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APPROXIMATE BAYESIAN INFERENCE OF A STOCHASTIC DISCRETE COMPARTMENTAL MODEL MOTIVATED BY COVID-19 PANDEMIC

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Abstract. In this paper we construct a stochastic discrete compartmental model from a set of hypotheses about the spread and evolution of an epidemic at the individual level. This model is motivated by the specificities of COVID-19 pandemic. Given the complexity of the likelihood of the model, an approximate Bayesian inference algorithm is proposed to estimate model parameters. Simulated datasets are used to test the efficiency of the proposed algorithm. We illustrate the introduced model on Morocco COVID-19 data.

Keywords: Approximate Bayesian Computation, Bayesian inference, SEIRD epidemic model, COVID 19 pandemic.

AMS Subject Classification: 62F15, 60E05, 92D30.

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1 Introduction

Covid 19 is a contagious disease caused by the SARS-COV2 virus. It was identified in Wuhan (Hubei), China for the first time Velavan et al. (2003). According to Wang et al. (2020), many transmissions occurred through human-to-human contact with individuals showing no or mild symptoms. To date, this epidemic has caused more than 2,917,595 deaths worldometers. According to studies Li (2021) and Bulut et al. (2020), severity of infection by SARS-COV2 virus varies from asymptomatic infection to critical disease. Clinical severity of COVID-19 was defined in Fang et al. (2020) and Wu et al. (2020) in 5 groups as asymptomatic, mild, moderate, severe, and critical.

Numerical modeling is a helpful tool for many phenomena Nachaoui et al. (2021, 2020); Rasheed et al. (2021). To consider the specificities of the Covid 19 pandemic, several epidemiological models have been proposed in the literature.

In Giordano et al. (2020), the authors introduced a deterministic compartment model. In their model, they extend the classic SEIR model Hethcote et al. (1980) and Kermack et al. (1927) by distinguishing 8 compartments considering the asymptomatic infected and the symptomatic infected detected and undetected. In Ivorra et al. (2020), Authors develop a model which considers the existence of infectious undetected cases and the different sanitary and infectiousness conditions of hospitalized people. S. He *et al* develop a model in He et al. (2020) based on classical SEIR model and considering control strategies, such as hospital, quarantine, and external input.

In this paper we introduce a discrete stochastic compartment model extending the classic SEIR model, applied in the literature to the epidemic caused by the SARS Cov 2 virus and its variants. The stochastic property considers the non-deterministic character of the contamination, the etiology of the disease caused by the virus (asymptomatic, symptomatic with severe symptoms...). This model was obtained from a set of hypotheses about the spread and evolution of an epidemic at the individual level. These hypotheses concern contacts between individuals, the process of generation of contaminations, the symptoms of the disease (mild or severe) and the evolution of individual's state (from susceptible to recovery from the disease or death).

The mathematical expectation of the introduced model generates the classical deterministic epidemic model: SEIRD. This model is described by a system of autonomous differential equations. Thus, the approximate Bayesian inference adopted in this paper can be seen for the deterministic model as a Bayesian optimization problem that searches for the parameters of the model that best fit the observed data.

The paper is organized as follows. In section 2, we derive a stochastic discrete compartmental epidemic model from individual level. An approximate Bayesian inference algorithm to estimate model parameters is proposed in section 3. We test the performance of the estimation algorithm introduced on simulated data in section 4. In section 5, we estimate the parameters of the model introduced from real data. Finally, Section 6 concludes the paper.

2 The stochastic discrete compartmental SEIRD model proposed

In this section, a discrete stochastic compartment model is derived from a set of assumptions about the diffusion and evolution of the epidemic at the individual level.
Following the classic SEIR model, we consider a compartment model with 6 compartments: Susceptible, Exposed (not yet infectious), Infected with mild symptoms, Infected with severe symptoms, Recovered and Death.

In Figure 1, we present the compartments considered and the possible transitions between the compartments.

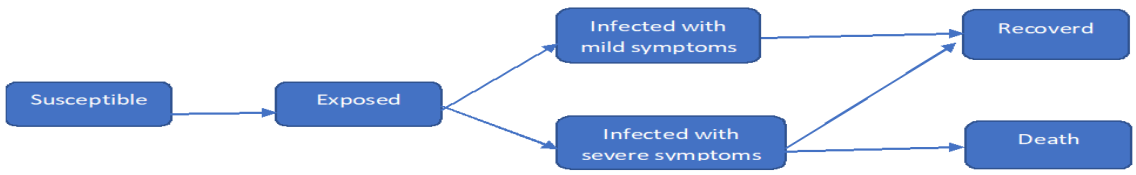

Figure 1: Compartments and possible transitions between compartments

At the individual level, the dynamics of the epidemic is modeled as follow:

At time t, let $\mathcal{S}_t$, $\mathcal{E}_t$, $\mathcal{I}_t^m$, $\mathcal{I}_t^s$, $\mathcal{R}_t$, $\mathcal{D}_t$ be respectively: the set of susceptible individuals, the set of exposed individuals, the set of infectious individuals with mild symptoms, the set of infectious individuals with serious symptoms, the set of recovered individuals and the set of deaths.

The dynamic of the disease in population is as follow:

- Let $i \in \mathcal{S}_t$ and $j \in \mathcal{I}_t^m \bigcup \mathcal{I}_t^s$, if i contacts j, then i becomes infected with probability β. At each time t, we assume that a contact between two individuals occurs with probability p.

- If the individual i is exposed at t ($i \in \mathcal{E}_t$), he becomes infectious after T_i^e times and develops severe symptoms with probability θ. We assume T_i^e is distributed as an exponential probability with parameter γ.

- An infectious individual i with severe symptoms ($i \in \mathcal{I}_t^s$) dies due to the disease with probability δ after $T_i^{s_1}$ times. We assume $T_i^{s_1}$ is distributed as an exponential probability with parameter η. Hence, with probability $1-\delta$ an infectious individual with severe symptoms recovers from the disease, we assume he is recovered after $T_i^{s_2}$ times where $T_i^{s_2}$ is distributed as an exponential probability with parameter μ_1.

- An infectious individual i with mild symptoms ($i \in \mathcal{I}_t^m$) recovers from the disease after T_i^m times. We assume T_i^m is distributed as an exponential probability with parameter μ_2.

Let S_t, E_t, I_t^m, I_t^s, R_t and D_t be respectively the size of sets: $\mathcal{S}_t$, $\mathcal{E}_t$, $\mathcal{I}_t^m$, $\mathcal{I}_t^s$, $\mathcal{R}_t$, $\mathcal{D}_t$.

Proposition 1. *Let i be an individual, then we have the following probabilities:*

1. $\mathbb{P}[i \in \mathcal{E}_{t+1} | i \in \mathcal{S}_t] = 1-(1-p\beta)^{I_t}$ *where* $I_t = I_t^m + I_t^s$
2. $\mathbb{P}[i \in \mathcal{I}_{t+1}^m | i \in \mathcal{E}_t] = (1-\theta)(1-e^{-\gamma})$
3. $\mathbb{P}[i \in \mathcal{I}_{t+1}^s | i \in \mathcal{E}_t] = \theta(1-e^{-\gamma})$
4. $\mathbb{P}[i \in \mathcal{D}_{t+1} | i \in \mathcal{I}_t^s] = \delta(1-e^{-\eta})$
5. $\mathbb{P}[i \in \mathcal{R}_{t+1} | i \in \mathcal{I}_t^s] = (1-\delta)(1-e^{-\mu_1})$
6. $\mathbb{P}[i \in \mathcal{R}_{t+1} | i \in \mathcal{I}_t^m] = (1-\delta)(1-e^{-\mu_2})$

Proof. 1. We have: $\mathbb{P}[i \in \mathcal{E}_{t+1} | i \in \mathcal{S}_t] = 1 - \mathbb{P}[i \in \mathcal{S}_{t+1} | i \in \mathcal{S}_t]$
as for $j \in \mathcal{I}_t$, $\mathbb{P}[j \text{ infects } i] = \mathbb{P}[i \text{ contact } j \text{ and } j \text{ infects } i] = p\beta$
then $\mathbb{P}[i \in \mathcal{S}_{t+1} | i \in \mathcal{S}_t] = (1-p\beta)^{I_t}$
hence $\mathbb{P}[i \in \mathcal{E}_{t+1} | i \in \mathcal{S}_t] = 1-(1-p\beta)^{I_t}$.

2. Let $\varepsilon_i = \inf\{s, i \in \mathcal{E}_s\}$ we have
$\mathbb{P}[i \in \mathcal{I}_{t+1}^m | i \in \mathcal{E}_t] = \mathbb{P}[T_i^e + \varepsilon_i < t+1 | T_i^e + \varepsilon_i \geq t; i \text{ develops mild symptoms}]$
$\times\, \mathbb{P}[i \text{ develops mild symptoms}]$
as $\mathbb{P}[T_i^e + \varepsilon_i < t+1 | T_i^e + \varepsilon_i \geq t; i \text{ develops mild symptoms}] = \mathbb{P}[T_i^e + \varepsilon_i < t+1 | T_i^e + \varepsilon_i \geq t] = 1-e^{-\gamma}$
and $\mathbb{P}[i \text{ develops mild symptoms}] = 1-\theta$
then $\mathbb{P}[i \in \mathcal{I}_{t+1}^m | i \in \mathcal{E}_t] = (1-\theta)(1-e^{-\gamma})$

3. In the same manner we prove the results 3., 4., 5. and 6.

□

Proposition 2. *For each t, we have:*

1. $S_{t+1} = S_t - X_t$
2. $E_{t+1} = E_t + X_t - (Y_t^m + Y_t^s)$
3. $I_{t+1}^m = I_t^m + Y_t^m - Z_t^m$
4. $I_{t+1}^s = I_t^s + Y_t^s - (Z_t^{s_1} + Z_t^{s_2})$
5. $R_{t+1} = R_t + Z_t^m + Z_t^{s_2}$
6. $D_{t+1} = D_t + Z_t^{s_1}$

Where:

- $X_t | S_t \sim Binomial(S_t, 1-(1-p\beta)^{I_t})$,

- $(Y_t^m, Y_t^s, E_t - (Y_t^m + Y_t^s))|E_t \sim$ *Multinomial*$(E_t, p_1, p_2, 1 - p_1 - p_2)$ *where* $p_1 = \theta(1 - e^{-\gamma})$ *and* $p_2 = (1 - \theta)(1 - e^{-\gamma)}$,
- $(Z_t^{s_1}, Z_t^{s_2})|I_t^s \sim$ *Multinomial*$(I_t^s, p_3, p_4, 1 - p_3 - p_4)$ *where* $p_3 = \delta(1 - e^{-\eta})$ *and* $p_4 = (1 - \delta)(1 - e^{-\mu_1})$,
- $Z_t^m|I_t^m \sim$ *Binomial*$(I_t^m, 1 - e^{-\mu_2})$.

Given S_t, E_t, I_t^m *and* I_t^s, *the random variables* X_t, $(Y_t^m, Y_t^s, E_t - (Y_t^m + Y_t^s))$, $(Z_t^{s_1}, Z_t^{s_2})$ *and* Z_t^m *are independents.*

The notation $X|Y \sim P$ *means that the random variable* X *given* Y *is distributed as* P.

Proof. 1. We have $X_t = S_{t+1} - S_t = \sum_{i \in \mathcal{S}_t} 1_{\{i \text{ is infected at } t\}}$.
By hypothesis, the variables $(1_{i \text{ is infected at t }})_{i \in \mathcal{S}_t}$ are independents.
Then, by proposition 2.1: $X_t|S_t \sim$ Binomial $(S_t, 1 - (1 - p\beta)^{I_t})$

2. For $i \in \mathcal{E}_t$, let:

$$\begin{cases} a_i, & \text{if i transit to infectious state with severe symptoms and 0 otherwise} \\ b_i, & \text{if i transit to infectious state with mild symptoms and 0 otherwise.} \end{cases}$$

We have:

$$E_{t+1} = E_t + X_t - \sum_{i \in \mathcal{E}_t} (a_i + b_i)$$

For every i, the random variables $(a_i, b_i, 1 - (a_i + b_i)) \sim$ Multinomial $(1, p_1, p_2, 1 - p_1 - p_2)$ given $i \in \mathcal{E}_t$ are independents.
Let $Y_t^s = \sum_{i \in \mathcal{E}_t} a_i$ and $Y_t^m = \sum_{i \in \mathcal{E}_t} b_i$
Then $(Y_t^m, Y_t^s, E_t - (Y_t^m + Y_t^s))|E_t \sim$ Multinomial $(E_t, p_1, p_2, 1 - p_1 - p_2)$

3. In the same manner, we prove the results 3., 4., 5. and 6.

□

Proposition 3. *Let* $(S_0, E_0, I_0^m, I_0^s, R_0, D_0) \in \mathbb{R}_+^6$, *then for every* t

$$\mathbb{P}[(S_t, E_t, I_t^m, I_t^s, R_t, D_t) \geq 0] = 1$$

Proof. Let $\Phi = (S_t, E_t, I_t^m, I_t^s, R_t, D_t)$
we have $\mathbb{P}[\Phi_{t+1} \geq 0] = \mathbb{P}[\Phi_{t+1} \geq 0 | \Phi_t \geq 0] \times \mathbb{P}[\Phi_t \geq 0]$.
From the proposition 2.2, we have $\mathbb{P}[\Phi_{t+1} \geq 0 | \Phi_t \geq 0] = 1$
as $\Phi_0 \geq 0$, by recurrence, we conclude: $\mathbb{P}[\Phi_t \geq 0] = 1$. □

3 Bayesian inference of model parameters

Given the complexity of the likelihood of the model (proposition 2.2), we opted for approximate Bayesian inference. Approximate Bayesian Computation (ABC) methods are a family of algorithms developed to perform Bayesian inference in the case of computationally intractable likelihood function. The steps of the basic ABC algorithm (see, Toni et al. (2009)) are as follows (Algorithme 1).

Algorithm 1: Basic ABC algorithm

Input: Observed data D_0, prior distribution π, threshold error e and discrepancy measure Δ

Output: a sample of size n from approximate posterior $P_a(\theta|D_0)$

1. Draw θ from the prior distribution $\pi(\theta)$.
2. Simulate data from the model, using parameters θ to get data D.
3. If $\Delta(D, D_0) < e$ accept θ otherwise reject.
4. Repeat 1.,2. and 3. until n values of θ are accepted.

To improve the efficiency of the basic algorithm, several algorithms have been developed such as ABC-MCMC, ABC-SMC (see Beaumont (2019),Sisson et al. (2018)). To estimate the parameters of the proposed stochastic discrete SEIRD model, we propose the following algorithm (Algorithm 2).

Algorithm 2:

Input: Observed data D_0, prior distribution π, a Kernel K, acceptance rate α, number of simulations m and discrepancy measure Δ

Output: a sample from approximate posterior $P_a(\theta|D_0)$

1. Draw a sample of $(\theta_i)_{i=1,...,m}$ from the prior distribution $\pi(\theta)$
2. For each θ_i, simulate data from the model, using parameters θ_i to get data D_i and $\Delta_i = \Delta(D_i, D_0)$
3. Compute $e = Q_\alpha(\{\Delta_i, i = 1, ..., m\})$ where Q_α is the α quantile
4. For each θ_i, compute $w_i = K_e(\Delta_i)$
5. Normalize $(w_i)_{i=1,...,m}$
6. Draw a sample from $(\theta_i, w_i)_i$ with replacement and probabilities $(w_i)_{i=1,...,m}$

4 Evaluation of the estimation algorithm

To evaluate the estimation algorithm introduced, we consider a population of size $N = 1000000$ individuals, 100 initial infectious individuals and $p = \frac{\zeta(\alpha-1)}{\zeta(\alpha)N}$ where ζ is the Riemann zeta function and $\alpha = 2.5$, this choice is based on the assumption that the network of contacts between individuals is a scale-free network with the fraction of nodes in the network having k connections to other nodes follow power law $P(k) \sim k^{-\alpha}$ with $2 < \alpha < 3$ (see, **?**).

We fix $\gamma = \frac{1}{5}$ days^{-1}, $\theta = 0.1$, $\delta = 0.5$, $\mu_1 = \frac{1}{7}$ days^{-1}, $\mu_2 = \frac{1}{14}$ days^{-1} and $\eta = \frac{1}{18}$ days^{-1}, choices motivated by epidemic parameters of Covid-19 (see, [8]). The introduced estimation algorithm is performed for different values of β.

We use the kernel $K(e - \Delta) = \max(e - \Delta, 0)$ and we test for the acceptation rates $\alpha = 1\%$ and $\alpha = 0.1\%$.

The discrepancy measure used is:

$$\Delta = \sum_t |S_t - S_t^0| + \sum_t |I_t^m - I_t^{m_0}| + \sum_t |I_t^s - I_t^{s_0}| + \sum_t |D_t - D_t^0| + \sum_t |R_t - R_t^0|$$

Where S_t^0, $I_t^{m_0}$, $I_t^{s_0}$, D_t^0 and R_t^0 are respectively: observed susceptible, observed mild infected cases, serious infected cases and observed recovered cases.

We perform the approximate Bayesian computation with the following priors in parameters (Table 1):

Table 1: Prior probability distributions considered

Parameter	Prior distribution considered
β	Uniform distribution on [0,1]
θ	Uniform distribution on [0,0.5]
δ	Uniform distribution on [0,1]

The estimations obtained are very close to the true values of parameters. The mean absolute error decreases with the value of the acceptance rate α.
The approximate posterior probability densities are generally concentrated on the true values of the parameters.

The table 2 below shows the estimates obtained and the credible intervals at the 5% threshold.

Table 2: Results obtained after 100000 simulations with acceptance rate $\alpha = 0.1\%$

Parameter	Value	Estimation	Credible interval (95%)
β	0.30	0.299	[0.292,0.312]
θ	0.10	0.100	[0.048,0.157]
δ	0.50	0.562	[0.283,0.992]
β	0.60	0.598	[0.579,0.619]
θ	0.10	0.090	[0.050,0.152]
δ	0.50	0.580	[0.333,0.949]
β	0.90	0.899	[0.868,0.928]
θ	0.10	0.097	[0.057,0.136]
δ	0.50	0.543	[0.378,0.840]

The Figures 2, 3 and 4 below present the approximate posterior densities of the parameters β, θ and δ according to different values of β with acceptance rate $\alpha = 0.1\%$.

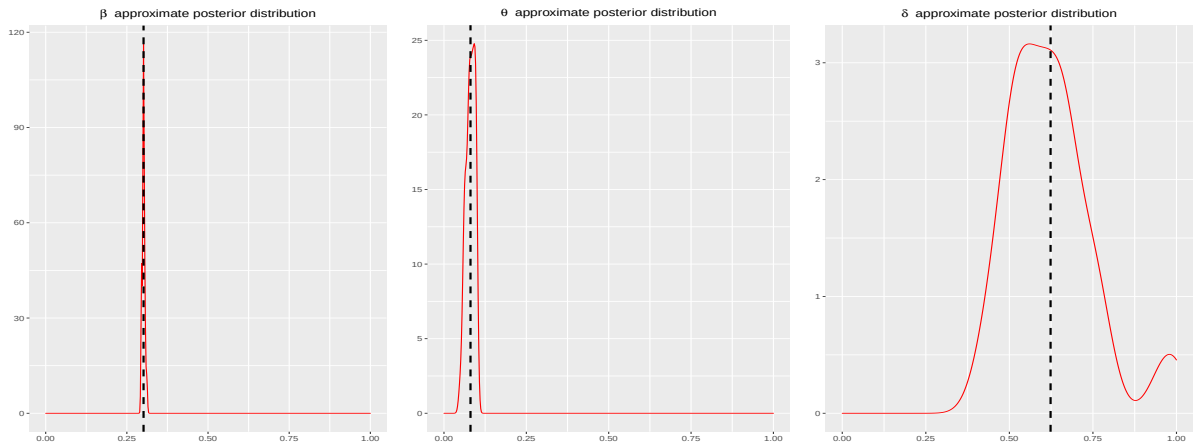

Figure 2: Approximate posterior distributions of parameters case $\beta = 0.3$. The dashed line refers to the posterior mean

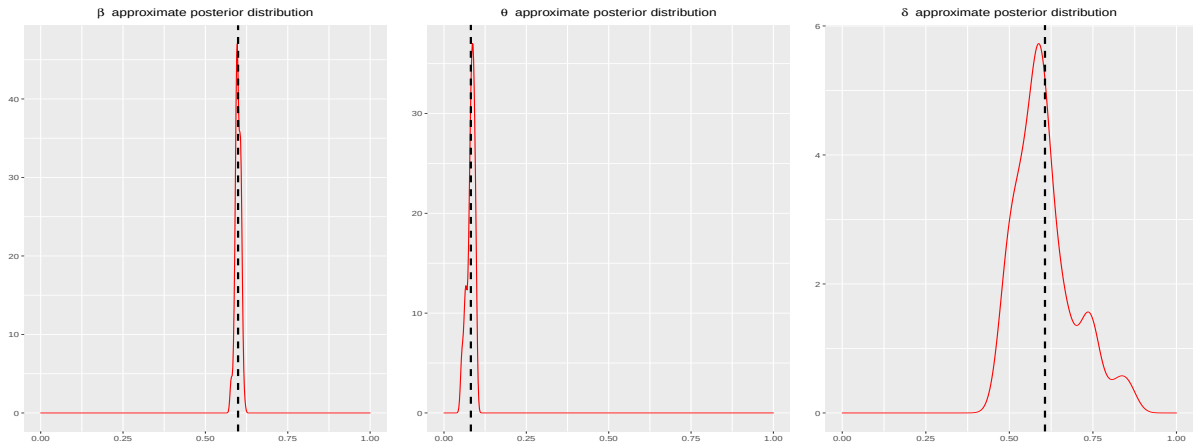

Figure 3: Approximate posterior distributions of parameters case $\beta = 0.6$. The dashed line refers to the posterior mean

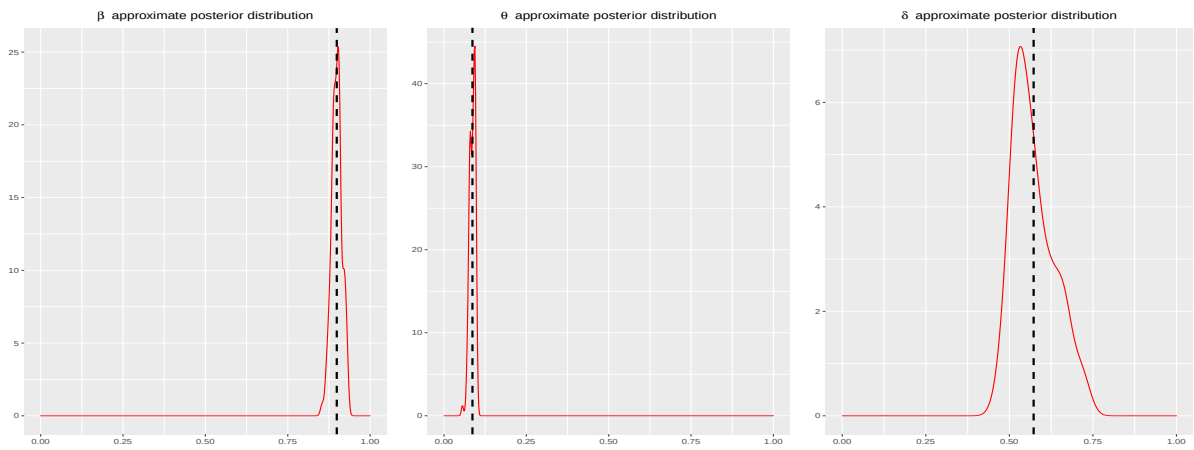

Figure 4: Approximate posterior distributions of parameters case $\beta = 0.9$. The dashed line refers to the posterior mean

5 Application

In this section we estimate the parameters of stochastic SEIRD model from Moroccan data concerning Covid 19 pandemic from 06/09/2020 to 02/03/2021. The data are taken from the official website of the Moroccan health ministry dedicated to the Covid 19 pandemic covidmaroc.

Motivated by the literature He et al. (2020) and Li (2021), $\gamma = \frac{1}{6}$ days^{-1}, $\mu_1 = \frac{1}{7}$ days^{-1}, $\mu_2 = \frac{1}{14}$ days^{-1} and $\eta = \frac{1}{18}$ days^{-1}, To perform the approximate Bayesian estimation, we use as summaries: active cases with severe symptoms and total deaths. These two statistics are more relevant given the limited number of PCR (The molecular test Reverse Transcription Polymerase Chain Reaction) tests to detect infected cases with the SARS COV 2 virus.

The Figure 5 below shows the evolution of active cases with severe symptoms and the cumulative number of deaths per day due to the pandemic Covid 19 over the period 06/09/2020 - 02/03/2021.

To model the prior information on parameters β, θ and δ, we adopt the following probability distributions (Table 3). We use as discrepancy measure:

$$\Delta = \sum_t |I_t^s - I_t^{s_0}| + \sum_t |D_t - D_t^0|$$

According to the results obtained, presented in the Table 4 below, the probability that an

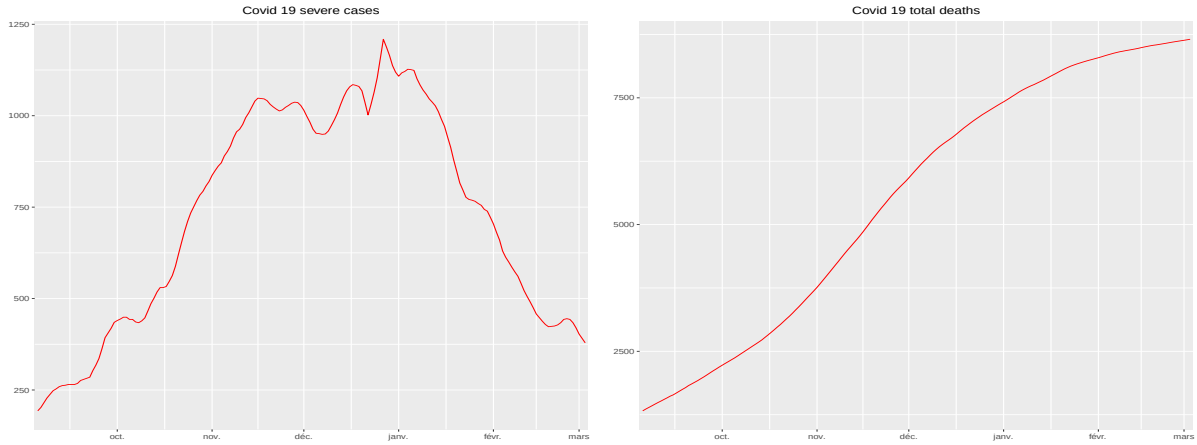

Figure 5: Active cases with severe symptoms and Total deaths from 06/09 to 02/03

Table 3: Prior probability distributions considered (Covid 19 Pandemic-Morocco)

Parameter	Prior distribution considered
β	Uniform distribution on [0,1]
θ	Uniform distribution on [0,0.1]
δ	Uniform distribution on [0,0.5]
I_0 : active cases in 06/09/2020 on [15 759,157 590] where 15 759 is the declared number	Uniform distribution

infected SARS COV 2 case will develop severe symptoms is estimated at 4.9%. The credible interval at the 5% threshold shows that this probability can be between 2% and 9.3%.

Given that a person is infected with severe symptoms, the probability of dying from the consequences of Covid 19 disease is estimated at 44.6%.

Table 4: Results obtained after 100000 simulations

Summaries used	Parameter	Estimation	Credible interval (95%)
Active cases with severe symptoms + Total deaths	β	0.054	[0.045,0.063]
	θ	0.049	[0.020,0.093]
	δ	0.446	[0.356,0.495]

The Figure 6 shows the approximate posterior distributions of model parameters. The dashed lines indicate the approximate posterior means of the model parameters: 0.054 for β, 0.049 for θ and 0.446 for δ.

6 Conclusion

In this paper we introduced a discrete stochastic epidemic model with compartments. This model was deduced from a set of hypotheses on the spread and evolution of the epidemic at the individual level. Given the complexity of the likelihood of the model, we opted for approximate Bayesian inference. We introduced an approximate Bayesian inference algorithm to estimate the model parameters. this algorithm was tested on simulated data and gave satisfactory results. In the last part of the paper, we illustrated the introduced model on Morocco COVID-19 data.

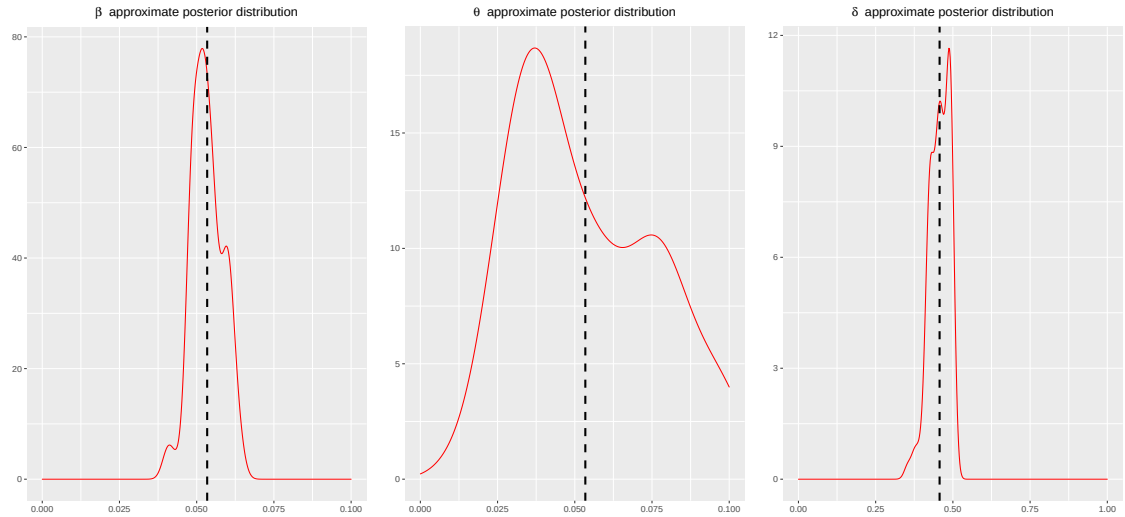

Figure 6: Approximate posterior distributions of parameters. The dashed line refers to the posterior mean (summaries: Active cases with severe symptoms and Total deaths)

Estimations obtained show in one hand, that an infected SARS COV 2 case will develop severe symptoms with probability 4.9%, this probability can vary between 2% and 9.3%. In the other hand, an infected person with severe symptoms can die from the consequences of Covid 19 disease with probability 44.6%.

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