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Stochastic approach of epidemic model using the SEIRS

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Abstract. The study of infectious diseases represents one of the oldest and richest sectors of biomathematics. The transmission dynamics of these diseases are still a major problem in mathematical epidemiology. In this work, we propose a stochastic version of a SEIRS epidemiological model for infectious diseases evolving in a random environment for the propagation of infectious diseases. This random model takes into account the rates of immigration and mortality in each compartment and the spread of these diseases follows a four-state Markovian process. We first study the stability of the model and then estimate the marginal parameters (means, variances and covariates) of each disease state over time. Real measles data are applied to the model.

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1. Introduction

Infectious diseases are of increasing concern to authorities and public health officials [2]. In the face of increasing bacterial resistance, the emergence of new pathogens and the rapid spread of the epidemic make surveillance and prevention of disease transmission particularly important and indispensable. Even with permanent and continuous surveillance of infectious diseases, it must be noted that their etiologies are still largely unknown. To combat this random phenomenon, in recent decades mathematical models have been developed and implemented to study the spread of infectious diseases since the early twentieth century in the field of mathematical epidemiology through the work of Daniel Bernoulli [1] . Stochastic and deterministic models of epidemics allow researchers to gain valuable knowledge about many infectious diseases and to study strategies to combat them.

The first stochastic epidemic models were presented by L. Reed and W, H. Frost in [3] to accurately describe the discrete-time spread of disease in a population. These models developed in 1928 and 1931[3] are based on the notion of probability and statistics. Later

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Bartlett [*M. Costa* 2011] proposed in 1949, the continuous time stochastic SIR model which serves as the basis for stochastic models. These last yeas, we can find in the literature several works but much remains to be done with the emergence of some of the new pathogens.

In this work, we are interested in the SEIRS model described in [7] for infectious diseases. We propose a stochastic version of this model using birth and death processes to describe the spread of infectious diseases in a random environment.

2. Stochastic probability of Birth and Mortality

In this section, we propose a stochastic version of the SEIRS model (fig 1) reviewed above. So, we assume that the spread of the disease follows a linear process of birth and death in continuous time and in four states in a variable environment. Moreover, we assume that the switching between environments follows a homogeneous Markov chain in continuous time.

A model of the dynamics of infectious disease transition can be formulated using a stochastic process $\{X_n, n = 1, 2, 3, ...\}$ as a Markov string with continuous time T and discrete state space $X_0, X_1, ..., X_n$ satisfying the following Markov property :

$$P(X_{n+1} = j_{n+1}/X_0 = j_0, X_1 = j_1, ..., X_n = j_n) = P(X_{n+1} = j_{n+1}/X_n = j_n). \quad (1)$$

That is, the evolution of the process at time n+1 depends only on the state of the process at time n but not on the past states $0, 1, 2, ..., n-1$ of the process. In biological modeling, a disease transmission process described with the states $X_0, ..., X_n$ can be seen as a Markov chain with a transition matrix $Q = (p_{ij})$ where the probabilities of the transitions are such as :

$$p_{ij} = P(X_{n+1} = j/X_n = i) \text{ for all } i, j = 1, 2, 3, ..., n. \quad (2)$$

The population of interest is divided into four compartments where each of them represents a specific stage of the epidemic. We have X_1 for susceptible or holy individuals, X_2 for lectures, X_3 for infected individuals and X_4 for healers. Add to this model the apparitions rates σ_i for $i = 1, 2, 3, 4$ independent of *lambda* and the natural death rates μ_i for all $i = 1, 2, 3, 4$ independent of the disease in the classes of persons susceptible to $X_1(t)$, exposed $X_2(t)$, infected $X_3(t)$ and healed $X_4(t)$ respectively at time t.

Moreover, let $Z(t) = X_1(t) + X_2(t) + X_3(t) + X_4(t)$ be the population size at a given time t. Assume that all rates are not time-dependent t and disease transmission occurs only by contact between susceptible and infectious individuals in a relatively small time interval dt. Once the vaccination is administered to the population, the immunized subjects against the disease and healed subjects enter the compartment X_4 and lose their immunity

rate	significance	
λ	the rate of newborns	
α	the rate of attacks of the disease	
β	The infection rate	
γ	recovery rate	
$\Theta\lambda$	the rate of newborns vaccinated and immunized against the disease	
τ	the tau of individuals healed but having lost temporary immunity	
η	the tau of holy individuals vaccinated and immunized against the disease	
Θ	the tau of unvaccinated newborns	
σ_i, $i = 1.4$	rates of immigrant individuals in different compartments	
μ_i, $i = 1.4$	mortality rates of the different compartments independent of the disease	
Xi, $i = 1, 4$	The steps in the process	

against this disease after a given latent period to become susceptible again. Newborn unvaccinated enter the susceptible compartment X_1 with a rate $\theta = 1 - \lambda$ and after contact with an infected subject first expose themselves to the disease and become infected, healed and susceptible again according to the diagram 1). In the case of infectious diseases, the ideal objective is to eradicate these diseases completely by preventive measures or by setting up a more effective mass vaccination program. Following the SEIR and SEIRS models with vital dynamics, Anderson and May studied vaccinations applied to the population [7].

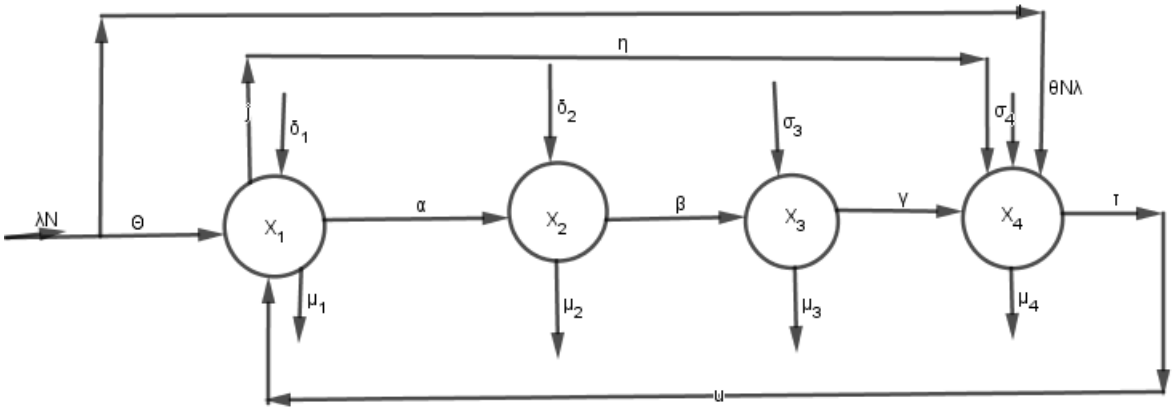

Figure 1: The propagation cycle of the SEIRS epidemic model

Transitions intensities are defined as a probability limit of transitions between times t and $t + dt$, when dt tends to zero [4]. Under the assumption of the existence of these limits, let's determine the infinitesimal probability laws of each process over a small time interval dt.

• Birth and emigration of S :

Once the population are vaccinated, the compartment S contains unimmunized indi-

viduals who are therefore susceptible to the disease. Among these individuals are immigrants with a rate of σ_1 from another locality and newborns not immune to the disease with a rate of λ. The probability that there will be a birth and then immigration of a susceptible person in the n process state is given by :

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n-1 \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix} = [\lambda(1-\theta)(n-1)+\sigma_1]dt+0(dt).$$

• Mortality of S :

The mortality rate of compartment S, independent of the cause of the disease, is μ_1. The probability of deaths in state n of the process is given by:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n+1 \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix} = \mu_1 dt+0(dt).$$

• Transition from S to E:

The individuals in compartment S come into contact with infected people at a rate of α and expose themselves to the disease. The probability of switching from the n state to the m state is given by:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n+1 \\ E(t+dt)=m/E(t)=m-1 \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix} = \alpha(n+1)dt+0(dt)$$

• Mortality of E :

The probability of deaths in the m state of the process is given by :

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m-1 \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix} = \mu_2 dt+0(dt)$$

• Mortality of I:

The probability that there will be deaths regardless of the cause of the disease among the infected in the $n^{'}$ state of the process is given by:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m+1 \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix}=\mu_3 dt+0(dt).$$

• Mortality of R :

The probability of deaths among people restored to the $m^{'}$ state of the process is given by:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'}+1 \end{pmatrix}=\mu_4 dt+0(dt).$$

3. Stochastic probability of migration and Transition

• Immigration of E:

The compartment E contains people exposed to the disease after contact with the patients. The probability of immigration at the m state of the process is therefore:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m-1 \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix}=\sigma_2 dt+0(dt)$$

• Transition from E to I:

The exposed individuals E, become infectious with a rate β and the probability of passing from the state m and to the state $n^{'}$ is given by:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m+1 \\ I(t+dt)=n^{'}/S(t)=n^{'}-1 \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix}=\beta(m+1)dt+0(dt)$$

• Immigration of I:

The probability of immigration to the state $n^{'}$ of the process in compartment I is:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'}-1 \\ R(t+dt)=m^{'}/S(t)=m^{'} \end{pmatrix}=\sigma_3 dt+0(dt)$$

• Transition from I to R:

Infected individuals I heal with a rate of *gammama*. The probability of switching from the state $n^{'}$ and to the state $m^{'}$ is given by :

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'}+1 \\ R(t+dt)=m^{'}/S(t)=m^{'}-1 \end{pmatrix}=\gamma(n_3+1)dt+0(dt)$$

• Immigration of R:

The probability of immigration in compartment R in the $m^{'}$ state of the process is:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'}-1 \end{pmatrix}=[\sigma_4+\theta\lambda]dt+0(dt)$$

• Transition from R to S:

Recovered people become susceptible again with a rate of *tau*. The probability of switching from the state $m^{'}$ and to the state $n^{'}$ is therefore:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n-1 \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/R(t)=m^{'}+1 \end{pmatrix}=\tau(n_4+1)dt+0(dt).$$

• Transition from S to R:

Individuals immunized against the disease with a rate of τ after direct vaccination coverage integrate the R compartments. The probability of transition from the n state to the $m^{'}$ state is therefore:

$$P\begin{pmatrix} S(t+dt)=n/S(t)=n+1 \\ E(t+dt)=m/E(t)=m \\ I(t+dt)=n^{'}/S(t)=n^{'} \\ R(t+dt)=m^{'}/S(t)=m^{'}-1 \end{pmatrix}=\eta(n+3)dt+0(dt).$$

4. Stochastic and Linear properties of the transition

The Markov property for the law of a multistate process is that the events $\{X(t)=j\}$, $j=0,...,n$ are independent on the past X_{n-1} given X(s). For Markov processes, the transition probability matrices satisfy the Chapman-Kolmogorov property [6]. The set of

transition intensities forms the matrix of transition intensity Q. The sum of the terms of each line of these matrices is equal to zero. We have the matrix of transmission probabilities Q such as .

$$Q = \begin{pmatrix} -M_1 + \mu_1 + \alpha & \alpha & 0 & \eta \\ 0 & -M_2 + \mu_2 & \beta & 0 \\ 0 & 0 & -M_3 + \mu_3 & \gamma \\ \tau & 0 & 0 & -M_4 + \tau + \mu_4 \end{pmatrix}$$

Where

$$\Rightarrow \begin{cases} M_1 = \lambda(1-\theta) + \sigma_1 + \eta \\ M_2 = \alpha + \beta + \sigma_2 \\ M_3 = \beta + \gamma + \sigma_3 \\ M_4 = \gamma + \eta + \theta\lambda + \sigma_4 \end{cases} \tag{3}$$

M_1, M_2, M_3 et M_4 are positive quantity.

The Kolmogorov equation gives the matrix of transition probabilities $Q(t)$ as a function of the exponential of a matrix :

$$P(t) = \exp\{Qt\}.$$

The exponential of a matrix is calculated relatively easily, particularly when the matrix can be diagonalized [4]. If Q has eigenvalues which are all different, it can be written as $Q = PDP^{-1}$, where D is the diagonal matrix of eigen-values, and P is the matrix of eigenvectors. In this case, the probability $P(t)$ at stable condition gives $P(t) = Pe^{tD}P^{-1}$ where the exponential of a diagonal matrix D is a diagonal matrix whose diagonal terms are the exponential of terms of D.

Using the cumulants generating function [5] , we then calculate the means, variances and covariances of the disease states as a function of time. For this purpose, the probability generating function is defined by :

$$\Phi(x_1, x_2, x_3, x_4, t) = \sum_{n,n',m,m' \geqslant 0} p(n, m, n', m', t) x_1^n x_2^m x_3^{n'} x_4^{m'}.$$

Using $A(t) = (A_{i,j}(t))_{1\leqslant i,j\leqslant 4} = (tA_{i,j})\,[i \leqslant, 4j \leqslant]$, the matrix of births with positive or null coefficients, such as :

$$A_{ij} = \begin{pmatrix} \lambda(1-\theta)+\sigma_1 & 0 & 0 & 0 \\ 0 & \sigma_2 & 0 & 0 \\ 0 & 0 & \sigma_3 & 0 \\ 0 & 0 & 0 & \sigma_4 \end{pmatrix};$$

and $B(t) = (B_{i,j}(t))$ the matrix of deaths given by:

$$B_{ij} = \begin{pmatrix} \mu_1+\alpha+\eta & -\alpha & 0 & -\eta \\ 0 & \mu_2+\beta & -\beta & 0 \\ 0 & 0 & \mu_3+\gamma & -\gamma \\ -\tau & 0 & 0 & \mu_4+\tau \end{pmatrix};$$

then, the joint generating function of the moments is defined by:

$$M(a_1,a_2,a_3,a_4,t) = \sum_{n,n',m,m'=0}^{\infty} p(n,n',m,m',t)e^{a_1 n}e^{a_2 n'}e^{a_3 m}e^{a_4 m'}. \tag{4}$$

By setting $x_k = e^{a_k}$, we get $\partial x_k = e^{a_k}\partial a_k$ for all $k = 1,2,3,4$

Let us define the generating function of the cumulants by:

$$K(a_1,a_2,a_3,a_4,t) = \sum_{n,n',m,m'=1}^{\infty} \frac{a_1^n}{n!}\frac{a_2^{n'}}{n'!}\frac{a_3^m}{m!}\frac{a_4^{m'}}{m'!}k_{nn'mm'}(a_1,a_2,a_3,a_4,t) \tag{5}$$

where $k_{nn'mm'}(a_1,a_2,a_3,a_4,t)$ are cumulative:

$$k_{nn'mm'}(a_1,a_2,a_3,a_4,t) = \frac{d^r K(a_1,a_2,a_3,a_4,t)}{dt^r}|_{t=0}. \tag{6}$$

Furthermore, the generating function of the cumulants is computed as follows:

$$K(a_1,a_2,a_3,a_4,t) = logM(a_1,a_2,a_3,a_4,t) \tag{7}$$

And

$$\partial M(a_1,a_2,a_3,a_4,t) = e^K \partial K(a_1,a_2,a_3,a_4,t). \tag{8}$$

By substituting $e^a = \sum_{i=0}^{\infty} \frac{a^i}{i!}$ in (5) and then, by derivating the functions $K(a_1, a_2, a_3, a_4, t)$, it comes that:

$$\begin{aligned}
\frac{\partial K(a_1,a_2,a_3,a_4,t)}{\partial t} &= \Big[\epsilon_1 \sum_{n=0}^{\infty} \frac{a_1^n}{n!} + \epsilon_3 \sum_{n=0}^{\infty} \frac{(-a_1)^n}{n!} - \epsilon_2\Big] \frac{\partial k_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{\partial a_1} \\
&+ \Big[\sigma_2 \sum_{n'=0}^{\infty} \frac{a_2^{n'}}{n'!} + \alpha \sum_{n=0}^{\infty} \frac{a_1^n}{n!} \sum_{n'=0}^{\infty} \frac{(-a_2)^{n'}}{n'!} - \epsilon_4 \\
&- \epsilon_5\Big] \frac{\partial k_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{\partial a_2} \\
&+ \Big[\sigma_3 \sum_{m=0}^{\infty} \frac{a_3^m}{m!} + \beta \sum_{n'=0}^{\infty} \frac{a_2^{n'}}{n'!} \sum_{m=0}^{\infty} \frac{(-a_3)^m}{m!} \\
&- \epsilon_7 \sum_{m=0}^{\infty} \frac{(-a_3)^m}{m!} - \epsilon_6\Big] \frac{\partial k_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{\partial a_3} \\
&+ \Big[\sigma_4 \sum_{m'=0}^{\infty} \frac{a_4^{m'}}{m'!} + \eta \sum_{n=0}^{\infty} \frac{a_1^n}{n!} \sum_{m=0}^{\infty} \frac{(-a_4)^{m'}}{m'!} + \gamma \sum_{m=0}^{\infty} \frac{a_3^m}{m!} \sum_{m'=0}^{\infty} \frac{(-a_4)^{m'}}{m'!} \\
&- \epsilon_9 \sum_{m'=0}^{\infty} \frac{(-a_4)^{m'}}{m'!} - \epsilon_8\Big] \frac{\partial k_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{\partial a_4}.
\end{aligned} \tag{9}$$

Moreover, knowing that:

$$\begin{cases} E(X) = \partial k_{nn'mm'}(a_1,a_2,a_3,a_4,t) \\ V(X) = \partial^2 k_{nn'mm'}(a_1,a_2,a_3,a_4,t). \end{cases} . \tag{10}$$

Which gives us:

$$\begin{cases} E(X_i(t)) = \dfrac{dk_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{da_i}|_{t=0} \\ V(X_i(t)) = \dfrac{d^2 k_{nn'mm'}(a_1,a_2,a_3,a_4,t)}{da_i^2}|_{t=0} \quad pour\ i = 1,2,3,4 \end{cases} \tag{11}$$

Using the moment generating function (5), we can determine the average and variance of each state.

The derivative of 5 gives:

$$\frac{\partial K(a_1,a_2,a_3,a_4,t)}{\partial t} = \sum_{n,n',m,m'=0}^{\infty} \frac{a_1^n}{n!} \frac{a_2^{n'}}{n'!} \frac{a_3^m}{m!} \frac{a_4^{m'}}{m'!} k'_{n,n',m,m'}(a_1,a_2,a_3,a_4,t). \tag{12}$$

By equalizing the two previous expressions (12) and (5) and using the relationship (11), we obtain a system of linear differential equations of the first degree whose variables are means of each state of the process defined by the relationship (13).

$$\begin{cases} \dfrac{dE(X_1)}{dt} = \rho_1 E(X_1) \\ \dfrac{dE(X_2)}{dt} = \rho_2 E(X_2) \\ \dfrac{dE(X_3)}{dt} = \rho_3 E(X_3) + \sigma_4 E(X_2X_3) + \rho_5 E(X_2) \\ \dfrac{dE(X_4)}{dt} = \rho_6 E(X_4) + \rho_7 E(X_2X_4) - \epsilon_5 E(X_3) \end{cases} . \tag{13}$$

With ρ_i, $i = 1, ..., 8$, the strictly positive constants defined by the system (14) :

$$\begin{cases} \rho_1 = \sigma_4 + \sigma_2 + \eta + \epsilon_8 - \epsilon_5 - \epsilon_4 + \epsilon_3 - \epsilon_2 + \gamma + \alpha \\ \rho_2 = \sigma_4 + \eta + \epsilon_8 - \epsilon_4 + \epsilon_3 - \epsilon_2 + \gamma + \alpha + \beta \\ \rho_3 = \sigma_4 + \sigma_3 + \sigma_2 + \eta - \epsilon_9 + \epsilon_8 - \epsilon_7 + \epsilon_6 - -\epsilon_5 - \epsilon_4 + \epsilon_3 - \epsilon_2 + \gamma + \alpha + \beta \\ \rho_4 = \sigma_3 - \epsilon_7 + \epsilon_6 - \beta \\ \rho_5 = \sigma_3 + \sigma_7 - \beta \\ \rho_6 = \sigma_4 + \sigma_3 + \sigma_2 + \eta - \epsilon_9 + \epsilon_8 - \sigma_7 + \epsilon_6 - \epsilon_5 - \epsilon_4 + \epsilon_3 - \epsilon_2 + \gamma + \alpha + \beta \\ \rho_7 = \sigma_3 + -\epsilon_7 + \epsilon_6 + \beta \end{cases} \tag{14}$$

The dispersion in turn of the average of each state of the process is given by the relationship (15). For a statistic with little dispersion, the observations are close to each other, and therefore to their average.

$$\begin{cases} \dfrac{dV(X_1)}{dt} = \frac{1}{2}(\sigma_2 + \eta + \epsilon_2 + \epsilon_3 + \gamma + \alpha)V(X_1) \\ \dfrac{dV(X_2)}{dt} = \frac{1}{2}(\sigma_4 + \sigma_2 + \eta + \epsilon_6 + \epsilon_3 + \epsilon_2 + \gamma + \beta)V(X_2) \\ \dfrac{dV(X_3)}{dt} = \frac{1}{2}(\sigma_4 + \sigma_3 + \sigma_2 + \eta + \epsilon_9 + \epsilon_3 + \epsilon_2 + \gamma + \beta)V(X_3) \\ \dfrac{dV(X_4)}{dt} = \frac{1}{2}(\sigma_4 + \sigma_3 + \sigma_2 + \eta + \epsilon_9 + \epsilon_8 + \epsilon_7 + +\epsilon_6 + +\epsilon_5 + \epsilon_3 + \alpha)V(X_4) \end{cases} . \tag{15}$$

The degree of the links between the different states of the process can be estimated from the co-variables by solving differential equations of the relationship (16).

$$\begin{cases} \frac{dCOV(X_1X_2)}{dt} = (\sigma_4+\sigma_2+\eta-\epsilon_9+\epsilon_8+\epsilon_3-\epsilon_2+\gamma+\alpha)COV(X_1X_2) \\ \frac{dCOV(X_1X_3)}{dt} = (\sigma_4+\sigma_3+\sigma_2+\eta-\epsilon_9+\epsilon_8-\epsilon_7+\epsilon_6-\epsilon_5-\epsilon_4+\epsilon_3-\epsilon_2+\gamma+\alpha+\beta)COV(X_1X_3) \\ \frac{dCOV(X_2X_3)}{dt} = (\sigma_4+\sigma_3+\sigma_2+\eta-\epsilon_9+\epsilon_8-\epsilon_5-\epsilon_4+\epsilon_3-\epsilon_2+\gamma+\alpha+\beta)COV(X_2X_3) \\ \frac{dCOV(X_2X_4)}{dt} = (\sigma_4+\sigma_2+\eta-\epsilon_9-\epsilon_5-\epsilon_4+\epsilon_3-\epsilon_2+\gamma+\alpha+\beta)COV(X_2X_4) \\ \frac{dCOV(X_3X_4)}{dt} = (\sigma_4+\sigma_3+\sigma_2-\epsilon_9+\epsilon_8+\epsilon_7+\epsilon_6-\epsilon_5-\epsilon_3-\epsilon_2+\alpha+\beta)COV(X_3X_4) \\ \frac{dCOV(X_1X_4)}{dt} = (\sigma_4+\sigma_2+\eta-\epsilon_9-\epsilon_5-\epsilon_4+\epsilon_3-\epsilon_2+\gamma+\alpha)COV(X_1X_4) \end{cases} \tag{16}$$

The resolution of the written equation system by the relationships (13), (15) and (16) have as initial conditions:

$$\begin{cases} S(0)=S_0>0, E(0)=E_0\geq 0, I(0)=I_0>0, R(0)=R_0\geq 0 \\ \Phi(x_1,x_2,x_3,x_4,0)=x_1^{S_0}x_2^{E_0}x_3^{I_0}x_4^{R_0}, M(a_1,a_2,a_3,a_4,0)=e^{a_1S_0}e^{a_2E_0}e^{a_3I_0}e^{a_4R_0} \\ K(a_1,a_2,a_3,a_4,0)=a_1S_0+a_2E_0+a_3I_0+a_4R_0 \\ E(X_1(0))=S_0, E(X_2(0))=E_0, E(X_3(0))=I_0, E(X_4(0))=R_0 \end{cases}. \tag{17}$$

5. Conclusions

In this study, we have proposed the stochastic approach of the deterministic SEIRS model with a vital dynamic and temporary immunity of [7]. whose balance and stability have been studied. The stochastic approach can be used to accurately describe the spread of infectious diseases in a random environment. This SEIRS model generalizes the SI, SIR and SEIR models and is therefore a valuable tool for stochastic modelling of epidemiological problems. The resulting systems of equations incorporate complexities and assume that randomness is important and explicitly include it in the behaviour of the system compared to the deterministic model that assumes that randomness has a negligible effect and considers only the average behaviour of the system. For good monitoring and prevention of transmission of epidemics, the results obtained provide more precision on the random

evolution of the disease over time. The main disadvantage of this approach is that in practice, it is often difficult to have data adapted to the model to be implemented. It is also clear that most of the results remain valid not only for a finite number of Markovian environments, but also for more general ergodic environments.

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