



A SIMPLE STOCHASTIC EPIDEMIOLOGICAL MODEL

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Abstract

In the present study, we introduce a simple stochastic differential equation based on the Susceptible-Infectious (SI) model to simulate the progression of COVID-19. For a detailed study, a cumulative number of individuals infected with COVID-19 in Norway from 26 Feb 2020 to 09 March 2023 is utilized. The Euler-Maruyama (EM) method is used to solve the problem. Computer codes are developed in Matlab for the solution process.

Keywords: Brownian Motion, Covid-19, Epidemiology, Euler-Maruyama (EM) Method, Stochastic Differential Equation (SDE).

I. Introduction

A mathematical model is a demonstration of a real-life situation using mathematical concepts and language with certain assumptions and approximations. Recently, it has gained more attention and awareness in the field of epidemiology and the medical sciences. Traditional compartmental models like SI, SIR, SEIR etc., which are deterministic in nature, involve knowledge of algebra, vector calculus, regression, differential equations and so on [III, IV, V].

The deterministic models do not consider uncertainty or noise involved in the process. So we develop a desirable model by including some stochastic noise components in a deterministic model [VI, X, IX]. In the present study, a stochastic differential equation (SDE) is used in the modelling of COVID-19 in Norway from 26 Feb 2020 to 09 March 2023.

II. Mathematical Model & Materials

A. S-I (or Susceptible-Infectious) based stochastic model for COVID-19.

First, we consider the two-compartment deterministic S-I epidemic model [I, II]

$$\frac{dx}{dt} = \lambda x(n - x) \quad (1)$$

where

$x(t)$: the number of infected and susceptible individuals at time t (in, days),

λ : constant of proportionality,

n : the total number of individuals in the community.

As usual, this model does not take into account the stochastic nature (or \white noise) that is often present in such situations. To establish a stochastic component in the model, the following SDE is considered:

$$dX(t) = \lambda X(t)(n - X(t))dt + \mu X(t)dW(t), \quad X(0) = X_0, \quad 0 \ll t \ll T \quad (2)$$

where

λ : constant,

μ : constant,

$W(t)$: random variable.

The first and second terms on RHS of the above equation are the drift and diffusion terms of the process. The deterministic portion of the model is denoted by the drift term, while the stochastic component is denoted by diffusion.

B. Solution Process

The Euler-Maruyama (EM) method [VII] is used to solve the eq (2) numerically. First, we construct the Brownian motion, $W(t)$, as a discrete function of t :

$$dW_j = dW_j - dW_{j-1}, \quad j = 1, 2, \dots, N \quad (3)$$

where

$$dW_j \sim \sqrt{\delta t} N(0, 1), \quad \delta t = \frac{T}{N}$$

The time scale is discretized as:

$$\Delta t = \frac{T}{L}$$

where L is a positive integer.

Applying the EM method to Equation (2) over an interval $[0, T]$, we get:

$$X_j = X_{j-1} + \lambda X_{j-1}(n - X_{j-1})\Delta t + \mu X_{j-1}(W(\tau_j) - W(\tau_{j-1})), \quad j = 1, 2, \dots, L, \quad \tau_j = j\Delta t \quad (4)$$

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where X_j is the numerical approximation to $X(\tau_j)$. We get back the deterministic model (1) when $\mu = 0$. Computer codes are written on Matlab. The user specifies the number of sample paths for each program run, with the final numerical solution being calculated as the average of all valid results.

C. Database

The analysis relies on the data that has been gathered and is accessible on the website [VIII]. It gives the cumulative number of individuals infected day wise in Norway from 26 Feb 2020 to 09 March 2023 as shown in Table 1.

Table 1: Total count of people who have been infected with COVID-19 in Norway from 26 Feb 2020 to 09 March 2023.

| Day | Cumulative number of individuals infected |
|------|---|
| 1 | 1 |
| 2 | 1 |
| 3 | 6 |
| ... | ... |
| ... | ... |
| 1107 | 1479453 |
| 1108 | 1479506 |

III. Simulation & Results

Using Matlab, a computer code was developed to replicate the spread of the outbreak according to the data outlined in Table 1. In the data set, we have $n = 1108$, $X_0 = 1$, $T = 1$ and $\lambda = 0.05$ in the simulation runs.

Based on the data outlined in the Table above, we run the code for $\mu = 0$ (with one path) and a sample case for $\mu = 0.25$ (with 500 paths) respectively, and display the results graphically in Figures 1 and 2 respectively along with the real data for comparison. We can get back the deterministic model if run the simulation with just one sample path and $\mu = 0$.

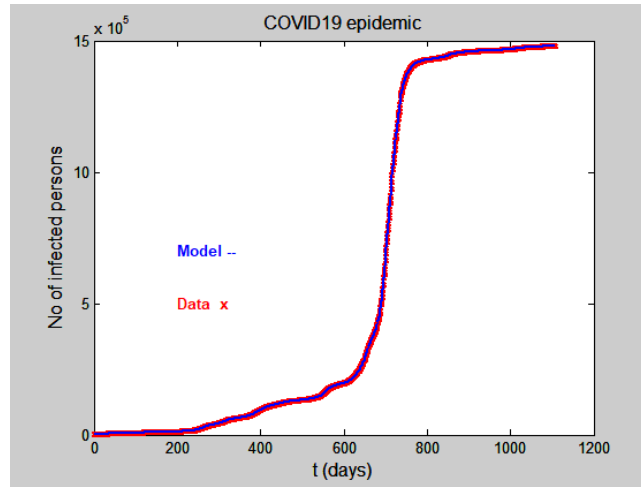


Fig. 1.

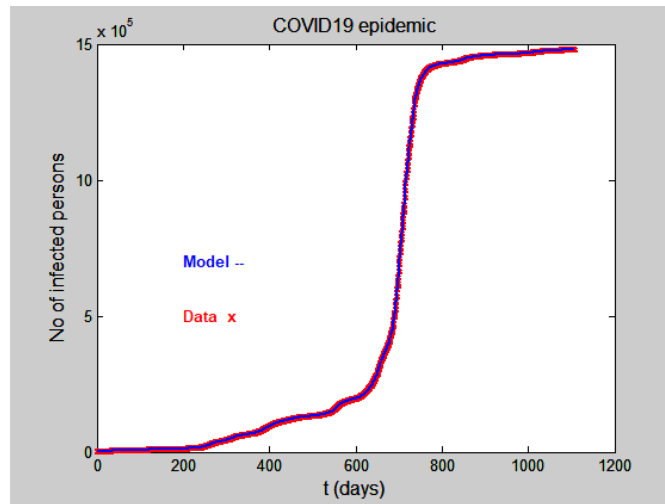


Fig. 2.

The calculation of the average error, denoted as E, for a simulation run, is as follows:

$$E = \sqrt{\frac{\sum_{i=1}^{1108} (\langle X_i \rangle - X_i)^2}{1108}}$$

where X_i and $\langle X_i \rangle$ are values obtained from the data and the model respectively. The code gives $E = 2.514$ for the case of the deterministic model (that is, when $\mu = 0$), and $E = 1.957$ with $\mu = 0.25$ and 500 paths. Since the process is stochastic in nature, the above results are samples and so, if we run the program again with the same values of μ and number of trials, we would get a different output with a different value for E.

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IV. Conclusion

In epidemiology, traditional compartmental models like SI, SIR or SEIR are fundamentally deterministic and do not have the ability to account for uncertainties or noise within the model.

In the present numerical study, a simple stochastic model for the spread of infectious disease along with the SI model is considered. A cumulative number of individuals infected with COVID-19 in Norway from 26 Feb 2020 to 09 March 2023 is used in the modelling.

It should be emphasized that the parameters used in the study (such as λ and μ) do not have any physical significance, they are arbitrary constants chosen carefully through experiments suitable to a particular set of data.

The present numerical study may motivate the readers to experiment with SDEs using a simple case of infectious disease outbreak.

Conflict of Interest:

The authors declare no conflicts of interest.

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