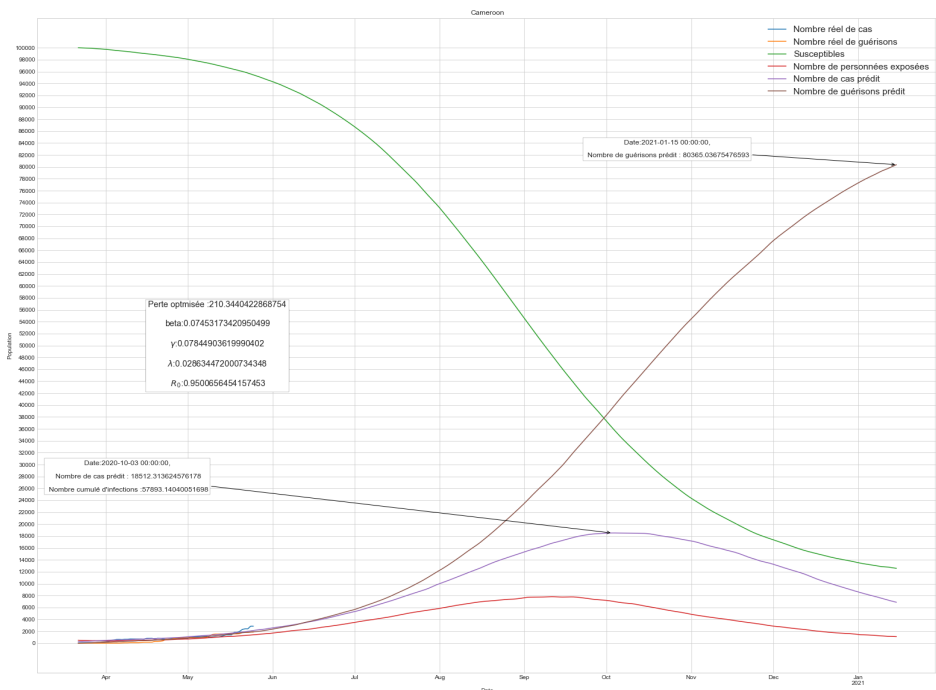
Figure 18. STOCHASTIC SEIR S_0=30000

Figure 19. STOCHASTIC SEIR S_0=10000

The summary of the main findings, limitations and implications of the model with the data from Cameroon is shown in Table 4.

Table 4. STOCHASTIC SEIR SUMMARY

S_0	Noise	Infection peak [Total cases]	Peak date	Model loss	R_0	Parameters (β, γ, λ)
10000	N(0,10),N(0,10), N(0,10),N(0,10)	2951 [7521]	22/06/2020	198.28	1.143	(0.12,0.105,0.034)
20000	N(0,10),N(0,10), N(0,10),N(0,10)	3712 [12608]	29/07/2020	206.71	1.24	(0.091,0.07,0.034)
30000	N(0,10),N(0,10), N(0,10),N(0,10)	6348 [16953]	09/08/2020	212.28	1.160	(0.077,0.067,0.027)
40000	N(0,10),N(0,10), N(0,10),N(0,10)	8497 [26614]	25/08/2020	210.173	1.29	(0.091,0.070,0.030)
100000	N(0,10),N(0,10), N(0,10),N(0,10)	18512 [57893]	03/10/2020	210.34	0.95	(0.074,0.0784,0.028)

3   Parameter Optimization

For the COVID-19 epidemic in Cameroon estimate the model parameters based on data from **22 March 2020 (day 1) to 25 May 2020 (day 61)**   and show how the progressive restrictions, including the most recent lockdown progressively enforced since 22 March 2020, have affected the spread of the epidemic. We also model possible longer-term scenarios illustrating the effects of noise on COVID-19 dynamic and also additionnal barrier measures such as social distancing and population-wide testing. The model parameters have been updated over time to reflect the progressive introduction of increased restrictions. In deterministic SIR R_0 was 2.44 in stochastic SIR R_0 was 2.32 , in determinstic SEIR R_0 was 4.15, in stochastic SEIR R_0 was 1.30. As we improve the model, the value of R_0 decreases as result of the introduction of basic social distancing, awareness of the epidemic, hygiene and behavioral recommendations, and early measures by the Cameroon government (for example, closing schools). Once the model parameters have been estimated on the basis of the available clinical data, the model enables us to reproduce and predict the dynamic evolution of the epidemic and to evaluate the possible underestimation or overestimation of the epidemic phenomenon based on current statistics, which are heavily subject to bias (for example, asymptomatic patients may get tested according to some protocols, not tested according to others). The model helps evaluate and predict the effect of the implementation of different guidelines and protocols (for example, more extensive screening for the disease or stricter social-distancing measures), which typically results in a change in the model parameters. The optimal values of the parameters can be found on the last column of each table.

Algorithm

We apply the The L-BFGS algorithm to find the optimal paramters of the model. The L-BFGS algorithm (Limited Memrory Broden-Fletcher-Goldfab-Shanno) is a very efficient algorithm for solving large scale problems. L-BFGS-B borrows ideas from the trust region methods while keeping the L-BFGS update of the Hessian and line search algorithms. Methods based completely on the trust region techniques exist and are freely available. The L-BFGS-B works for one iteration as follows :

1. Find the approximation of the Cauchy point for objective function as a quadratic form
2. Minimize the quadratic form
3. Perform a line search along new search direction
4. Update and check if the convergence is obtained

Stopping Criterion

There are three different stopping criteria for the L-BFGS-B algorithm. First the program stops when the maximum number of iterations is reached. Or, the program stops when the decrease of the objective function becomes small enough. Or, the program stops when the norm of the projected gradient is small enough.

Selection Criterion

We will apply a criterion based on error bound to select the best model. The model with te smallest error bound is considered as the best model.

$$Err(N) = \frac{1}{N}\sqrt{\sum_i (X_{realised}(i) - X_{predicted}(i))^2} \tag{9}$$

Stability

The stability analysis in the present paper shows that despite the incorporation noise in the model, of the environmental variables, there is a similar pattern of stability exchange at $R_0 = 1$. Specifically, we establish the following results for the Covid 19 model: For $R_0 < 1$, there is a unique disease-free equilibrium which is both locally and globally asymptotically stable; this equilibrium becomes unstable when $R_0 > 1$. Meanwhile, there is a unique positive equilibrium which is locally asymptotically stable when $R_0 > 1$. A complete study of the epidemic global asymptotic stability for the full Covid 19 model is challenging, and we plan to pursue it in a separate paper.We will also briefly discuss the global asymptotic stability of the epidemic equilibrium for a simplified, linear case in the next section.

3.1 Sensitivity Analysis with Respect to the Parameters (β, λ, γ)

We now investigate the sensitivity of the model to parameter variations, focusing in particular on the parameters that can be influenced by policymakers: transmission parameters, related to lockdown measures (β, λ, γ). To illustrate the effect of changing the parameter values in the model, our sensitivity analysis results are reported in Extended Table 5, 6, 7 and 8. Interestingly, the model is particularly sensitive to variations in the value of α and of ε. Increasing the parameters will increase the cumulative amount of infected individuals and the date affect the pic significantly.

We have also observed that if we increase the parameters of the model, from +5% , +15% and +20% we obtain a slight increase in the number of infected persons, the pic date but a decrease in R_0. Conversely, if we decrease the parameters of the model from -5% , -15% and -20% ,we also obtain a slight decrease in the number of infected persons, the pic of infection but an increase of R_0.

Table 5. DETERMINISTIC SIR parameters sensitivity

S_0	P.s	Infection Peak [Total cases]	Peak date	Model Loss	R_0	Parameters (β, γ)
30000	+10%	5490 [16221]	02/07/2020	199.32	2.15	(0.0975,0.045)
30000	-10%	5486 [16085]	24/07/2020	199.32	2.15	(0.079,0.037)
30000	-15%	5486 [16221]	01/08/2020	199.32	2.15	(0.075,0.0349)
30000	+15%	5489 [16073]	27/06/2020	199.32	2.15	(0.101,0.047)
30000	-20%	5486 [16176]	09/08/2020	199.32	2.15	(0.07,0.03)
30000	+20%	5489 [16082]	23/06/2020	199.32	2.15	(0.106,0.049)

Table 6. STOCHASTIC SIR parameters sensitivity

S_0	P.s	Noise	Infection Peak [Total cases]	Peak date	M. Loss	R_0	Parameters (β, γ)
30000	-10%	N(0,10),N(0,10), N(0,10)	3178[11738]	11/07/2020	275.45	1.71	(0.089,0.052)
30000	+10%	N(0,10),N(0,10), N(0,10)	5332 [15638]	05/07/2020	195.77	2.125	(0.090,0.042)
30000	+5%	N(0,10),N(0,10), N(0,10)	5841[17754]	14/07/2020	197.23	2.20	(0.090,0.040)
30000	-20%	N(0,10),N(0,10), N(0,10)	4816 [16043]	15/08/2020	193.256	1.93	(0.064,0.033)

Table 7. DETERMINISTIC SEIR parameters sensitivity

S_0	Parameters sensitivity	Infection Peak [Total cases]	Peak date	M. Loss	R_0	Parameters (β, γ, λ)
30000	-5%	6444.52 [19639]	07/08/2020	192.176	2.95	(0.126,0.043,0.033)
30000	+5%	6444 [19674]	25/07/2020	192.176	2.95	(0.139,0.0472,0.037)
30000	-15%	6049 [18338]	22/09/2020	192.176	1.024	(0.073,0.072,0.0277)
30000	+15%	6444.85 [19640]	14/07/2020	192.176	1.677	(0.152,0.051,0.040)
30000	-20%	6442 [19661]	02/09/2020	192.176	2.948	(0.106,0.0358,0.02)
30000	+20%	6444 [19844]	10/07/2020	192.176	2.948	(0.159,0.054,0.042)

Table 8. STOCHASTIC SEIR parameters sensitivity

S_0	P.s	Noise	Infection Peak [Total cases]	Peak date	M. Loss	R_0	Parameters (β, γ, λ)
30000	-5%	N(0,10),N(0,10), N(0,10),N(0,10)	5892 [18090]	16/08/2020	216.56	1.08	(0.083,0.076,0.030)
30000	+5%	N(0,10),N(0,10), N(0,10),N(0,10)	5457 [16260]	27/06/2020	237.37	1.00	(0.414,0.025,0.053)
30000	-15%	N(0,10),N(0,10), N(0,10),N(0,10)	5937 [18895]	05/09/2020	201.008	1.07	(0.077,0.072,0.028)
30000	+15%	N(0,10),N(0,10), N(0,10),N(0,10)	6492 [19540]	16/07/2020	204.08	1.36	(0.111,0.082,0.037)
30000	-20%	N(0,10),N(0,10), N(0,10),N(0,10)	3712 [12608]	29/07/2020	206.71	1.24	(0.091,0.07,0.034)
30000	+20%	N(0,10),N(0,10), N(0,10),N(0,10)	6124 [19627]	16/07/2020	192.95	1.2	(0.111,0.093,0.040)

− **P.s**: Parameters sensitvity
− **M. Loss**: Model loss

3.2 Asymptotic behaviour of state variables (Stochastic SEIR Model)

With fixed S_0, E_0 and defined I_0 as the initial number of infected patients which is known and $R_0 = 0$. Since $0 \leq S(t) \leq S(0) \leq N$ and $0 \leq R_0 \leq R(t) \leq N$. This implies that $\lim_{t\to\infty} S(t) = S_\infty, \lim_{t\to\infty} R(t) = R_\infty, \lim_{t\to\infty} E(t) = E_\infty$, therefore $I(\infty) = \lim_{t\to\infty} I(t) = N - S(\infty) - E(\infty) - R(\infty)$ exists.

Remarks

1. The disease will die out when $I(\infty) = 0$, $S_\infty = 1 - \epsilon$, ($\epsilon \in [0,1]$) and $R_\infty = \infty$
2. If $R_0 \leq 1$, Then $I(t)$ decreases monitically to zero as $t \to \infty$.
3. If $R_0 > 1$, Then $I(t)$ starts increasing , reaches a maximumn then decreases to zero as $t \to \infty$. This caracterises an epidemic

4   Results and Discussion

Our findings provide researchers with a tool to assess the consequences of possible strategies, including lockdown and social distancing, as well as testing and contact tracing. Our simulation results, achieved by combining the model with the available data about the COVID-19 epidemic in Cameroon, suggest that enforcing strong social-distancing measures is urgent, necessary and effective, in line with other reports in the previous papers. The earlier the lockdown is enforced, the stronger the effect obtained. The model results also confirm the benefits of mass testing, whenever facilities are available. We believe these indications can be useful to manage the epidemic in Cameroon and other countries in Africa that are still in the early stages of outbreak. This article highlights the findings below:

1. The initial number of infected individuals is one of the key parameter for the COVID 19 propagation
2. By Adding noise to covid19 models we improve the results significantly.
3. The peak of the infected people strongly depends on the optimization of the parameters
4. The model selection relies only on the error bound of the model.

Assuming that the virus does not mutate and no vaccine is found, and we largely forgo testing and quarantining procedures, the number of deaths that would occur due to COVID-19 in Cameroon varies, and is improved as we improved the model. The peak value of active cases in a day and cumulative number of cases is calculated. The pandemic would affect a total of 15000 crore individuals by July.

There can be multiple reasons for this. Even though lock down has been imposed, it is not strictly followed. Violation of lock down means that temporary curbing of the pandemic does not occur. So the number of cases will continue to rise. Also testing and quarantining of the infected remains very poor in Cameroon The above results are what our deterministic an stochastic models predicts which are subject to the simplifying assumptions made while deriving them. Actual numbers are totally different in case stochasticity is important, which the present study ignores. Future deleterious mutations of COVID-19 may exacerbate the situation whereas development of an effective vaccine may mitigate the problem.

Practically, however, the strength and the success of the control measures would be limited by social and economic factors and available resources, and the combination of different prevention and intervention approaches would possibly achieve the best result. Other types of control measures, such as sanitation, sewage treatment, and water cleaning, can be also incorporated into the model and the resulting values of R_0 can be similarly calculated. Such information would provide useful guidelines for the public health administrations to effectively design disease control strategies and to properly scale their efforts.

5   Limitations

There are a few limitations in this study. As mentioned before, the model (1-5) is based on the assumption that S_0 is chosen large enough to solve the problem. This may not be true in the real world, especially when a long period of time is concerned. Next, the disease-induced mortality is not included in the model. the models do not account for migration; Datas were not collected by ourself; Model's parameters are limited (2 to 4 parameters);The computational time was short with determinstic models and longer with stochastic models; The current models are only suitable for countries with an acceptable number of infected people; Therefore, part of the results can be improved; Any factor that is not included in the models is considered as part of the noise; This research has been done under the pressure and the urgency of the current covid-19 situation.

6   Conclusion and Recommendations

In this article we have provided a rough quantification of the error in estimating the actual number of infected people due to COVID-19 in Cameroon. Also, Our models can explain and predict the long-term effects of underdiagnosis, including the (apparently surprising) increased number of infections and fatalities, with sudden outbreaks after long silent periods. Our results demonstrate that restrictive social-distancing measures will need to be combined with widespread testing and contact tracing to end the ongoing COVID-19 pandemic. The model predictions in the long run remain sensitive to the initial conditions, but they are sensitive to the parameter values (and in particular extremely sensitive to some of these, as our sensitivity analysis has indicated), which are deeply uncertain and can vary due to several factors, such as population density, cultural habits, environmental conditions and age distribution of the population. The predictions must also consider parameter variations due to the measures imposed by the government. This is a fundamental aspect: in the long term, not imposing drastic measures leads to catastrophic outcomes, even when the initially affected population is a small fraction.(low). Social-distancing measures are modeled by reducing the infection coefficients β, λ and γ. The infection peak time is not monotonic with increasing restrictions. Partial restrictions on population movements postpone the peak, while strong restrictions anticipate the peak. The modified version of mathematical model proposed and studied in this paper been proved more practical than the usual SIR model as it gives a better insight into covid 19 diseases and consequently enhances struggle against the spread of those diseases. It also revealed some remarkable result such as the effect of S_0 on the infection peak, the slight variation of parameters and the nature of the noise (homogenous vs heterogeneous). The modified version of the model can be used to study and describe more complex spread of disease

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