Mikailalsys Journal of Mathematics and Statistics

e-ISSN : 3030-816X
p-ISSN : 3030-8399

Index : Harvard, Boston, Sydney University, Dimensions, Lens, Scilit, Semantic, Google, etc

https://doi.org/10.58578/MJMS.v3i3.6136

Mathematical Analysis of *Cryptosporidium* Outbreak

Ayanrinola O. W[1], Odebiyi O. A[2], Ogidiolu O. M[3], Fagbemiro O[4], Ogidiolu O. O[5], Adeyemi M. O[6]

[1,2,3,5,6]Ladoke Akintola University of Technology, Ogbomoso, Oyo State, Nigeria
[4]Federal University of Agriculture, Abeokuta, Ogun State,Nigeria
solaayanrinola2020@gmail.com

Article Info:

Submitted:	Revised:	Accepted:	Published:
Apr 22, 2025	May 21, 2025	Jun 2, 2025	Jun 7, 2025

Abstract

Cryptosporidium is a waterborne pathogen that transmits through various routes, including contact with the feces of infected individuals, contaminated environments, unsafe water, unsanitized food, raw or unpasteurized milk, animal exposure, and recreational water bodies. This study formulates and analyzes five compartmental models to propose effective strategies for controlling the spread of cryptosporidiosis. The models were assessed for biological and mathematical validity using the theory of positivity and were confirmed to be epidemiologically well-posed. The basic reproduction number was derived using the next generation matrix method and found to be less than unity, suggesting that the infection has the potential to be eliminated from the population. Stability analysis of the disease-free equilibrium was conducted using the Jacobian matrix method and confirmed local asymptotic stability. Sensitivity analysis identified the contact rate between susceptible and infected individuals as the most influential parameter affecting the basic reproduction number. This highlights the importance of reducing contact rates as a key intervention strategy. Numerical simulations performed using Maple 22 provided supportive insights and interpretations of the model dynamics, reinforcing the analytical findings.

MJMS Journal is licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International License

Keywords: Cryptosporidiosis; Cryptosporidium; Gastrointestinal; Basic Reproduction Number; Asymptotically Stable

Introduction

Human cryptosporidiosis is caused by infection with apicomplexan protozoa of the genus cryptosporidium hominis, which humans are the only natural host and cryptosporidium parvum which infects a range of mammals, including humans. This mainly affects children and causes a self-limited diarrhea illness in otherwise healthy adults. It is also recognized as a cause of prolong diarrhea in children, which can lead to malnutrition. Cryptosporidiosis is primarily a childhood disease. Daycare Center –related outbreaks have a high rate (30% - 60%). Risk groups includes child-care workers, parents of infected children, hikers who drink unfiltered untreated water, swimmers who swallow contaminated recreation water, people who handle infected animals, and people exposed to human feces through sexual contact [1-4]

All hands are on desk in United Kingdom as Water Minister Robbie Moore, Anthony Mangnall, MP for Totnes and South Devon-where the outbreak was noticed, Laura Flowerdew, South West Water's chief customer and digital officer, groups of scientists and researchers are out, on the means of combating the outbreak of the cryptosporidium. Cryptosporidium is a parasite (a tiny organism) that causes an infection called cryptosporidiosis [5]. Cryptosporidiosis affects people and farm animals [6]. Cryptosporidium is found in lakes, streams and rivers, untreated drinking water and sometimes in swimming pools. It can infect anyone, but it is most common in children aged between one and five years. People who care for, or work with children are more vulnerable to the infection than others. For most people, the illness is unpleasant but self-limiting. However, it can be a serious illness in people who have immune systems that have been compromised. The incubation period is average of 7 days (range between 2-10days) [8].

Cryptosporidiosis can be contacted directly from infected person or infected animal, by touching

feaces, (for example when changing a nappy) and putting the hands near or in the mouth without washing them thoroughly. It can still be contacted from infected animals or by

swimming in contaminated pool, or drinking contaminated water [8]. Occasionally you can be infected by eating and drinking contaminated food, particularly unpasteurized milk, meat not properly boiled and diseases which can also be transmitted by contaminated food, poor hygiene or turning compost in a local compost site [10,13]. The people who are at risk of contacting the infection are child-care workers, the less vulnerable, Parents of infected children, people caring for other people with cryptosporidiosis, backpackers, hikers, and campers who drink unfiltered, untreated water, People who visit petting farms and open farms, including swimmers, who swallow water from contaminated sources People handling infected animals, People exposed to human faeces, People who turn compost that has not gone through its phase where temperatures is over 50°C. Cryptosporidiosis can be very contagious [11], and the infected person can infect others when the symptoms begin and for several weeks after the symptoms disappear, and the infected person who does not have symptoms can still infect others. The infection is characterized with severe watery diarrhea [12]; however, asymptomatic infection may arise which becomes the source of infection [13]. There has not been any approved vaccine against cryptosporidiosis and there is possibility of re-infection of an individual who have been cured of Cryptosporidiosis [14]

This study is organized as follows: Section 2 explains the formulation of model, including the model's positivity of solution. Section 3 presents an in-depth mathematical examination of the model, encompassing key aspects such as the basic reproduction, local stability analysis of the disease-free equilibrium, and computation of the sensitivity analysis of the basic reproduction number was carried out. Section 4 focuses on numerical simulations and discussions while Section 5 summarizes the findings.

Mathematical Model Formulation and Analysis

Some essential background information about cryptosporidiosis needs to be clearly understood before a meaningful model can be formulated or before already formulated model be re-modified. Some of these important background pieces of information have been clearly explained under the introduction. [21] Formulated SIR model where he investigates the probable approximate solution of integer and non-integer systems of nonlinear ordinary differential equations representing cryptosporidiosis dynamics. The approximate or estimate solution is derived through recent developed analytic method, the homortopy decomposition method (HDM). Several researchers have also worked on the

cryptosporidiosis with aim of providing solution to the spread of the infections among human population. Some of the researchers view the infections as zoonotic (i.e.) infection spread from animal to human, among them were [20] where he described cryptosporidiosis as zoonotic, he developed and analyzed a mathematical model using ordinary differential equation with a nonlinear incidence function called Beddington –De Angelis Function, where he worked on both human and animal population as infection primarily transmitted from animal to human.

Recent research reveals that the infection is not only zoonotic; the germs can be contacted from other source apart from animals. A system of ordinary differential equation if formulated and analyzed here revealing that the infection is not only contacted from animals [16]. This could be possible if the research aimed to eradicate the infection from both human animal population, but animal population is enormous as some are Pet and some are non-pet and most of the pet hosting the cryptosporidium are herbivores pets [17]. Research revealed that, the microbes are on vegetables and grass which may be contacted directly by farmers [18]. The total population is denoted by N(t)=S(t)+I(t)+T(t)+P(t) and the source of the germs causing infection can be termed as reservoir R(t)

Model Formulation Assumption

The system of equation comprises of S(t) representing susceptible human, I(t) infected human T(t) treated people while P(t) represents the recovered population and R(t) denoted the reservoir where the cryptosporidium can be contacted, this maybe through the infected pet, contaminated water, faeces of infected person, vomit from infected person, faeces of infected animals, consumption of uncooked not fully cooked of infected animals, consumption of unwashed raw vegetables, contaminated fruits, and including even grasses that herbivores consume.

$\beta(1-\theta I)$ represents the recruitments rate of susceptible, as some proportions were born into the population with the infections. α_1 denotes the rate by which susceptible individual contact the cryptosporidiosis from infected individual (internal source), α_2 denotes the rate by which susceptible individual contacts the infection from the reservoir (external source) μ_1, μ_2, μ_3 and μ_4 represents the natural death rate of susceptible individual, natural death rate of infected individual, natural death rate of individual under treatment,

and natural death rate of individual recovered from the infection, in which its numerical value can be assumed to be equal and natural death rate of microbes in the surrounding (reservoir) can be by their life span between two months [19]. Also μ_5 represents other means of eradicating the microbes from the environments such as water bodies, vegetables, fruits and other items consumed by human or pet that have close relationship with man. δ_1, δ_2 Represent death rate of infected individuals and the death rate of individual under treatment. γ, the rate by which infected individual move for treatment, σ is the rate of recovery of individual under treatment while π denotes loss of immunity from the infection.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \beta_1(1-\theta I) - \alpha_1 SI - \alpha_2 SR - \mu_1 S + \pi P \\
\frac{dI}{dt} &= \alpha_1 SI + \theta I\beta_1 - \mu_2 I - \delta_1 I - \gamma I \\
\frac{dT}{dt} &= \gamma I - \mu_3 T - \delta_2 T - \sigma T \\
\frac{dP}{dt} &= \sigma T - \mu_4 P - \pi P \\
\frac{dR}{dt} &= n\beta_2 - \mu_5 R - \delta_3 R
\end{aligned}\right\} \qquad (1)$$

$$S(0) \geq 0,\ I(0) \geq 0,\ T(0) \geq 0, P(0) \geq 0,\ R(0) \geq 0$$

Tabel 1. Definition of terms used in the modified model

Parameters	Descriptions
$\beta_1(1-\theta I)$	The recruitment rate of the susceptible with proportion infected during pregnant
α_1	Disease transmission coefficient from infected human to susceptible human
α_2	Disease transmission coefficient from reservoir to susceptible human
μ_1	Natural death of susceptible individual
μ_2	Natural death of infected individual
μ_3	Natural death of individual on treatment
μ_4	Natural death of just recovered individual
μ_5	Natural expiration of the protozoa (Life expectancy)
δ_1	Disease death rate of infected individual

δ_2 Disease death rate of individual under treatment

δ_3 Other means of eradicating the germs from the surrounding

$n\beta_2$ Recruitment rate of the germs in the surrounding

γ Progressive rate of moving individual infected to treated class

σ Progressive rate of moving individual treated and recovered to recovered class

π Progressive rate of discharging individual recovered back to susceptible class

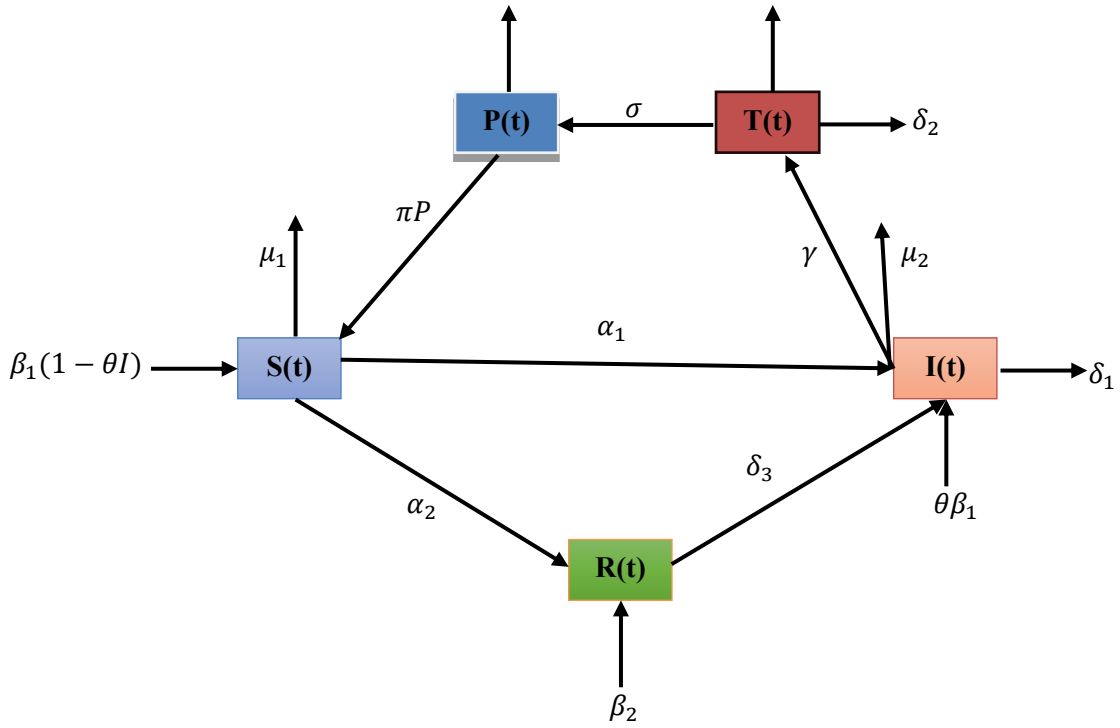


Figure 1: Schemeatic diagram of the model

Positivity of the model

The formulated model of the system of equation (1.0) is subjected into test through the theory of positivity.

Theorem 1.0

Let the initial conditions of the variables be such that $S(0) \geq 0,\ I(0) \geq 0, T(0) \geq 0, P(0) \geq 0, R(0) \geq 0$

Proof:

Positivity of S(t) from the first equation in (1)

$$\frac{dS}{dt} = \beta_1(1-\theta I) - \alpha_1 SI - \alpha_2 SR - \mu_1 S + \pi P \qquad (2)$$

The model (1) can be express without loss of generality after eliminating the positive term $\beta_1(1-\theta I)+\pi P$ as we have it in (2), it implies

$$\frac{dS}{dt} \geq -(\alpha_1 I + \alpha_2 R + \mu_1)S \qquad (3)$$

Using variable separable, we have

$$\frac{dS}{S} \geq -(\alpha_1 I + \alpha_2 R + \mu_1)dt \qquad (4)$$

Integrating both sides of (4) we have

$$\int \frac{dS}{S} = -\int (\alpha_1 I + \alpha_2 R + \mu_1)dt \qquad (5)$$

$$\ln S \geq -(\alpha_1 I + \alpha_2 R + \mu_1)t + C_1$$

$$S(t) \geq e^{(\alpha_1 I+\alpha_2 R+\mu_1)t}.e^{c_1}$$

$$S(t) \geq A_1 e^{-(\alpha_1 I+\alpha_2 R+\mu_1)t}$$

$$S(0) = S_0$$

$$S(0) \geq A_1$$

$$S(t) \geq S_O e^{-(\alpha_1 I+\alpha_2 R+\mu_1)t} \qquad (6)$$

Irrespective of sign with exponential function, it is always positive, therefore $S(t) \geq 0$ since $S_0 \geq 0$

Similarly, it can be shown that $I(t) \geq 0, T(t) \geq 0, P(t) \geq 0, R(t) \geq 0$ for all $t \geq 0$

Thus the solutions $S(t), I(t), T(t), P(t), R(t)$ of the system remain positive forever. This proves

that the model's variables are biologically meaningful and Mathematically well posed.

Disease free equilibrium points

The disease free equilibrium points is a situation whereby there is no disease in the system

Recall the system of equation (1)

$$\left.\begin{aligned}
\frac{dS}{dt} &= \beta_1(1-\theta I) - \alpha_1 SI - \alpha_2 SR - \mu_1 S + \pi P \\
\frac{dI}{dt} &= \alpha_1 SI + \theta I\beta_1 - \mu_2 I - \delta_1 I - \gamma I \\
\frac{dT}{dt} &= \gamma I - \mu_3 T - \delta_2 T - \sigma T \\
\frac{dP}{dt} &= \sigma T - \mu_4 P - \pi P \\
\frac{dR}{dt} &= n\beta_2 - \mu_5 R - \delta_3 R
\end{aligned}\right\} \quad (7)$$

Let

$$I(t) = 0,\ T(t) = 0, P(t) = 0,\ R(t) = 0 \quad (8)$$

We have

$\frac{dS}{dt} = \beta_1(1-\theta I) - \mu_1 S$ This implies that $\frac{dS}{dt} = \beta_1 - \theta\beta_1 I - \mu_1 S$

Then, let $\frac{dS}{dt} = 0 \Rightarrow\ \beta_1 - \mu_1 S = 0$

$$S = \frac{\beta_1}{\mu_1} \quad (9)$$

Therefore, we have $S^0, I^0, T^0, P^0, R^0 = \left[\frac{\beta_1}{\mu_1}, 0,0,0,0\right]$ (10)

Basic Reproduction Number

Basic reproduction number is the measure of the effect created on a system, when a single infected individual is introduced into the system of fully susceptible population over a particular time interval. The basic reproductive number (R_0) of an infectious agent such as rabies virus is defined as the average number of secondary infections produced by an infected individual in an otherwise susceptible host population [19]. R_0 determines whether a pathogen can persist in such a population and is valuable for assessing control options. When R_0 is less than 1, on average each infectious individual infects less than one other individual, and the pathogen will die out in the population. In contrast, when R_0 exceeds 1, numbers of cases will on average rise over time, and an epidemic can result. R_0 is consistently estimated to be between 1 and 2 from rabies outbreaks in dog populations around the world [24], which is relatively close to the extinction. It is the threshold

parameter that determines or governs the spread of disease. Considering only the infection classes in the system,

this can be obtained by generating the Jacobian Matix, the Jacobian matrix FV^{-I}.

And F is transition matrix and V is transmission Matrix (i.e.) gaining and losing according to the infectious classes

$$\begin{aligned}\frac{dI}{dt} &= \alpha_1 SI + \theta I\beta_1 - \mu_2 I - \delta_1 I - \gamma I \\ \frac{dT}{dt} &= \gamma I - \mu_3 T - \delta_2 T - \sigma I \\ \frac{dR}{dt} &= n\beta_2 - \mu_5 R - \delta_3 R\end{aligned} \qquad (11)$$

Let F be the number of new infection coming into the system and V be the number of infections

that are leaving the system either by death or birth, then

$$V = \begin{bmatrix} (\mu_2 + \delta_1 + \gamma)I \\ (\mu_3 + \delta_2 + \sigma)T \\ (\mu_5 + \delta_3)R \end{bmatrix} \quad \text{And} \quad F = \begin{bmatrix} (\alpha_1 SI + \theta I\beta_1) \\ \gamma I \\ n\beta_2 \end{bmatrix}$$

By simplifying V and F, we arrive the characteristics equation

$$\left[\frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)} - \lambda\right](-\lambda) = 0$$

This becomes

$$-\lambda\frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)} + \lambda^2$$

$$\lambda^2 - \lambda\frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)} = 0$$

Factoring out the λ we have

$$\lambda\left[\lambda - \frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)}\right] = 0 \tag{12}$$

$$\lambda = 0 \text{ or } \lambda = \frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)}$$

Therefore

$$R_O = \left[\frac{\beta_1(\alpha_1 + \theta\mu_1)}{\mu_1(\mu_2 + \delta_2 + \gamma)}\right] \tag{13}$$

The extent at which the disease spread and the extent at which the disease can be control is determined by the basic reproduction number. Basic reproduction number determines the extent at which the infection can be controlled. The implication of the basic reproduction number is that, if

$R_0 < 1$, it means the infection will die out, $R_0 > 1$, it means the infection will spread and $R_0 = 1$, it means that the infection will remain in the population at a consistent rate since one infected individual can transmit the disease to the susceptible population.

Stability of disease free equilibrium points

Theorem 2.0

The disease free equilibrium of the model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof

Evaluating the Jacobian Matrix at the disease free equilibrium point E^0,

$$J(E^0) = \begin{vmatrix} -\mu_1 & -(\theta\beta_1 + \frac{\alpha_1\beta_1}{\mu_1}) & 0 & \pi & 0 \\ 0 & (\frac{\alpha_1\beta_1}{\mu_1} + \theta\beta - \mu_2 - \delta_1 - \gamma) & 0 & 0 & 0 \\ 0 & \gamma & -(\mu_3 + \delta_2 + \sigma) & 0 & 0 \\ 0 & 0 & \sigma & -(\mu_4 + \pi) & 0 \\ 0 & 0 & 0 & 0 & -(\mu_5 + \delta_3) \end{vmatrix} = 0 \tag{14}$$

Solving the Jacobian matrix (14) by introducing the eigen values, we have

$$\begin{vmatrix} -(\mu_1)-\lambda & -(\theta\beta_1+\frac{\alpha_1\beta_1}{\mu_1}) & 0 & \pi & 0 \\ 0 & (\frac{\alpha_1\beta_1}{\mu_1}+\theta\beta-\mu_2-\delta_1-\gamma)-\lambda & 0 & 0 & 0 \\ 0 & \gamma & -(\mu_3+\delta_2+\sigma)-\lambda & 0 & 0 \\ 0 & 0 & \sigma & -(\mu_4+\pi)-\lambda & 0 \\ 0 & 0 & 0 & 0 & -(\mu_5+\delta_3)-\lambda) \end{vmatrix} = 0 \quad (15)$$

Then, we obtained

$$[-(\mu_1)-\lambda]\left[(\frac{\alpha_1\beta_1}{\mu_1}+\theta\beta-\mu_2-\delta_1-\gamma)-\lambda\right][-(\mu_3+\delta_2+\sigma)-\lambda][-(\mu_4+\pi)-\lambda][-(\mu_5+\delta_3)-$$

That is,

$$-(\mu_1)-\lambda=0$$
$$\lambda_1=-\mu_1 \quad (16)$$

$$(\frac{\alpha_1\beta_1}{\mu_1}+\theta\beta-\mu_2-\delta_1-\gamma)-\lambda=0$$
$$-(\frac{\alpha_1\beta_1}{\mu_1}-\theta\beta+\mu_2+\delta_1+\gamma)-\lambda=0$$
$$\lambda_2=-(\frac{\alpha_1\beta_1}{\mu_1}-\theta\beta+\mu_2+\delta_1+\gamma) \quad (17)$$

$$-(\mu_3+\delta_2+\sigma)-\lambda=0$$
$$\lambda_3=-(\mu_3+\delta_2+\sigma) \quad (18)$$

$$-(\mu_4+\pi)-\lambda=0$$
$$\lambda_4=-(\mu_4+\pi) \quad (19)$$

$$-(\mu_5+\delta_3)-\lambda=0$$
$$\lambda_5=-(\mu_5+\delta_3) \quad (20)$$

Therefore, the model is locally asymptotically stable, since all the eigenvalues are all negative.

Sensitivity Analysis of the model

The aim of sensitivity analysis is to determine the most sensitive parameter of the basic reproduction number or control reproduction number R_o which enable us to know how to control the infection within the population or suggesting the possible approach to the control of the infection for other researchers on the clinical and chemical support. In this section, we investigated the sensitivity of the parameters for the basic reproduction number of the model using the notion from [16]. It is important to carry out the sensitivity of the basic reproduction number R_o for its parameters. This will give parameters with a high quality impact on the Cryptosporidiosis model (1) and therefore allow us to target on control measures to reduce the transmission rate of the disease. To determine the sensitivity index of R_0,

Following the approach used in [25-26], the sensitivity indices of the parameters relative to the basic reproduction number (R_0), (13) is established. Therefore, the normalized forward sensitivity indices of the basic reproduction number (R_0) associated with parameters, ρ, is calculated with respect to each of the parameters involved in R_0 as computed in table 2 below:

Table 2: Sensitivity Analysis on the basic reproduction number

Parameters	**Values**	**Sensitivity index**
β_1	0.004	1.0000
γ	0.04	-0.9174
μ_1	0.005	-0.9999
μ_2	0.003	-0.0688
θ	0.0001	1.1×10^{-4}
α_1	0.045	9.999×10^{-1}
δ_2	0.0006	-0.00793

Numerical Simulations of the model

The numerical simulations of the model (1) were performed to support some of the analytical results. We use the set of parameters values given on Table 2 below and the initial values of the

model are set as: $S(0) = 1000$ $I(0) = 10, T(0) = 5, P(0) = 50, R(0) = 500$. Maple software application was used to implements the simulations to generate the results below.

Table 3. Table of Parameters and their values

Parameters	Values	Source
β_1	0.0004	[20]
μ_1	0.0005	[20]
δ_1	0.0006	[18]
δ_2	0.0001	Assumed
α_1	0.045	[17]
α_2	0.5	[19]
β_2	1000	[19]
π	0.7	[20]
θ	0.0001	[18]
γ	0.03	Assumed
σ	0.04	Assumed
μ_2	0.005	Assumed
μ_3	0.0005	Assumed
μ_4	0.0005	Assumed
μ_5	0.0009	Assumed
δ_3	0.5	Assumed

Presentation of Results

Simulation of the model was performed for better understanding of dynamical spread and transmission of cryptosporidium outbreak using Maple software. The result of the model equations are presented below in form of graphs and are discussed in the figure below to

illustrate the changes in the compartments. The infected population, treated population and the reservoir population were checked in order to observe their impact on the numerical spread of the disease using a set of reasonable parameters.

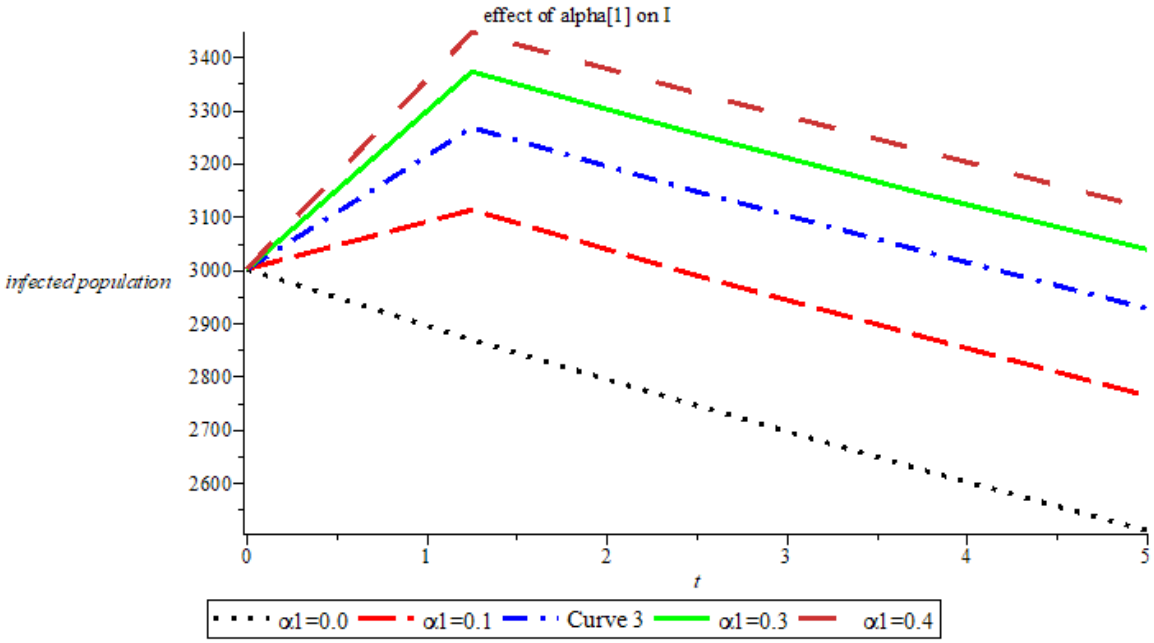


Figure 2. Effect of Contact rate of subsceptibe individual with infected individual on the infected Population

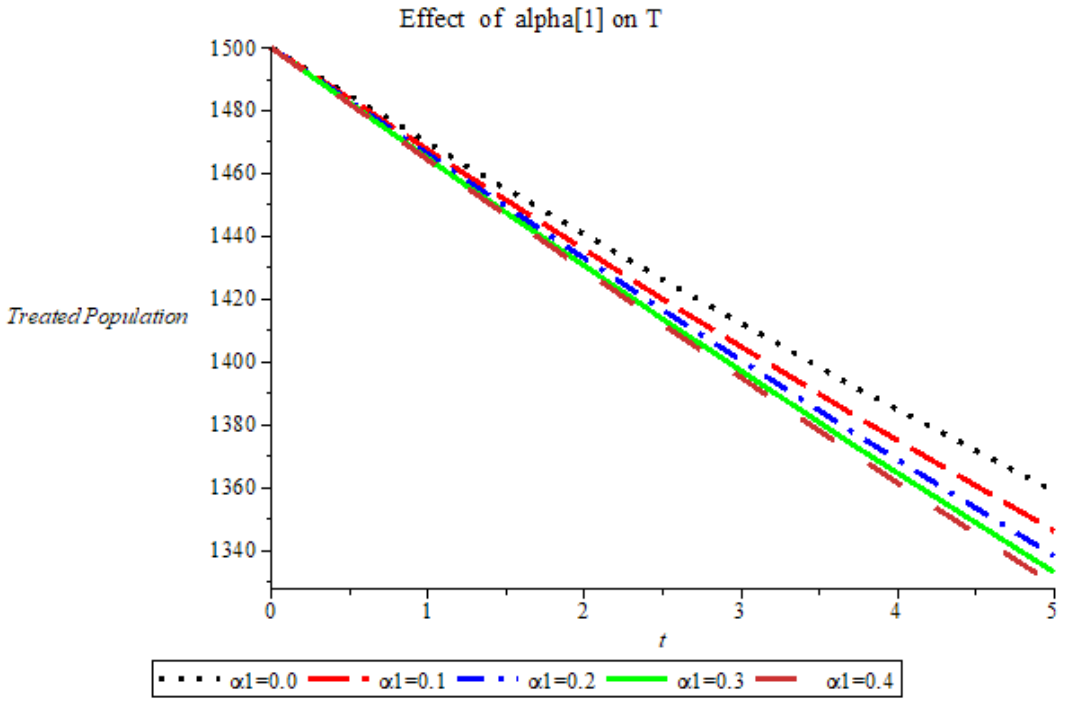


Figure 3. Effect of Contact rate of subsceptibe individual with Reservoir on the Treated Population

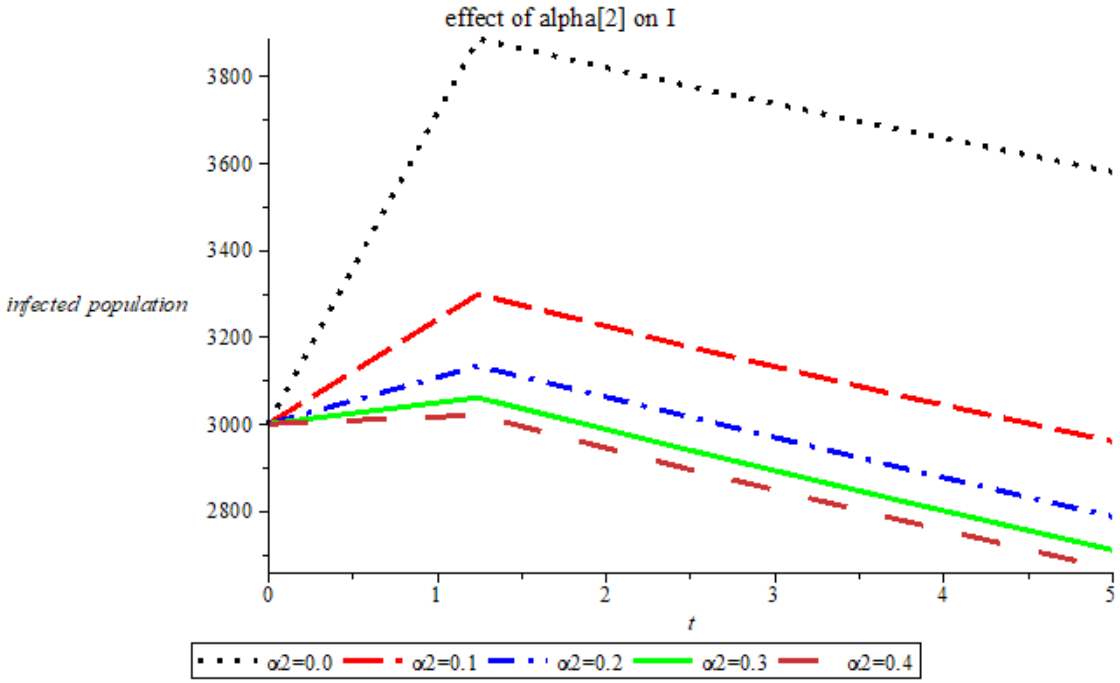


Figure 4: Effect of Contact rate of subsceptibe individual with Reservoir on the infected Population

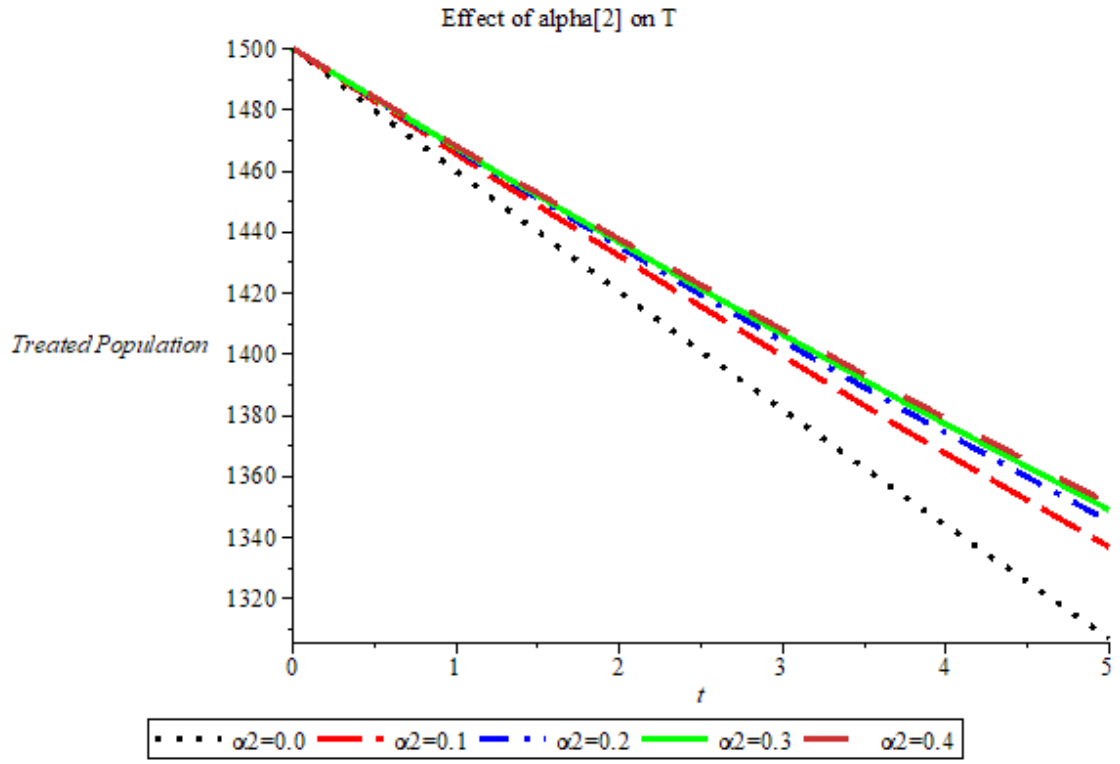


Figure 5. Effect of Contact rate of subsceptibe individual with Reservior on the Treated Population

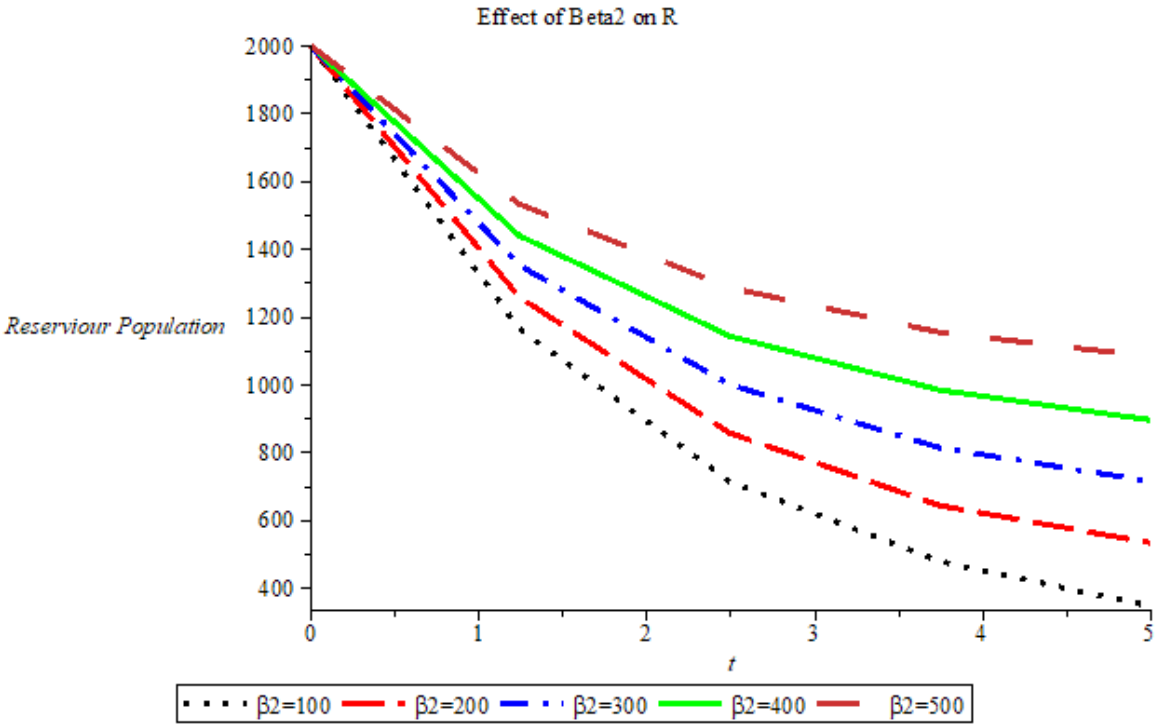


Figure 6. Effect ofrecruitment rate of germs on the Reservior Population

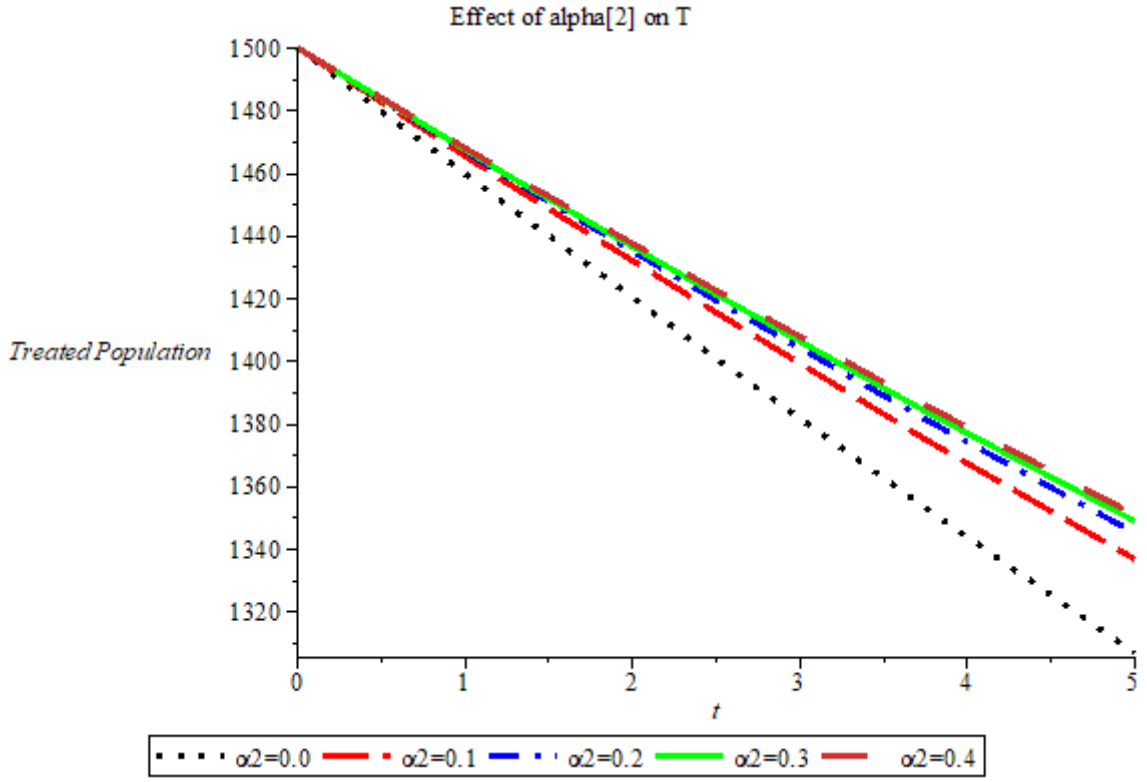


Figure 7. Effect of Contact rate of recruitment rate of germs on the Treated Population

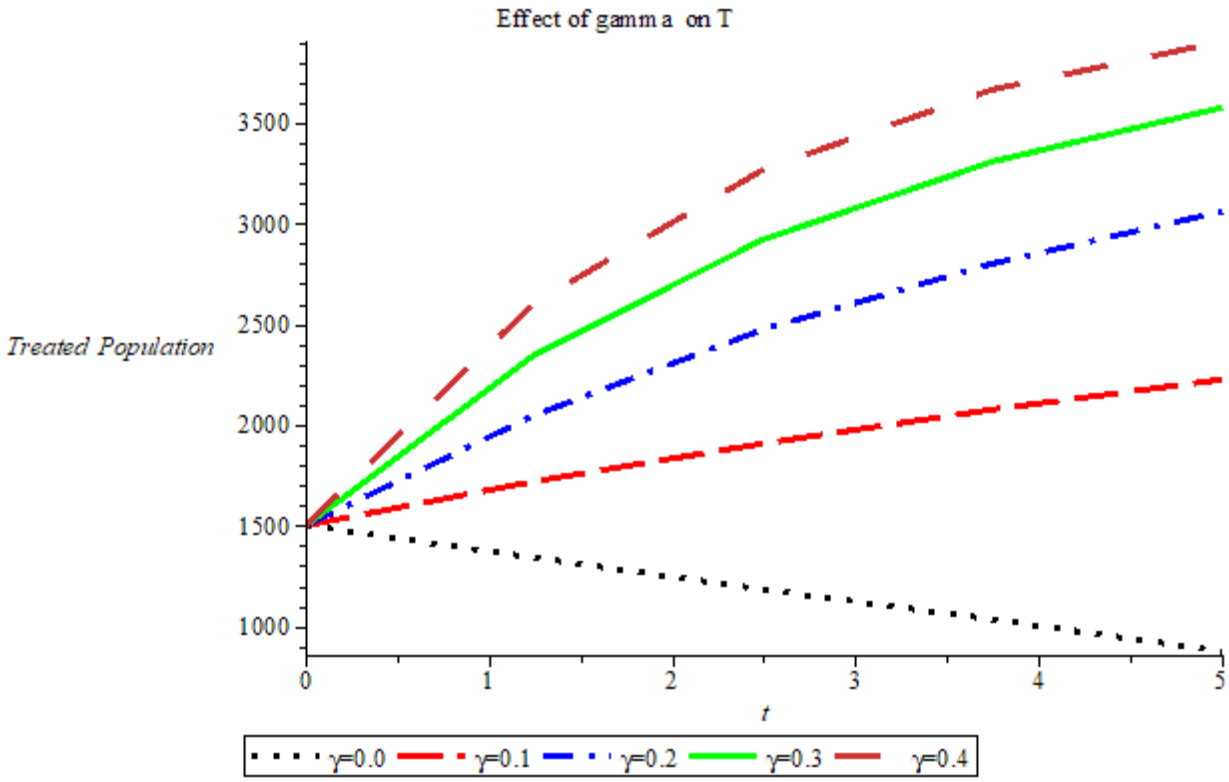


Figure 8. Effect of the rate of movement from infected population to Treatment(Hospitalize) on the Treated Population.

Discussions of the results

From equation (13), the numerical value of the basic reproduction number of this model is lesser than unity, as carried out with the help of maple ssoftware application, this indicates that, the infection will die out from the society with time.

The stabilty ananlysis of the model considered is locally asymptotically stable, since all the Eigenvalues are negative.

From table 2: the sensitivity analysis of the model, we can deduce that only the parameter α_1 has the most positive influence on the basic reproduction number. Increase of this parameter will lead to increase in the value of R_0 while keeping other parameters constant and in the same way leading to an increase of the spread of Cryptosporidiosis among the susceptible population.

Figure 2: Effect of Contact rate of subsceptibe individual with infected individual (α_1) on the infected Population, this indicates that**,** as contacts rate increases the infection increases in the population, more awareness is needed to reduce the infection most especially by the health worker on the proper need of personal protective equipment before treatment is administered to the infected individuals.

Figure 3: Effect of Contact rate of subsceptibe individual with Reservoir (α_2) on the Treated Population, it was estabished that the germs can be contacted by other means (Reservior) such as contaminated water and swuiming pool apart from infected person, as this contact rate increases, the infection also increases. The quality of treatment administered reduces the treated population as clearly observed on the graph.

Figure 4: Effect of Contact rate of subsceptibe individual with Reservoir (α_2) on the infected Population. **A**s the contact rate increases, the infection also increases within the population. Good sensitization must be put in place on varrious ways of maintaining hygienic environment and treatment of water body such as (swiming pool, pipe born water supply for human consumption) is highly essential.

Figure 5: Effect of Contact rate of subsceptibe individual with Reservior (α_2) on the Treated Population: As contact rate increases, infection also increases indicating that more people are subjected to treatment

Figure 6: Effect of recruitment rate of cryptosporodiosis (β_2) on the Reservior Population: As the germs reproduces within the environment, if not combated by sanitization and fumigation, the environment might be contaminated with germs and most especially moistly areas as illustrated in the figure.

Figure 7: Effect of recruitment rate of germs (β_2) on the Treated Population: As the germs reproduces within the environment, more infection will likely spread and thereby increases the population of treated people as illustrated in the figure.

Figure 8: Effect of the rate of movement of infected to the Treated Population, the more people are infected, the more hospital become congested, and posses more risk to health workers if appropriate control measures are not quickly put in place.

Conclusion and recommendations

Mathematical analysis of cryptosporidium outbreak is a research undertaken purposely to suggest a likely solution to combat the spread of the infection. The followings are thereby recommended to:

1. create an awareness campaign on the spread of the infection on the need to wash hands thoroughly with soap and warm water before preparing and eating food after handling raw food and after going to the toilet or changing a baby's nappy, feeding, grooming or playing with pets and other animals.
2. sensitize general public on the need not to drink untreated water and to sound the note of warning not use ice or drinking water in countries where the water supply might be unsafe
3. always wash or peel fruits and vegetables before eating them.
4. sensitize people on the need not to go for swimming if have diarrhea, then If anyone have had cryptosporidiosis, it is not advisable to go for swimming until you have been cleared of diarrhea for at least two weeks.
5. avoid swallowing water in lakes and swimming pools.
6. pay special attention to hygiene during farm visits, washing hands after making any contact with animals in the farm, and eat only in designated areas.
7. cryptosporidiosis is highly infectious so there is need to scrupulously clean the toilet seats, toilet bowls, flush handles, taps and wash hand basins after use with disinfectants.
8. make sure all members of household wash their hands thoroughly with soap and hot water after going to the toilet and after handling soiled clothing or bedding and avoid sharing towel and clothing and ensure that all soiled clothes and linen are properly washed.

References

1. White, A. C. Jr. (2020). Cryptosporidiosis (Cryptosporidium species). In J. E. Bennett, R. Dolin, & M. K. Blaser (Eds.), *Principles and practice of infectious diseases* (pp. 3410–3420). Elsevier Inc.
2. Checkley, W., White, A. C. Jr., Jaganath, D., Arrowood, M. J., Chalmers, R. M., Chen, X. M., et al. (2015). A review of the global burden, novel diagnostics, therapeutics, and vaccine targets for Cryptosporidium. *The Lancet Infectious Diseases, 15*(1), 85–94.

3. Khalil, I. A., Troeger, C., Rao, P. C., et al. (2018). Morbidity, mortality, and long-term consequences associated with diarrhea from Cryptosporidium infection in children younger than 5 years: A meta-analysis study. *The Lancet Global Health, 6*(7), e758–e768.
4. Centers for Disease Control and Prevention. (2019). *Nationally notifiable infectious diseases and conditions, United States: Annual tables*. https://wonder.cdc.gov/nndsss/nndss_annual_tables_menu.asp
5. Tzipori, S., & Griffiths, J. (1998). Natural history and biology of Cryptosporidium parvum. *Advances in Parasitology, 40*, 5–36. https://doi.org/10.1016/S0065-308X(08)60116-5
6. Brookhart, M. A., Hubbard, A. E., van der Laan, M. J., et al. (2002). Statistical estimation of parameters in a disease transmission model: Analysis of a Cryptosporidium outbreak. *Statistics in Medicine, 21*, 3627–3638.
7. Boehmer, T. K., Alden, N. B., Ghosh, T. S., & Vogt, R. L. (2009). Cryptosporidiosis from a community swimming pool: Outbreak investigation and follow-up study. *Epidemiology and Infection, 137*(11), 1651–1654.
8. Black, M., & McAnulty, J. (2006). The investigation of an outbreak of cryptosporidiosis in New South Wales in 2005. *New South Wales Public Health Bulletin, 17*(5–6), 76–79.
9. Centers for Disease Control and Prevention. (2007). Cryptosporidiosis outbreaks associated with recreational water use—Five states, 2006. *Morbidity and Mortality Weekly Report, 56*(29), 729–732.
10. Stanford University. (n.d.). *Cryptosporidiosis*. https://web.stanford.edu/class/Cryptosporidiosis
11. Food Safety News. (2024, May). Cryptosporidium outbreak affects dozens in England. https://www.foodsafetynews.com/2024/05/cryptosporidium-outbreak-affects-dozens-in-england/
12. NHS Direct. (n.d.). Retrieved from http://www.nhsdirect.nhs.uk or http://www.nhsdirect.wales.nhs.uk
13. Heymann, D. L. (Ed.). (2008). *Control of communicable diseases manual* (19th ed.). American Public Health Association.
14. Insulander, M., Lebbad, M., Stenström, T. A., & Svenungsson, B. (2005). An outbreak of cryptosporidiosis associated with exposure to swimming pool water. *Scandinavian Journal of Infectious Diseases, 37*(5), 354–360.
15. Sponseller, J. K., Griffiths, J. K., & Tzipori, S. (2014). The evolution of respiratory cryptosporidiosis: Evidence for transmission by inhalation. *Clinical Microbiology Reviews, 27*(3), 575–586. https://doi.org/10.1128/CMR.00115-13
16. Lemmon, J. M., McAnulty, J. M., & Bawden-Smith, J. (1996). Outbreak of cryptosporidiosis linked to an indoor swimming pool. *Medical Journal of Australia, 165*(11–12), 613–616.
17. McAnulty, J. M., Fleming, D. W., & Gonzalez, A. H. (1994). A community-wide outbreak of cryptosporidiosis associated with swimming at a wave pool. *Journal of the American Medical Association, 272*(20), 1597–1600.
18. Puech, M. C., McAnulty, J. M., Lesjak, M., Shaw, N., Heron, L., & Watson, J. M. (2001). A statewide outbreak of cryptosporidiosis in New South Wales associated with swimming at public pools. *Epidemiology and Infection, 126*(3), 389–396.
19. Anderson, R. M., & May, R. M. (1991). *Infectious diseases of humans: Dynamics and control*. Oxford University Press.

20. Brookhart, M. A., Hubbard, A. E., van der Laan, M. J., et al. (2002). Statistical estimation of parameters in a disease transmission model: Analysis of a Cryptosporidium outbreak. *Statistics in Medicine, 21*, 3627–3638. https://doi.org/10.1002/sim.1258
21. Bonyah, E., Zakari, A., & Bakari, L. (2016). Qualitative analysis of malaria dynamics with nonlinear incidence function. *Asia Pacific Journal of Computer Engineering, 3*(2). https://doi.org/10.1186/s40540-016-0018-2
22. Wikipedia contributors. (n.d.). *Cryptosporidium life cycle*. Wikipedia. https://www.en.wikipedia.org/wiki/Cryptosporidiosis
23. Stanford University. (n.d.). *Cryptosporidiosis*. https://web.stanford.edu/class/Cryptosporidiosis
24. Hampson, K., Dushoff, J., Bingham, J., Bruckner, G., Ali, Y. H., & Dobson, A. (2007). Synchronous cycles of domestic dog rabies in sub-Saharan Africa and the impact of control efforts. *Proceedings of the National Academy of Sciences, 104*(18), 7717–7722.
25. Olaniyi, S., & Obaniyi, O. S. (2014). Qualitative analysis of malaria dynamics with nonlinear incidence function. *Applied Mathematical Sciences, 8*(78), 3889–3904.
26. Olusola, A. O., Oladejo, J. K., Salahu, W. O., Taiwo, A. A., & Ayanrinola, O. W. (2025). Stability and sensitivity analysis of HIV/AIDS model with saturated incidence rate. *Transpublika International Research in Exact Sciences, 4*(2). https://doi.org/10.55047/tires.v4i2.1650