

## NONLINEAR MATHEMATICAL MODEL FOR THE TRANSMISSION OF CORONAVIRUS IN CHEBYSHEV POLYNOMIAL AND EULER SENSE

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Received Dec. 2, 2024

**ABSTRACT.** Recently, many studies offered the population dynamic and analysis of various problems phenomena. Among these cases can be seen in the modeling of the Coronavirus. Implementing mathematical pattern has become a crucial tool in the characterization and understanding of the dynamics associated with infectious diseases. In this effort, we present an efficient model based on the develop the Chebyshev integral of first order quadrature polynomial to estimate the infected cases of Coronavirus disease in the sense of ordinary differential equation. The Chebyshev polynomials of the first kind is utilised to approximate the solvability that estimate the transmissibility of the virus. We test the proposed system by using live data provided by World Health Organization (WHO) outbreak of the disease in Malaysia in 2020 and then we compare the outcomes with the Euler's transform model. The proposed approach was sufficient in dealing with the ODE problems of nonlinear modes and a MATLAB code is developed to obtain the numerical results of the work. The numerical examples assert the theoretical results with agreement action on the graphs in describing transmission processes.

2020 Mathematics Subject Classification. 05C78.

Keywords and phrases. nonlinear equation; Chebyshev integral; Chebyshev quadrature polynomial; ordinary differential equations (ODEs); Jacobian representation; data analysis.

### 1. INTRODUCTION

The Severe Acute Respiratory Syndrome Novel Coronavirus 2, abbreviated as (SARS CoV-2) or otherwise popularly known as COVID-19 is a new type of Coronavirus that can potentially cause severe respiratory illnesses very much like very similar viruses such as Severe Acute Respiratory Syndrome

Associated Coronavirus (SARS) and Middle East respiratory syndrome (MERS). COVID-19 has spread to almost all countries and all continents of the globe except for Antarctica (World Health Organisation (WHO) 2020) ([1]- [2]). Those with underlying medical conditions and the elderly have shown to develop acute respiratory distress syndrome [3]. In early December 2019, cases of pneumonia with an unknown cause began to emerge in Wuhan City, Hubei Province of China [4]. Several of these cases have been traced back to person-to-person transmission in the Huanan Seafood Market where other wildlife species have been sold [5]. Based on past cases, the likelihood that initial infections were from animals to humans increased and later the wet market was identified as the origin of this new virus.

The second phase of the outbreak began on January 13, where cases of nosocomial infections (spread of the virus within medical facilities) and family transmission (close contact transmission) started to emerge (see [5]- [10]). On January 22, 2020, COVID-19 was declared to have originated from wild bats and belongs to the same Coronavirus group as SARS [3], [6]. By January 23, 29 provinces and six other countries other than China had reported cases of COVID-19 infections with a total of 846 confirmed cases [10]. The outbreak would be difficult to curb as these events occurred during the Spring festival where Chinese locals would go back to their hometowns in China or even travel to foreign countries for their holidays.

The World Health Organisation (WHO) declared the viral outbreak a public health emergency of international concern (PHEIC) on January 30, 2020 [9]. Up until January 31, 2020, COVID-19 had spread to 19 countries aside from China reporting 11,791 infections and 213 deaths. In the months to follow, this new strain of Coronavirus would spread all over the world and be announced by WHO that the ongoing crisis be regarded as a pandemic on March 12, 2020. By April 14, 2020, there were a total of 1,844,683 confirmed cases and 177,021 deaths reported globally (WHO).

Several growth strategies have been very recently engaged in the time rise of the Corona infection [11]. Mostly, by employing the following ordinary differential equation:

$$\frac{df(t)}{dt} = f(t), \quad t \geq 0 \quad (1)$$

where  $f$  signifies the number of infected persons, the rampant phase, the growing number of asymptomatic infected individuals are labelled. Currently, there are diverse numerical investigations and analytic surveys in corona have been obtained (see [12]- [16]).

The current effort deals with the extended dynamic formula of the growth laws by employing the polynomials concept. We present an approximate solution by utilizing Chebyshev polynomials of the first kind (see [17]- [20]). Our method is based on the Chebyshev integral of first order, which indicates significant outcomes in the system of ordinary differential equation. We test the suggested system by considering live data form Malaysia, which is normalized to fit the propagation of the analysis. We found agreement action on the graphs.

## 2. METHODOLOGY

**2.1. Infected system.** The system is given by the ordinary differential equations

$$\frac{df(t)}{dt} = f(t),$$

where  $f$  indicates the number of infected individuals. In our study, we shall use the Chebyshev's differential equation, where it is the second order linear differential equation [17]

$$(1 - t^2) \frac{d^2 f}{dt^2} - t \frac{df}{dt} + \rho^2 f = 0$$

where  $\rho$  is a real constant. The solutions can be indicated by power series, which converges for  $t < 1$

$$f(t) = \sum_{n=0}^{\infty} b_n t^n$$

where the coefficients have the recurrence formula

$$b_{n+2} = \frac{(n - \rho)(n + \rho)}{(n + 1)(n + 2)} (b_n).$$

The statute is frequently known Chebyshev's theorem (CT), about the change of standard deviations about the mean, in statistics [22]. The CT has excessive usefulness because it can be employed to any probability distribution in which the mean and variance are well-defined [20], [21]. For example, it can be utilized to study a huge data such as the COVID-19.

**2.2. The Chebyshev polynomials (CP).** The Chebyshev quadrature polynomials are two sequences of polynomials indicated by the sine and cosine functions, constructed as  $T_n(t)$  and  $U_n(t)$ . They can be formulated by numerous conducts that have the same end consequence. Our study is based on the the Chebyshev polynomials of the first kind ( $T_n$ ) which are formulated by [20], [23].

$$T_n(\cos(\omega)) = \cos(n\omega).$$

The CPs of the first kind are known from the recurrence formula

$$T_0(t) = 1$$

$$T_1(t) = t$$

$$T_2(t) = 2t^2 - 1$$

$$\vdots$$

$$T_{n+1}(t) = 2tT_n(t) - T_{n-1}(t).$$

The ordinary generating function for  $T_n$  is

$$\sum_{n=0}^{\infty} T_n(t) z^n = \frac{1 - tz}{1 - 2tz + z^2}.$$

Since a Chebyshev series is a special case of a Fourier cosine series through a transformation of variables, all of the formula, identities, etc. that employ to Fourier series have a Chebyshev equivalent. These characteristics contain:

- The CPs arrange a complete orthogonal construction.
- The Chebyshev series converges to  $f(t)$  when the function is piece-wise continuous and continuous.

The analytic behavior requirement can be conformed in furthestmost suitcases whenever there are a finite number of discontinuities in  $f(t)$  and its derivatives.

- At a discontinuity case, all the series will be converged to the normal of the right and left limits.

**2.3. Nonlinear equations with incidence rate of Coronavirus.** This research method will be modelled on

$$\begin{aligned} V &= \delta - \kappa v - \frac{\epsilon}{1 + \mu A^2} VA, \\ A &= \frac{\epsilon}{1 + \mu A^2} VA - (\kappa + \mu)A, \\ D &= \mu A - \kappa D. \end{aligned} \quad (2)$$

where  $V, A$  and  $D$  in Eq. (2) states the vulnerable to affected and those discharged population, respectively. The parameters  $\delta$  denotes new birth,  $\epsilon$  denotes the bits transfers the virus and  $\eta$  denotes represents the prevention effect such as to prevent the spread of Coronavirus such as governing system or isolated contacts. Here, we implemented Euler's method for sensitive time computation of the numerical solution where it acts sensitively for finding the numerical results of the problem. By using Euler's method [15], [17], [18] the above  $V, A$  and  $D$  expressions of Eq. (2) are expressed as

$$\begin{aligned} \frac{V_{m+1} - V_m}{r} &= \delta - \kappa V_m - \frac{\epsilon}{1 + \eta A_m^2} V_m A_m, \\ \frac{A_{m+1} - A_m}{r} &= \frac{\epsilon}{1 + \eta A_m^2} V_m A_m - (\kappa + \mu)A_m, \\ \frac{D_{m+1} - D_m}{r} &= \mu A_m - \kappa D_m. \end{aligned} \quad (3)$$

The Eqs. in (2) can also be re-written as

$$\begin{aligned} V_{m+1} &= V_m + \delta r - \kappa r V_m - \frac{\epsilon}{1 + \eta A_m^2} r V_m A_m, \\ A_{m+1} &= A_m + \frac{\epsilon}{1 + \eta A_m^2} r V_m A_m - (\kappa + \mu)r A_m, \\ D_{m+1} &= D_m + \mu r A_m - \kappa r D_m. \end{aligned} \quad (4)$$

The equation shows the mathematical model to get the reproduction number of an infectious case that occurs during or after treatment for another infection is  $D_0 = \frac{\delta\epsilon}{\kappa(\kappa + \mu)}$ . let  $(V^*, A^*, D^*)$  be the constant solution to the differential equation, yields,

$$\begin{aligned} V^* &= V^* + \delta r - \kappa r V^* - \frac{\epsilon}{1 + \mu A^{*2}} r V^* A^*, \\ A^* &= A^* + \frac{\epsilon}{1 + \eta A^{*2}} r V^* A^* - (\kappa + \mu) r A^*, \\ D^* &= D^* + \mu r A^* - \kappa r D^*. \end{aligned} \quad (5)$$

By applying substitution method to solve (5),

$$\begin{aligned} 0 &= \delta r - \kappa r V^* - \frac{\epsilon}{1 + \mu A^{*2}} r V^* A^*, \\ 0 &= \frac{\epsilon}{1 + \eta A^{*2}} r V^* A^* - (\kappa + \mu) r A^*, \\ 0 &= \mu r A^* - \kappa r D^*. \end{aligned} \quad (6)$$

By equating the Eqs. (6) we get

$$\begin{aligned} 0 &= \frac{\epsilon}{1 + \eta A^{*2}} r V^* A^* - (\kappa + \mu) r A^*, \\ &= r A^* \left( \frac{\epsilon}{1 + \eta A^{*2}} V^* - (\kappa + \mu) \right), \quad \text{where } r > 0. \end{aligned} \quad (7)$$

If we substitute each cases into the remaining equation, it gives the result that either;

$$A^* = 0$$

or

$$V^* = (\kappa + \mu) \frac{1 + \eta A^{*2}}{\epsilon}.$$

If we substitute each cases into the remain equation then we have 2 adjustable points such as  $w_0 = (\frac{\delta}{\kappa}, 0, 0)$  and  $w_1 = (\frac{\delta - (\kappa + \mu)}{\mu}, A_w, \frac{\mu}{\kappa} A_w)$  where  $A_w = \frac{-\epsilon + \sqrt{\epsilon^2 - 4\kappa^2\eta(1 - D_0)}}{2\kappa\eta}$ . The equation figure outs that  $D_0 > 1$  then  $A_w > 0$ .

Note that the Eqs. in (7) are all independent from D, then the equation is re-written as:

$$\begin{aligned} A(V, A) &= \delta - \kappa V - \frac{\epsilon}{1 + \eta A^{*2}} V A, \\ B(V, A) &= \frac{\epsilon}{1 + \eta A^2} V A - (\kappa + \mu) A. \end{aligned} \quad (8)$$

The Eq. in (8) can be expressed in Jacobian form, the Jacobian Representation  $J(V,A)$  is defined as follow:

$$\begin{pmatrix} \frac{\partial A}{\partial V} & \frac{\partial A}{\partial A} \\ \frac{\partial B}{\partial V} & \frac{\partial B}{\partial A} \end{pmatrix}$$

where  $\frac{\partial A}{\partial V} = 1 - r(\kappa + f(A))$

$$\begin{aligned} \frac{\partial A}{\partial V} &= -rV \frac{\partial f}{\partial A}, \\ \frac{\partial B}{\partial V} &= rf(A), \end{aligned} \tag{9}$$

$$\frac{\partial B}{\partial V} = 1 + r \left( V \frac{\partial f(A)}{\partial A} - (\kappa + \mu) \right).$$

where  $f(A) = \frac{\epsilon}{1 + \eta A^2}$

$$\Rightarrow J(w_0) = J\left(\frac{\delta}{\kappa}, 0\right) = \begin{pmatrix} 1 - \kappa r & \frac{\delta \epsilon}{\kappa} r \\ 0 & 1 - r(\kappa + \mu)(1 - D_0) \end{pmatrix}$$

$$\Rightarrow r \leq \min(r_1, r_2)$$

where  $r_1 = \frac{2}{\kappa}$ ,  $r_2 = \frac{2}{(\kappa + \mu)(1 - D_0)}$

If the coronavirus has presented previously then we concentrate the cases consistently presented but limited to a particular region that is  $D_0 > 1$ .

Represent the model into graphical representation to focus its mathematical structure and its solution. Thus the parameters  $\delta = 0.1$ ,  $\kappa = 0.1$ ,  $\epsilon = 0.5$ ,  $\eta = 0.5$ ,  $\mu = 0.15$ ,  $r = 0.1$ , with the condition that the reproduction number  $D_0 = 2$ .

### 3. GENERATIVE MODEL

In machine learning, generative models are a classes of invariables and these models are Markov Chains, the part of science concerned with the physical and mathematical basis of engineering and machine technology. The spread of pandemic similar to the COVID virus is a generative model [19] in which the change in concentration as a function of time is specified by differential equation.

In Figure (1), we consider three factors that alter the champers, the three classes are

- New Nurslings
- New Recuperation
- Necrotic Frequencies

The differential equations for all the three classes is given by

$$\begin{aligned} \frac{dN(x)}{dx} &= F_N - L_N N(x), \\ \frac{dR(x)}{dx} &= F_R - L_R R(x), \end{aligned} \tag{10}$$

$$\frac{dF(x)}{dx} = F_F - L_F F(x).$$

where  $F_N, F_R$  and  $F_F$  are the factors that alters the champers of the new Nurslings, new recuperation and necrotic frequencies respectively.  $L_N, L_R$  and  $L_F$  are subsequent sets of results of these champers. Also, the forces are usually changes from up and downs and it represents the first order differential equation;

$$\begin{aligned} \frac{du_i(x)}{dx} &= \frac{a_i - b_i u_i(x)}{w_i}, \\ \frac{dv_i(x)}{dx} &= \frac{d_i - e_i v_i(x)}{f_i}, \quad i = N, R, F. \end{aligned} \tag{11}$$

where  $u_i$  and  $v_i$  represents isolated contacts and the maximum that a clinic can hold for each classes. The multiplied variables is given by  $\varphi(x) = u_i(x)v_i(x)$  and it provides the entire status of the isolated contacts and the maximum that a clinic can hold and for each classes the first order linear differential equation is given by,

$$\begin{aligned} \frac{dN(x)}{dx} &= \lambda \varphi_N(x) - (1 - \varphi_N(x))N(x), \\ \frac{dR(x)}{dx} &= \mu \varphi_R(x) - (1 - \varphi_R(x))R(x), \\ \frac{dF(x)}{dx} &= \gamma \varphi_F(x) - (1 - \varphi_F(x))F(x). \end{aligned} \tag{12}$$

The new variables  $L_N, L_R, L_F$  and  $1 - \varphi_i(t)$  are decreased when the three factors alter the chambers is high and vice versa. The Flow chart for the generative model is structured by the following architecture;

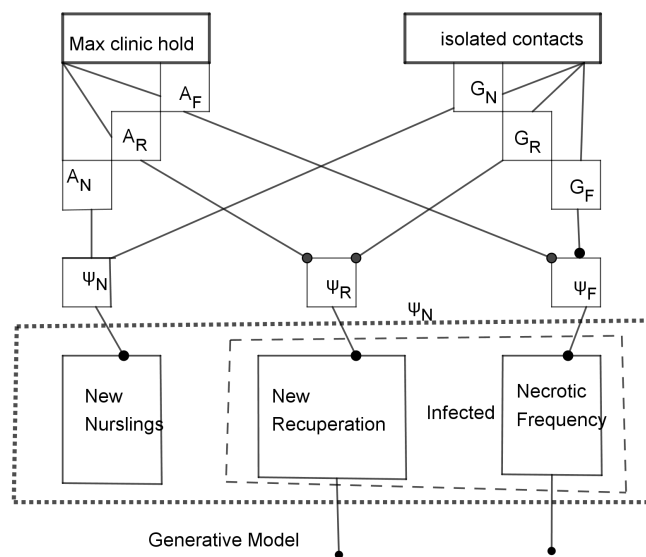


FIGURE 1. Flow Chart for the Proposed Generative Model

Figure 2. shows the table of the values of Eq. (13) that represent the virus upsurge predicting in Malaysia for 1 year from 20 January 2020 to 26 November 2021.

X (day)	Parameter	1			2			3			4			5			6		
	i	N	R	F	N	R	F	N	R	F	N	R	F	N	R	F	N	R	F
x < 10	0.003	0.002	0.002	0	0	0	1	1	1	0	0	0	0	0	0	0	1	1	1
10 < x < 29	0.003	0.002	1	0	0	1	1	1	40	0	0	0	0	0	1	1	1	1	40
29 < x < 40	1	1	1	1	1	1	40	90	30	0	0	0	1	0	1	30	1	25	
40 < x < 70	2	2	2	2	2	2	40	40	70	0	0	0	2	2	2	20	20	40	
70 < x < 90	2	2	2	2	2	2	300	500	90	2	2	0	2	2	2	220	220	40	
90 < x < 110	2	2	2	2	2	2	300	500	100	2	2	2	2	2	2	240	240	220	
110 < x < 150	2	2	2	2	2	2	1100	1100	60	2	2	2	2	2	2	2400	2400	300	
150 < x < 195	0	0	0	2	2	2	70	70	60	2	2	2	2	2	2	300	300	200	
195 < x < 245	2	2	2	2	2	2	150	300	110	2	2	2	2	2	2	240	240	200	
245 < x < 270	2	2	2	2	2	2	30	100	90	2	2	2	2	2	2	240	240	200	
270 < x < 285	2	2	2	2	2	2	110	25	100	0	0	0	2	2	2	900	150	55	
285 < x < 300	2	2	2	2	2	2	110	10	100	0	0	0	2	2	2	50	150	55	
300 < x < 320	2	2	2	2	2	2	110	10	100	0	0	0	2	2	2	50	100	55	
320 < x < 335	2	2	2	2	2	2	110	10	100	0	0	2	2	2	2	450	450	200	
x > 335	0	0	0	2	2	2	600	100	110	2	2	2	2	2	2	450	450	200	

FIGURE 2. Table 1. Predicting the new Coronavirus upsurge in Malaysia.

4. PREDICTING THE NEW CORONA VIRUS UPSURGE IN MALAYSIA THROUGH THE PROPOSED DIFFUSION MODEL

Human behavior is proportional to the change in the hospitals capacity, which is influenced by social distancing. The continual change over is, therefore, understood with the parameters  $(a_i, b_i, c_i, d_i, e_i, f_i)$ . As the units change over time with the dominance of human (mis)behavior, so does the second equation. The presented Table 1 interprets the values of the censures occurring within 335 days. This is derived based on information from the speculated time period of the outbreak from 20 January 2020 to 26 November 2021 and is represented by a first-order differential equation. Since the growth of the proportions is rapid, vis-à-vis, the newly affected, recovery rate, and daily casualties, the system of equations (4) is rewritten as:

$$\begin{aligned} \frac{dN(x)}{dx} &= D\varphi_N(x) - (1 - \varphi_N(x)), \\ \frac{dR(x)}{dx} &= 0.86D\varphi_R(x) - (1 - \varphi_R(x))R(x), \\ \frac{dF(x)}{dx} &= 0.09D\varphi_F(x) - (1 - \varphi_F(x))F(x). \end{aligned} \tag{13}$$

The graphs of the DEs. in (13), Figures (3-5) represent the speculated diffusion model expected for new admissions, discharges, and mortalities within a time frame of 335 days in Malaysia. The proposed model closely aligns with Malaysia’s real-time data. However, for the left-out data of the remaining couple of months, a variation predicting a novel small wave is proposed.

The earlier outbreak of the Malaysian pandemic is also forecasted. In the changing variables, which are represented in a graph, the parameters reflecting the management style in Malaysia during the



year 2021 are considered. Relatively, the decline in communal distancing during the first wave is also depicted, which has significantly impacted the graphs of the studied conditions.

The imbalance in the incremental admittance capacity of hospitals in Malaysia, combined with a fall in social distancing (shown by the variables  $A_i$ :  $A_N$ ,  $A_R$ , and  $A_F$ ), has induced the upsurge of the subsequent wave. The disproportion in the graph can be explained as follows: first, the increase in variables is limited again in proportion to  $A_i$ , due to another factor—growing fatigue among medical staff.

This results in a consecutive third wave, this time striking with a significant number of casualties. To mitigate this large-scale pandemic, strategic measures were applied by the Malaysian government. Therefore, the variables  $A_i$  and  $G_i$  visibly reflect the outcome of the management style during the pandemic blaze of COVID-19.

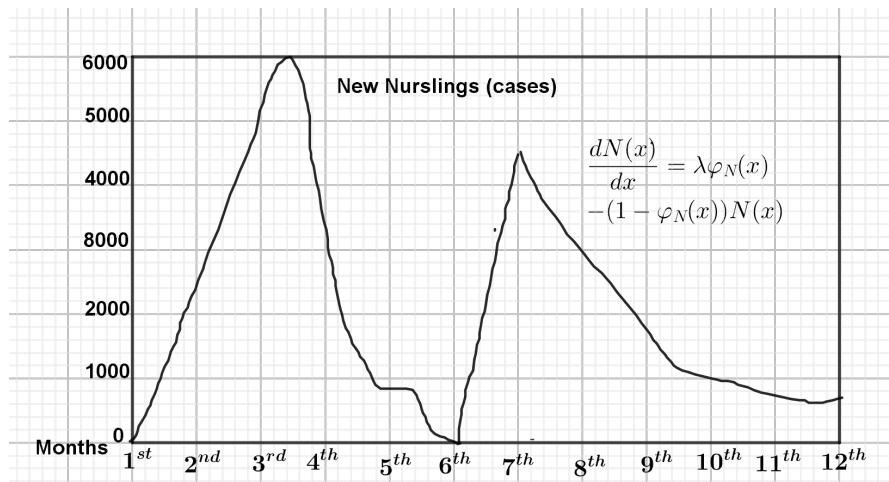


FIGURE 3. New cases

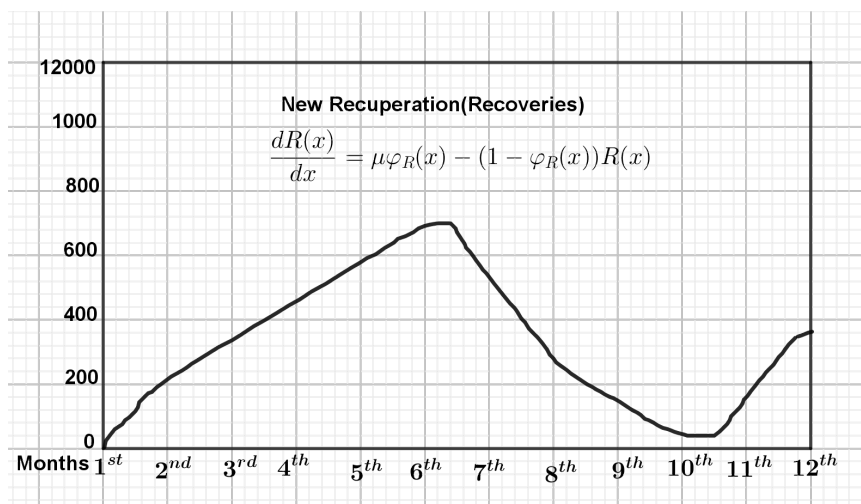


FIGURE 4. Rate of Recoveries

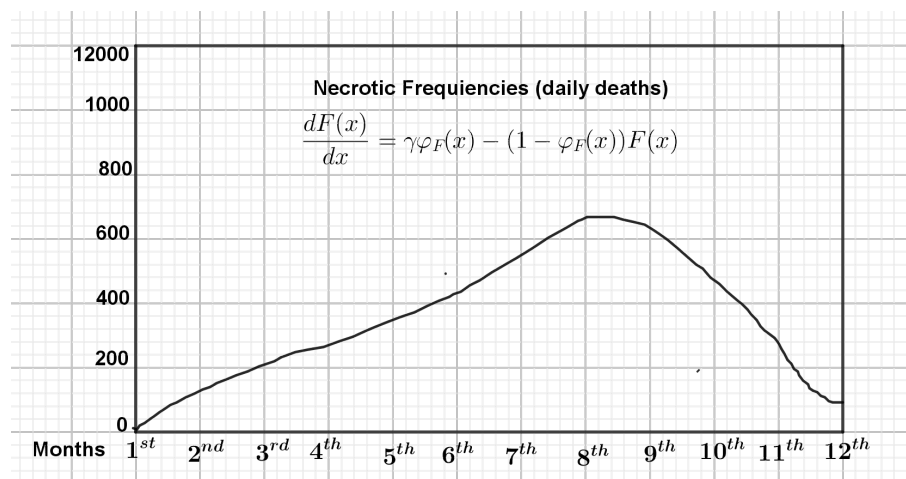


FIGURE 5. Death Rate

The results of the generative model shows for predicting the dead cases, new cases and recovery cases(5),(3) and (4) for 1 year from 20 January 2020 to 26 November 2021.

## 5. DISCUSSION AND CONCLUSION

In this place, we indicate that the usage of Chebyshev polynomial has the edibility to control the path of the outcome (data) for the infected system in COVID-19. The Chebyshev polynomial operation includes the organizer term with different kinds of network functions. The existence of the dynamical construction of the growth is given by utilizing self-function.

Moreover, the error function is determined for the second order Chebyshev polynomial ( $T_2$ ) for the constructed data, and then we determined the root of the convergence followed by the interval of the compact infected data using the approximated law  $\epsilon = \text{root-integrator of the root}$ .

This study can be applied for different data of COVID-19 depending on the suitable selection of the order of Chebyshev polynomial. In our next study we shall employ the concept of fractional calculus to present a generalization of Chebyshev equation to evaluate a fractional Chebyshev polynomials.

## 6. FUTURE WORKS

For future works, we advice researchers and investigators to modify, extend and generalize this effort. We have the following suggestions, which may consider as open problems for future researches

- One can modify our technique by using other types of polynomials, where this field is very rich in special polynomials recorder. Comparisons can be added to recognize different analysis, such as stability and fast convergence to the equilibrium point of the dynamic system.

- Moreover, one can extend this work by using any recent calculus, such as local fractional calculus, fractional calculus and quantum calculus. By utilizing these specialties of calculus, researchers can realize the growth history and the future rising of the virus.
- One can generalize this work by using derivative of chains to discuss the multi-face COVID-19. In this case, we provide the following system

$$\frac{df(t)}{dt} = f(f(f(f\dots f(t))), \quad t \geq 0. \quad (14)$$

For example, the recent growth of COVID-19 is delta types, therefore, System (14) is defined for four iterations.

- Combining items two and three, one can study the fractional system (generalized system)

$$\frac{d^\alpha f(t)}{dt^\alpha} = f(f(f(f\dots f(t))), \quad t \geq 0, \alpha \in [0, 1], \quad (15)$$

where  $\frac{d^\alpha f(t)}{dt^\alpha}$  indicates any type of fractional calculus (see [21]).

## 7. APPENDIX

In this section, we give the code of the computation. The first part is the normalization computation and the second part is the normalized data under the CP ( $T_2$ ).

```
AN = normalize(A,'range')
xn1 = AN(1 : 28, 1);first column-October
xn2 = AN(1 : 28, 2);first column- Nov
xn3 = AN(1 : 28, 3);first column- Dec
n = 2;
yn1 = chebyshevT(n,xn1);
yn2 = chebyshevT(n,xn2);
yn3 = chebyshevT(n,xn3);
```

**Availability of Data and Material.** <https://www.statista.com/statistics/1110785/malaysia-covid-19-daily-cases/>.

**Acknowledgement.** This research was sponsored by the Universiti Malaya, and it is funded by the RMF 12067-2024 grant, and the National Defense University of Malaysia grant.

**Authors' Contributions.** Concepts, S.J.O. and N.A.J.; methodology, S.J.O and G.U.M.; software, S.J.O.; validation, N.A.A. and N.A.J.; formal analysis, S.J.O. and N.A.A.; draft preparation and editing, S.J.O.; All authors have read and approved the final version of the manuscript.

**Conflicts of Interest.** The authors declare that there are no conflicts of interest regarding the publication of this paper.

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