

Mathematical Model for the Control of Typhoid Fever with Effects of Early Treatment

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ABSTRACT

In this paper, we develop a mathematical model on the transmission dynamics of typhoid fever using the concept of differential equation. The Next Generational Matrix (NGM) method is used to calculate the basic reproduction number necessary for the disease control. The findings of the study show that if the basic reproduction number is less than one, the disease can be controlled. Finally, numerical simulations to demonstrate our findings and brief discussions are provided.

(Keywords: transmission dynamics, typhoid fever, differential equations, transmission model, Next Generational Matrix, NGM)

INTRODUCTION

Typhoid fever is one of the deadliest diseases in Africa, especially where there is a poor sanitation, poor standards of personal hygiene, and the prevalence of contaminated water (Kariuki, 2004). It is endemic in developing countries and remains a substantial public health concern despite recent progress in water sanitation coverage. Advances have been made towards the fight against the infection such as treatment with drugs, vaccination, and environmental sanitation (Moffact, 2014).

Typhoid bacteria are passed in the feces and urine of infected individuals and people become infected after eating food or drinking beverages that have been handled by a person who is infected, or by drinking water that has been contaminated by sewage containing the bacteria. Once the bacteria enters the body it travels in the human intestines, and then enters the bloodstream. The bacteria enter to the blood

through lymph nodes, gallbladder, spleen, liver, etc. Abdominal pain, fever, and general ill feeling are the symptoms of this disease. High fever (103° F or 39.5 C) or higher and severe diarrhea occur as the disease gets worse (Mushayabasa, et al., 2014 and Mushayabasa, 2017).

In 2001, it is estimated that the disease caused 21.6 million illnesses and 216,500 deaths globally (WHO, 2004). Modelling the spread of typhoid fever and its transmission is an important and interesting area for a many computational mathematical researchers. The study of infectious diseases in the past has mainly focused on impacts within the human population (Watson and Edmunds, 2015).

In recent years, data indicating that typhoid fever is a major cause of mortality among the urban and peri-urban population. For instance, several community-based studies have emerged from South Asia, where the incidence rate seems to be high among young children, with rates exceeding 500-1000 cases per 100,000 (Mushayabasa, et al., 2013).

When dealing with large populations, as in the case of typhoid fever, compartmental mathematical models are used. In the deterministic model, individuals in the population are assigned to different subgroups, each representing a specific stage of the epidemic. Mathematical models are used in science and engineering to help understand complex systems and optimize industrial processes. There are numerous examples of the fruitful applications of mathematical principles to problems in typhoid vaccines and in the recent years, there have been increasing interests in applying the transmission models (Peter, et al., 2021; Ojo, et al., 2022; Ayoade, et. al., 2019; Peter, et. al.,

2021; Peter, et. al., 2021; Adebisi, 2019; Peter et. al., 2020; and Ayoola, et al., 2021).

Various studies including mathematical models of the spread of typhoid fever, dynamic models for analyzing and predicting process of typhoid fever, among others, have been conducted by many researchers globally. For instance, according to Peter, et al. (2017) constructed mathematical model of the type *PSITR* in which added a recovered compartment in which all treated individuals recovered but after some time the recovered individuals lose immunity and return back to a susceptible class.

Several authors have also worked in this area, and few among them are Lauria, et al. (2009) and Nithiri, et al. (2016). In Lauria, et al. (2009) an optimization model for reducing typhoid cases in developing countries without increasing public spending. In Nithiri et al. (2016), mathematical modelling of typhoid fever disease incorporating protection against the disease was studied.

Thus, in this work, we test for the existence and uniqueness of a solution for the model using Lipschitz condition, and compute the basic reproduction number necessary for the disease control.

MODEL FORMULATION

The compartment used in this model consists of three classes, namely:

- Susceptible Class $S(t)$: these are individuals who are susceptible to the disease or are prone to the disease.
- Infected $I(t)$: these are individuals who are infected with the disease and are capable of transmitting the disease to these in the susceptible class.
- Recovered class $R(t)$: these are who have recovered from the disease.

Recruitment rate to susceptible class is either by immigration or by birth at a rate (π). Susceptible individuals get infected through interaction with the infected individuals at a rate (β), γ represent rate of recovery from infection. In each of the classes, individual can die naturally at a rate (μ), the disease induced death rate is given as (δ),

the above illustration can be represented by the system of differential-equations given below:

$$\frac{dS}{dt} = \pi - \beta SI - \mu S \quad (1)$$

$$\frac{dI}{dt} = \beta SI - (\mu + \delta + \gamma)I \quad (2)$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad (3)$$

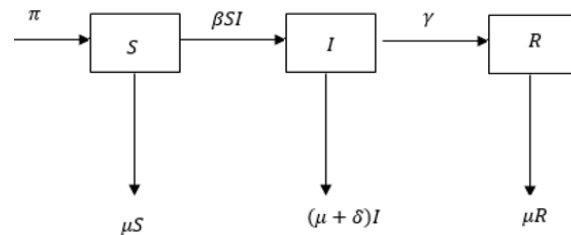


Figure 1: The Model 's Flow Diagram.

Table 1: Description of Parameters/Variables.

Variable	Description
$S(t)$	Susceptible class at time t
$I(t)$	Infected individual at time t
$R(t)$	Recovered individuals at time t
Parameter	Description
π	Recruitment rate
β	Force of infection
μ	Natural death rate
δ	Disease induced death rate
γ	Recovered rate

The model assumptions:

- 1) We assume direct transmission between two individuals by showing contaminated food or drinks.
- 2) All parameters used are positive.
- 3) Susceptible individuals cannot be infected simultaneously

Existence and Uniqueness of Solution

Existence and uniqueness theorem is the tool which makes it possible for us to conclude that there exists only one solution to a first order differential equation which satisfies a given initial condition.

Theorem 1: Let $f(x,y)$ be a real valued function which is continuous on the rectangle $R = \{(x,y); |x-x_0| \leq a, |y-y_0| \leq b\}$. Assume f has a partial derivative with respect to y and that $\frac{\partial f}{\partial y}$ is also continuous on the rectangle R . Then there exists an interval $I = [x_0 - h, x_0 + h]$ (with $h \leq a$) such that the initial value problem $\begin{cases} y' = f(x,y) \\ y(x_0) = y_0 \end{cases}$ has a unique solution $y(x)$ defined on the interval I .

Note that the number h may be smaller than a . In order to understand the main ideas behind this theorem, assume the conclusion is true. Then if $y(x)$ is a solution to the initial value problem, we must have:

$$y(x) = y_0 + \int_{x_0}^x f(t, y(t)) dt \quad (4)$$

It is not hard to see that if a function $y(x)$ satisfies the equation (called functional equation):

$$y(x) = y_0 + \int_{x_0}^x f(t, y(t)) dt \quad (5)$$

on an interval I , then it is solution to the initial value problem:

$$y' = f(x, y) \quad y(x_0) = y_0 \quad (6)$$

Lipschitz Condition

The term is used for a bound on the modulus of continuity a function. In particular, a function $f: [a, b] \rightarrow \mathcal{R}$ is said to satisfy the Lipschitz condition if there is a constant M such that:

$$|f(x, y_1) - f(x, y_2)| \leq M |y_1 - y_2| \quad (7)$$

$$x \in [a, b], y \in (-\infty, \infty)$$

The smallest constant M satisfying Equation (7) is called Lipschitz constant.

Theorem 2: Let D represents the region $0 < \alpha < R$, Therefore the solution of model in (1) – (3) is unique if we are able to establish that $\frac{\partial x_i}{\partial y_j};$ for $i, j = 1, 2, 3$ are bounded in D and continuous in D for x_1 , we have:

$$\left| \frac{\partial x_1}{\partial s} \right| = |\beta I - \mu| < \infty \quad (8)$$

$$\left| \frac{\partial x_1}{\partial I} \right| = |\beta I| < \infty \quad (9)$$

$$\left| \frac{\partial x_1}{\partial R} \right| = 0 < \infty \quad (10)$$

For x_2

$$\left| \frac{\partial x_2}{\partial s} \right| = |\beta I| < \infty \quad (11)$$

$$\left| \frac{\partial x_2}{\partial I} \right| = |\beta S - (\mu + \delta + \gamma)| < \infty \quad (12)$$

$$\left| \frac{\partial x_2}{\partial R} \right| = 0 < \infty \quad (13)$$

For x_3

$$\left| \frac{\partial x_3}{\partial s} \right| = 0 < \infty \quad (14)$$

$$\left| \frac{\partial x_3}{\partial I} \right| = |\gamma| < \infty \quad (15)$$

$$\left| \frac{\partial x_3}{\partial R} \right| = |-\mu| < \infty \quad (16)$$

These partial derivatives exist, are continuous and bounded, and from theorem 2, we conclude that the solution of the model is unique and it exists.

Equilibrium State

An equilibrium of a dynamical system is a value of the state variables where the state variables do not change. In other words, an equilibrium is a solution that does not change with time. This

means if the systems start at an equilibrium, the state will remain at the equilibrium forever.

In a discrete dynamical system, such as:

$$x_{n+1} = f(x_n) \quad (17)$$

In function iteration form or:

$$x_{n+1} - x_n = g(x_n) \quad (18)$$

In difference form, one can find the equilibria by substituting in the same quantity for x_n and x_{n+1} such as substituting $x_{n+1} = x_n = E$

$$E = f(E) \text{ or } 0 = g(E)$$

to determine the value E such that $x_n = E$ is an equilibrium of the dynamical system.

In a continuous dynamical system, such as:

$$\frac{dx}{dt} = f(x) \quad (19)$$

One can find the equilibrium by setting $\frac{dx}{dt} = 0$.

One must then solve the equation:

$$0 = f(E) \quad (20)$$

to determine values E such that $x(t) = E$ is an equilibrium of the dynamical system.

Disease Free-Equilibrium State

This is the equilibrium state in the absence of infection. Recall from Equations (1)- (3):

$$\frac{ds}{dt} = \pi - \beta SI - \mu S \quad (21)$$

$$\frac{dI}{dt} = \beta SI - (\mu + \delta + \gamma)I \quad (22)$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad (23)$$

To calculate the Disease free-equilibrium state, we equate the right-hand side of Equations (21) – (23) to zero, Also, in the absence of infection, we set the infected class to zero. Following the above, (21) – (23) reduced to:

$$\pi - \mu S = 0 \quad (24)$$

From (24), $S = \frac{\pi}{\mu}$, also $I = 0$ and $R = 0$.

Therefore, the disease free-equilibrium denoted by ϕ_{DFE} is given as:

$$\phi_{DFE}(S, I, R) = \left(\frac{\pi}{\mu}, 0, 0\right). \quad (25)$$

Basic Reproduction Number

The basic reproduction number R_0 of an infection is the expected number of cases directly generated by one case in a population where all individuals are susceptible to infection (Diekmann, et al., 1990). Thus, whether a disease persistent or eradicated in the population, it depends on the value of the basic reproduction number, when the basic reproduction number $R_0 < 1$, it means the disease is under control, but when the value of the basic reproduction number is greater than one, then the disease will invade the entire population.

Computation of the Basic Reproduction Number

The basic reproduction number R_0 is obtained by using the next generation matrix technique. This method was first used by Diekman, et al. (1990) and has been by many researchers. The procedure is given as follows:

Let $F_i(a)$ represent the appearance of new infection, in the class I

Let V_i^+ represent the movement of individuals to the class I by other mode of disease transmission.

V_i^- represent movement rate of people out of compartment I.

The transmission model consists of non-negative initial condition together with the system of equation given below:

$$a_i = F_i(a) - V_i(a), i = 1, 2, 3, \dots, n$$

$$\text{where } V_i(a) = V_i^- - V_i^+$$

F and V represents n x n matrix defined by:

$$F = \frac{\partial F(a_0)}{\partial a_j} \text{ and } V = \frac{\partial V(a_0)}{\partial a_j}$$

Following the method of Diekman, et al. (1990) the product of the matrix FV^{-1} is called the next generation matrix for the model and the basic reproduction number R_0 is the spectral radius $\rho(FV^{-1})$ that is, $R_0 = \rho(FV^{-1})$. However, the largest eigenvalue represents the next generation matrix.

Following the above procedure, we shall calculate the basic reproduction number for the model. We shall apply the procedure above to get the basic reproduction number. It has been mentioned that only the infected class are needed in the computation of R_0 . Hence $n = 1$ that is, the number of infected compartments is one from (1)-(3).

According to Diekman, et al. (1990) F and V are computed by finding the partial derivatives of the matrices with respect to infected compartment.

$$f_i = (\beta SI)$$

$$dv = (\mu + \delta + \gamma)I$$

F and V are the Jacobian matrix which shall be computed at the Disease free-equilibrium such that:

$$F = \frac{\partial f}{\partial I}, V = \frac{\partial v}{\partial I}$$

$$F = \beta S, V = (\mu + \delta + \gamma)$$

$$V^{-1} = \frac{1}{\mu + \delta + \gamma}; FV^{-1} = \frac{\beta S}{\mu + \delta + \gamma} \quad (26)$$

Substituting the value of S at Disease free-equilibrium that is, $S = \frac{\pi}{\mu}$. Therefore, the

spectral radius of the matrix ρFV^{-1} which is the highest eigenvalue is the basic reproduction number R_0 .

$$R_0 = \frac{\pi\beta}{\mu(\mu + \delta + \gamma)} \quad (27)$$

SIMULATION AND RESULTS

In this section, we present the simulation and results obtained from the computation of the basic reproduction number, which demonstrates the findings from the proposed model. This is achieved by using the set of parameter values given in the Table 1 which are obtained from the literature. We also perform numerical simulations to describe graphically the long-term impact of early treatment on the dynamics of typhoid fever. We used the following assumed initial condition for the simulation. $S_0=10, I_0=200, R_0=30$.

Table 2: Parameters Values for Model.

Parameter	Value	Source
π	10	Lauria <i>et al.</i> ,(2009)
β	0.10	Peter, <i>et al.</i> ,(20017)
μ	0.142	Mushayabasa, (2014)
δ	0.75	Nthiiri, (2016)
γ	0.01	Mushayabasa, (2014)

Recal from (27) that the basic reproduction number which is necessary for the control of the disease is given as:

$$R_0 = \frac{\pi\beta}{\mu(\mu + \delta + \gamma)}$$

We substitute the values of the parameter in Table 2 to get the actual value of the basic reproduction number necessary for the control of the disease:

$$R_0 = \frac{10 \times 0.01}{0.142(0.142 + 0.75 + 0.01)}$$

$$\frac{0.1}{0.128084}$$

$$\therefore R_0 = 0.78$$

DISCUSSION OF RESULTS

Figure 2 shows the susceptible population against time. The population of Infected individual is on the increase. Once preventive measures are put in place such as sanitation, personal hygiene, etc., transmission rates will be low and the number of susceptible individuals will increase as seen in Figure 2.

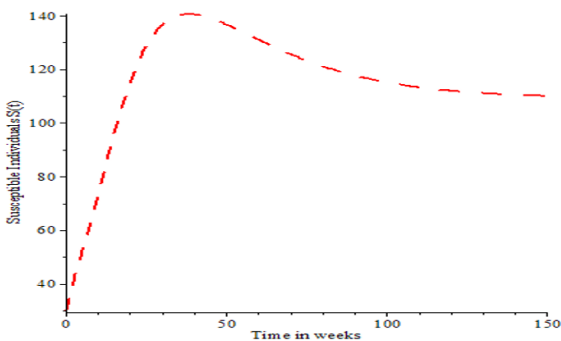


Figure 2: Susceptible Population.

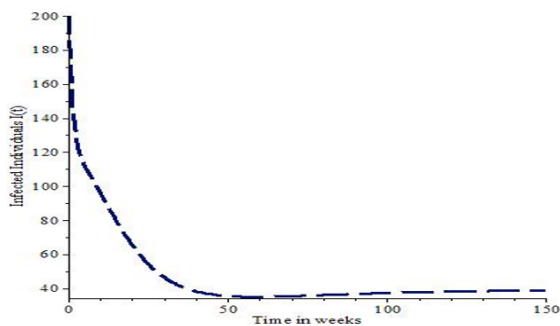


Figure 3: Infected Population.

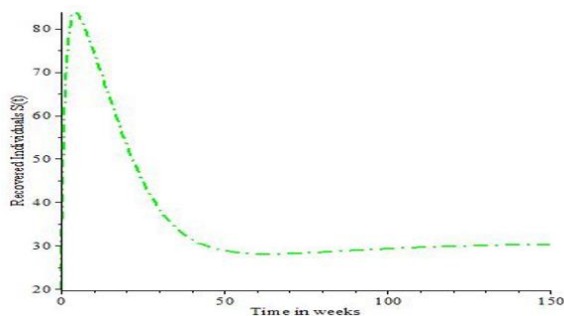


Figure 3: Recovered Population.

Figure 3 shows Infected population against time. We have proved that when the basic reproduction number is less than one the disease can be controlled. The population of the infected individual reduced drastically due to the fact that the basic reproduction number is less than one, when this happened then we can control the spread of the disease.

Figure 4 shows the recovered population against time, the population of the recovered class increased but the population tends to decrease as the 25th week this is as results of incomplete treatment. It is recommended that for treatment to be effective, it must be completed

CONCLUSION

We developed a mathematical model on the transmission dynamics of typhoid fever disease. The existence and uniqueness theorem using the Lipchitz criteria is used to check the validity of the model, we proceeded to calculate the disease-free equilibrium and we compute the basic reproduction number. Whether a disease dies out or persists in a population, depends on the value of the basic reproduction number. The results obtained from the basic reproduction number shows that the disease can be control if some necessary measures are put in place. It is recommended that early treatment should be implemented as this will reduced the number of infected individuals.

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