

Parametrization of the Stochastic SIRD Model for COVID-19 Outbreak Using Markov Chain Monte Carlo Method

Muhammad Fahmi^{1, a)}, Norhayati Rosli^{1, b)} and Noryanti Muhammad^{1,2, c)}

Author Affiliations

¹*Centre for Mathematical Sciences, College of Computing and Applied Sciences, Universiti Malaysia Pahang, Lebuhraya Tun Razak, 26300 Gambang, Kuantan, Pahang, Malaysia.*

²*Centre of Excellence for Data Science & Artificial Intelligence, Universiti Malaysia Pahang, 26300, Gambang, Kuantan, Pahang.*

Author Emails

^{a)} *mfahmi.aor@gmail.com*

^{b)} Corresponding author: *norhayati@ump.edu.my*

^{c)} *noryanti@ump.edu.my*

Abstract. The susceptible-infectious-recover-death SIRD deterministic compartmental model is the most frequent mathematical model of the epidemic outbreak. The model consists of four states, susceptible, infected, recovered and death. Pandemic outbreak is highly influenced by the uncontrolled factors of the environmental noise. This paper is aimed to extend the deterministic model of SIRD to a stochastic SIRD counterpart. The epidemiological parameters are perturbed with the noisy behavior of the Wiener process to gain insight of the noisy behaviour of the outbreak. The parameters representing the rate between the four states (infection rate, recovery rate, fatality rate and immune lost rate) are estimated using the Markov Chain Monte Carlo (MCMC) method using 200, 400 and 1000 simulations. The result shows that as the number of sample paths is increased (1000 simulations), the parameter estimated from the model provide low value of the Monte-Carlo error and root mean square error (RMSE), hence indicate 1000 simulation of the MCMC provide acceptable estimated value of the epidemiological parameter for model simulation.

INTRODUCTION

Pandemic outbreaks give a great impact worldwide. Coronavirus disease (2019), COVID 19 spread for example has resulted in large number of human lives being lost. Public health analytics on the infectious disease spread is a great concern all over the world. Designing the strategies for managing disease threats to humans is possible through a mathematical model. The present paper is based on the most well-known deterministic SIRD epidemiological model. This model is an extension of the SIR model introduced by Kermack and McKendrick in 1927 [1]. Deterministic models do not consider the effects of the environment in the SIRD model. Stochastic models produce more realistic results as the same set of parameter values and initial conditions for deterministic counterpart models lead to different outputs. From [2], the main difference between the deterministic and stochastic epidemic model is stochastic epidemic model will eventually converge to a disease-free equilibrium state even though the deterministic counterpart converges to endemic equilibrium. Ultimately, the aim of modeling pandemic outbreaks is to forecast the spreading of the disease and predict a situation of disease extinction.

Among researchers that use the stochastic epidemiological model is [3-6]. Further than modeling the epidemic, a model inference could only be done by first estimating the epidemiological parameter. Method such as Maximum Likelihood Estimation (MLE) and Monte Carlo Markov Chain (MCMC) are used as the stochastic epidemiological