

A SPECIAL TYPE OF MARKOV BRANCHING PROCESS MODEL FOR THE NOVEL CORONAVIRUS (COVID-19) OUTBREAK

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ABSTRACT. *Mathematical modeling has been an important tool to estimate key factors of the transmission and investigate the dynamical system of evolutionary nature in epidemics. More precisely, the outbreaks of the virus or epidemiology is generally considered as an application of branching process. Therefore, in this paper, we propose a special type of Markov branching process model to examine and explore some problems of the novel coronavirus (COVID-19) infectious disease with the aims of reducing the effective reproduction number of an infection below unity. Since the COVID-19 has been recognized as a global pandemic, we have assessed a big amount of data such as hourly contagious, hospitalized patients, recovered and deaths. However, these data are necessary to be further processed to produce useful information for people and authorities when they make an efficient and optimal decisions. In such a decision-making process, we establish a special type of Gama Markov branching process model which has been successfully applied in other research areas such as queueing and waiting lines problems, stochastic reservoir problems, inventory controls and operation research. Specifically, we develop a three parameter Gama Markov branching process model that is structured in two parts, initial and latter transmission stages, so as to provide a comprehensive view of the virus spread through basic and effective reproduction numbers respectively, along with the probability of an outbreak sizes and duration. As an illustration, we have performed some simulations based on the daily data appearing on WHO dashboard in order to analyze the first semiannual spread of the ongoing coronavirus pandemic in the region of Myanmar. The results show that the proposed model can be utilized for the real-life applications.*

Keywords: Novel coronavirus, Markov branching process model, Spreads in Myanmar, Reproduction rate, Outbreak sizes

1. Introduction. The exponential spread of the novel coronavirus (COVID-19) around the world has made millions of lives loss and created an unprecedented lockdown in many countries pushing the world to the brink of global pandemic alert. Consequently, it caused an immense economic and social impact. Since the virus was first discovered in December 2019, variety of measures such as mask wearing campaigns, social distance movements, and mass vaccination programs were taken globally to stop this pandemic as soon as possible. In other words, almost all countries around the world are fighting against the pandemic to reduce the effective reproduction number of an infection below unity. Thus, many researchers investigate methods to stop this epidemic as soon as possible [1-4]. The

struggle involves researchers from various fields such as bioinformatics, epidemiology, sociology, mathematics, and computer science. A sizable number of studies have already explored the dynamics of the spread of COVID-19 in different countries with various methodologies [5-7]. In these days, COVID-19 vaccines are being deployed worldwide, and it is necessary to take consideration of available therapeutic measures, vaccination of susceptible and treatment of hospitalized/infected individuals when we establish a mathematical model to deal with COVID-19 [8,9]. We all know that mathematical models are not a cure for the infectious disease; however, they can be used to analyze possible trends and the dynamic spreads of the disease. Currently, almost all professionals in various disciplines are putting efforts to stop the spread of COVID-19. Mathematicians have also developed new mathematical models that can be used for simulation to flatten the infection and death curve, predict the future behavior of its spread, make decisions to control it, and are trying to create new optimal models every day. Many studies have been conducted in the literature on the mathematical model of the COVID-19 pandemic in a short time [10-12]. Although there are some mathematical models that have been proposed for new coronavirus disease prediction, some of them can be further improved. In this context, [10] proposed a new mathematical model by taking the vaccinating effects into account. However, their approach is mostly based on deterministic models. We thought that it would be more realistic if we can take the probability concepts which we have included in our model. Moreover, in [11], the authors used deep learning method by utilizing an Artificial Neural Network (ANN)-based and data-stream driven real-time learning algorithm to predict the parameters of the non-competitive, intelligent adaptive and online analytical model of COVID-19 disease. Although their approach is an excellent one, it involves more parameters for estimations than our proposed model. In [12], the authors reviewed and introduced some models for the COVID-19 that can address important questions about the global health care and suggest important notes. They suggested three well known numerical techniques, namely, Euler's method, Runge-Kutta method of order two and of order four. However, we thought that some deep insight information could be achieved by using the Markov Chain Monte Carlo (MCMC) method to fit the model to the data that we utilize in our proposed model. It is worthwhile to investigate the pandemic as much as possible from various perspectives. Therefore, we propose a branching process model of special type named as Gama Markov model to derive the reproduction rate which is a key factor to reduce the spread of any infectious disease. The main contributions of the paper are

- (i) To show how Gama Markov branching model can effectively provide the reproduction rate of COVID-19,
- (ii) The utilization of Markov branching process is new and novel for a framework of coronavirus infectious disease,
- (iii) In addition, due to the Markovian property, the proposed model can provide some realistic results.

The rest of the paper is organized as follows. In Section 2, we introduce Gama Markov branching process to model and analyze the dynamic spreads of COVID-19. The model simulation procedures are described in Section 3 followed by the illustrative example shown by using real life data along with discussions in Section 4. Finally, we give concluding remarks in Section 5.

2. Gama Markov Branching Process and COVID-19. In this section, we introduce a Gama Markov branching process model to investigate the spreads of novel coronavirus (COVID-19). In order to do so, we assume that each case infects a random X other, known as the offspring of the case who infected them. The distribution of X is called the

offspring distribution, and we shall assume that it belongs to the Gama Type distribution family. In particular, we shall consider a special type of Gama Markov density function shown in Equation (1): The conditional probability density of $X_{t+1} = x_{i+1}$ given $X_t = x_i$ is defined as

$$p(X_{t+1} = x_{i+1} | X_t = x_i) = \beta e^{-\alpha x_{i+1} - \beta x_i} \sum_{j=0}^{\infty} \frac{(\alpha x_i)^j (\beta x_{i+1})^{j+r-1}}{r! \Gamma(r+j)} \tag{1}$$

$0 < x_{i+1}, x_i < \infty$ where $r > 0, 0 < \alpha < \beta$

An extensive investigation of the processes (i) Gama Markov sequence and (ii) negative binomial Markov chain has been carried out by Lampard [13] and Phatarfod [14], who obtained them as output processes of a counter system. Among other results, they show that the stationary distributions of the two processes are given by Gama density.

$$f(x) = \frac{(\beta - \alpha)^r}{\Gamma(r)} x^{r-1} e^{-(\beta-\alpha)x} \text{ where } x > 0 \tag{2}$$

Now let us define the total number of cases up to the n th generation as the partial sum.

$$S_n = X_0 + X_1 + \dots + X_n \tag{3}$$

We then have the moment generating function of the partial sum as shown in Equation (4).

$$M_n(\theta) = E(\theta S_n) = \left[\frac{(1 - \rho)(\mu_1 - \mu_2)}{\mu_1(1 - \mu_2)^2 \mu_1^n - \mu_2(1 - \mu_1)^2 \mu_2^n} \right]^r \tag{4}$$

where $\mu_1(\theta), \mu_2(\theta) = \frac{(1 + \rho) \pm \sqrt{(1 + \rho)^2 - 4\rho e^\theta}}{2}$

In this case, we have $\theta < \log \frac{(1-\rho)^2}{4\rho}$, $\mu_1(\theta) > \mu_2(\theta) > 0$ and $\mu_2(\theta) < 1$.

Hence, when $n \rightarrow \infty$, we have

$$M_n(\theta) \sim C(\theta) \lambda_1^n(\theta) \text{ where } C(\theta) = \left[\frac{(1 - \rho)(\mu_1 - \mu_2)}{\mu_1(1 - \mu_2)^2} \right]^r, \lambda_1(\theta) = \mu_1^{-r}(\theta) \tag{5}$$

We will be mainly interested in deriving the asymptotic behavior of the number $N(T)$ of new cases occurring in $(0, T)$.

According to [14], the least positive integer n is such that $S_n \geq T$. From Equation (5), it is given by

$$\begin{aligned} E(N(T)) &\sim \frac{\beta - \alpha}{r} T \\ \text{Var}(N(T)) &\sim \frac{\alpha + \beta}{r^2} T \end{aligned} \tag{6}$$

Thus, by using Equation (6), we can estimate the number of new cases during a given time interval and time to no new occurrence of a case.

3. Model Simulation Procedure. The characteristics of a population of infectious cases are given by parameters. A population of infectious disease variables is not always exactly known. Therefore, we use samples taken from the world pandemic COVID-19 cases. Parameters estimated from a sample are called statistics, which are functions of the elements of the sample and reflect the properties of the whole population. In statistics, there are many different methods to estimate the parameters and simulate the variables. In here we will consider two methods namely (i) method of moments and (ii) modified maximum likelihood estimation for simulation purposes.

3.1. Methods of moments. This is one of the oldest and the most useful methods of parameter estimation. The method of moments uses relations between the central moments and parameters of the distribution. Parameter estimation is given for the Gama Markov model defined in Equation (1). The corresponding moments of the distribution by a little calculation can be obtained as follows:

$$\begin{aligned} E(X) &= \frac{r}{\beta - \alpha} \\ \text{Corr}(X_t, X_{t+1}) &= \rho = (\alpha/\beta) \\ E(X_{t+1}|X_t) &= \rho X_t + (1 - \rho)E(X) = (\alpha/\beta)X_t + (r/\beta) \\ \text{Vov}(X_{t+1}|X_t) &= 2(\rho/\beta)X_t + (r/\beta^2) \end{aligned} \quad (7)$$

The shape and scale parameters of the Gamma distribution (α and β) are determined from the daily sample data of a particular location in a monthly time interval, by Equation (7). Once we obtain the parameters, we can predict the time at which the pandemic will be wiped out by using Equation (6).

3.2. Maximum likelihood method. In the maximum likelihood method, values maximizing the maximum likelihood function of the distribution are taken as estimates of the parameters. The density function described in Equation (1) can be considered as a Poisson-Gamma mixture probability density function, i.e., X_{t+1} has a Gama $G(u + r, \alpha(1 - (\alpha/\beta)))$ distribution where u is a Poisson variable with mean $\lambda = X_t/(\beta - \alpha)$. This result allows us to simulate the sequence X_0, X_1, X_2, \dots as follows.

Generate a value of a Poisson random variable with $\lambda = X_0/(\beta - \alpha)$ and call it u . Now generate a value of a Gamma random variable with parameters $\{u + r, \alpha(1 - (\alpha/\beta))\}$. The value so obtained is X_1 . This procedure is repeated n times to give the sequence, $X_0, X_1, X_2, \dots, X_n$.

We then define the likelihood function as

$$L(\alpha, \beta, r) = \prod_{i=0}^{n-1} \left[\beta e^{-\alpha x_{i+1} - \beta x_i} \sum_{j=0}^{\infty} \frac{(\alpha x_i)^j (\beta x_{i+1})^{j+r-1}}{r! \Gamma(r+j)} \right] \quad (8)$$

Let us denote the estimators by r^*, α^*, β^* .

The estimate r^* is obtained iteratively using a Newton-Raphson method as follows.

From the sequence $X_0, X_1, X_2, \dots, X_n$, we find

$$E(X) = r/(\beta - \alpha) \text{ and } (\alpha/\beta) = \text{Corr}(X_t, X_{t+1})$$

Taking a preliminary value for r , we obtain the new value as

$$\begin{aligned} r(\text{new}) &= r - f(r)/f'(r) \\ \text{where } f(r) &= \partial \text{Log} L / \partial r \end{aligned} \quad (9)$$

The procedure is used recursively where at each stage we use

$$\begin{aligned} E(X) &= r/(\beta - \alpha) \\ \text{Corr of sample} &= \alpha/\beta \end{aligned} \quad (10)$$

4. Illustrative Example. To illustrate the model developed in this paper, we utilize the daily data for COVID-19 in Myanmar. A key limitation in our understanding of the COVID-19 pandemic is that we do not know the true number of infections. Instead, we only know infections that have been confirmed by a test – the confirmed cases. Specifically, we use the data we have confirmed cases and deaths data issued by WHO Statistics

from 1st January 2021 to 14th November to estimate true infections and other important metrics. Some sample data are shown in Table 1. We also note that a COVID-19 forecasting model has been used for Indonesia data [15].

By using the data from WHO Statistics, we estimated the new cases as described in Section 3. We find that the observed data and the estimated data are very close enough as shown in terms cumulative function in Figure 1. Probability density function comparison between simulated data and observed data is shown in Figure 2.

As a discussion, we make some remarks. There are many strategies and prevention measures under global efforts to reduce the impact of the COVID-19 around the world. All clinical and theoretical studies give a great effort to control this disease. One of the

TABLE 1. Sample data: COVID-19 in Myanmar

Date	Country code	WHO region	New cases	Cumulative cases	New deaths	Cumulative deaths
1/1/21	MM	SEARO	423	125053	15	2697
1/2/21	MM	SEARO	563	125616	14	2711
1/3/21	MM	SEARO	729	126345	17	2728
1/4/21	MM	SEARO	590	126935	16	2744
1/5/21	MM	SEARO	647	127582	22	2766
1/6/21	MM	SEARO	596	128178	19	2785
1/7/21	MM	SEARO	594	128772	14	2799
1/8/21	MM	SEARO	711	129483	13	2812
1/9/21	MM	SEARO	566	130049	14	2826
1/10/21	MM	SEARO	555	130604	20	2846
—	—	—	—	—	—	—
11/10/21	MM	SEARO	1180	509771	14	18869
11/11/21	MM	SEARO	954	510725	13	18882
11/12/21	MM	SEARO	992	511717	17	18899
11/13/21	MM	SEARO	831	512548	14	18913
11/14/21	MM	SEARO	714	513262	16	18929

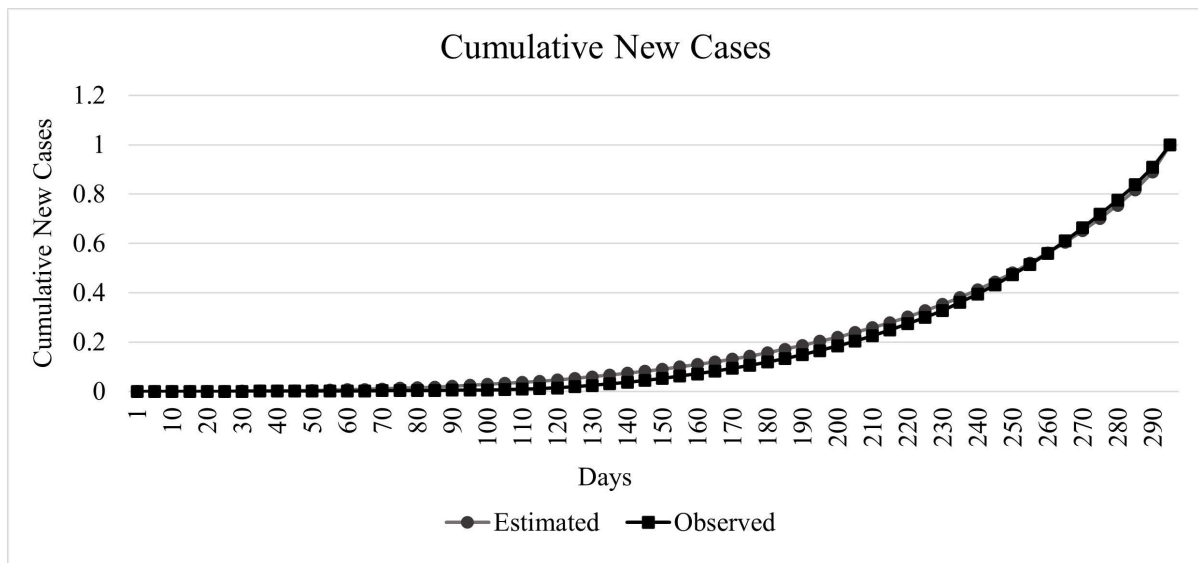


FIGURE 1. Cumulative comparative graph

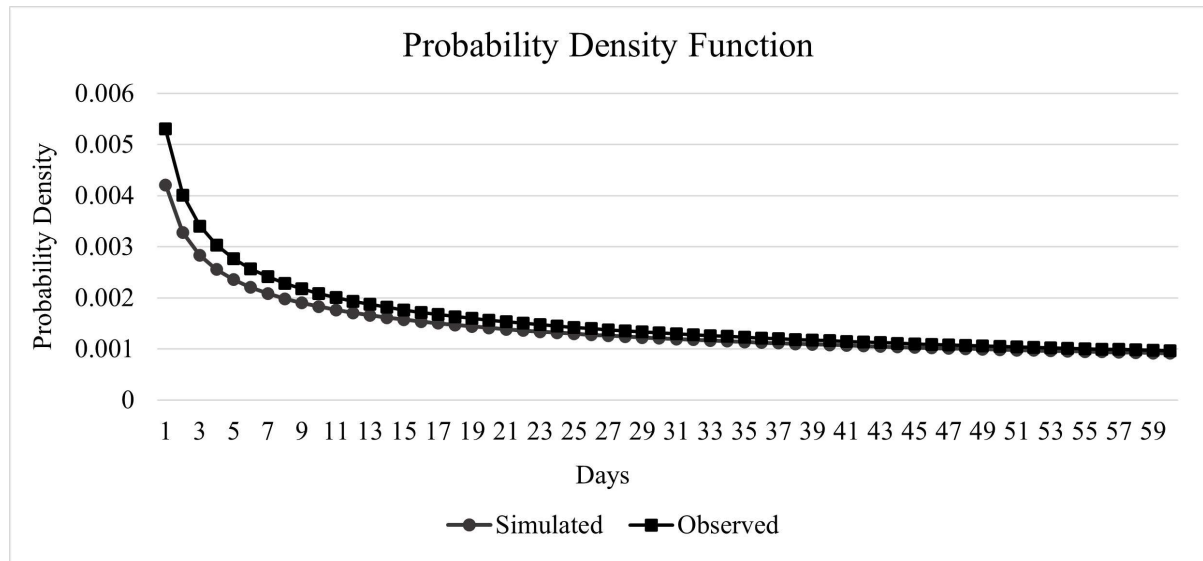


FIGURE 2. Probability density function comparison

theoretical tools that provide a wide range of predictions and estimations about this issue is mathematical modelling. Mathematical modeling with computational simulation models predicts and identifies key critical parameters. Our proposed method provides an essential way to suggest more preventions compared to the previous approaches. Compared to all previous studies, our Gama Markov branching process modelling approach gives another significant step forward to understand the model dynamics and predict the spreading of coronavirus disease on the community.

5. Conclusions. In this paper, we had proposed a Gama Marko Model to study some behavior patterns of infectious disease particularly for COVID-19. The proposed model could be used for prediction and trend analysis for the pandemic case. Although it can be applied for any location, we have given an illustration by using the data issued by WHO Statistics. We hope the proposed model would be beneficial for the researchers in epidemiology. So far, we have not yet considered the migration data explicitly in our proposed model. However, migrants – particularly in lower paid jobs and in irregular situations – may be both more affected by and vulnerable to the spread of COVID-19, but migrants also play an important role in the response to COVID-19 by working in critical sectors. Therefore, in our future works, we would like to consider a new model taking migration data into account.

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