

ROLE OF REINFECTION IN TRANSMISSION DYNAMICS OF COVID-19: A SEMI-ANALYTICAL APPROACH USING DIFFERENTIAL TRANSFORM METHOD

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ABSTRACT

Reinfection of a recovered individual either as a result of relapse or new contact no doubt poses a major threat to the eradication of an infection within the host community. In this work, the role of re-infection in the transmission dynamics of COVID-19 was considered and analysed using the semi-analytical tool Differential Transform Method (DTM). COVID-19 (also known as Coronavirus) has shut down the economy of the world since it became a global pandemic. A mathematical model was constructed with consideration of multiple pathways of infection transmission, the treatment strategies and policies adopted (social distancing, wearing of face mask and so on) to limit the spread of the infection globally. The non-linear system of equations governing the model was solved using DTM and the resulting series solution was compared with the standard numeric Runge-Kutta order 4 (RK4). It was discovered that re-integration of a recovered individual into the susceptible community without observing the prevention guidelines such as social distancing, washing of hands and proper sanitizing could increase the spread of the infection since the recovered individuals are not guaranteed of immunity against the infection after recovery. The study concluded that families of recovered patients must ensure adequate preventive measure while integrating their recovered loved ones back to their midst.

Keywords: COVID-19, DTM, Re-infection, Relapse, RK4, and Pandemic.

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1. Introduction

COVID-19 (Coronavirus disease) is a viral infection that causes mild to moderate respiratory illness, which may also lead to serious illness in the body of an infected individual with underlying health problem (WHO, 2020a). It has several transmission pathways but transmits primarily through droplets (discharge while sneezing and/or coughing) from an infected individual. Like other viral infections, the disease is highly contagious even at an asymptomatic stage. From the time of contact with the virus, it has an incubation period of 1 – 14 days within the host and it was declared a world pandemic by the World Health Organization on January 30, 2020 (WHO, 2020a). Globally, the total number of confirmed cases of this infection is 7,805,148 with total death due to COVID-19 related issues is at 431,192 as of 15th June, 2020. It was also reported that America has the largest number of cases of infection and fatality from the disease (WHO, 2020a). Furthermore, it was reported that it took 98 days for Africa as a continent to report its first one hundred thousand cases whereas the next hundred thousand cases were reported in just 18 days (WHO, 2020b). This shows that the spreading rate of the

disease in these developing countries is alarming compared with developed countries which have started recording lower cases.

The recurrence of an infection is considered as the second phase that arises after the patient was treated and cured (Portal, 2014). This recurrence can occur either as a result of reinfection or relapse. Reinfection is defined as a second infection of a body (or an organ) by the same agent (or a different agent/strain) while relapse is defined as “insufficient” cure of the first episode of an infection (Portal, 2014). The role of reinfection in the transmission dynamics of COVID-19 shall be discussed in this work. What accounts for the rapid one hundred thousand new cases in just 18 days in Africa is not a result of newly imported cases since borders have been closed, but it is due to contact already made within the population by the infected as well as contact made with relapsed and re-infected individuals. Thus, the aim of this research work is to analyze the impact of relapse and reinfection on the transmission dynamics of COVID-19 especially in a developing country like Nigeria. This is to ascertain the necessary steps to take in order to stop the further spread of the infection within the population while also looking for effective and efficient ways of maintaining immunity for the recovered. To achieve this aim, a mathematical model for the transmission dynamics of the infection was developed and solved using Differential Transform Method (DTM) to obtain the semi-analytic solution (in time dependent series form). The result obtained from the above method is graphically compared with Runge-Kutta order 4 method and tables of approximate result was also presented.

Mathematical modeling is an applied branch of mathematics that deals with representing, analyzing and evaluating physical (biological, economical, ecological etc.) problems using mathematical equations (arithmetic, difference and differential equation) with the purpose of interpreting the outcome of the analyses to proffer solution(s) to the problem. The most elementary model developed is the *Susceptible-Infected-Recovered* (SIR) model where human population is sub-divided into three epidemiological classes (also called compartments). This model was developed by Kermack and McKendrick (1927) and has been widely studied and analyzed by mathematical epidemiologist (Akinyemi et al., 2016). Since then, several modifications and extensions to their model have been developed to suit the dynamics of the disease under consideration. Alqahtani (2021) adopted the fractional-order SIR model to study COVID-19 dynamics and obtained the stability analysis, bifurcation and numerical simulation of the model. Ivorra et al. (2020) developed a new θ -SEIHRD model which takes into account the known special characteristics of this disease, such as the existence of infectious undetected cases and the different sanitary and infectiousness conditions of hospitalized people. Thus, in this work, a new SI_1I_2QRM non-linear deterministic model for the transmission dynamics of COVID-19 infection is proposed. The model was developed with consideration of intervention mechanisms such as social distancing, proper sensitization and quarantine as a preventive means of reducing secondary infection. The effect of asymptomatic carrier of the disease on the overall new cases is investigated as well as the effect of immunity loss and relapse.

2. Material and Methods

It is important to state here that deterministic mathematical model was used in this study. This is to enable adequate analysis of the non-linear nature of physical problems being formulated. Also, it is easy to interpret the result to other agencies that are not-mathematically inclined, as they will use the result of the analysis to make decisions on what best practices to employ in eliminating the virus. Furthermore, this study relies on data obtained majorly from WHO website and other recent data from literature.

A non-linear mathematical model was formulated by dividing the total human population at time t , denoted by $N(t)$ into six disjoint epidemiological sub-populations, which are, Susceptible (S), Asymptomatic-Infected (I_1), Symptomatic-Infected (I_2), Quarantine (Q), Recovered (R) and Partial Immunity (M). Thus, at any time (t), the total human population is:

$$N(t)=S(t)+I_1(t)+I_2(t)+Q(t)+R(t)+M(t)$$

Each epidemiological sub-populations of the model accept the inflow and outflow of human population as a result of several factors like birth, death, contact with the disease, treatment, death caused by infection, relapse, reinfection and so on. Greek letters were used to denote the passage rate of human from one compartment to another, for instance, π denote the recruitment into susceptible class, μ is the natural mortality rate, λ is the force of infection which denotes the rate at which uninfected individual becomes infected and it depends on so many factors. One of those factors include contact with people infected (β). Table 1 shows the definition of the parameters used in the model together with the numerical values used to solve the series solution of DTM. The system of equations governing the model is given as:

$$\left. \begin{aligned} \frac{dS}{dt} &= \pi + \gamma M - \lambda S - \mu S \\ \frac{dI_1}{dt} &= \varepsilon \lambda S + \theta_1 R + \omega_2 I_2 - (\mu + \omega_1 + \phi_1) I_1 \\ \frac{dI_2}{dt} &= (1 - \varepsilon) \lambda S + \theta_2 R + \omega_1 I_1 - (\mu + \omega_2 + \phi_2 + \delta_1) I_2 \\ \frac{dQ}{dt} &= \phi_1 I_1 + \phi_2 I_2 - (\mu + \delta_2 + \eta) Q \\ \frac{dR}{dt} &= \eta Q - (\mu + \theta_1 + \theta_2 + \alpha) R \\ \frac{dM}{dt} &= \alpha R - (\gamma + \mu) \end{aligned} \right\} \quad (1)$$

where the force of infection is given as:

$$\lambda = \beta_1 I_1 + \beta_2 I_2 + \beta_3 Q \quad (2)$$

Table 1. Table Parameter Definition and Values.

Symbol	Meaning	Value used	Source of value
π	Recruitment rate	$\mu \times 10^5$	(Okuonghae, 2013)
λ	Force of infection	Estimated	Estimated
ε	Education parameter (hand sanitizing, social distancing etc.)	0.0975	(NCDC, 2020)
μ	Natural mortality rate	0.02041	(Okuonghae, 2013)
γ	Immunity loss after recovery with reinfection possibility	0.04	Assumed
α	Partial immunity obtained from effective treatment	0.05	Assumed
η	Recovery rate	0.01958	(NCDC, 2020)
$\beta_i, i = 1,2,3$	Contact rate with I_1 , I_2 and Q classes respectively	[0, 0.75]	(Ivorraa, et al., 2020)
$\delta_i, i = 1,2$	Fatality case for I_2 and Q classes respectively	[0.01, 0.02]	(Ivorraa, et al., 2020)
$\phi_i, i = 1,2$	Rate of quarantine of detected cases	[0.15, 1.43]	(Ivorraa, et al., 2020)
$\theta_i, i = 1,2$	Relapse rate to I_1 and I_2 classes respectively	[0.01, 0.08]	(Ivorraa, et al., 2020)
ω_1	Deterioration rate of I_1	0.18	(Ivorraa, et al., 2020)

ω_2	Improvement rate of I_2 classes due to personal hygiene	[0.08, 0.14]	(Ivorraa, et al., 2020)
$S(t)$	Susceptible sub-population	Varied	State Variable
$I_1(t)$	Asymptomatic (Carrier) sub-population	Varied	State Variable
$I_2(t)$	Symptomatic sub-population	Varied	State Variable
$Q(t)$	Quarantine sub-population	Varied	State Variable
$R(t)$	Recovered sub-population	Varied	State Variable
$M(t)$	Recovered with partial immunity sub-population	Varied	State Variable

3. Theory/ Calculations

Differential transform method shall be used to obtain the series solution of the system of equations governing the model formulated. This is a semi-analytical method that transforms system of linear or non-linear differential equations into an infinite time dependent series so that an approximate solution for the differential equation is obtained. Table 1 of Akinboro et al. (2014) gives some fundamental operations on differential transformation method and it shall be adopted to transform the system of Eq. (1) into its DTM equivalent. Thus, for finite step k , the system of Eq. (1) can be written as Eq. (3):

$$\begin{aligned}
 & \left. \begin{aligned}
 S(k+1) &= \frac{1}{k+1} \left[\pi \cdot \delta(k, 0) + \gamma M(k) - \beta_1 \sum_{i=0}^k S(i) I_1(k-i) - \beta_2 \sum_{i=0}^k S(i) I_2(k-i) \right. \\
 & \quad \left. - \beta_3 \sum_{i=0}^k S(i) Q(k-i) - \mu S(k) \right] \\
 I_1(k+1) &= \frac{1}{k+1} \left[\varepsilon \left(\beta_1 \sum_{i=0}^k S(i) I_1(k-i) + \beta_2 \sum_{i=0}^k S(i) I_2(k-i) + \beta_3 \sum_{i=0}^k S(i) Q(k-i) \right) \right. \\
 & \quad \left. + \theta_1 R(k) + \omega_2 I_2(k) - (\mu + \omega_1 + \phi_1) I_1(k) \right] \\
 I_2(k+1) &= \frac{1}{k+1} \left[\varepsilon \left(\beta_1 \sum_{i=0}^k S(i) I_1(k-i) + \beta_2 \sum_{i=0}^k S(i) I_2(k-i) + \beta_3 \sum_{i=0}^k S(i) Q(k-i) \right) \right. \\
 & \quad \left. + \theta_1 R(k) + \omega_2 I_2(k) - (\mu + \omega_1 + \phi_1) I_1(k) \right] \\
 I_1(k+1) &= \frac{1}{k+1} \left[\varepsilon \left(\beta_1 \sum_{i=0}^k S(i) I_1(k-i) + \beta_2 \sum_{i=0}^k S(i) I_2(k-i) + \beta_3 \sum_{i=0}^k S(i) Q(k-i) \right) \right. \\
 & \quad \left. + \theta_1 R(k) + \omega_2 I_2(k) - (\mu + \omega_1 + \phi_1) I_1(k) \right] \\
 R(k+1) &= \frac{1}{k+1} [\eta Q(k) - (\mu + \theta_1 + \theta_2 + \alpha) R(k)] \\
 M(k+1) &= \frac{1}{k+1} [\alpha R(k) - (\gamma + \mu) M(k)]
 \end{aligned} \right\} \quad (3)
 \end{aligned}$$

An initial population of 10,550 was used for analysis in this work and was distributed into each compartment as follows: $S(0)=10,250$, $I_1(0)=100$, $I_2(0)=60$, $Q(0)=60$, $R(0)=50$ and

$M(0)=30$. The initial conditions together with the value of parameter in Table 1 was used to iterate Eq. (2) to obtain the series solution given in Eq. (4) below:

$$\left. \begin{aligned} S(t) &= 10250 + \\ &1719.39400t - 59.89529345t^2 - 8.963911503t^3 - 2.095788193t^4 - .3008733754t^5 + \\ &\quad h.o.t \\ I_1(t) &= \\ &100 - 58.94925000t + 60.02903380t^2 - 20.77850350t^3 + 7.933624672t^4 - 1.932203854t^5 + h.o.t \\ I_2(t) &= \\ &100 - 58.94925000t + 60.02903380t^2 - 20.77850350t^3 + 7.933624672t^4 - 1.932203854t^5 \\ &\quad h.o.t \\ Q(t) &= \\ &60 + 167.45540t - 41.88881676t^2 + 28.81151164t^3 - 5.992018388t^4 + 1.753659319t^5 + \\ &\quad h.o.t \\ R(t) &= \\ &50 - 20.52050t + 13.81490920t^2 - 3.838815887t^3 + 1.229324375t^4 - 0.2502495560t^5 + \\ &\quad h.o.t \\ M(t) &= \\ &30 + 1.97950t - 0.4062032975t^2 + 0.1823107517t^3 - 0.03799468025t^4 + 0.009733790400t^5 + \\ &\quad h.o.t \end{aligned} \right\} \quad (4)$$

where *h.o.t.* denotes higher order terms in the series.

4. Numerical Solution of the Model by Runge-Kutta Fourth Order (RK4)

The system of equation in Eq. (1) was solved numerically using the fourth order of Runge-Kutta method. This method is widely accepted as a numerical scheme with greater accuracy and it is also easy to use. The method was postulated by German Mathematician Carl Runge (1856 – 1927) and German Engineer Wilhelm Kutta (1867 – 1944). The method has been widely used to solve both linear and non-linear mathematical problems. Side *et al.* (2018) used the method to solve SIR tuberculosis model. The scheme is of the form:

$$y_{r+1} = y_r + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4) \quad (5)$$

such that:

$$\left. \begin{aligned} k_1 &= hf(x_r, y_r) \\ k_2 &= hf\left(x_r + \frac{1}{2}h, y_r + \frac{1}{2}k_1\right) \\ k_3 &= hf\left(x_r + \frac{1}{2}h, y_r + \frac{1}{2}k_2\right) \\ k_4 &= hf(x_r + h, y_r + k_3) \end{aligned} \right\} \quad (6)$$

where *h* denotes the step length; x_r and y_r are the initial conditions for both the independent and dependent variable respectively. It is sufficed to re-write Eq. (1) in standard form as:

$$\left. \begin{aligned} \frac{dS}{dt} &= g_1(t, S, I_1, I_2, Q, R, M) = \pi + \gamma M - \lambda S - \mu S \\ \frac{dI_1}{dt} &= g_2(t, S, I_1, I_2, Q, R, M) = \varepsilon \lambda S + \theta_1 R + \omega_2 I_2 - (\mu + \omega_1 + \phi_1) I_1 \\ \frac{dI_2}{dt} &= g_3(t, S, I_1, I_2, Q, R, M) = (1 - \varepsilon) \lambda S + \theta_2 R + \omega_1 I_1 - (\mu + \omega_2 + \phi_2 + \delta_1) I_2 \\ \frac{dQ}{dt} &= g_4(t, S, I_1, I_2, Q, R, M) = \phi_1 I_1 + \phi_2 I_2 - (\mu + \delta_2 + \eta) Q \\ \frac{dR}{dt} &= g_5(t, S, I_1, I_2, Q, R, M) = \eta Q - (\mu + \theta_1 + \theta_2 + \alpha) R \\ \frac{dM}{dt} &= g_6(t, S, I_1, I_2, Q, R, M) = \alpha R - (\gamma + \mu) M \end{aligned} \right\} \quad (7)$$

The RK4 scheme for Eq. (7) based on Eqs. (5) and (6) is given in Eq. (8) below:

$$\left. \begin{aligned} S_{r+1} &= S_r + \frac{1}{6} (k_1 + 2k_2 + 2k_3 + k_4) \\ I_{1r+1} &= I_{1r} + \frac{1}{6} (l_1 + 2l_2 + 2l_3 + l_4) \\ I_{2r+1} &= I_{2r} + \frac{1}{6} (m_1 + 2m_2 + 2m_3 + m_4) \\ Q_{r+1} &= Q_r + \frac{1}{6} (n_1 + 2n_2 + 2n_3 + n_4) \\ R_{r+1} &= R_r + \frac{1}{6} (p_1 + 2p_2 + 2p_3 + p_4) \\ M_{r+1} &= M_r + \frac{1}{6} (q_1 + 2q_2 + 2q_3 + q_4) \end{aligned} \right\} \quad (8)$$

With

$$\left. \begin{aligned} k_1 &= \pi + \gamma M_r - \lambda S_r - \mu S_r \\ l_1 &= \varepsilon \lambda S_r + \theta_1 R_r + \omega_2 I_{2r} - (\mu + \omega_1 + \phi_1) I_{1r} \\ m_1 &= (1 - \varepsilon) \lambda S_r + \theta_2 R_r + \omega_1 I_{1r} - (\mu + \omega_2 + \phi_2 + \delta_1) I_{2r} \\ n_1 &= \phi_1 I_{1r} + \phi_2 I_{2r} - (\mu + \delta_2 + \eta) Q_r \\ p_1 &= \eta Q_r - (\mu + \theta_1 + \theta_2 + \alpha) R_r \\ q_1 &= \alpha R_r - (\gamma + \mu) M_r \\ k_2 &= \pi + \gamma \left(M_r + \frac{h}{2} q_1 \right) - \lambda \left(S_r + \frac{h}{2} k_1 \right) - \mu \left(S_r + \frac{h}{2} k_1 \right) \quad etc \end{aligned} \right\} \quad (9)$$

Each equation in Eq. (8) was iterated based on RK4 scheme with the help of Maple 18 software.

5. Result

The series in Eq. (4) was numerically simulated and the result was compared with the solution of Runge-Kutta order 4 method for Eq. (8). For each sub-population class of the model, the solutions obtained for both methods were graphically plotted and shown in Figure 1 – 6.

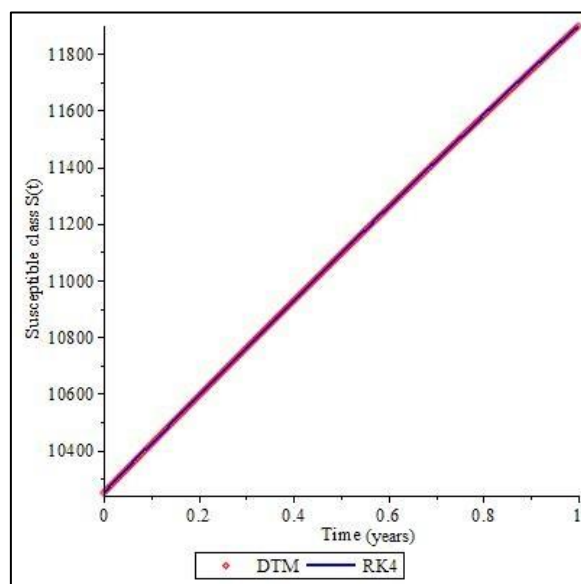


Figure 1. Dynamics of Susceptible class with time.

The population of the susceptible grow as time t increases. The result for both methods (DTM and RK4) agreed as seen in Figure 1. This implies that DTM also gives a reliable approximation that can be used to solve non-linear problems that may arise from modelling of physical problems. From the model result display in Figure 1, the susceptible sub-population will maintain a steady increase if there is early diagnosis, removal of the infected individual through quarantine, effective treatment and sensitization towards maintaining proper hygiene.

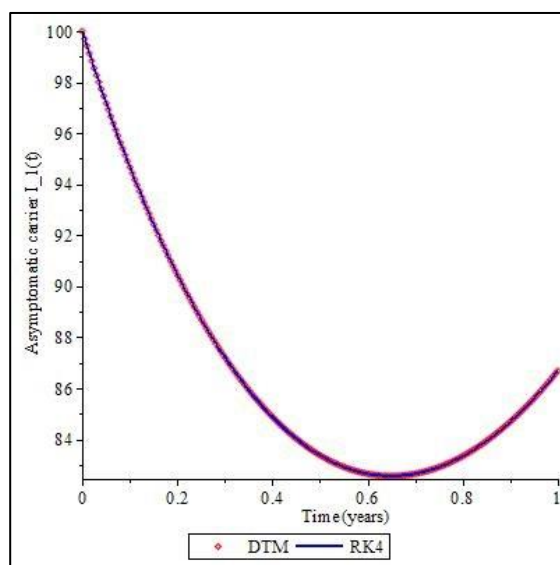


Figure 2. Dynamics of Asymptomatic carrier class with time.

From Figure 2, the sub-population of asymptomatic carrier keep decreasing for a period of time before increasing over time of simulation. This is due largely to people moving from no/mild symptoms to developing severe symptoms as a result of negligence or non-testing due to lack of adequate intervention from the government in developing countries. After some period ($t=7$ months), it rises again due to emergence of new cases as a result of non-compliance with best practices that can reduce the risk of infection (social distancing, regular hand washing/sanitizing, and use of recommended face mask).

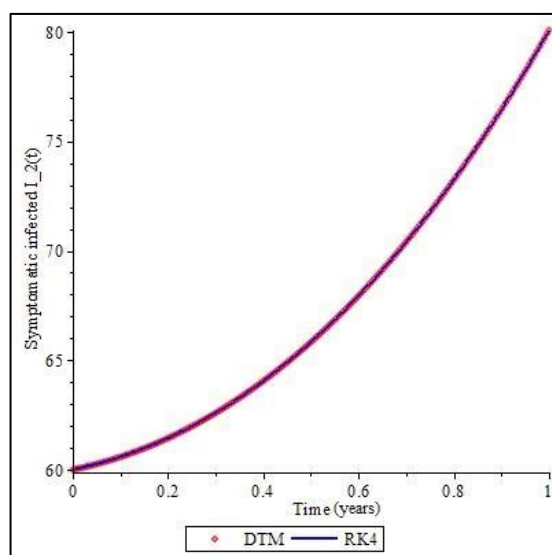


Figure 3. Dynamics of Symptomatic Infected class with time.

Figure 3 shows that symptomatic infected compartment increases over the period of time. This confirms the high-infectivity nature of the disease. The more the asymptomatic carrier stays without testing, the more it deteriorates into severe infection, in which case leads to more people being infected most especially the health workers.

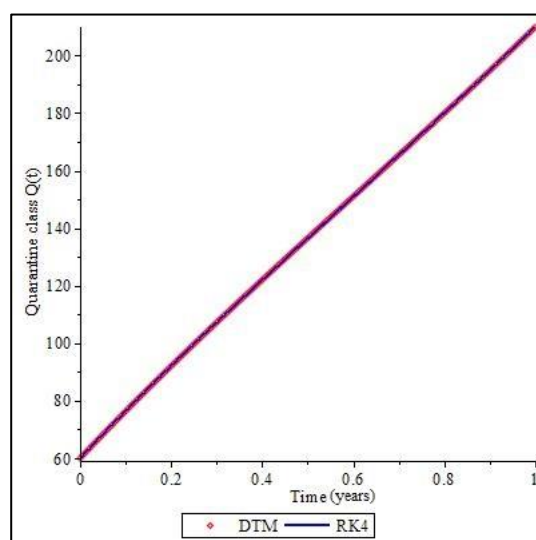


Figure 4. Dynamics of Quarantine class with time.

Quarantine sub-population also increases with time due to discovery of more people from the symptomatic class and less people from the asymptomatic class (the high-income socio-economic group that can afford to go for routine check). The vast majority of people in this

class are discovered at critical stage of the infection due to symptoms. Also, from Figure 4, the result for both methods used have almost the same degree of accuracy.

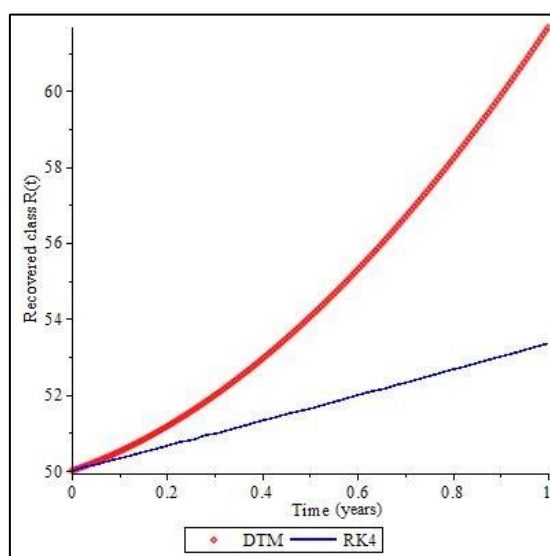


Figure 5. Dynamics of Recovered class with time.

The recovered sub-population slowly but consistently increases despite no confirmed effective treatment strategy for COVID-19 according to Figure 5. This is due to several efforts directed towards eliminating the infection as well as body immunity of some individuals. It was reported that the majority of the fatality due to the disease is associated with underlying ailment (like diabetes and hypertension) of an infectious individual. However, the approximate solution for DTM differs from the numerical result of RK4 for this sub-population. This variation may arise from the value of initial condition chosen for the recovered sub-population.

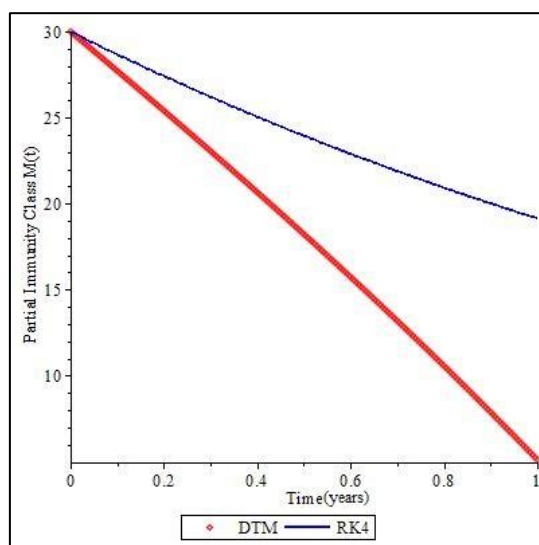


Figure 6. Dynamics of individuals with Partial Immunity

The partially immune population due to recovery from treatment slowly and consistently reduces over time according to Figure 6. This is a result that ascertain that immunity from COVID-19 due to treatment is not guaranteed. Also, the rate of losing the immunity differs (0.08219 in DTM to 0.0274 in RK4) both cases. Thus, COVID-19 prevalence is further

increased due to the possibility of reinfection and relapse (which are higher in DTM solution than RK4 solution as obtained from Figure 6). For a stable and minimal infection community, there has to be an intervention that guarantees protection against least contact with the infection.

The following Table 2 shows the result obtained for both methods (DTM and RK4) together with the modulus of the error in the two methods.

Table 2. Result Values for DTM and RK4 Compared

Susceptible Compartment				
Time (t)	DTM Value	RK4 Value	Approximate Error	% Error
0	10250	10250	0	0
0.1	10421.27677	10421.2976050359	0.0208350359389442	$1.9993 \times 10^{(-4)}$
0.2	10591.18943	10591.2752148022	0.0857848021969403	$8.0996 \times 10^{(-4)}$
0.3	10759.67539	10759.8739881044	0.198598104427219	$1.8457 \times 10^{(-5)}$
0.4	10926.66595	10927.0291049432	0.363154943173868	0.0033
0.5	11092.08576	11092.6693229912	0.583562991228973	0.0053
Asymptomatic Carrier Compartment				
0	100	100	0	0
0.1	94.68594829	94.6859082052910	0.0000400847090418210	$4.2334 \times 10^{(-5)}$
0.2	90.45941352	90.4592426820865	0.000170837913501032	$1.8886 \times 10^{(-4)}$
0.3	87.22144905	87.2210179270702	0.000431122929811067	$4.9429 \times 10^{(-4)}$
0.4	84.88817158	84.8873153398327	0.000856240167308897	0.00100
0.5	83.38913663	83.3876936457131	0.00144298428688217	0.0017
Symptomatic Infected Compartment				
0	60	60	0	0
0.1	60.58120235	60.5811706854506	0.0000316645494109480	$5.2268 \times 10^{(-5)}$
0.2	61.44142143	61.4412591663590	0.000162263641001914	$2.6410 \times 10^{(-4)}$
0.3	62.59501408	62.5945869517748	0.000427128225155116	$6.8237 \times 10^{(-4)}$
0.4	64.05586266	64.0550143677824	0.000848292217597191	0.0013
0.5	65.83789217	65.8364492622422	0.00144290775780576	0.0022
Quarantine Compartment				
0	60	60	0	0
0.1	76.35492491	76.3549279371374	0.00000302713743849381	$3.9646 \times 10^{(-6)}$
0.2	92.03730962	92.0372939058907	0.0000157141092813617	$1.7074 \times 10^{(-5)}$
0.3	107.2011486	107.201068877237	0.0000797227628623887	$7.4368 \times 10^{(-5)}$
0.4	121.9898293	121.989619951491	0.000209348509400797	$1.7161 \times 10^{(-4)}$
0.5	136.5378135	136.537359734028	0.000453765971514031	$3.2334 \times 10^{(-4)}$
Recovered Compartment				
0	50	50	0	0
0.1	50.50450687	50.3239952161646	0.180511653835410	0.3587

0.2	51.16699875	50.6500898903303	0.516908859669691	1.0205
0.3	51.98098230	50.9782976267836	1.00268467321636	1.9669
0.4	52.94147000	51.3086321179699	1.63283788203005	3.1824
0.5	54.04487727	51.6411071450522	2.40377012494782	4.6548
Partial Immunity Compartment				
0	30	30	0	0
0.1	27.71207592	28.6745970793992	0.962521159399181	3.3567
0.2	25.39755107	27.4089924223092	2.01144135230918	7.3386
0.3	23.04938440	26.2004963048879	3.15111190488793	12.0269
0.4	20.66079596	25.0465400026505	4.38574404265052	17.1504
0.5	18.22520053	23.9446704619974	5.71946993199740	23.8862

6. Discussion

A new mathematical model to study the dynamics of COVID-19 infection was presented for analysis. The infected class was further sub-divided into asymptomatic and symptomatic classes to establish the effect of early diagnosis and quarantine on the overall new case within a population. The non-linear system of equations from the developed SI/I_2QRM was solved using DTM. Secondary data from the literature and W.H.O. reports were relied upon for the numerical simulation of the model. Figure 1 shows the population change for the Susceptible class over a period of one year. Also, Figure 1 give the results for both DTM and RK4 solution of the $S(t)$ class. The graph in Figure 1 established that the DTM method adopted to solve the model equations is efficient in solving non-linear differential equations. According to W.H.O. situation report 209, total confirmed cases for Nigeria as at August, 2020 were 48,770 with 325 of the number occurring within the previous 24 hours (WHO, 2020c). Based on the result obtained from the developed model, the susceptible class will increase if the preventive measures such as early diagnosis, social distancing, regular surface and hand sanitizing is properly kept by all. The results for other sub-population of the model as obtained were given in Figure 2 to Figure 6 respectively.

7. Conclusion

A mathematical model for the study of the reinfection role in the transmission dynamics of COVID-19 was proposed and analyzed. Semi-analytical method of solution using DTM for the non-linear system of equations of the model was presented to describe the non-linear nature of the model. The efficacy of DTM to solve non-linear mathematical equation was established by comparing the result obtained with RK4 standard numerical scheme, and the error was tabulated in Table 2. The method of solution employed was found to be relatively accurate since we are considering a physical problem with several properties. Some of the results obtained from the model include: (i) effective treatment of the infection does not guarantee an immunity against reinfection as the graph of the partially immune class reduces with time; (ii) recovery class increases steadily and progressively not because of a standard treatment strategy but due to the immune system of the individuals infected; and (iii) asymptomatic class reduces as obtained in the graph not because of self-recovery (without treatment) but because they moved to symptomatic class due to non-testing and no adequate knowledge. Thus, from the findings, it is recommended that: (a) sensitization be taken seriously especially among the uneducated and poor classes; (b) proper treatment strategy be obtained that will effectively cure those with low immune system (or with underlying ailments like diabetes, hypertension etc.)

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