Original Research Article

# MATHEMATICAL MODEL FOR ROTAVIRUS INFECTION INCORPORATING TIME DELAY ON THE EFFECTIVENESS OF VACCINATION WITH TREATMENT

## Abstract

Rotavirus is the most common cause of severe gastroenteritis infection in infants and young children, occurring even with very high standard of hygiene. The disease spreads by contact with infected faeces and might also be transmitted through faecesically-contaminated: food, water and respiratory droplets. A Rotavirus vaccine was developed in 1998. The vaccine has helped to reduce fatalities due to rotavirus. However , it takes time for vaccine induced immunity to take place, hence the need to investigate the impact of this time delay on the dynamics of rotavirus. The purpose of the study was to focus on developing and analysing a mathematical model incorporating time delay on effectiveness of vaccination with treatment on rotavirus infection, The developed model was shown to be positively invariant and bounded. The disease free equilibrium point and endemic equilibrium were shown to exist and shown to be asymptotically stable when some conditions are met. The basic reproduction number was shown to exist, when the basic reproduction number is less than 1 ($R_0 < 1$) or ($R_0 \to 1$), rotavirus dies out in the community but when the basic reproduction number is greater than 1 ($R_0 > 1$), rotavirus spreads and becomes endemic. Numerical simulation using MATLAB were carried out; when ($R_0 > 1$) and was big, a bigger time delay would make the population to oscillate, meaning that the population was not predictable. The findings of this study is useful to the government, ministry of Health stakeholders and policy developers and further provides baseline information for studies of this nature.

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**keywords**{Rotavirus, Stability analysis, delay, Disease Free Equilibrium, Endemic Equilibrium point.}

## 1 Introduction

Diarrheal disease is the second leading cause of under-five mortality worldwide [13]. Rotavirus is the most common cause of severe diarrheal disease in young children globally, attributing to more than 25 million clinic visits, an estimated 2 million hospitalizations, and approximately 527,000 deaths of children under 5 each year [31]. However, the great proportion of the burden of rotavirus is borne by young children in developing countries.

Rotaviruses were discovered in the 1960s in animals. It was first discovered in humans by electron microscopy in duodenal biopsies from children with acute gastroenteritis [2]. It gets its name from the fact that under microscope, the virus resembles a wheel [16, 27]. Rotaviruses are 70-nm icosahedral viruses that belong to the family Reoviridae [7]. There are seven serogroups of rotavirus namely A, B, C, D, E, F and G. Most human pathogens belong to groups A, B, and C. Group A rotaviruses are most commonly found in humans and hence important from a public health standpoint. The virus is composed of three protein shells, an outer capsid, an inner capsid, and an internal core, that surround the 11 segments of double-stranded RNA. Four major structural and nonstructural proteins are of interest in vaccine development: VP6, NSP4, VP7, and VP4. VP6, the most abundant viral structural protein, is found in the inner capsid [1].

Rotavirus spreads by contact with infected faeces and might also be transmitted through faecally-contaminated: food, objects or surfaces, water, hands and respiratory droplets. The incubation period is about two days [3, 5, 27]. Once ingested, the virus that is not neutralized by stomach acid attaches to the proximal small intestine. During the incubation period of 1836 hours, the virus enters epithelial cells where it first elaborates a potent enterotoxinNSP4that can cause diarrhoea, and then goes on after 1836 hours to destroy the epithelial surface leading to blunted villi, extensive damage, and shedding of massive quantities of virus (more than 10 particles per gram) in stools [27]. The outcome is a profuse watery diarrhea with loss of fluid and electrolytes that can last 27 days and might lead to severe or fatal dehydration. The diagnosis of rotavirus infection is commonly done clinically, although a rapid antigen stool test is available. Children between 6 to 24 months of age can be infected with rotavirus several times during their lives, and infection can occur despite very high standards of hygiene [16]. Few clinical or epidemiological features distinguish a child with rotavirus from a child with diarrhea of any other cause. Newborn babies can be infected in the nursery, but these infections are often asymptomatic, perhaps because of the protective effect of circulating maternal antibodies of 2730. However, first infections in children 324 months of age most often lead to vomiting, then watery diarrhoea that is sometimes accompanied by fever. In temperate climates, rotavirus has a distinct peak in the cooler winter months when it is the predominant pathogen causing up to 70 percent of hospital admissions for diarrhea [**?**].

After a single natural infection, 38 percent of children are protected against any subsequent rotavirus infection, 77 percent are protected against rotavirus diarrhoea and 87 percent are protected against severe diarrhoea. Malnutrition or co-infection with multiple enteric pathogens, common in developing countries, can further hinder effective rotavirus treatment, delay recovery, and lead to further sequelae, such as growth and developmental delays and susceptibility to re-infection which can occur at any age. Therefore, prevention of rotavirus through immunization is considered a global priority to manage the disease. However, with each infection immunity develops and this makes subsequent infections less severe [5, 13, 16].

Vaccination is the administration of antigenic material (vaccine) into the body to stimulate an individuals immune system to develop adaptive immunity to a pathogen [29, 24]. To date, vaccination is considered the most effective and cost-beneficial intervention for protection against infectious diseases. The introduction of variolation in the 17th century and the intense vaccination programs that followed led to the worldwide eradication of smallpox by 1980. Further vaccinations that followed lead to more than 90 percent reduction of polio outbreaks as well as a significant reduction of pertussis, diphtheria, varicella, measles, and tetanus cases, saving millions of lives from preventable diseases, such as influenza, worldwide [9]. Immunizations have led to drastic improvements not only in developing and emerging countries but also in developed countries [9, 10, 15].

Rotavirus vaccine is a vaccine used to protect against rotavirus infections. The vaccine contains a weakened strain of rotavirus. This helps the body to build up immunity to fight off the disease in the event of an infection[6, 17, 19, 21, 25]. There are two types of rotavirus vaccines namely Rota teq (pentavalent human bovine reassortant) and Rotarix (Glaxosmithkline human monvalent) currently licensed for use. In addition, several developing country manufacturers are developing a new pipeline of rotavirus vaccines [7]. Introduction of rotavirus vaccine should be accompanied by measures to ensure high vaccination coverage and timely administration of each dose [23, 26, 28, 30].

In 2007, the World Health Organization (WHO) [31] recommended routine vaccination against rotavirus worldwide. Due to concern for infolding of one segment of the intestine within the other, a rare adverse event associated with an early-generation rotavirus vaccine no longer in use, WHO initially recommended that the first and last doses of RV5 and RV1 be given by 15 and 32 weeks of age, respectively. In January 2013, after re-evaluating the potential benefits and risks of rotavirus vaccination, WHO recommended removing these age restrictions [30]. However, it is anticipated that implementation of this recommendation has been challenging in both already existing and subsequent rotavirus vaccination programs as countries would need to adopt this recommendation, update their national immunization program guidelines, and retrain vaccinators [18].

A study on delayed vaccination and its predictors among children under 2 years in India has been done. The study reported that the vaccine timeliness is an under-recognised problem in India despite high proportion of Indian children having delayed vaccination. The targeted groups with higher chances of delayed vaccination included children delivered at home, low birth weight new-borns, poorer households, children of mothers with lower education, children from Muslim families which are integral when designing routine immunization micro-plan in the primary care settings [4]. A study of the timeliness of rotavirus vaccination at sentinel sites in four early-adopter African countries has been done. The study focused on age-eligible children to have received rotavirus vaccine that were enrolled in Ghana, Zimbabwe, Rwanda and Burkina Fasso using logistic regression technique. It was noted that delayed administration of first dose pentavalent vaccine was significantly associated with missing first dose of rotavirus vaccine in 3 of the 4 countries studied, although delays in administration were rare (14) percent and that age restrictions had minimal impact on rotavirus vaccine use due to timely vaccine administration[18, 4].

Investigations of delayed pertussis vaccination in infants using mathematical modeling, a methodology that involves the use of data collected from vaccination centres and an age-structured deterministic mathematical model for pertussis transmission was developed. The results obtained showed that strategies that avoid delays in vaccination have a strong impact on incidence reduction in the most vulnerable population (infants less than 1 year). In regions with high vaccination coverage (95) percent the elimination of delays in the three primary doses decreased pertussis incidence in infants by approximately 20 percent. In regions where delays in the administration of vaccines was higher, the combined action to reduce delays and improve coverage lead to a significant improvement in disease control in infants [8, 11, 12, 20].

In order to mitigate the diarrhoeal hazards of rotavirus, it is therefore necessary to employ both the prevention and precaution measures and the treatment methods available. The proposed study hence seeks to use a mathematical model to uncover and predict the dynamics of rotavirus infection by considering both vaccination and treatment parameters.

## 2 Model description and analysis

The assumptions in the model development were;
(i) Recruitment into the population is by birth or migration. (ii)The population under study is homogeneous. (iii) The mass action incidence transmission is defined by $\beta SI$

The model subdivided the total population at a time t given as N(t) into five compartments. The first compartment has the individuals that are susceptible to Rotavirus infections, it is denoted by S(t). The second compartment has the individuals infected with Rotavirus infection, it is denoted by I(t). The number of Individuals seeking treatment from Rotavirus infection and the individuals who have recovered from Rotavirus infection are denoted by T(t) and R(t), respectively.The individuals vaccinated from Rotavirus infection are represented by V(t).

The total population is; N(t)=S(t)+I(t)+T(t)+R(t)+V(t).

The parameters used in the formulated model include $(1-\rho)\wedge$ which denotes the recruitment rate into susceptible compartment. Recruitment rate into vaccination is denoted by $\rho\wedge$ while the rate at which vaccinated individuals become susceptible to Rotavirus is denoted by $\gamma$. Vaccination rate of the susceptible class is denoted by $\omega$ while $\varepsilon$ denotes the expected decrease in the risk of infection. Rate of flow from I to T is denoted by $k$ while $\beta$denotes transmission rate. Natural death rate of human is denoted by $\mu$ while $\delta$ denotes rotavirus induced deaths on compartment I. Time delay in completion of vaccination immunity is denoted by $\tau$ while $a$ denotes Rotavirus induced death on compartment T. Recruitment rate from R to S is denoted by $b$ while $c$ denotes recruitment rate from T to R.

The proposed model is represented by the following system of equations .

$$\begin{aligned}
\frac{dS}{dt} &= (1-\rho)\wedge + \gamma V + bR - (\omega + \beta I + \mu)S \\
\frac{d\vee}{dt} &= \rho \wedge + \omega S - \vee(\mu + \gamma) - ((1-\varepsilon)\beta \vee (t-\tau) I) \\
\frac{dI}{dt} &= \beta S I - (\mu + \delta + k - (1-\varepsilon)\beta \vee (t-\tau))\, I \\
\frac{dT}{dt} &= kI - (\mu + a + c)T \\
\frac{dR}{dt} &= cT - (\mu + b)R \qquad (2.1)
\end{aligned}$$

## 2.1 Invariant Region

The invariant region gives the region of study. The model in equation 2.1 was analysed in a feasible bounded region $\Pi$ that was defined as: $\Pi = \left\{ (S(t), V(t), I(t), T(t), R(t) \in \Re^5_+ : N(t) \leq \frac{\Lambda}{\mu} \right\}$
To show that the region $\Pi$ is a bounded set, the time derivative of $N$ was taken as follows;

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dI}{dt} + \frac{dT}{dt} + \frac{dR}{dt} \qquad (2.2)$$

Substituting the right-hand of equation 2.2 with its equivalence from equation 2.1 and simplifying we have:

$$\begin{aligned}
\frac{dN}{dt} &= \wedge - \mu(S + V + I + T + R) - \delta I - aT \\
\frac{dN}{dt} &= \wedge - \mu N - (\delta I + aT) \qquad (2.3)
\end{aligned}$$

For any increasing population $(\delta I + aT) > 0$ holds. Thus, if rotavirus induced deaths were not considered then;

$$\begin{aligned}
&\frac{dN}{dt} \leq \wedge - \mu N \\
&\frac{dN}{dt} + \mu N \leq \wedge \qquad (2.4)
\end{aligned}$$

Solving equation 2.4 by separation of variables we get;

$$N(t) \leq \frac{\wedge}{\mu} + N(0)e^{-\mu(t)} \qquad (2.5)$$

From inequality in equation 2.5, and since $N(t) \geq 0$, then

$$0 \leq \ N(t) \leq \frac{\wedge}{\mu} + N(0)e^{-\mu(t)} \qquad (2.6)$$

where $N(0)$ is initial population. Thus as $t \to \infty$, we have ;

$$0 \leq \ N(t) \leq \frac{\wedge}{\mu}. \tag{2.7}$$

This implies that the total population is bounded. Therefore the model is well posed and biologically meaningful .

## 2.2 Positivity of solutions

The model dealt with rotavirus infection in a varying human population size. Therefore the associated state variables were to be shown that they were non-negative for all time $t \geq 0$.

**Theorem 2.1.** *Given the model in equation 2.1 with conditions* $V(0) \geq 0, I(0) \geq 0, T(0) \geq 0, S(0) \geq 0, R(0) \geq 0$ *then the solutions set* $S(t), V(t), I(t), T(t), R(t)$ *of the model remain positive for all time* $t \geq 0$ *in the feasible region* $\Pi$

*Proof.* Given the initial conditions $V(0) \geq 0, I(0) \geq 0, T(0) \geq 0, S(0) \geq 0, R(0) \geq 0$ for $t \geq 0$ it is shown that the solutions of equation 2.1 will remain to be positive . This is done by showing that each of the trajectories of the system in equation 2.1 was non-negative for all $t \geq 0$. Considering the first equation of 2.1, we had:

$$\frac{dS}{dt} = (1-\rho)\wedge + \gamma V + bR - (\omega + \beta I + \mu)S \tag{2.8}$$

The resulting differential inequality was given as ;

$$\frac{dS}{dt} \geq -(\omega + \beta I + \mu)S \tag{2.9}$$

Using separation of variables method, you get;

$$\begin{aligned} \int \frac{dS}{S} &\geq -\int (\omega s + \beta I + \mu)dt \\ S(t) &\geq S_0 e^{-(\omega+\beta I+\mu)(t)} \end{aligned} \tag{2.10}$$

which is positive. Repeating the same process of integration for $V(t), I(t), T(t), R(t)$ in equation 2.1 we get;

$$\begin{aligned} V(t) &\geq V_0 e^{-(\mu+\gamma)-(1-\varepsilon)\beta(t-\tau)(t)} \\ I(t) &\geq I_0 e^{-(\mu+\delta+k)(t)} \\ T(t) &\geq T_0 e^{-(\mu+a+c)(t)} \\ R(t) &\geq R_0 e^{-(\mu+b)(t)} \end{aligned} \tag{2.11}$$

respectively.
Hence all the solutions of the model in equation 2.1 remained positive in the feasible bounded region $\Pi$ ☐

## 2.3 Disease-Free Equilibrium Point (DFE)

It is denoted by $E^0$. Olaniyi and Obabiyi [14] defined it as a steady-state solution for which there is no disease or infection in the population. To obtain disease-free equilibrium point, we set the system in equation 2.1 equal to zero and solve for $S(t), V(t), I(t), T(t), R(t)$. We set $I(t) = T(t) = R(t) = 0$ since there were no infections and obtained $E^0$ of model 2.1 as

$$E^0 = [S^0, V^0, 0, 0, 0]$$

$$\begin{aligned}(1-\rho)+\gamma V^0-\mu S^0-\omega S^0=0\\ \rho\wedge+\omega S^0-\mu V^0-\gamma V^0=0\end{aligned}\tag{2.12}$$

Solving for $S^0$ and $V^0$ from the system in equation 2.12, we get;

$$S^0 \quad = \quad \frac{(1-\rho)\wedge+\gamma V^0}{\mu+\omega}\tag{2.13}$$

$$V^0 \quad = \quad \frac{\rho\wedge+\omega S^0}{\mu+\gamma}\tag{2.14}$$

Substituting equation 2.14 into equation 2.13 and solving for $S^0$ ,we get;

$$S^0=\frac{(1-\rho)\wedge(\mu+\gamma)+\gamma\rho\wedge}{(\mu+\omega)(\mu+\gamma)-\gamma\omega}\tag{2.15}$$

Substituting equation 2.15 into to equation 2.14 and solving for $V^0$, we get;

$$V^0=\frac{\rho\wedge+\omega(1-\rho)\wedge(\mu+\gamma)+\gamma\rho\wedge}{(\mu+\gamma)(\mu+\omega)(\mu+\gamma)-\gamma\omega}\tag{2.16}$$

### 2.3.1 The Basic Reproduction Number $R_0$

The next generation matrix approach was used to determine the basic reproduction number denoted by $R_0$. According to [14] , it is defined as the number of secondary infections produced by a single typical infection introduced into a completely susceptible population . $R_0$ is used to measure the ability of an infection reproducing itself. The basic reproduction number was obtained as;

$$R_0=Spectral\ \ radius\ \ of\ \ the\ \ matrix\ \ FV^{-1}\tag{2.17}$$

which are the dominant eigenvalues of $FV^{-1}$. F and V are computed and given as in the following $5\times5$ matrices by first determining f and v.
f(a new infection terms) was defined as;

$$f=(F_1,F_2,F_3,F_4,F_5)^T$$

and was given by ;

$$f=(0,0,\beta SI+(1-\varepsilon)\beta V(t-\tau)I,0,0)^T$$

V(transition terms) was given as;

$$v=(0,0,kI+\mu I+\delta I,0,0)^T$$

To obtain F and V , the partial derivatives of f and v were evaluated at the disease free equilibrium point. F and V were given as follows;

$$F=\beta S+(1-\varepsilon)\beta V(t-\tau)\ V=k+\mu+\delta$$

On computing the inverse of $V$,$V^{-1}$ we have;

$$V^{-1}=\frac{1}{k+\mu+\delta}\tag{2.18}$$

$$FV^{-1}=\frac{\beta}{k+\mu+\delta}S+(1-\varepsilon)V(t-\tau)\tag{2.19}$$

substituting $S_0$ and $V_0$ at DFE,we get;

$$R_0=\frac{\beta}{k+\mu+\delta}S_0+(1-\varepsilon)V_0(t-\tau)\tag{2.20}$$

In the absence of the disease then the delay $\tau=0$, thus;

$$R_0=\frac{\beta}{k+\mu+\delta}S_0+(1-\varepsilon)V_0(t)\tag{2.21}$$

### 2.3.2 Local Stability of the Disease Free Equilibrium Point

**Theorem 2.2.** *The DFE is asymptotically stable if :*

$$\beta[S^0 + (1-\varepsilon)] < \gamma + \delta + k \tag{2.22}$$

*Proof.* The Jacobian matrix of the models in Mathematics is used to evaluate the local stability of the system at $E^0$ using the signs of determined corresponding eigen-values. The Jacobian matrix of 2.1 was given by ;

$$J = \begin{pmatrix} -(A_1+\beta I) & \gamma & \beta S & 0 & b \\ \omega & -A_2 - A_3\frac{dV(t-\tau)}{dV(t)}\beta I & A_3V(t-\tau)\beta I & 0 & 0 \\ \beta I & A_3\frac{dV(t-\tau)}{dV(t)}\beta I & \beta S + A_3V(t-\tau)\beta - A_4 & 0 & 0 \\ 0 & 0 & k & -A_5 & 0 \\ 0 & 0 & 0 & c & -A_6 \end{pmatrix} \tag{2.23}$$

Where $A_1 = \omega + \mu$, $A_2 = \gamma + \mu$, $A_3 = 1 - \varepsilon$, $A_4 = \mu + \delta + k$, $A_5 = \mu + a + c$ and $A_6 = \mu + b$

At $E^0$,the Jacobian matrix a bove becomes;

$$J_1 = \begin{pmatrix} -A_1 & \gamma & \beta S^0 & 0 & b \\ \omega & -A_2 & 0 & 0 & 0 \\ 0 & 0 & \beta S^0 + \beta A_3 V - A_4 & 0 & 0 \\ 0 & 0 & k & -A_5 & 0 \\ 0 & 0 & 0 & c & -A_6 \end{pmatrix} \tag{2.24}$$

Whose eigenvalues are found to be: $\lambda_1 = -A_6, \lambda_2 = -A_5, \lambda_3 = -A_2, \lambda_4 = -A_1 and \lambda_5 = \beta S^0 + \beta A_3 V - A_4$ which are negative if:

$$\beta S^0 + \beta A_3 < A_4 \tag{2.25}$$

Therefore the eigenvalues are negative if the condition in the inequality in equation 2.25 holds,implying that the disease free equilibrium system is asymptotically stable as long as$R_0 < 1$. ☐

## 2.4 Endemic Equillibrium Point

It is denoted by $E^*$. Olaniyi and Obabiyi [14] defined it as a steady-state solution for which there exists a constant occurence of disease within the population . It occurs when the disease persists in the community . To obtain the endemic equilibrium point , the system in equation 2.1 was equated to zero and solved for $(S(t), V(t), I(t), T(t), R(t)$ which were denoted by;

$$E^* = S^*(t), V^*(t), I^*(t), T^*(t), R(t) \tag{2.26}$$

The points are generated;

$$\begin{aligned} S^* &= \frac{k + \mu + \delta - (1-\varepsilon)\beta V^*(t-\tau)}{\beta} \\ V^* &= \frac{\beta S^* I^* + \mu S^* - bR^* - (1-\rho)\wedge}{\gamma} \\ I^* &= \frac{\rho}{\wedge} + \omega S^* - \mu V^* - \gamma V^*(1-\varepsilon)\beta V^*(t-\tau) \\ T^* &= \frac{kI^*}{\mu + a + c} \\ R^* &= \frac{cT^*}{\mu + b} \end{aligned} \tag{2.27}$$

### 2.4.1 Local Stability of the Endemic Equilibrium Point

The Jacobian matrix of equation 2.1 at endemic state $E^* = S^*, V^*, I^*, T^*, R^*$ was given by:

$$J_2 = \begin{pmatrix} -(A_1 + \beta I^*) & \gamma & \beta S^* & 0 & b \\ \omega & -A_2 - A_3 e^{-\lambda\tau}\beta I^* & -A_3 V^*(t-\tau)\beta & 0 & 0 \\ \beta I^* & A_3 e^{-\lambda\tau}\beta I^* & \beta S^* + A_3 V^*(t-\tau)\beta - A_4 & 0 & 0 \\ 0 & 0 & k & -A_5 & 0 \\ 0 & 0 & 0 & c & -A_6 \end{pmatrix} \tag{2.28}$$

Therefore

$$J_2 = \begin{pmatrix} -G_1 & \gamma & G_2 & 0 & b \\ \omega & -G_3 & -G_4 & 0 & 0 \\ G_5 & G_6 & G_7 & 0 & 0 \\ 0 & 0 & k & -A_5 & 0 \\ 0 & 0 & 0 & c & -A_6 \end{pmatrix} \tag{2.29}$$

Where $G_1 = (A_1 + \beta I^*), G_2 = \beta S^*, G_3 = A_2 + A_3 e^{-\lambda\tau}\beta I^*, G_4 = A_3 V^*(t-\tau)\beta G_5 = \beta I^*, G_6 = A_3 e^{-\lambda\tau}\beta I^*, G_7 = \beta S^* + A_3 V^*(t-\tau)\beta - A_4$

From matrix $J_2$ goven in equation 2.29, the trace:

$traJ_2 = -G_1 - G_3 + G_7 - A_5 - A_6$

Which is negative if

$$G_7 < G_1 + G_3 + A_5 + A_6 \tag{2.30}$$

The determinant for Equation 2.29 is given by: $detJ_2 = bckG_3G_5 + A_5A_6G_2G_3G_5 - \gamma A_5A_6G_4G_5 + bck\omega G_6 + \omega A_5A_6G_2G_6 - A_5A_6G_1G_4G_6 - \gamma\omega A_5A_6G_7 + A_5A_6G_1G_3G_7$

Which becomes $bckG_3G_5 + A_5A_6G_2G_3G_5 + bck\omega G_6 + \omega A_5A_6G_2G_6 - A_5A_6[\gamma G_4G_5 + \gamma\omega G_7 + G_1G_4G_6 - G_1G_3G_7]$

Which is positive if

$$bckF_3G_5 + A_5A_6G_2G_3G_5 + bck\omega G_6 + \omega A_5A_6G_2G_6 > A_5A_6[\gamma G_4G_5 + \gamma\omega G_7 + G_1G_4G_6 - G_1G_3G_7] \tag{2.31}$$

From stability theory [19], if the inequalities in equation 2.30 and equation 2.31 hold , then the system in equation 2.1 is asymptotically stable.

# 3 Numerical simulation And Analysis

Through the use of numerical simulations, we examine the behaviour of transmission dynamics of Rotavirus as given in the formulated model. The parameter values, adapted from [1, 22], are used in simulating the graphs of the formulated model. These parameter values are varied and their impact on the model explored. In this section, Matlab software is used to illustrate the numerical simulations describing the theoretical results for the system in equation 2.1.

## 3.1 Model in equation 2.1 with no vaccination and $\tau = 0$

In this subsection, we will numerically simulate equation 2.1 with no vaccination and $\tau = 0$. The initial populations are given by S(0)=12, I(0)=5, T(0)=2, R(0)=1. The parameter values used are $\Lambda = 4$, b =0.3, $\mu = 0.1$ $\delta = 0.04$, k=0.4, a=0.8 and c=0.2. For Figure 1, $\beta = 0.001$. For Figure 2, $\beta = 0.03$. For Figure 3, $\beta = 0.6$.

The following graphs are obtained:

In figure 1, when $R_0 < 1, (R_0 = 0.02)$; the susceptible population grows boundedly because the secondary infections from one infected individual are very few. Hence the infected, treated and

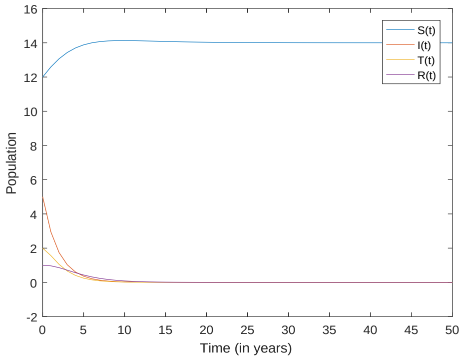

Figure 1:*No vaccination and* $R_0 < 1$

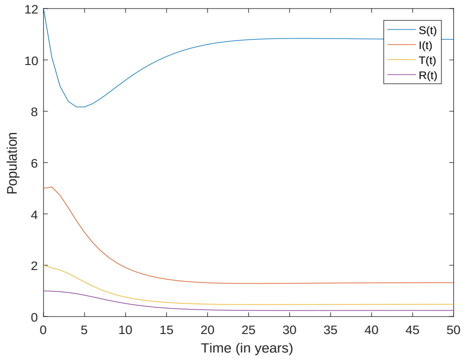

Figure 2:*No vaccination and* $R_0 \to$ *1*

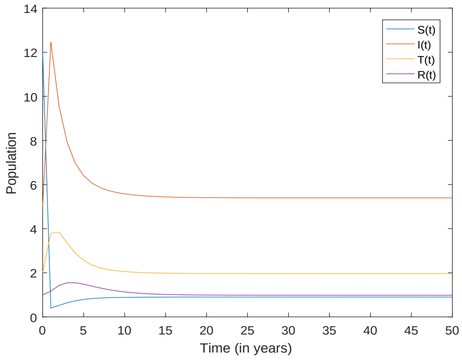

Figure 3:*No vaccination and* $R_0 > 1$

recovered populations tend to zero.
In figure 2, when the $R_0 \to 1, (R_0 = 1.07)$; the susceptible population reduces slightly then increases and stabilizes after some time . The infected , treated and recovered population reduces gradually and stabilizes. All the four classes co-exist because $R_0 \to 1$, meaning that the secondary infections from one primary infection are not many.
In figure 3, when the $R_0 > 1$ and big $(R_0 = 13.73)$; the susceptible population reduces sharply because the number of secondary infections are many from one primary infection, it stabilizes with time . The infected population increases sharply, and decreases before stabilizing. The treated and recovered population behave in the same manner as the infected population. This shows that when $R_0 > 1$ and big meaning that the disease will persist and therefore it is necessary to have $R_0 < 1$ and $R_0 \to 1$.

## 3.2 Model in equation 2.1 with $\tau = 0$

In this subsection, we will numerically simulate the model in equation 2.1 with $\tau = 0$. The initial populations are given by S(0)=12, V(0)=4, I(0)=5, T(0)=2, R(0)=1. The parameter values used are $\rho = 0.3$, $\Lambda = 4$, b =0.3, $\omega = 0.1$ $\mu = 0.1$ $\delta = 0.04$, k=0.4, a=0.8, c=0.2, $\gamma = 0.3$ and $\varepsilon = 0.9$. For Figure 4, $\beta = 0.001$. For Figure 5, $\beta = 0.03$. For Figure 6, $\beta = 0.6$. The following graphs are obtained: In figure 4, when $R_0 < 1, (R_0 = 0.42)$, the susceptible population grows boundedly because the secondary infections from one infected individual are few. Due to this

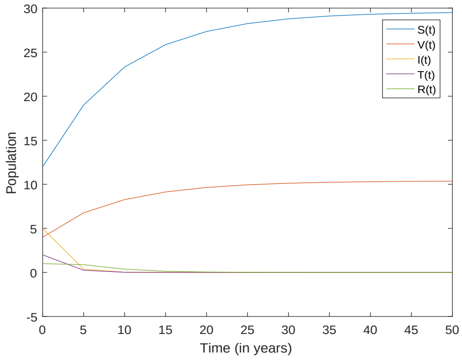

Figure 4:$\tau = 0$ *and* $R_0 < 1$

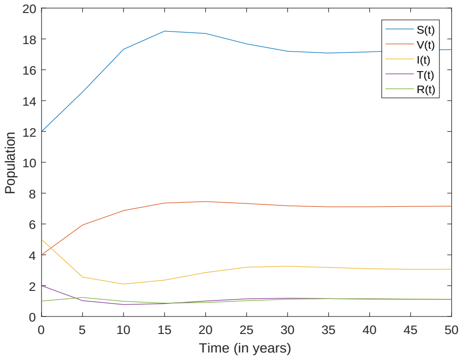

Figure 5:$\tau = 0$ *and* $R_0 \rightarrow$ *1*

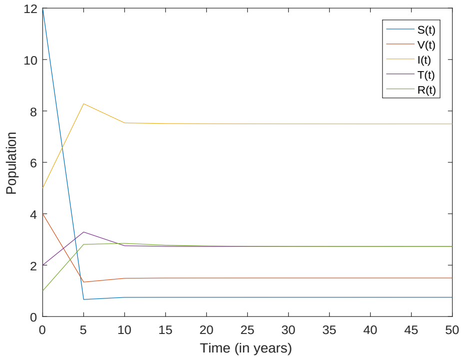

Figure 6:$\tau = 0$ *and* $R_0 > 1$

fact,the infected,treated and recovered individuals tend to zero. The vaccinated population depends on the value of $\omega$ i.e it is a fraction of the susceptible population.

In figure 5, when $R_0 \rightarrow 1$, ($R_0 = 1.07$); the susceptible population increases and then slightly decreases after some time. The vaccinated population also increases. These two populations are increasing because $R_0 \rightarrow 1$. The infected and treated slightly decreases and stabilizes. The recovered population also stabilizes with time. All the five compartments co-exist because $R_0 \rightarrow 1$, meaning that the secondary infections from one primary infection are not many.

In figure 6, when $R_0 > 1$ and big ($R_0 = 13.73$); the susceptible population decreases sharply because the number of secondary infections are many from one primary infection. However the susceptible population stabilizes with time. This in turn affects the vaccinated population which decreases sharply and stabilizes. The infected population increases before stabilizing which affects the treated and recovered population in the same manner. This shows that when $R_0 > 1$ and big, the infected population will grow and therefore we need to have $R_0 < 1$ or $R_0 \rightarrow 1$.

## 3.3 Model in equation 2.1

In this section, we will numerically simulate equation 2.1 with either a small delay $(\tau = 0.01) \approx 4$ days or a large delay $(\tau = 0.1) \approx 37$ days. The initial populations are given by S(0)=12, V(0)=4, I(0)=5, T(0)=2, R(0)=1. The parameter values used are $\rho = 0.3$, $\Lambda = 4$, b =0.3, $\omega = 0.1$ $\mu = 0.1$ $\delta = 0.04$, k=0.4, a=0.8, c=0.2, $\gamma = 0.3$ and $\varepsilon = 0.9$. For Figure 7 and 8, $\beta = 0.001$. For Figure

9 and 10, $\beta = 0.03$. For Figure 11 and 12, $\beta = 0.6$. For Figure 7, 9 and 11, $\tau = 0.01$ whereas for Figure 8, 10 and 12, $\tau = 0.1$ The following graphs are obtained:

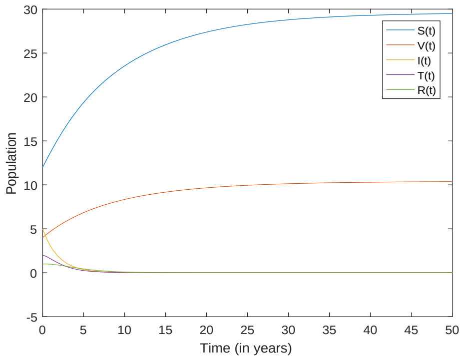

Figure 7:$R_0 < 1$ *and* $\tau = 0.01$

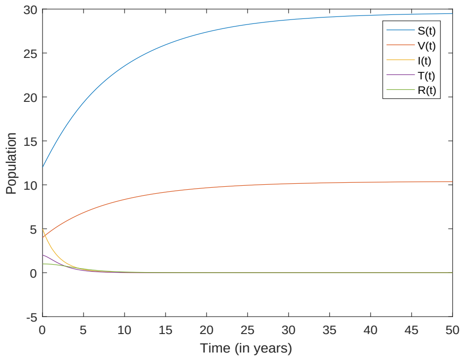

Figure 8:$R_0 < 1$ *and* $\tau = 0.1$

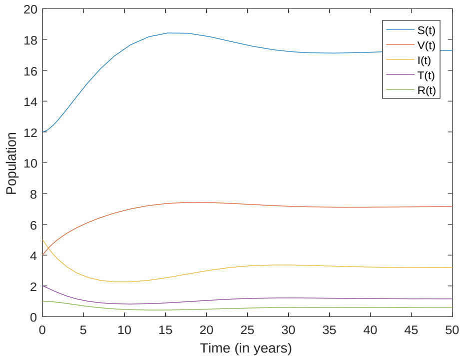

Figure 9:$R_0 \rightarrow$ *1 and* $\tau = 0.01$

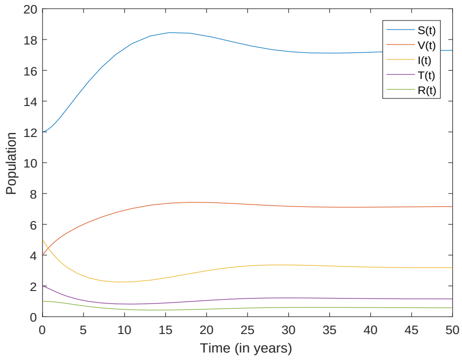

Figure 10:$R_0 \rightarrow$ *1 and* $\tau = 0.1$

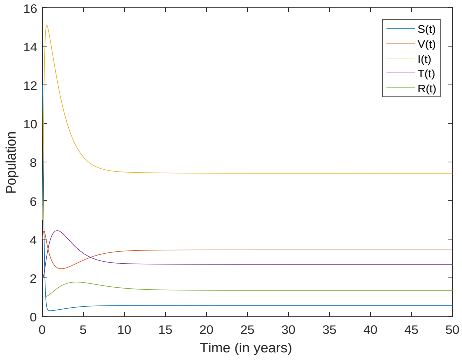

Figure 11:$R_0 > 1$*and* $\tau = 0.01$

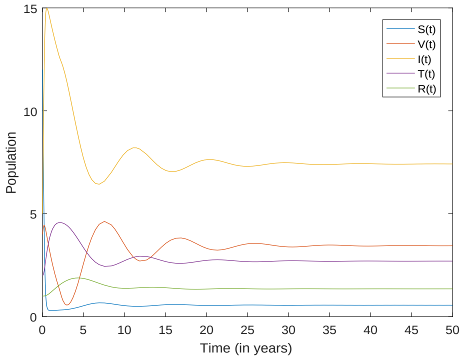

Figure 12:$R_0 > 1$*and* $\tau = 0.1$

In figures 7 and 8 when $R_0 < 1$ ($R_0 = 0.42$); the susceptible population grows boundedly because the secondary infections from one infected individual are few. Due to this fact, the infected, treated and recovered individuals ted to extinction. The vaccinated population depends on $\omega$ i.e it is a fraction of the susceptible. The impact of delay is not seen because $R_0 < 1$ i.e secondary number of infections are few.

In figure 9 and 10 when $R_0 > 1$ ($R_0 = 1.07$); the susceptible population increases and it then slightly decreases after some time before stabilizing. The vaccinated population increases and stabilizes after some time. The two populations are increasing because $R_0 \to 1$. The infected and treated population slightly decreases and stabilizes. The recovered population also stabilizes with time. All the five classes co-exist because $R_0 \to 1$, meaning that the secondary infections from one primary infection are not many. The impact of delay is also not felt because $R_0 \to 1$.

In figure 11 and 12 $R_0 > 1$ ($R_0 = 13.73$), when $\tau = 0.01$; the susceptible population decreases sharply because the number of secondary infections are many from one primary infection. However the susceptible population stabilizes with time. This in turn affects the vaccinated population which decreases sharply and stabilizes. The infected population increases before stabilizing. The treated and recovered population behave in the same way as the infected population. This shows that when $R_0 > 1$ and big, the infected population will grow and therefore we need to have $R_0 < 1$ or $R_0 \to 1$. When $\tau = 0.1$, the compartments behave in the same way, but it takes a longer time to stabilize showing that when $\tau$ is large the population will be greatly affected and therefore there is need to have $\tau = 0.1$ reduced for favourable environment in the system.

# 4 Conclusion

A model to determine Rotavirus infection incorporating time delay on the effectiveness of vaccination with treatment was formulated and shown to be positively invariant as well as bounded. The basic reproduction number $R_0$ corresponding to Rotavirus was determined. $R_0$ which plays the role in controlling the spread of the infection of the disease was determined by use next generation matrix. The existence and analysis of equilibrium points were established. The disease free equilibrium point was shown to be asymptotically stable,implying that the disease outbreak for life was not expected. By use of Routh-Hurwitz criterion, the endemic equilibrium point was shown to be locally asymptotically stable . The disease transmission levels could be kept quite low with minimal deaths and interferences at the peak times of re-occurrences if $R_0$ is maintained at $R_0 < 1$ or $R_0 \to 1$.

Numerical simulation showed that, when $R_0 < 1$ or $R_0 \to 1$, the susceptible population would not decrease drastically neither would the infected population rise drastically unlike when $R_0 > 1$($R_0$ is big). When $R_0$ is big a bigger time delay would make the population to oscillate meaning that the population was not predictable.

# 5 Recommendation

Authorities in the public health, health practitioners and epidemiologists can use the formulated model to understand the spread and control of the infection of the Rotavirus. The health agencies can get better understanding on the role of delay on the effectiveness of vaccination with treatment associated to Rotavirus in order to respond to the associated infection.

Recommendations for future studies; even though the results obtained were in improving the health status of Rotavirus infection,there still improvements that were related to the research that could be implemented since the research could serve as the baseline for further studies. For instance,different geographical regions can be considered, since each region is affected by different dynamics.

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