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Research Article

A Stochastic Approach in the Analysis of Compartmental Models in Epidemiology

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Abstract: The spread of infectious diseases is a significant public health issue. Mathematical modeling is being used to find appropriate answers to this question. In this paper we propose a stochastic approach to compartmental models. A new model allows to rely on the fokker-planck equation with a SEIR model, with constant rates, to take into account the random environment in the propagation of a disease, markov and kolmogorov properties have been used in the modeling of the process. We have also determined the basic reproduction rate R_0 of our new stochastic model using the new generation matrix.

***Keywords*:** compartimental models, SEIRS, kolmogorov equation, fokker planck equation, epidemiology

MSC: 93E03, 68Q30, 92D30, 60G20

1. Introduction

Epidemiology is the study of the distribution of diseases and the factors that influence them. It aims to understand the causes of disease and to improve treatment and means of prevention. The contribution of mathematics,because of the great complexity of epidemiological systems,is focused on data acquisition, the construction of deterministic and stochastic compartmental models describing the dynamics in these systems and the analysis of the stability of equilibria. The equations formulated in a stochastic framework are realistic but much more complex to analyze. In the last few years number of authors worked on stochastic models in the literature [1–5] Gray and al. proposed a stochastic SIS (susceptible-infectious-susceptible) model and studied an SDE version of the classical SIS epidemic model, with noise introduced in the disease transmission term while Tornatore et al. designed a stochastic SIR (susceptible-infectious-recovery) framework and demonstrated the presence of a limit on the incentive to reproduce.

The SIR compartmental model can be represented by the following equation:

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$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

The birth of epidemiology is attributed to Daniel Bernoulli [6], who presented a model whose main objective was to find out whether variolization (the inoculation of the pus of a person with smallpox) was more advantageous or more risky for people who had contracted the disease. The latter developed more appropriate methods which are the foundations of modern epidemiology. An epidemiological model is based on two concepts: compartments and rules. Compartments divide the population into various possible states with respect to the disease.

Emergence of a random dimension is conceived from the impossibility of knowing the behavior of a system down to its smallest details. Thus we have stochastic differential equations (SDE). This offers a first motivation for the stochastic approach of epidemiological models. Moreover, stochastic models are important when the number of affected individuals is small compared to the population size or when transmission, infection, births and deaths are highly variable. In particular the progressive Kolmogorov equation is widely used in modeling. In one dimension this equation (of Fokker-Planck) has the following form [7].

$$\frac{\partial}{\partial t}P(x,\, t) = -\frac{\partial}{x}[D_1(x,\, t)P(x,\, t)] + \frac{1}{2}\frac{\partial^2}{\partial x^2}[D_2(x,\, t)p(x,\, t)]. \tag{1}$$

where $P(x,\, t)$ is the probability of finding the particle at point x and time t.

In this paper, our objective is to use the Fokker-Planck equation to determine the intercompartmental transfer rates in a deterministic compartmental model, specifically the SEIR model.

Our major contribution is to have introduced a new approach including Fokker-Planck equation (progressive Kolmogorv) in compartmental methods such as SEIR to describe the propagation of a disease in time. The rest of the paper is organized as follows. Section 2 provides a brief overview of stochastic differential equation (SDE) and Survey of SEIRS necessery to build our model. In section 3 we propose our main results, a stochastic model of the propagation of desease in SEIR model determided about deterministe. The last section present a conclusion.

2. Methods and materials

In this section we recall necessary tools which are used in our study, such as stochastic differential equations and the compartmental epidemiological models SEIRS.

2.1 *An overview of stochastic differential equation*

The kolmogorov equations are tools for solving stochastic differential equations.

Let's note L the Kolmogorov operator associated to the stochastic differential equation (SDE) defined for $x \in \mathbb{R}^d$ and $\phi \in C^\infty(\mathbb{R}^d)$ by [8]

$$L\phi(x) = \frac{1}{2}\sum_{j,\ i=1}^{d} a_{i,\ j}(x)\frac{\partial^2\phi}{\partial x_i \partial x_j}(x) + \sum_{i=1}^{d} f_i(x)\frac{\partial\phi}{\partial x_i}(x); \tag{2}$$

with

$$a_{i,\ j} = (\sigma(x)\sigma(x)^T)_{i,\ j} = \sum_{l=1}^{m} \sigma_{il}(x)\sigma_{jl}(x).$$

Let $d \in \mathbb{N}$, the space $C^{\infty}_{pol}(\mathbb{R}^d)$ denotes the set of functions C^{∞} which are polynomial and such that all their derivatives are polynomial.

In particular, the retrograde kolmogorov equation is such that [8];

$$\frac{\partial P(t,\ x,\ y)}{\partial t} = a_1 x\frac{\partial P(t,\ x,\ y)}{\partial x} + \frac{1}{2}a_2 x\frac{\partial^2 P(t,\ x,\ y)}{\partial x^2}; \tag{3}$$

where the first term of the right-hand members are known as drift and the second one as diffusion [9]. It can be defined as follows, for $i,\ j = 1,\ 2,\ 3$ ...

$$\frac{dP_{ij}(t)}{dt} = \sum_{k\neq j} q_{ik}(t)P_{kj};$$

Writting in matrix form, one have; $\frac{dP_{ij}(t)}{dt} = QP(t)$ where Q is the transition generator matrix. Moreover, if S is a set of finite states and $Q = (q_{ij})_{i,\ j\in S}$ then they satisfy the following properties:

The elements of the matrix that are not on the diagonal are all positive, and the elements on the diagonal are all negative.

The sum of the elements in a row is equal to the opposite of the element on the diagonal of that row [11]. The sum of all elements in a row is zero.

The progressive equation can be defined by

$$\frac{\partial P(t,\ x,\ y)}{\partial t} = -\frac{\partial(a_1 yP(t,\ x,\ y))}{\partial y} + \frac{1}{2}\frac{\partial^2(a_2 yP(t,\ x,\ y))}{\partial y^2} \tag{4}$$

In the same vein, the progressive differential equation can be defined as follows:

$$\frac{dP_{ij}(t)}{dt} = \sum_{k\neq j} P_{ik}(t)q_{kj}.$$

for $i,\ j = 1,\ 2,\ 3$ ... With the associated matrix form $\frac{dP_{ij}(t)}{dt} = P(t)Q$. A stochastic differential equation is of the form

$$X_t = x + \int_0^t b(s,\ X_s)ds + \int_0^t \sigma(s,\ X_s)dB_s \tag{5}$$

or in condensed form:

$$\begin{cases} dX_t = b(s,\ X_s)ds + \sigma(s,\ X_s)dB_s \\ \\ X_0 = x \end{cases}$$

B_s is a standard Brownian motion (SBM), and s is a strictly positive real.

2.2 *An overview of SEIRS models*

Recall that SEIRS models are the principles of a compartmental model in epidemiology. A SEIRS epidemic is introduced by infecting an individual. With the disease, the population is divided into four compartments according to the status of the individuals, linked to the disease. The S compartment of susceptible individuals, the E compartment of latent or exposed individuals exposed individuals, the I compartment of infectious individuals, and the R compartment of (those who have recovered from the disease with a non-permanent immunity) [9–22].

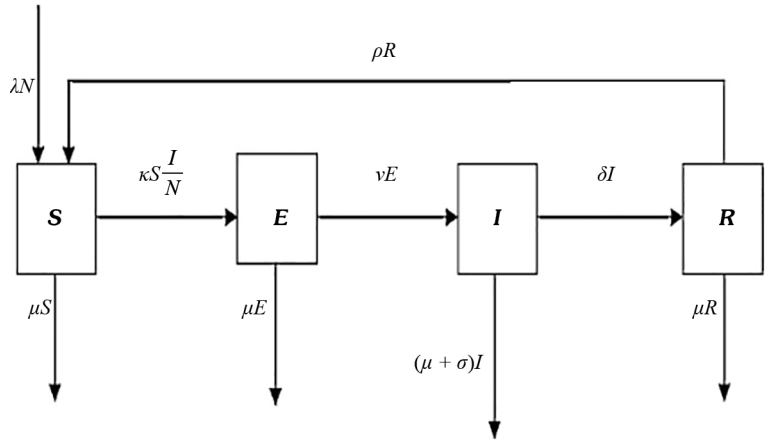

Figure 1. SEIRS graph of transfert

In this model, $S,\ E,\ I,\ R,\ S$ and N represent numbers such that $N = S + E + I + R$. So N represents the total number of the population. The progression through the compartments is illustrated in Figure 1.

The system differential equation governing the SEIRS can then be written as follows [14]

$$\begin{cases} \dfrac{dS}{dt} = \rho R + \lambda N - \mu S - kS\dfrac{I}{N} \\ \dfrac{dE}{dt} = kS\dfrac{I}{N} - (\mu + v)E \\ \dfrac{dI}{dt} = vE - (\mu + \sigma)I - \delta I \\ \dfrac{dR}{dt} = \delta I - (\mu + \rho)R \end{cases} \tag{6}$$

We have the following proportions:
λ: birth rate in the total population;
μ: death rate independent of disease;
σ: death rate due to disease;
δ: cure rate from disease;
ρ: rate of loss of temporary immunity;
κ: rate of contact;
υ: infection rate as well as non-negative initial conditions.

3. Main results

In our model we do not take into account the elements of demography since we estimate the time of study relatively short so that it has births and deaths for other causes than the disease, which means that the population remains constant during the study. We consider the disease introduced in the population as a particle charged with energy and which must follow a well defined route through the different states.

3.1 *Modelling of inter compartment transfer*

The Fokker-Planc Equation [23] will enable us to follow the evolution of the disease in each compartment of the SEIR model seen above.By applying the Foker-Planck Equation (FPE) on the inter-compartmental flow we obtain the following result

Proposition 1 Let N be the size of the population and $X_1(t)$, $X_2(t)$, $X_3(t)$ *and* $X_4(t)$ the numbers of compartments 1, 2, 3, 4 respectively.

Then, it follows that

$$\begin{cases} \dfrac{dX_1}{dt} = N - p(X_1,\, t_0)N \\ \dfrac{dX_2}{dt} = p(X_1,\, t_0)N - p(X_2,\, t)p(X_1,\, t_0)N \\ \dfrac{dX_3}{dt} = p(X_2,\, t)p(X_1,\, t_0)N - p(X_3,\, t)p(X_2,\, t)p(X_1,\, t_0)N \\ \dfrac{dX_4}{dt} = p(X_3,\, t)p(X_2,\, t)p(X_1,\, t_0)N \end{cases} \tag{7}$$

Where $N = X_1(t) + X_2(t) + X_3(t) + X_4(t)$.

proof. Consider the Fokker-Planc equation given by the relation (1).

$$\frac{\partial}{\partial t}p(x,\, t) = \frac{-\partial}{\partial x}[D_1(x,\, t)p(x,\, t)] + \frac{1}{2}\frac{\partial^2}{\partial x^2}[D_2(x,\, t)p(x,\, t)]; \tag{8}$$

where p is the probability of finding the particle at point x and time t.

Let us integrate $\dfrac{\partial}{\partial t}p(x,\, t)$ since by assumption it defined and continuous on the domain of study [15]. So, it comes that

$$\int \frac{\partial}{\partial t}p(x,\, t) = \int \frac{-\partial}{\partial x}[D_1(x,\, t)p(x,\, t)] + \frac{1}{2}\int \frac{\partial^2}{\partial x^2}[D_2(x,\, t)p(x,\, t)], \tag{9}$$

where

$$p(x,\, t) = -[D_1(x,\, t)p(x,\, t)] + \frac{1}{2}\frac{\partial}{x}[D_2(x,\, t)p(x,\, t)]. \tag{10}$$

Moreover the SEIR model described in section 1 and $X_1,\, X_2,\, X_3$ and X_4 be the different states [9–11]. So,

- $\dfrac{dX_1}{dt}$ denotes the number of susceptible, $p(x_1,\, t_0)$ is the probability of finding an exposed individual in state 1 at time t_0 and $p(x_1,\, t_0)N$ the number of exposed individuals leaving the susceptible class.
- $\dfrac{dX_2}{dt}$ is the number of exposed individuals and $p(x_2,\, t)$ is the probability of finding an infectious individual in state 2 at time t. The number of infectious individuals leaving the exposed class is $p(x_1,\, t_0)p(x_2,\, t)N$.
- $\dfrac{dX_3}{dt}$ is the number of infectious individuals. $p(x_3,\, t)$ is the probability of finding a cured individual in state 3 at time t, while,the number of cured leaving the infectious class is $p(x_1,\, t_0)p(x_2,\, t)p(x_3,\, t)N$.
- $\dfrac{dX_4}{dt}$ is the number of cured individuals,and the number of healed individuals is $p(x_1,\, t_0)p(x_2,\, t)p(x_3,\, t)N$.

By referring to equation (4) we have a probability system of the progression of a sick individual in state X_1 towards his certain cure in state X_4 by passing by the states X_2 and X_3. So, we have a system of probability.

$$\begin{cases} p(X_1,\, t) = -[D_1(X_1,\, t)p(X_1,\, t)] + \dfrac{1}{2}\dfrac{\partial}{\partial x}[D_2(X_1,\, t)p(X_1,\, t)] \\ p(X_2,\, t) = -[D_1(X_2,\, t)p(X_2,\, t)] + \dfrac{1}{2}\dfrac{\partial}{\partial x}[D_2(X_2,\, t)p(X_2,\, t)] \\ p(X_3,\, t) = -[D_1(X_3,\, t)p(X_3,\, t)] + \dfrac{1}{2}\dfrac{\partial}{\partial x}[D_2(X_3,\, t)p(X_3,\, t)] \\ p(X_4,\, t) = -[D_1(X_4,\, t)p(X_4,\, t)] + \dfrac{1}{2}\dfrac{\partial}{\partial x}[D_2(X_4,\, t)p(X_4,\, t)] \end{cases} \tag{11}$$

However the inter-compartment transfer can be obtained by:

$$\begin{cases} \dfrac{dX_1}{dt} = N - p(X_1,\, t_0)N \\ \dfrac{dX_2}{dt} = p(X_1,\, t_0)N - p(X_2,\, t)p(X_1,\, t_0)N \\ \dfrac{dX_3}{dt} = p(X_2,\, t)p(X_1,\, t_0)N - p(X_3,\, t)p(X_2,\, t)p(X_1,\, t_0)N \\ \dfrac{dX_4}{dt} = p(X_3,\, t)p(X_2,\, t)p(X_1,\, t_0)N \end{cases} \tag{12}$$

So, the result is obtained as disserted. □

Let E be the set of all possible states of the process. Markov property and the measures $P(x;\, t)$ represent the transition probabilities of the process.Where $x \in E$ and $t \geq 0$ represent the time. By applying Kolmogorov property, we obtain a stochasttic approach through a deterministic model in the following result [19].

Proposition 2 Consider a deterministic model SEIR. A stochastic approach based on the model can be obtained,for $c_i,\ i = 1,\ ...,\ 8$

$$\begin{cases} \dfrac{dS(t)}{dt} = c_1 e^{\kappa t} S - \left(c_2 e^{-\kappa t} + c_3 e^{-v}\right) SI \\ \dfrac{dE(t)}{dt} = \left(c_2 e^{-\kappa t} + c_3 e^{-v} + c_4 e^{-vt}\right) SI - \left(c_5 e^{-\delta t} + c_6 e^{-v}\right) E \\ \dfrac{dI(t)}{dt} = \left(c_5 e^{-\delta t} + c_6 e^{-v}\right) E + c_7 e^{-\delta t} E - c_8 e^{-\delta t} I \\ \dfrac{dR(t)}{dt} = c_8 e^{\delta t} I \end{cases} \tag{13}$$

where c_i is a constant.

proof. The proof of this proposition is based on the kolmogorov properties.

The process being Markovian and also fulfilling the kolmogorov properties [8], we obtain the following transition matrix:

$$M = \begin{pmatrix} 1-M_1 & M_1 & 0 & 0 \\ 0 & 1-M_2 & M_2 & 0 \\ 0 & 0 & 1-M_3 & M_3 \\ 0 & 0 & 0 & M_4 \end{pmatrix}. \tag{14}$$

Where

$$\begin{cases} M_1 = p(X_1,\, t_0) \\ M_2 = p(X_1,\, t_0)p(X_2,\, t) \\ M_3 = p(X_1,\, t_0)p(X_2,\, t)p(X_3,\, t) \\ M_4 = 1 \end{cases} \tag{15}$$

The state X_4 is an absorbing state because if the individual penetrates it he does not come out of it any more either by death or by cure. Using the progressive differential equation of Kolomogorov we have $\frac{dP_{ij}(t)}{dt} = MQ$ where Q the transition generating matrix, the sum of the elements of each row is equal to zero such that [11]

$$Q = \begin{pmatrix} -\kappa & \kappa & 0 & 0 \\ 0 & -\upsilon & \upsilon & 0 \\ 0 & 0 & -\delta & \delta \\ 0 & 0 & 0 & 0 \end{pmatrix}; \tag{16}$$

while

δ: is the rate of healing;

κ: is the contact rate;

υ: is the rate of infection.

Let's that the progressive equation of Kolmogorow we obtain the following operation

$$\left(\frac{dP_{ij}(t)}{dt}\right) = \begin{pmatrix} 1-M_1 & M_1 & 0 & 0 \\ 0 & 1-M_2 & M_2 & 0 \\ 0 & 0 & 1-M_3 & M_3 \\ 0 & 0 & 0 & M_4 \end{pmatrix} \begin{pmatrix} -\kappa & \kappa & 0 & 0 \\ 0 & -\upsilon & \upsilon & 0 \\ 0 & 0 & -\delta & \delta \\ 0 & 0 & 0 & 0 \end{pmatrix}. \tag{17}$$

Which gives, by identificat,the following system

$$\begin{cases} \dfrac{dP_{11}(t)}{dt} = -(1-M_1)\kappa \\ \dfrac{dP_{12}(t)}{dt} = (1-M_1)\kappa - \upsilon M_1 \\ \dfrac{dP_{13}(t)}{dt} = \upsilon M_1 \\ \dfrac{dP_{22}(t)}{dt} = -(1-M_2)\upsilon \\ \dfrac{dP_{23}(t)}{dt} = (1-M_2)\upsilon - \delta M_2 \\ \dfrac{dP_{24}(t)}{dt} = \delta M_2 \\ \dfrac{dP_{33}(t)}{dt} = -(1-M_3)\delta \\ \dfrac{dP_{34}(t)}{dt} = \delta M_3 \end{cases} \tag{18}$$

with the time-dependent stochastic transition matrix t and the time-independent transition rate matrix t we obtain the system (18) which represents the propagation of the disease through the different states taking into account the stochastic.

Let's determine now, the probabilities P_{ij} for $i,\ j = 1,\ ...,\ 4$.

Consider that: $P_{11} = 1 - M_1$, $P_{12} = M_1$, $P_{13} = 0$, $P_{22} = 1 - M_2$, $P_{23} = M_2$, P_{24}, $P_{33} = 1 - M_3$, $P_{34} = M_3$

Determining of P_{11} and P_{12}

Let the first two equations be

$$\begin{cases} \dfrac{dP_{11}(t)}{dt} = -(1-M_1)\kappa \\ \dfrac{dP_{12}(t)}{dt} = (1-M_1)\kappa - \upsilon M_1 \end{cases} \tag{19}$$

So, by using (18) one obtains the following system;

$$\begin{cases} \dfrac{dP_{11}(t)}{dt} = -P_{11}\kappa \\ \dfrac{dP_{12}(t)}{dt} = P_{11}\kappa - \upsilon P_{12} \end{cases} \tag{20}$$

Which gives, after

$$\begin{cases} DP_{11} = -P_{11}\kappa \\ \\ DP_{12} = P_{11}\kappa - \upsilon P_{12} \end{cases} \tag{21}$$

Then to determine P_{11},
Consiste multiply in the first equation by $P_{12}(D+\upsilon)$ and the second one by $-P_{11}(D+\kappa)$ if so, it follows that;

$$\begin{cases} P_{11}(D+\kappa)P_{12}(D+\upsilon) = 0 \\ \\ -P_{11}(D+\kappa)P_{12}(D+\upsilon) + P_{11}(D+\kappa)P_{11}\kappa = 0 \end{cases} \tag{22}$$

And by solving the system by a linear combination we have: $P_{11}^2(D\kappa+\kappa^2) = 0$ and $D = -\kappa$ and finally $P_{11} = C_1 e^{-\kappa t}$.
Determining of P_{12}.
Consider the following system and multiply the first equation by κ and the second by $D+\kappa$

$$\begin{cases} P_{11}(D+\kappa) = 0 \\ \\ -P_{12}(D+\upsilon) - P_{11}\kappa = 0 \end{cases} \tag{23}$$

We obtain

$$\begin{cases} \kappa P_{11}(D+\kappa) = 0 \\ \\ P_{12}(D+\upsilon)(D+\kappa) - P_{11}\kappa(D+\kappa) = 0 \end{cases} \tag{24}$$

By a linear combination we obtain

$$P_{12}(D+\kappa)(D+\upsilon) = 0$$

$$P_{12}[(D^2 + D(\kappa+\upsilon) + \upsilon\kappa] = 0$$

$$D^2 + D(\kappa+\upsilon) + \upsilon\kappa = 0,\ \Delta = (\kappa+\upsilon)^2 - 4(\upsilon\kappa)$$

$$w_1 = \frac{-(\kappa+\upsilon) - (\kappa-\upsilon)}{2} \text{ and } w_2 = \frac{-(\kappa+\upsilon) + (\kappa-\upsilon)}{2}$$

$$w_1 = -\kappa \text{ et } w_2 = -\upsilon$$

So $p_{12} = c_2 e^{-\kappa t} + c_3 e^{-\upsilon t}$
Determining of P_{13}
Lest's consider the third equation of the system (18)

$$\frac{dP_{13}}{dt} = \upsilon M_1 \Longrightarrow \frac{dP_{13}}{dt} = \upsilon P_{12}$$

$$\frac{dP_{13}}{dt} = \upsilon(c_2 e^{-\kappa t} + c_3 e^{-\upsilon t})$$

So finally, one obtains P_{13} such as

$$P_{13} = -\upsilon(c_2 \frac{e^{-\kappa t}}{\kappa} + c_3 \frac{e^{-\upsilon t}}{\upsilon})$$

Determining of P_{22}
Consider the following system

$$\begin{cases} \frac{dP_{22}}{dt} = -P_{22}\upsilon \\ \frac{dP_{23}}{dt} = P_{22}\upsilon - \delta P_{23} \\ \frac{dP_{23}}{dt} = P_{22}\upsilon - \delta P_{23} \end{cases}. \tag{25}$$

After transformation we obtain the following system

$$\begin{cases} P_{22}P_{23}(D+\upsilon)(D+\delta) = 0 \\ -P_{22}P_{23}(D+\upsilon)(D+\delta) + P_{22}^2\upsilon(D+\upsilon) = 0 \end{cases}. \tag{26}$$

By a linear combination we have $P_{22}^2\upsilon(D+\upsilon) = 0$ which implies that $D = -\upsilon$
$P_{22} = c_4 e^{-\upsilon t}$
Determining of P_{23}
Consider the following system

$$\begin{cases} P_{22}(D+\upsilon) = 0 \\ P_{23}(D+\delta) - P_{22}\upsilon = 0 \end{cases} \tag{27}$$

After transformation and by a linear combination we have $P_{23}(D+\delta)(D+\upsilon) = 0$, $D_1 = -\delta$ and $D_2 = -\upsilon$. Then $P_{23} = c_5 e^{-\delta t} + c_6 e^{-\upsilon t}$

Determining of P_{24}
After get P_{23} one obtains P_{24} by;

$$\frac{P_{24}}{dt} = \delta p_{23} = \delta(c_5 e^{-\delta t} + c_6 e^{-\upsilon t})$$

Then

$$P_{24} = -\delta(c_5 \frac{e^{-\delta t}}{\delta} + c_6 \frac{e^{-\upsilon t}}{\upsilon})$$

Determining of P_{33} and P_{34}
Consider the following system which represents the last two equations of the system(18)

$$\begin{cases} \dfrac{dP_{33}(t)}{dt} = -(1 - M_3)\delta \\ \\ \dfrac{dP_{34}(t)}{dt} = \delta M_3 \end{cases} \tag{28}$$

by replacing $(1 - M_3)$ with P_{33} and M_3 with P_{34}, we obtain

$$\begin{cases} \dfrac{dP_{33}(t)}{dt} = -P_{33}\delta \\ \\ \dfrac{dP_{34}(t)}{dt} = \delta P_{34} \end{cases} \tag{29}$$

we thus obtain the following results

$$\begin{cases} DP_{33} + P_{33}\delta = 0 \\ \\ DP_{34} - \delta P_{34} = 0 \end{cases} \tag{30}$$

$D_1 = -\delta$ and $D_2 = \delta$ which gives the following values $P_{33} = c_7 e^{-\delta t}$ and $P_{34} = c_8 e^{-\delta t}$
Thus, the probabilities P_{11}, ..., P_{31} are computed as disserted. □

3.2 *Modelling the basic reproduction rate*

The epidemiological definition of R_0 [9] is the average number of secondary infections which are infections that occur during or after treatment of another infection, produced by an infected individual introduced into a population of susceptible individuals, where an infected individual has contracted the disease, and the susceptible individuals are healthy but can contract the disease. R_0 is a critical threshold that determines whether the disease will persist or disappear.

If $R_0 < 1$ then the infection rate will decrease and the disease will eventually disappear, but if $R_0 > 1$ the disease will persist in the population.

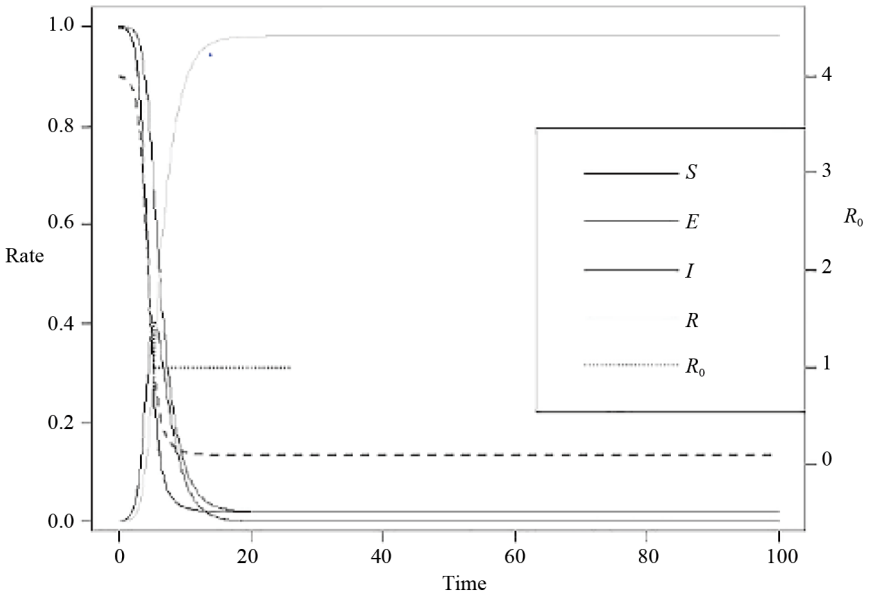

Figure 2. graph of R_0

Proposition 3 According to the system of equation (13) the reproduction rate R_0 is obtained by

$$R_0 = \frac{(c_2 e^{-\kappa\tau} + c_3 e^{\upsilon\tau}) S_0 c_7 e^{-2\delta\tau}}{(c_5 e^{-\delta\tau} + c_6 e^{-\upsilon\tau}) c_8} \tag{31}$$

where c_1, c_2, c_3, c_4, c_5, c_6, c_7 and c_8 are constant.

Proof. This proof is based on the new generation matrix. Let's consider that the process is stationary, that is $\tau = [t, t+\tau]$. Let us consider the matrix of the new generation associated with our system

$$\mathscr{F} = \begin{pmatrix} 0 \\ (c_2 e^{-\kappa\tau} + c_3 e^{-\upsilon\tau}) SI \\ 0 \end{pmatrix}; \tag{32}$$

where $\mathscr{F}$ is the flow of newly infected individuals into the compartment

$$\mathscr{V}^+ = \begin{pmatrix} c_1 e^{\kappa\tau} S \\ c_4 e^{-\upsilon\tau} SI \\ c_7 e^{-\delta\tau} E \end{pmatrix}; \tag{33}$$

$\mathscr{V}^+$ is the set of incoming flows related to the compartments

$$\mathscr{V}^- = \begin{pmatrix} (c_2e^{-\kappa\tau} + c_3e^{-\upsilon\tau})SI \\ (c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau})E \\ c_8e^{\delta\tau}I \end{pmatrix}. \tag{34}$$

and $\mathscr{V}^-$ is the set of outgoing flows related to the compartment.

Then by calculus we get

$$\mathbb{F} = \begin{pmatrix} 0 & (c_2e^{-\kappa\tau} + c_3e^{-\upsilon\tau})S_0 \\ 0 & 0 \end{pmatrix}; \mathbb{V} = \begin{pmatrix} -(c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau}) & 0 \\ c_7e^{-\delta\tau} & -c_8e^{\delta\tau} \end{pmatrix} \tag{35}$$

The matrix $K = -\mathbb{F}\mathbb{V}^-$

So, $K =$

$$\begin{pmatrix} 0 & (c_2e^{-\kappa\tau} + c_3e^{-\upsilon\tau})S_0 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau}} & 0 \\ \frac{c_7e^{-\delta\tau}}{(c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau})(c_8e^{\delta\tau})} & \frac{1}{c_8e^{\delta\tau}} \end{pmatrix} \tag{36}$$

which gives, after calculus, the following matrix

$$K = \begin{pmatrix} \frac{(c_2e^{-\kappa\tau} + c_3e^{-\upsilon\tau})S_0c_7e^{-\delta\tau}}{(c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau})(c_8e^{\delta\tau})} & \frac{(c_2e^{-\kappa\tau} + c_3e^{\upsilon\tau})S_0}{c_3e^{\delta}} \\ 0 & 0 \end{pmatrix}. \tag{37}$$

Then, R_0 corresponds to the spectral radius of K :

$$R_0 = \rho(K) = \frac{(c_2e^{-\kappa\tau} + c_3e^{-\upsilon\tau})S_0c_7e^{-2\delta\tau}}{(c_5e^{-\delta\tau} + c_6e^{-\upsilon\tau})c_8}. \tag{38}$$

The R_0 thus obtained represents our basic reproduction. □

4. Dicussion

Many authors have worked on compartimental models in epidemiology, some like Hay Yoba Talkibing, Barro Diakarya and Ouoba Fabrice [12] propose a stochastic version of the SEIRS model in epidemiolgy using Markov processes, other authors such as Qun Liu, Daquing Jiang Ningzhong Shi, Tasawar Hayat and Bashir Ahmad [3] propose a suitable stochastic Lyapunov funtions, he establish sufficient conditions for the existence of ergodic stationary distribution to the model. Taking randomness into account in the modeling of compartmental models remains a major challenge. The uniqueness of our paper is to propose a stochastic SEIRS model using the Fokker-Planck equation. This paper being more theoretical.

5. Conclusion

The objective of this work was to introduce a stochastic approach to compartmental models through the SEIR model. Using the Fokker-planck equation and the Kolmogorov properties we could build a stochastic model and also determine R_0 the basic reproduction rate. Our model allows transitioning from a model with constants rates to stochastic model.

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Conflict of interest

The authors declare there is no conflict of interest at any point with reference to research findings.

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