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ABSTRACT

The disease is still endemic in many parts in the world, we need to raise up an awareness to the community to control and eliminating the dynamic transmission of this disease, To eliminate the disease in the community we have to maintain the effectiveness of reproduction number by achieving and maintaining low levels of susceptibility $R_0 < 1$.

In this project, we concentrated on the mathematical model for control and elimination of transmission dynamics of paragonimiasis. We have obtained disease free equilibrium (DFE) point, basic reproduction number for the model and interpreted them epidemiologically.

Also, we performed sensitivity analysis to examine parameters which have great impacts on the spread of disease and we saw that recruitment into susceptible snails and crabs both are directly proportional to the spread of disease since both expands reproductive number.

Simulation of different parameters to see the variation of the populations in the model has been done by using MATLAB codes of the Ordinary differential equations (ODES) to observe the effectiveness of interventions in disease controlling and concludes that, education efficacy and treatment both have significant impacts in controlling and eliminating paragonimiasis in the community.

DECLARATION

We hereby declare to the senate of the University of Dodoma that this project is our own original work and that it has neither been submitted nor being con-currently submitted for degree award in any other institution.

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CERTIFICATION

The undersigned certify that have read and hereby recommend for acceptance by the University of Dodoma a project report entitled: **A mathematical model for controlling and eliminating paragonimiasis disease in the community**, in partial fulfillment of the Mathematical Project Course (MT 3200) for the degree of Bachelor of Science in Mathematics and Statistics of the University of Dodoma (2021/22-2023/24).

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First, we would like to thank our almighty God for giving us good health and strength which helped us to accomplish our mathematical project effectively. In fact, without him we couldn't finish this project successfully.

Secondly, special thanks to several researchers in the field of Mathematics who developed different models on paragonimiasis, because their materials and ideas helped us to complete this project.

Also, our gratitude to the department of Mathematics and Statistics, panel of Mathematics which accepted our concept note and gave us permission to go ahead with our project.

Our heartfelt thanks go to our supervisor **Dr. Stephen Edward Mwaijande** a lecturer at the University of Dodoma (UDOM) who has always been there to help us and give us direction on what to do in our project. Honestly, without him our project couldn't be this successful.

We would like to thank our families for their support, prayers and encouragement in our studies though we are far from them but they always encourage us in whatever we do.

Since it is not possible to mention everyone who participated to this work, we want to take this opportunity to thank everyone who has contributed in our project in one way or another towards the accomplishment of this project. May the lord bless them.

DEDICATION

To our families, supervisors and lecturers for their continuous and unconditional support towards the accomplishment of the degree of Bachelor of Science in Mathematics and Statistics of the University of Dodoma (2021/2022-2023/2024)

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ABBREVIATIONS

DFE	-	Disease Free Equilibrium
DVC-ARC	-	Deputy Vice Chancellor for Academic Research and Consultancy
EE	-	Equilibrium Endemic
MATLAB	-	Matrix Laboratory
MDA	-	Mass Drug Administration
ODEs	-	Ordinary Differential Equations
UDOM	-	University of Dodoma

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CHAPTER ONE

INTRODUCTION AND BACKGROUND

1.1 Background of Paragonimiasis

Paragonimiasis or lung fluke infection is a food-borne disease and is the one of the re-emerging neglected tropical diseases, which commonly infects the lungs caused by parasite known as **paragonimus genus** or fluke lung of flat-worm. The infection occurs primarily in the lungs and pleura of humans and animals. When the parasite infects the lungs, it can cause a pulmonary disease resembling tuberculosis. However, it frequently involves other visceral organs, including the brain, spinal cord, and abdominal organs.

There are over 40 species in the *Paragonimus* genus. Over ten of these infect humans. There were 53 species in 21 genera of freshwater crustaceans and 40 species of freshwater snails, which are intermediate hosts of *Paragonimus*. This parasite's infection is transmitted to a person in indirect way after eating raw or undercooked infected crabs or crayfish.

One of the first cases of paragonimiasis was reported in Vietnam, in 1906. From 1906 to 1992, over 30 cases of paragonimiasis in Vietnam were reported. The National Institute of Malariology, Parasitology, and Entomology, Ha Noi, commenced studies on the epidemiology, pathology, diagnosis, and treatment of paragonimiasis in some northern mountainous provinces of Vietnam in early 1994.

Paragonimiasis is a fatal disease, it was estimated that there were about 23.2 million cases of paragonimiasis worldwide in 2005, including about 5 million who were heavily infected patients and these cases resulted in death.

1.2 Symptoms of Paragonimiasis Disease

Symptoms of paragonimiasis are often vague and non-specific. Some of those symptoms are, first in the early stage of infection (2-15 days), symptoms include fever, diarrhoea or abdominal pain but in the later stages a patient experiences, bloody cough, seizure, chest pain, headache, visual disturbances, motor and sensory disturbances and fatigue.

1.3 Risk Group

Paragonimiasis is a parasitic disease caused by lung flukes of the genus *Paragonimus*. People become infected by consuming raw or undercooked freshwater crabs or crayfish that harbor the parasites. The risk group for Paragonimiasis includes individuals who live in or visit areas where the disease is endemic, especially those who consume raw or undercooked freshwater crustaceans.

This group also includes individuals who engage in activities such as fishing, farming, or hunting that involve contact with freshwater crabs or crayfish. Additionally, populations with limited access to clean water and proper sanitation are at higher risk due to their reliance on potentially contaminated water sources. Understanding and targeting these risk factors are essential for developing effective control and elimination strategies for Paragonimiasis.

1.4 Modes of Transmission of Paragonimiasis

At the first stage, parasites infect snails which are the first intermediate hosts, and later on the snails infect freshwater crabs which are the second intermediate host. Finally, in the third stage, they infect humans and cause paragonimiasis (Pan and Zhang, 2023).

The infection is transmitted to an individual in indirect way through consumption of raw or undercooked crustaceans such as crabs. The larval stages of the parasite (*Paragonimus*) are released when the crab or crayfish is digested in human body after eating that undercooked crabs. It is well described in the diagram below.

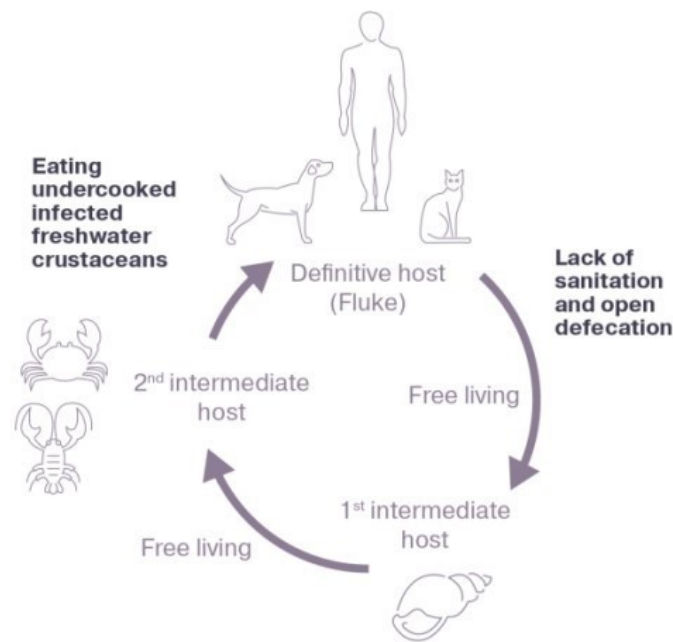


Figure 1: Paragonimus life cycle. Source: <https://www.who.int/health-topics/foodborne-trematode-infections>

1.5 Disease Diagnosis and Treatment

Paragonimiasis disease has treatment. A disease is treatable with antiparasitic medications e.g praziquantel. Having symptoms as stated above does not implies a person suffer from paragonimiasis disease he or she may take the diagnosis so as to detect whether he or she suffers paragonimiasis. The diagnosis is usually done through, clinical evaluation (identifying Paragonimus eggs in the sputum or sometimes in the stool), through imaging studies (like chest X-rays), laboratory tests to check the existence of the disease after symptoms occurred and confirming is a paragonimiasis patient.

1.6 Preventive measures and Immunization

A disease has no a specific vaccine. But it has treatment (ant parasitic Medication e.g praziquantel) A person re-infected when and only when he or she is exposed to the parasite again through consumption of raw or undercooked freshwater. Preventive Measures of the disease includes, freshwater crustaceans such as crabs are well cooked at least $145^{\circ}F$ before consumptions, proper hygiene e.g washing hands with soap especially after handling raw seafood, avoiding contaminated water from untreated water from freshwater sources and public health education.

1.7 Statement of the Problem

Different researchers have conducted several studies about paragonimiasis disease on its transmission, prevention and control measures in biological aspect and discovered paragonimiasis' treatment. Despite the availability of treatment, still the disease exist in the community.

This might be attributed due to lack of education about the disease transmission in the population. It is uncommon disease. The study aims to develop a mathematical model to provide awareness to the community to understand the disease transmission and taking effective preventive measures about the disease.

1.8 Objectives of the Study

1.8.1 Main Objective:-

To develop a mathematical model for controlling and eliminating Paragonimiasis disease in the community.

1.8.2 Specific Objectives

- (i) To formulate a mathematical model for paragonimiasis control and elimination
- (ii) To determine the disease equilibrium points of the formulated model.
- (iii) To determine a basic reproductive number of the formulated model.
- (iv) To interpret a basic reproductive number of the formulated model epidemiologically.
- (v) To assess the impact of control measures on the disease transmission numerically.

1.9 Research Questions

- (i) How can a mathematical model for paragonimiasis control and elimination be formulated?
- (ii) How can the disease equilibrium points of the formulated model be determined?
- (iii) How can the basic reproductive number of the model be determined?
- (iv) How can the basic reproductive number interpreted epidemiologically?
- (v) How can the impact of control measures on the disease transmissions be assessed?

1.10 Significance of the study

- The study will help individual/readers to understand the disease how it's caused/transmitted and how to take measures (Public awareness).
- Population dynamics by analyzing the impact of paragonimiasis on humans and host populations by considering factors like demographics, migration and environment changes.
- This study will adds to the body of knowledge on paragonimiasis and parasitic diseases, providing a valuable reference for future research and helping to advance the field of infectious disease modelling in Mathematics.
- The results from this study can inform and influence health policies related to parasitic diseases, contributing to the development of advanced control and preventive strategies at local, national and international levels.

CHAPTER TWO

LITERATURE REVIEW

Paragonimiasis is a neglected tropical disease caused by a parasitic infection with the lung fluke *Paragonimus*. This disease affects millions of people worldwide, particularly in rural communities where the consumption of raw or under-cooked freshwater crabs and crayfish is common. Traditional methods of controlling and eliminating paragonimiasis have been largely ineffective. However, mathematical modeling has emerged as a valuable tool in understanding the dynamics of disease transmission and designing effective control strategies. This literature review aims to explore the mathematical models that have been developed previously for controlling and eliminating paragonimiasis in the community and the results includes:

Li, Wang, Huang, & Chen,(2017) developed a mathematical model to investigate the impact of different control strategies on the transmission dynamics of paragonimiasis in the community. The model incorporated various factors such as host population dynamics, infection rates, and treatment interventions. The study suggested that a combination of chemotherapy, health education, and snail control could effectively reduce the prevalence of paragonimiasis in the community.

Wang, Li, & Chen, (2018) proposed a mathematical model in order to assess the impact of mass drug administration (MDA) in controlling paragonimiasis. They also considered factors such as drug efficacy, treatment coverage, and migration rates of infected individuals in the model. The study concluded that MDA, when implemented with high treatment coverage and effective drugs, could significantly reduce the transmission of paragonimiasis.

Keiser & Utzinger, (2009) developed a model on the life cycle of *Paragonimus* specie where, a few years earlier, paragonimus fluke were recovered from animals including otter, tiger and mongoose. Also, they spoke about symptoms which have been associated with lung fluke infections depending on the infection intensity. Where in the early stage of Pulmonary infections, symptoms include cough, fever, bloody sputum, loss of appetite, chest pain and headache. A chronic, productive cough with brownish sputum, chest pain and night sweats occur once the infection is established.

Fischer & Weil, (2015) developed a model on the transmission of paragonimiasis infection where they said the frequency of transmission to humans depends on dietary practices, especially on whether people consume raw or under-cooked freshwater crustaceans which includes crabs or crayfish.

Richter, (2022) developed a model of the treatment of paragonimiasis where he identified cases of paragonimiasis were treated by praziquantel where the dose of Praziquantel was administered in a dose of 3*25mg/kg/d for three days. After treatment with praziquantel there was high rate of recovery and hence he concluded that praziquantel is effective for treatment of paragonimiasis.

Yakoko, Momoh, Abdulkadir, & Micah, (2024) developed a mathematical models SIR (Susceptible Infectious- Recovered) framework that are commonly used to simulate disease spread and assess the effectiveness of interventions. Specifically highlighted the application of compartmental models in predicting paragonimiasis outbreaks and evaluating intervention outcomes.

CHAPTER THREE

MODEL FORMULATION AND ANALYSIS

3.1 Description of the Mathematical Compartmental Model.

Under this section we formulated a mathematical model to describe the transmission dynamics of paragonimiasis disease in the community which is just increased by natural birth rate (b_3) which is constant over time. Paragonimiasis fatal disease and is denoted by σ_3 and the natural mortality rate is denoted by μ_3 which is constant over time.

In this study we will consider two models, first **SICRS** model for human population, where **S** represents susceptible individuals (not yet infected, they are at risk of getting disease), **I** for individuals who are infected, **C** for carrier individuals (as it is to infectious human do not transmit disease to human, because, this disease is not directly transmitted from human to human) and **R** for recovered individuals. Second **SIRS** model for snails and crabs, where **S** for susceptible, **I** for Infected and **R** naturally recovered.

There are two ways for snails population to leave a susceptible class first through contact with infected snails at a rate denoted by β_1 and the second way through a natural mortality rate denoted by μ_1 and this rate is constant over time. Snails recover naturally at a rate α_1 and may return to Susceptible class at a rate ρ_1 because there is no permanent immunity.

For the second intermediate host which are crabs, they have three ways to leave a Susceptible class which are, through a direct contact with infected crabs at a rate β_2 , contact with infected first intermediate host (snails) at a force of infection $\lambda_1 = \beta_{12}I_1$ and lastly through a natural mortality at a rate μ_2 and assumed to be constant over time for all three crabs' classes. Also, the infected crustaceans recover naturally at a rate α_2 and returning to Susceptible class at a rate ρ_2 since they have no permanent immunity.

We assume that, the susceptible population (S_3) get disease's agent (parasites) through consumption of inadequately cooked (infected) crustaceans (crabs). The force of infection through consumption of crustaceans is $\lambda_2 = \beta_{23}I_2$. Susceptible individuals (S_3) moves to infected class at decreasing function $(1 - \epsilon)$ of education efficacy and also leaves this class through a natural mortality at a rate μ_3 and this is constant for all human population classes.

Infected individuals may become a parasite's carrier (chronically infected) at a rate ω who moves by a proportion of $(1-\theta)$ to a carrier class. Infected and carrier individuals are assumed to recover through treatments at a different rate of η_1 and η_2 respectively in which infected individuals moves to recovered class (through treatment) with θ proportion.

On the other hand, recovered individuals may return to susceptible class (the risk to be infected again) at a rate ρ_3 when he or she is introduced to causative environment that is eating again inadequately cooked infected crustaceans (crabs).

3.2 Variables and Parameters Description.

Tables below provides a clear definitions of the parameters and variables used in the models.

Table 1: Variables used in the models.

Variable	Definition
S_1	The number of susceptible snails at time t
S_2	The number of susceptible crustaceans at time t
S_3	The number of susceptible individuals at time t (Assumed not educated)
I_1	The number of infected snails at time t
I_2	The number of infected crustaceans at time t
I_3	The number of infected individuals at time t
R_1	The number of recovered snails at time t
R_2	The number of recovered crustaceans at time t
C_3	The number of carrier individuals at time t
R_3	The number of recovered individuals at time t

Table 2: Parameters used in the models

Parameter	Definition
b_1	Recruitment rate into susceptible snails population .
b_2	Recruitment rate into susceptible crustaceans population.
b_3	Birth rate for human population at time t.
β_1	Infectious rate among the snails.
β_2	Infectious rate between Susceptible crabs and infected crabs.
β_{12}	Infectious rate between a susceptible crabs and infected snails.
β_{23}	Infectious rate from infected crabs to human through consumption.
α_1	Recovery rate of the snails.
α_2	Recovery rate of the crustaceans.
η_1	Recovery rate for infectious individuals through treatment.
η_2	Recovery rate for a parasite individual carrier.
ω	Rate of infected individuals who become carriers.
ε	Educational efficacy.
θ	Proportion of an infectious individuals who directly recover.
$1 - \theta$	Proportion of chronic infected individuals(infected to carrier class).
μ_1	Natural mortality rate for snails.
μ_2	Natural mortality rate for crustaceans.
μ_3	Natural mortality rate for human population.
ρ_1, ρ_2, ρ_3	Rate at which recovered snails, crabs and human respectively lose immunity and become susceptible again.
σ_3	Disease-induced death rate.

3.3 Compartmental Diagram.

All of the explained above on *SICRS* and *SIRS* models can be well summarized by the diagram below.

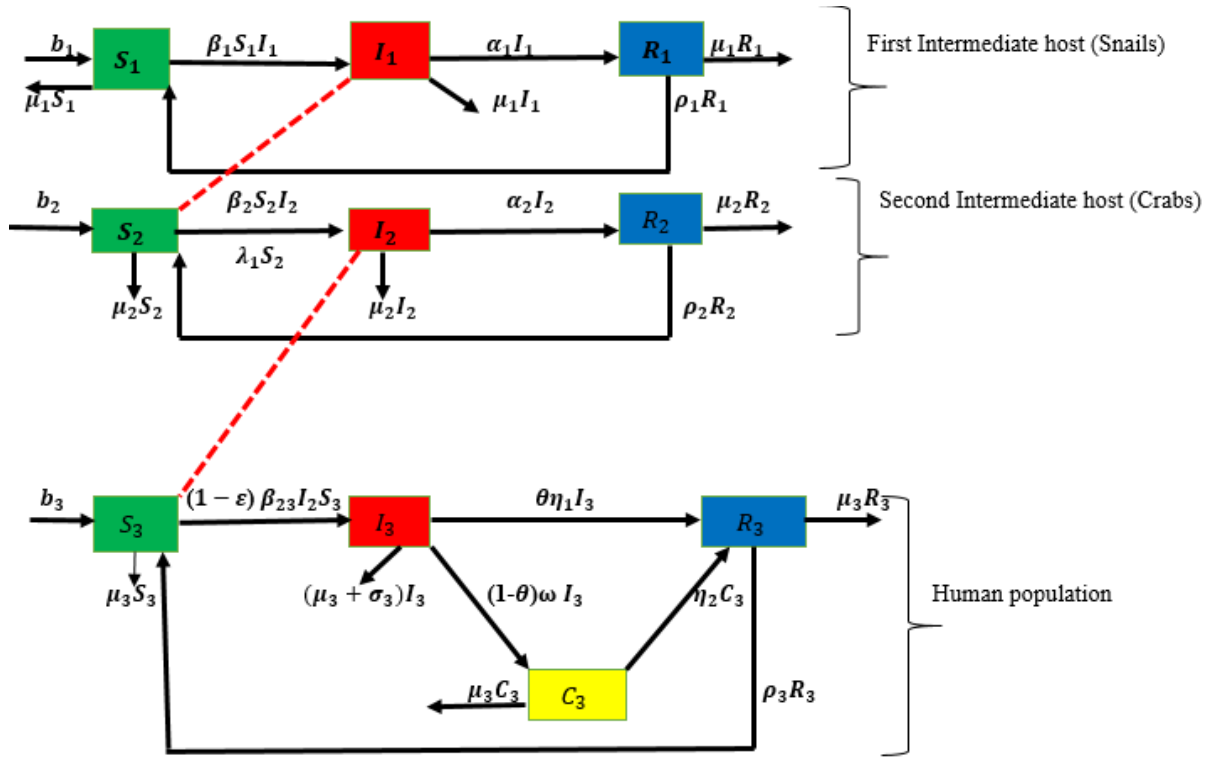


Figure 2: Flow chart for a transmission dynamics of paragonimiasis disease. Red dotted lines indicates parasite flow between compartments

3.4 Differential Equations.

From the above compartmental diagram which describes the transition between the compartments we formulate differential equations as follows;

Ordinary Differential equations for Snails (First Intermediate host)

$$\frac{dS_1}{dt} = b_1 + \rho_1 R_1 - \beta_1 S_1 I_1 - \mu_1 S_1 \quad (1)$$

$$\frac{dI_1}{dt} = \beta_1 S_1 I_1 - \mu_1 I_1 - \alpha_1 I_1 \quad (2)$$

$$\frac{dR_1}{dt} = \alpha_1 I_1 - \mu_1 R_1 - \rho_1 R_1 \quad (3)$$

Ordinary Differential equations for Crabs (Second Intermediate host).

$$\frac{dS_2}{dt} = b_2 + \rho_2 R_2 - \beta_2 S_2 I_2 - \beta_{12} I_1 S_2 - \mu_2 S_2 \quad (4)$$

$$\frac{dI_2}{dt} = \beta_2 S_2 I_2 + \beta_{12} I_1 S_2 - \alpha_2 I_2 - \mu_2 I_2 \quad (5)$$

$$\frac{dR_2}{dt} = \alpha_2 I_2 - \rho_2 R_2 - \mu_2 R_2 \quad (6)$$

Ordinary Differential equations for Human Population.

$$\frac{dS_3}{dt} = b_3 + \rho_3 R_3 - (1 - \epsilon)\beta_{23} I_2 S_3 - \mu_3 S_3 \quad (7)$$

$$\frac{dI_3}{dt} = (1 - \epsilon)\beta_{23} I_2 S_3 - (\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1) I_3 \quad (8)$$

$$\frac{dC_3}{dt} = (1 - \theta)\omega I_3 - (\mu_3 + \eta_2) C_3 \quad (9)$$

$$\frac{dR_3}{dt} = \theta\eta_1 I_3 + \eta_2 C_3 - (\mu_3 + \rho_3) R_3 \quad (10)$$

Upon simplification of the ordinary differential equations (1-10) above we obtained the followings simplified equations:

$$\begin{aligned} \frac{dS_1}{dt} &= b_1 + \rho_1 R_1 - (\beta_1 I_1 + \mu_1) S_1, \\ \frac{dI_1}{dt} &= \beta_1 S_1 I_1 - (\mu_1 + \alpha_1) I_1, \\ \frac{dR_1}{dt} &= \alpha_1 I_1 - (\mu_1 + \rho_1) R_1, \\ \frac{dS_2}{dt} &= b_2 + \rho_2 R_2 - (\beta_2 I_2 + \beta_{12} I_1 + \mu_2) S_2, \\ \frac{dI_2}{dt} &= (\beta_{12} I_1 + \beta_2 I_2) S_2 - (\alpha_2 + \mu_2) I_2, \\ \frac{dR_2}{dt} &= \alpha_2 I_2 - (\rho_2 + \mu_2) R_2, \\ \frac{dS_3}{dt} &= b_3 + \rho_3 R_3 - ((1 - \epsilon)\beta_{23} I_2 + \mu_3) S_3, \\ \frac{dI_3}{dt} &= (1 - \epsilon)\beta_{23} I_2 S_3 - (\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1) I_3, \\ \frac{dC_3}{dt} &= (1 - \theta)\omega I_3 - (\mu_3 + \eta_2) C_3, \\ \frac{dR_3}{dt} &= \theta\eta_1 I_3 + \eta_2 C_3 - (\mu_3 + \rho_3) R_3. \end{aligned}$$

with the initial conditions:

$$S_1(0) \geq 0, I_1(0) \geq 0, R_1(0) \geq 0, S_2(0) \geq 0, I_2(0) \geq 0, R_2(0) \geq 0, S_3(0) \geq 0, I_3(0) \geq 0, R_3(0) \geq 0, C_3(0) \geq 0 \text{ and } S_E(0) \geq 0$$

3.5 Basic properties of the model

3.5.1 Positivity of the solution

The model differential equations (11-20) above has the solution set $\{S_1, S_2, S_3, I_1, I_2, I_3, R_1, R_2, R_3, C_3\}$ with the initial conditions which always remains non-negative (positive) $\forall_t > 0$, since they represents population (snails, crabs and human). We need to verify that $S_1(t) \geq 0, I_1(t) \geq 0, R_1(t) \geq 0, S_2(t) \geq 0, I_2(t) \geq 0, R_2(t) \geq 0, S_3(t) \geq 0, I_3(t) \geq 0, R_3(t) \geq 0$ and $C_3(t) \geq 0 \forall_t > 0$.

For

$$\begin{aligned} \frac{dS_1}{dt} &= b_1 + \rho_1 R_1 - (\beta_1 I_1 + \mu_1) S_1 \\ \Rightarrow \frac{dS_1}{dt} &\geq -(\beta_1 I_1 + \mu_1) S_1 \end{aligned}$$

Solving equation 13 above we obtain

$$S_1(t) \geq S_1(0) e^{-(\beta_1 I_1 + \mu_1)t} \quad (11)$$

as $t \rightarrow \infty, S_1(t) \geq 0$

For

$$\frac{dI_1}{dt} = \beta_1 S_1 I_1 - \mu_1 I_1 - \alpha_1 I_1 \quad (12)$$

$$\Rightarrow \frac{dI_1}{dt} \geq -(\mu_1 + \alpha_1) I_1 \quad (13)$$

Solving equation (16) above we get

$$I_1(t) \geq I_1(0) e^{-(\mu_1 + \alpha_1)t} \quad (14)$$

as $t \rightarrow \infty, I_1(t) \geq 0$

For

$$\frac{dR_1}{dt} = \alpha_1 I_1 - \mu_1 R_1 - \rho_1 R_1 \quad (15)$$

$$\Rightarrow \frac{dR_1}{dt} \geq -(\mu_1 + \rho_1) R_1 \quad (16)$$

Solving equation (19) above we get

$$R_1(t) \geq R_1(0) e^{-(\mu_1 + \rho_1)t} \quad (17)$$

as $t \rightarrow \infty, R_1(t) \geq 0$

For

$$\frac{dS_2}{dt} = b_2 + \rho_2 R_2 - \beta_2 S_2 I_2 - \beta_{12} I_1 S_2 - \mu_2 S_2 \quad (18)$$

$$\Rightarrow \frac{dS_2}{dt} \geq b_2 - \mu_2 S_2 \quad (19)$$

Solving equation (22) above we obtain

$$S_2(t) \geq \left(\frac{b_2}{\mu_2} \right) + \left(S_2(0) - \frac{b_2}{\mu_2} \right) e^{-\mu_2 t} \quad (20)$$

as $t \rightarrow \infty, S_2(t) \geq 0$

For

$$\frac{dI_2}{dt} = \beta_2 S_2 I_2 + \beta_{12} I_1 S_2 - \mu_2 I_2 - \alpha_2 I_2 \quad (21)$$

$$\Rightarrow \frac{dI_2}{dt} \geq -(\mu_2 + \alpha_2) I_2 \quad (22)$$

Solving equation (25) above we get

$$I_2(t) \geq I_2(0) e^{-(\mu_2 + \alpha_2)t} \quad (23)$$

as $t \rightarrow \infty, I_2(t) \geq 0$

For

$$\frac{dR_2}{dt} = \alpha_2 I_2 - \mu_2 R_2 - \rho_2 R_2 \quad (24)$$

$$\frac{dR_2}{dt} \geq -(\mu_2 + \rho_2) R_2 \quad (25)$$

Solving equation (28) above we get

$$R_2(t) \geq R_2(0)e^{-(\mu_2+\rho_2)t} \quad (26)$$

as $t \rightarrow \infty, R_1(t) \geq 0$

For

$$\frac{dS_3}{dt} = b_3 + \rho_3 R_3 - (1-\varepsilon)\beta_{23}I_2 S_3 - \mu_3 S_3 \quad (27)$$

$$\Rightarrow \frac{dS_3}{dt} \geq b_3 - \mu_3 S_3 \quad (28)$$

Solving equation (31) above we get

$$S_3(t) \geq \left(\frac{b_3}{\mu_3}\right) + \left(S_3(0) - \frac{b_3}{\mu_3}\right)e^{-\mu_3 t} \quad (29)$$

as $t \rightarrow \infty, S_3(t) \geq 0$

For

$$\frac{dI_3}{dt} = (1-\varepsilon)\lambda_3 S_3 - (\mu_3 + \sigma_3 + (1-\theta)\omega + \theta\eta_1)I_3 \quad (30)$$

$$\Rightarrow \frac{dI_3}{dt} \geq -(\mu_3 + \sigma_3 + (1-\theta)\omega + \theta\eta_1)I_3 \quad (31)$$

Solving equation (34) above we get

$$I_3(t) \geq I_3(0)e^{-(\mu_3+\sigma_3+(1-\theta)\omega+\theta\eta_1)t} \quad (32)$$

as $t \rightarrow \infty, I_3(t) \geq 0$

For

$$\frac{dC_3}{dt} = (1-\theta)\omega I_3 - (\mu_3 + \eta_2)C_3 \quad (33)$$

$$\Rightarrow \frac{dC_3}{dt} \geq -(\mu_3 + \eta_2)C_3 \quad (34)$$

Solving equation (37) above we get

$$C_3(t) \geq C_3(0)e^{-(\mu_3+\eta_2)t} \quad (35)$$

as $t \rightarrow \infty, C_3(t) \geq 0$

For

$$\frac{dR_3}{dt} = \theta\eta_1 I_3 + \eta_2 C_3 - (\mu_3 + \rho_3)R_3 \quad (36)$$

$$\Rightarrow \frac{dR_3}{dt} \geq -(\mu_3 + \rho_3)R_3 \quad (37)$$

Solving equation (40) above we get

$$R_3(t) \geq R_3(0)e^{-(\mu_3+\rho_2)t} \quad (38)$$

as $t \rightarrow \infty, R_3(t) \geq 0$

All the variables are non-negative as shown above.

3.6 Disease Free Equilibrium (DFE)

The disease free equilibrium for a transmission dynamics of paragonimiasis disease model obtained when we assume that, no disease in the population (snails, crabs and Human). We set model differential equations in model 1 equals 0 such that:

$$\frac{dS_1}{dt} = \frac{dI_1}{dt} = \frac{dR_1}{dt} = \frac{dS_2}{dt} = \frac{dI_2}{dt} = \frac{dR_2}{dt} = \frac{dS_3}{dt} = \frac{dI_3}{dt} = \frac{dC_3}{dt} = \frac{dR_3}{dt} = 0 \text{ we have}$$

$$\begin{aligned} 0 &= b_1 + \rho_1 R_1 - (\beta_1 I_1 + \mu_1) S_1, \\ 0 &= \beta_1 S_1 I_1 - (\mu_1 + \alpha_1) I_1, \\ 0 &= \alpha_1 I_1 - (\mu_1 + \rho_1) R_1, \\ 0 &= b_2 + \rho_2 R_2 - (\beta_2 I_2 + \beta_{12} I_1 + \mu_2) S_2, \\ 0 &= (\beta_{12} I_1 + \beta_2 I_2) S_2 - (\alpha_2 + \mu_2) I_2, \\ 0 &= \alpha_2 I_2 - (\rho_2 + \mu_2) R_2, \\ 0 &= b_3 + \rho_3 R_3 - ((1 - \varepsilon) \beta_{23} I_2 + \mu_3) S_3, \\ 0 &= (1 - \varepsilon) \beta_{23} I_2 S_3 - (\mu_3 + \sigma_3 + (1 - \theta) \omega + \theta \eta_1) I_3, \\ 0 &= (1 - \theta) \omega I_3 - (\mu_3 + \eta_2) C_3, \\ 0 &= \theta \eta_1 I_3 + \eta_2 C_3 - (\mu_3 + \rho_3) R_3. \end{aligned}$$

Solving the equations above when $I_1 = I_2 = I_3 = R_1 = R_2 = R_3 = C_3 = 0$ we obtain:

$$P_1(S_1^*, 0, 0) = \left(\frac{b_1}{\mu_1}, 0, 0 \right) \text{ for snail compartments, } P_2(S_2^*, 0, 0) = \left(\frac{b_2}{\mu_2}, 0, 0 \right) \text{ for crabs compartments and}$$

$$P_3(S_3^*, 0, 0, 0) = \left(\frac{b_3}{\mu_3}, 0, 0, 0 \right) \text{ for Human population, when we combine them we obtain}$$

$$P_0 = (S_1^*, S_2^*, S_3^*, I_1^*, I_2^*, I_3^*, R_1^*, R_2^*, R_3^*, C_3^*) = \left(\frac{b_1}{\mu_1}, \frac{b_2}{\mu_2}, \frac{b_3}{\mu_3}, 0, 0, 0, 0, 0, 0, 0 \right) \text{ for all populations (snails, crabs and human)}$$

3.7 Endemic Equilibrium Point (EE)

The disease persist in the community when endemic point of the model exists.

By setting $I_1^* \neq I_2^* \neq I_3^* \neq R_1^* \neq R_2^* \neq R_3^* \neq C_3^* \neq 0$, we obtain paragonimiasis endemic points of the model equations (11-20) as follows per population under study:

$$P_1 = (S_1^*, S_2^*, S_3^*, I_1^*, I_2^*, I_3^*, R_1^*, R_2^*, R_3^*, C_3^*)$$

Endemic equilibrium point for snails we have;

$$P_1^* = (S_1^*, I_1^*, R_1^*) \text{ where,}$$

$$S_1^* = \frac{\mu_1 + \alpha_1}{\beta_1}$$

$$I_1^* = \frac{(\mu_1 + \rho_1)(\mu_1 + \alpha_1)}{\beta_1(\mu_1 + \alpha_1 + \rho_1)} (R_1 - 1)$$

$$R_1^* = \frac{\alpha_1(\mu_1 + \alpha_1)}{\beta_1(\mu_1 + \alpha_1 + \rho_1)} (R_1 - 1)$$

$$R_1 = \frac{\beta_1 b_1}{(\alpha_1 + \mu_1) \mu_1}$$

Endemic equilibrium point for crabs.

$$E_2^* = (S_2^*, I_2^*, R_2^*) \text{ where,}$$

$$S_2^* = \frac{\mu_2 + \alpha_2}{\beta_2}$$

$$I_2^{**} = \frac{(\mu_2 + \rho_2)(\lambda_1 + \mu_2)(\mu_2 + \alpha_2)}{\beta_2[(\mu_2(\mu_2 + \alpha_2) + \rho_2\mu_2)]}(R_2 - 1)$$

$$R_2^{**} = \frac{\alpha_2(\lambda_1 + \mu_2)(\mu_2 + \alpha_2)}{\beta_2[(\mu_2(\mu_2 + \alpha_2) + \rho_2\mu_2)]}(R_2 - 1)$$

$$R_2 = \frac{\beta_2 b_2}{(\alpha_2 + \mu_2)(\mu_2 + \lambda_1)}, \lambda_1 = \beta_{12} I_1^*$$

3.8 Basic Reproductive number of the paragonimiasis model, R_0

Basic reproductive number is the secondary infections cases brought on when a single infectious agent is introduced into a susceptible population (free disease population). This threshold parameters tells that whether the disease will persist or die in the population. It is one of the most important threshold parameters in mathematical epidemiology. It is clearly described quantitatively as follows:

If $R_0 < 1$, disease dies out (an infected crustaceans can not transmit the disease to any person, similarly infected snails can not transmit the disease to crabs as well as person will not release pathogens into environment where snails are mostly found and live), that is a transmission dynamics of paragonimiasis disease in a population will perish out.

If $R_0 > 1$, indicates epidemic situation will occurs where the disease spread quickly to the community. This will be mostly happen when the DFE is unstable in the context that no education efficacy in controlling the disease transmission.

If $R_0 = 1$, then endemic situation will occurs where an infected crabs can transmit the disease to only one person and thus the disease progresses slowly (at very small rate) to the community.

We calculated R_0 by using the technique imposed by Dieckmann *et al* (1990) called the next generation matrix, in which R_0 is obtained as the maximum eigenvalue of the product F and V^{-1} where F is the new infections of the disease classes and V represents other infections (outflow) from the compartment.

Let's consider the model differential equations for disease classes below:

$$\begin{aligned}\frac{dI_1}{dt} &= \beta_1 S_1 I_1 - (\mu_1 + \alpha_1) I_1, \\ \frac{dI_2}{dt} &= (\beta_{12} I_1 + \beta_2 I_2) S_2 - (\alpha_2 + \mu_2) I_2, \\ \frac{dI_3}{dt} &= (1 - \epsilon) \beta_{23} I_2 S_3 - (\mu_3 + \sigma_3 + (1 - \theta) \omega + \theta \eta_1) I_3, \\ \frac{dC_3}{dt} &= (1 - \theta) \omega I_3 - (\mu_3 + \eta_2) C_3,\end{aligned}$$

from which we have

$$F_i = \begin{pmatrix} \beta_1 S_1 I_1 \\ \beta_2 S_2 I_2 + \beta_{12} I_1 S_2 \\ (1 - \epsilon) \beta_{23} I_2 S_3 \\ 0 \end{pmatrix}$$

$$V_i = \begin{pmatrix} (\mu_1 + \alpha_1) I_1 \\ (\alpha_2 + \mu_2) I_2 \\ (\mu_3 + \sigma_3 + (1 - \theta) \omega + \theta \eta_1) I_3 \\ (\mu_3 + \eta_2) C_3 - (1 - \theta) \omega I_3 \end{pmatrix}$$

Taking partial derivative for each F_i and V_i with respect to infections classes (that is I_1, I_2, I_3, C_3) we obtain F and V as:

$$F = \begin{pmatrix} \beta_1 S_1 & 0 & 0 & 0 \\ \beta_{12} S_2 & \beta_2 S_2 & 0 & 0 \\ 0 & (1-\varepsilon)\beta_{23} S_3 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \mu_1 + \alpha_1 & 0 & 0 & 0 \\ 0 & \alpha_2 + \mu_2 & 0 & 0 \\ 0 & 0 & \mu_3 + \sigma_3 + (1-\theta)\omega\theta\eta_1 & 0 \\ 0 & 0 & -(1-\theta)\omega & \mu_3 + \eta_2 \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu_1 + \alpha_1} & 0 & 0 & 0 \\ 0 & \frac{1}{\alpha_2 + \mu_2} & 0 & 0 \\ 0 & 0 & \frac{1}{\mu_3 + \sigma_3 + (1-\theta)\omega\theta\eta_1} & 0 \\ 0 & 0 & \frac{(1-\theta)\omega}{(\mu_3 + \sigma_3 + (1-\theta)\omega\theta\eta_1)(\mu_3 + \eta_2)} & \frac{1}{\mu_3 + \eta_2} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1 S_1}{\mu_1 + \alpha_1} & 0 & 0 & 0 \\ \frac{\beta_{12} S_2}{\mu_1 + \alpha_1} & \frac{\beta_2 S_2}{\alpha_2 + \mu_2} & 0 & 0 \\ 0 & \frac{(1-\varepsilon)\beta_{23} S_3}{\alpha_2 + \mu_2} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

Computing the eigenvalues of FV^{-1} we have

$$\lambda_1 = 0, \quad \lambda_2 = 0, \quad \lambda_3 = \frac{\beta_1 S_1^*}{\mu_1 + \alpha_1}, \quad \lambda_4 = \frac{\beta_2 S_2^*}{\alpha_2 + \mu_2}$$

where $S_1^* = \frac{b_1}{\mu_1}$ and $S_2^* = \frac{b_2}{\mu_2}$ from Disease Free Equilibrium, **DFE** Thus

$$R_0 = \max\{\lambda_3, \lambda_4\} = \max\left\{\frac{\beta_1 S_1^*}{\mu_1 + \alpha_1}, \frac{\beta_2 S_2^*}{\alpha_2 + \mu_2}\right\} = \max\left\{\frac{\beta_1 b_1}{\mu_1(\mu_1 + \alpha_1)}, \frac{\beta_2 b_2}{\mu_2(\alpha_2 + \mu_2)}\right\}$$

It can be noted that

$$R_1 = \frac{\beta_1 b_1}{\mu_1(\mu_1 + \alpha_1)},$$

$$R_2 = \frac{\beta_2 b_2}{\mu_2(\alpha_2 + \mu_2)}.$$

where R_1 is the basic reproduction number associated with the snails population, whereas R_2 is the reproduction number associated with crustacea populations.

CHAPTER FOUR

MODEL ANALYSIS

4.1 Local Stability Analysis

Here it is needed to compute the Jacobian at disease free for the system (), we get

$$J = \begin{pmatrix} -\mu_1 & -\beta_1 S_1 & \rho_1 & 0 & 0 & 0 & 0 \\ 0 & \beta_1 S_1 - (\mu_1 + \alpha_1) & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_1 & -(\mu_1 + \rho_1) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -(\beta_2 S_2 + \mu_2) & 0 & \rho_2 & 0 \\ 0 & 0 & 0 & \beta_2 S_2 & -(\alpha_2 + \mu_2) & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha_2 & -(\rho_2 + \mu_2) & 0 \\ 0 & 0 & 0 & 0 & -(1 - \varepsilon)\beta_{23} S_3 & 0 & -((1 - \varepsilon)\beta_{23} S_2 + \mu_3) \\ 0 & 0 & 0 & 0 & (1 - \varepsilon)\beta_{23} S_3 & 0 & (1 - \varepsilon)\beta_{23} S_2 & -(\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1) - \lambda \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -(\mu_3 + \eta_2) - \lambda \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -(\mu_3 + \rho_3) - \lambda \end{pmatrix}$$

First block

$$J_1 = \begin{pmatrix} -\mu_1 - \lambda & -\beta_1 S_1 & \rho_1 \\ 0 & \beta_1 S_1 - (\mu_1 + \alpha_1) - \lambda & 0 \\ 0 & \alpha_1 & -(\mu_1 + \rho_1) - \lambda \end{pmatrix}$$

Eigenvalues for the first block:

$$\lambda_1 = -\mu_1, \quad \lambda_2 = \beta_1 S_1 - (\mu_1 + \alpha_1), \quad \lambda_3 = -(\mu_1 + \rho_1)$$

The second block is

$$J_2 = \begin{pmatrix} -(\beta_2 S_2 + \mu_2) - \lambda & 0 & \rho_2 \\ \beta_2 S_2 & -(\alpha_2 + \mu_2) - \lambda & 0 \\ 0 & \alpha_2 & -(\rho_2 + \mu_2) - \lambda \end{pmatrix}$$

Eigenvalues for the second block:

$$\lambda_4 = -(\beta_2 S_2 + \mu_2), \quad \lambda_5 = -(\alpha_2 + \mu_2), \quad \lambda_6 = -(\rho_2 + \mu_2)$$

The third block is

$$J_3 = \begin{pmatrix} -((1 - \varepsilon)\beta_{23} S_2 + \mu_3) - \lambda & 0 & 0 & \rho_3 \\ (1 - \varepsilon)\beta_{23} S_2 & -(\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1) - \lambda & 0 & 0 \\ 0 & (1 - \theta)\omega & -(\mu_3 + \eta_2) - \lambda & 0 \\ 0 & \theta\eta_1 & \eta_2 & -(\mu_3 + \rho_3) - \lambda \end{pmatrix}$$

Eigenvalues for the third block:

$$\lambda_7, \lambda_8, \lambda_9, \lambda_{10}$$

where $\lambda_7, \lambda_8, \lambda_9, \lambda_{10}$ are the roots of the characteristic polynomial:

$$\det \begin{vmatrix} -((1 - \varepsilon)\beta_{23} S_2 + \mu_3) - \lambda & 0 & 0 & \rho_3 \\ (1 - \varepsilon)\beta_{23} S_2 & -(\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1) - \lambda & 0 & 0 \\ 0 & (1 - \theta)\omega & -(\mu_3 + \eta_2) - \lambda & 0 \\ 0 & \theta\eta_1 & \eta_2 & -(\mu_3 + \rho_3) - \lambda \end{vmatrix} = 0$$

characteristic polynomial:

$$\det \begin{vmatrix} -a-\lambda & 0 & 0 & \rho_3 \\ (1-\varepsilon)\beta_{23}S_2 & -b-\lambda & 0 & 0 \\ 0 & (1-\theta)\omega & -c-\lambda & 0 \\ 0 & \theta\eta_1 & \eta_2 & -d-\lambda \end{vmatrix} = 0$$

$$\lambda^4 + c_1\lambda^3 + c_2\lambda^2 + c_3\lambda + c_4 = 0$$

where

$$\begin{aligned} c_1 &= a + b + c + d, \\ c_2 &= a(b + c + d) + c(b + d) + bd, \\ c_3 &= a(bc + bd + cd) + bcd, \\ c_4 &= abcd. \end{aligned}$$

such that

$$\begin{aligned} a &= (1 - \varepsilon)\beta_{23}S_2 + \mu_3, \\ b &= (\mu_3 + \sigma_3 + (1 - \theta)\omega + \theta\eta_1), \\ c &= (\mu_3 + \eta_2), \\ d &= (\mu_3 + \rho_3). \end{aligned}$$

CHAPTER FIVE

SENSITIVITY ANALYSIS

5.1 Sensitivity Analysis and Discussion.

Sensitivity analysis in mathematical models used to determine how the output of a model is affected by the changes in its input parameters. The goal of sensitivity analysis is to decide qualitatively which parameters are most influential in the model output (Martcheva, 2015). We use sensitivity indices so as to determine which parameters have higher impacts on a basic reproductive number R_1 and R_2 of the model and should be preventive to the spread of the disease. It has two kinds of results, positive and negative. If sensitivity index of the parameter is positive then parameter has much impact of expanding the disease in the population if their values increases. Also, if sensitivity index is negative then parameter has the great chance of minimizing the spread of disease in the population as when their values increases. It is usually calculated as follows:

$$\gamma_{\chi}^{R_o} = \frac{\partial R_o}{\partial \chi} \times \frac{\chi}{R_o}.$$

Where:

R_o Is the reproductive number,

χ Is the parameter of interest (in the reproductive number).

Let's consider our basic reproductive numbers to find parameter's sensitivity indices.

For

$$R_1 = \frac{\beta_1 b_1}{\mu_1(\mu_1 + \alpha_1)}.$$

We get the following indices

$$\begin{aligned}\gamma_{\beta_1}^{R_1} &= \frac{\partial R_1}{\partial \beta_1} \times \frac{\beta_1}{R_1} = +1, \\ \gamma_{b_1}^{R_1} &= \frac{\partial R_1}{\partial b_1} \times \frac{b_1}{R_1} = +1, \\ \gamma_{\alpha_1}^{R_1} &= \frac{\partial R_1}{\partial \alpha_1} \times \frac{\alpha_1}{R_1} = - \left(\frac{\alpha_1}{\alpha_1 + \mu_1} \right) = - \left(\frac{0.01}{0.01 + 0.01} \right) = -0.5, \\ \gamma_{\mu_1}^{R_1} &= \frac{\partial R_1}{\partial \mu_1} \times \frac{\mu_1}{R_1} = - \left(\frac{2\mu_1 + \alpha_1}{\alpha_1 + \mu_1} \right) = - \left(\frac{2 \times 0.01 + 0.01}{0.01 + 0.01} \right) = -1.5.\end{aligned}$$

For

$$R_2 = \frac{\beta_2 b_2}{\mu_2(\alpha_2 + \mu_2)}.$$

We have the following indices.

$$\begin{aligned}\gamma_{\beta_2}^{R_2} &= \frac{\partial R_2}{\partial \beta_2} \times \frac{\beta_2}{R_2} = +1, \\ \gamma_{b_2}^{R_2} &= \frac{\partial R_2}{\partial b_2} \times \frac{b_2}{R_2} = +1, \\ \gamma_{\alpha_2}^{R_2} &= \frac{\partial R_2}{\partial \alpha_2} \times \frac{\alpha_2}{R_2} = - \left(\frac{\alpha_2}{\alpha_2 + \mu_2} \right) = - \left(\frac{0.002}{0.002 + 0.02030} \right) = -0.09, \\ \gamma_{\mu_2}^{R_2} &= \frac{\partial R_2}{\partial \mu_2} \times \frac{\mu_2}{R_2} = - \left(\frac{2\mu_2 + \alpha_2}{\alpha_2 + \mu_2} \right) = - \left(\frac{2 \times 0.02030 + 0.002}{0.002 + 0.02030} \right) = -1.9.\end{aligned}$$

As calculated above for each parameters we have the followings indices in table below:

Table 3: Sensitivity indices.

Parameter	Description	Index
β_1	Infectious rate among the snails	+1
b_1	Recruitment rate into susceptible snails population	+1
μ_1	Natural mortality rate for snails	-0.5
α_1	Recovery rate of the snails	-1.5
β_2	Infectious rate between Susceptible crabs and infected crabs	+1
b_2	Recruitment rate into susceptible crustaceans population	+1
μ_2	Natural mortality rate for crustaceans	-0.09
α_2	Recovery rate of the crustaceans	-1.9

Parameter β_1 is directly proportional to reproductive number that is, an increase in births for snails increase secondary infectious since there will be closer contacts between susceptible snails and infected snails.

Similarly, parameter β_2 is directly proportional to the disease outbreak since it increase the reproductive number for crabs as contacts between infected crabs and susceptible crabs increases and this speed up disease spread.

Natural mortality rate for crabs and snails both are inversely proportional to their respective reproductive number this means that, an increase in deaths for snails and crabs decreases the dynamic transmission of paragonimiasis.

Also, an increase in recover rates for snails and crabs minimizes dynamic transmission of paragonimiasis because both are inversely proportional to their reproductive number (negative sensitivity index).

CHAPTER SIX

MODEL SIMULATION

A mathematical model for controlling and eliminating dynamics transmission of paragonimiasis disease in the community was formulated and well analyzed. The main objective of this study was to provide public education to the community to aware the society about this disease which is very negligible and assessing the impact of education efficacy as the strategy of controlling and eliminating paragonimiasis in the community.

Table 4: Parameter's initial values.

Parameter	Definition	Value	Source
b_1	Recruitment rate into susceptible snails population	3.12×10^6	Yakoko <i>et al.</i> (2024)
b_2	Recruitment rate into susceptible crustaceans population	1×10^3	Yakoko <i>et al.</i> (2024)
b_3	Recruitment rate into human population at time t	5×10^6	Yakoko <i>et al.</i> (2024)
β_1	Infectious rate among the snails	5.54×10^{-4}	Yakoko <i>et al.</i> (2024)
β_2	Infectious rate between Susceptible crabs and infected crabs	3.59×10^3	(Yuan, Huang, Zhang, & Ruan, 2018)
α_1	Recovery rate of the snails	0.01 per year	Assumed
α_2	Recovery rate of the crustaceans	0.002 per year	Assumed
η_1	Recovery rate for infectious individuals through treatment	0.05	Assumed
η_2	Recovery rate for a parasite individual carrier	0.73	Yakoko <i>et al.</i> (2024)
β_{12}	Infectious rate between a susceptible crabs and infected snails	0.0125	Assumed
β_{23}	Infectious rate from infected crabs to human through consumption	5.54×10^{-1}	Assumed
ω	Rate of infected individuals who become carriers	0.125	Yakoko <i>et al.</i> (2024)
π	Efficacy rate of person hygiene through education	0.8	Assumed
ε	Education efficacy	(0.0-1.0) varies with scenario	Assumed
θ	Proportion of an infectious individuals who directly recover	0.3	Yakoko <i>et al.</i> (2024)
μ_1	Natural mortality rate for snails	0.01	Yakoko <i>et al.</i> (2024)

Parameter	Definition	Value	Source
μ_2	Natural mortality rate for crustaceans	0.02030	Assumed
μ_3	Natural mortality rate for human population	1.4×10^{-2}	Yakoko <i>et al.</i> (2024)
ρ_1	Rate at which recovered snails lose immunity and become susceptible again	0.003	Assumed
ρ_2	Rate at which recovered crabs lose immunity and become susceptible again	0.003	Assumed
ρ_3	Rate at which recovered individual lose immunity and become susceptible again	0.045	Assumed
σ_3	Disease-induced death rate	0.1 per year	Yakoko <i>et al.</i> (2024)

We plotted different figures to aid easy understanding in variations for populations in respect to exposure rates provided in the table above. Simulation for population dynamics are as follows:

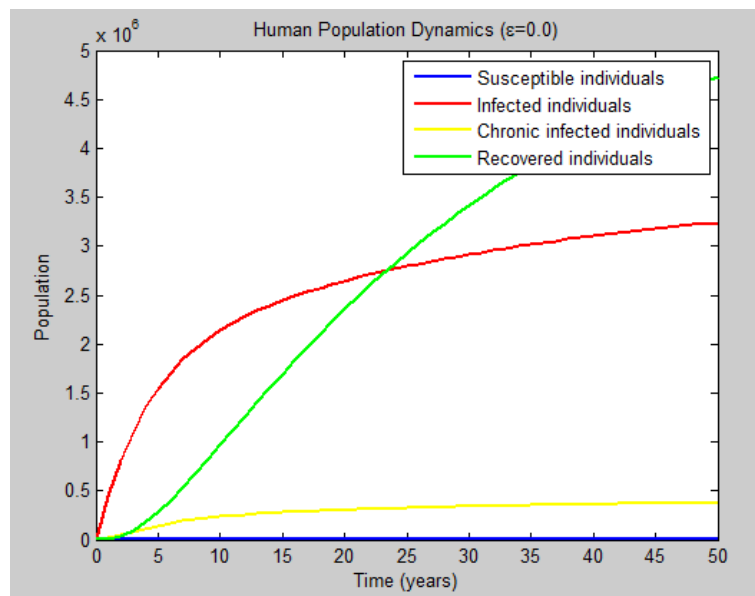


Figure 3: Dynamics of human population when no educational efficacy ($\epsilon = 0.0$)

In figure 2 above indicates that, in absence of person hygiene (lack of awareness) leads to fewer susceptible human while a lot of individuals get infections in which after a moment due to a speed recover through treatments most of them recovers and reduces number of infected individuals.

On the other hand the maximum provision of education (person hygiene) eliminates or minimizes the infectious individuals in a community as shown in the figure 3 below when all other parameter values are constant and this proves that the effective provision of education to create awareness to the community eliminates the dynamics transmission of that disease.

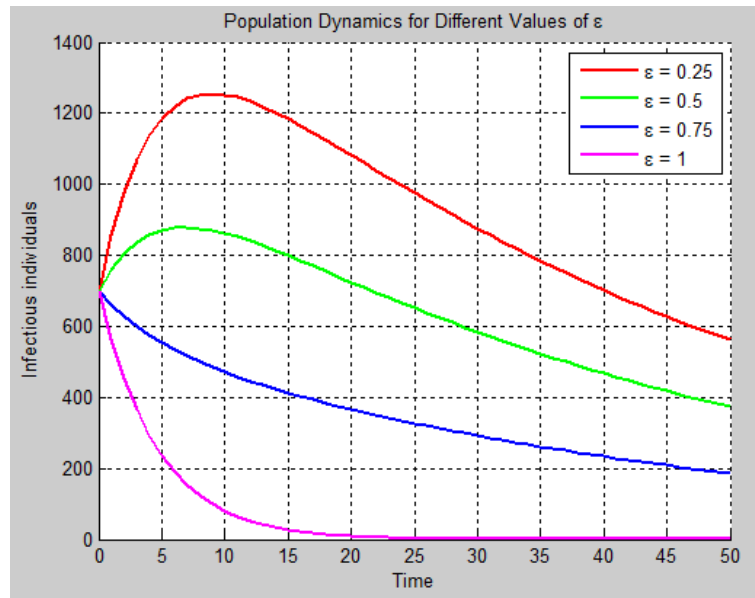


Figure 4: Dynamics of infected human with varied education efficacy

We can observe from figure 4 above that, number of infections decreases as per increase in education efficacy in the community once education is well structured (provided) as intervention method for disease controlling and elimination and this may concludes that education is effective method in controlling paragonimiasis in the community.

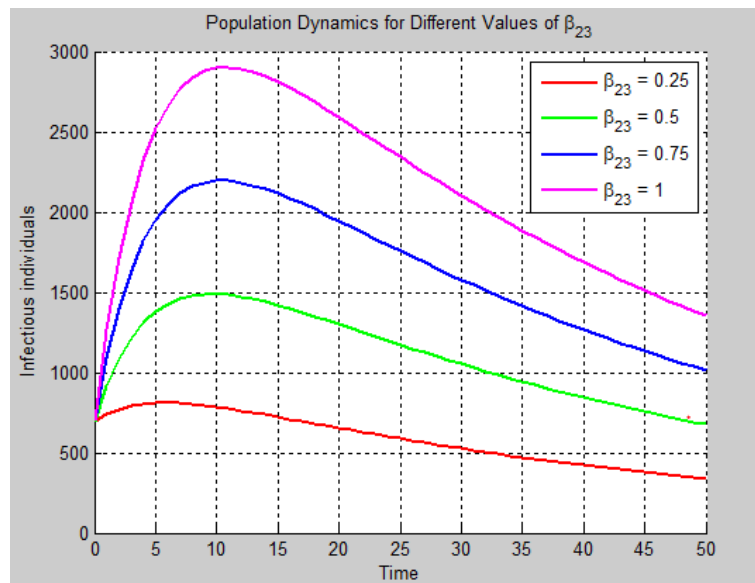


Figure 5: Dynamics of infected human with varied crustaceans consumption rate.

Figure 5 above, indicates that an increase in consumption rate of inadequately cooked crabs increases infectious individuals from the susceptible population who leaves the compartment and this progress to chronic class (carriers) and this is when there is no any interventions for disease control in the community.

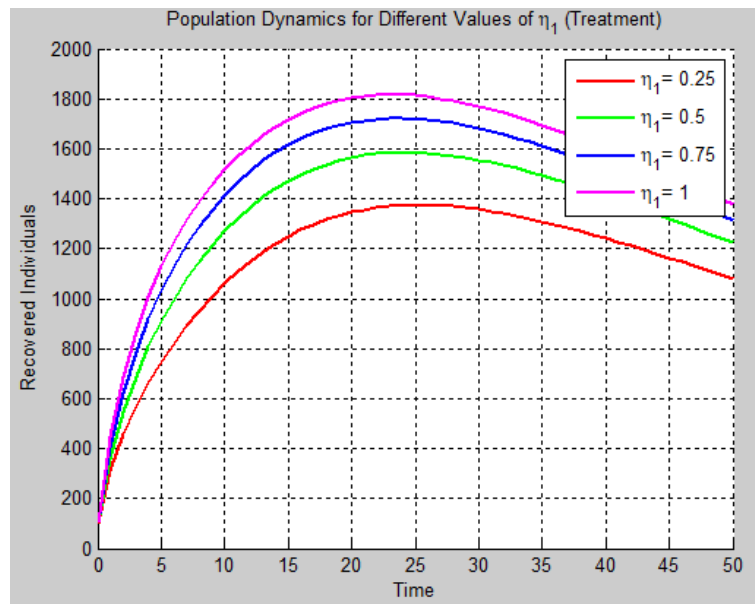


Figure 6: Recovered Individuals through Treatment.

From figure 6 above, we see the effectiveness of treatment in controlling paragonimiasis in the community. Infected humans are cured very fast as increase in dose of praziquantel and this concludes that praziquantel is effective treatment of paragonimiasis

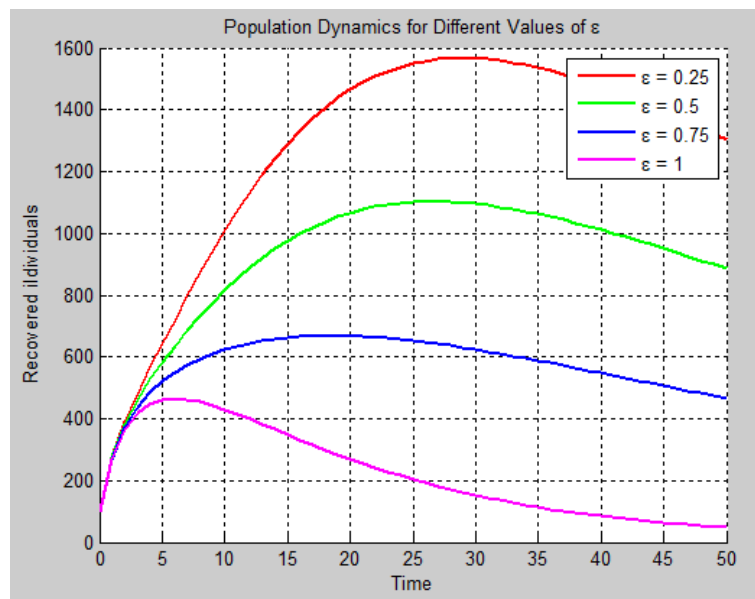


Figure 7: Reduction on recovered individual as the impact of education efficacy

Since education efficacy reduces number of infectious probably number for individuals to recover will decrease as there is few infectious, still education is more important in fighting against this neglected disease.

CHAPTER SEVEN

CONCLUSION AND RECOMMENDATIONS

7.1 Conclusion.

From the model we developed, the model succeeded to show that the rate of transmission of paragonimiasis disease to human largely depend on the contact rate with infected snails and crabs where the increase in infection among snails increase the rate of secondary infection among crabs and thus to human.

Also, the model indicated that the increase in education efficacy about paragonimiasis disease decreases the number of infected individuals in the community but decrease in level of education about paragonimiasis increases the number of infected individuals in the community hence education should be given to the members of community about the transmission of the disease so as to create awareness to people and hence reduce the number of infected individuals in the community.

The model also pointed out that dose called praziquantel has positive impact in reduction of paragonimiasis disease. So, once an individual is infected by paragonimus specie should use this dose so as to cure the disease as it is seen from the model that infected people are cured very fast as increase in dose of praziquantel.

7.2 Recommendations.

We have developed a mathematical model that incorporates education efficacy and the use of treatment in controlling and eliminating paragonimiasis in the community. We encourage other researchers to build upon this work by incorporating additional factors to further improve disease control and elimination efforts. The other factors may include:

- Economic factors; Assessing the economic burden of the disease and the cost-effectiveness of different intervention strategies.
- Behavioral change; Implementing and evaluating programs that promote behavior changes to reduce infection risks, such as proper food preparation techniques.
- Healthcare access; Evaluating the availability and accessibility of healthcare facilities and resources for diagnosis and treatment

References

- [1] Chai, J.Y.,Jung, B.K and Robertson, L., (2018). Paragonimus spp. Global Water Pathogens Project. Part, 3, pp.1-18.
- [2] Chituis, N., Hyman, J.M and Cushing , J.M. (2008). Determining important parameters.
- [3] Dieckmann, O., Heesterbeek, J.,and Roberts, M. (2010). The Construction of Next Generation Matrices for Compartmental Epidemic Models. Journal of The Royal Interface, 873-885.
- [4] Fischer, P. U., and Weil, G. J. (2015). North American Paragonimiasis: epidemiology and diagnostic strategies. Expert Review of Anti-Infective Therap. pp. 779-786.
- [5] Keiser, J., and Utzinger, J. (2009, July). Food-Borne Trematodiasis. Clinical microbiology reviewa, 22(3), pp. 466-483.
- [6] Li, Y., Wang, Q., Huang, Y., and Chen, X. (2017). Mathematical Model for controlling and eliminating paragonimiasis. Mathematical Bioscience and Engineering,pp. 643-660
- [7] Martcheva, M. (2015).An Introduction to Mathematical Epidemiology. New York: Springer.
- [8] Pan, S. and Zhang, Y. (2023). Modelling and analyzing dynamic system for transmission of Paragonimiasis. Theoretical and Natural Science, 20(1), pp.90-96. Available at:<http://dx.doi.org/10.54254/2753-8818/20/20230726> [Accessed 20 December 2023]
- [9] Yakoko, J. J., Momoh, A. A., Abdulkadir, H. O., and Habila, M. (2024). Mathematical Model for the Dynamics of Paragonimiasis Disease in Human, Snails and Crustaceans Populations. International Journal of Development Mathematics (IJDM), 1(1).
- [10] Yuan RuiXia., Y.R., Huang JiCai., H.J., Zhang XiNan.,Z.X., and Ruan ShiGui.,R.S. (2018). Modeling the Transmission Dynamics of Paragonimus in Foshan, China.
- [11] Ritcher, J. (2022). Current status of the treatment of Paragonimiasis.Lung cancer, 8(10).

APPENDICES

APPENDIX I. A MATLAB code for plotting figure 3.

```
function dy = paragonimusA3(t, y)
    % Parameters values
    epsilon = 0.0; % Proportional education efficacy
    b1 = 3.12*10^6; % Recruitment into susceptible snails
    b2 = 4*10^6; % Recruitment into susceptible crustaceans
    b3 = 5*10^5; % Recruitment into human population
    betal = 5.54*10^-1; % Infectious rate among snails
    beta2 = 3.59*10^-1; % Contact rate between susceptible crabs and infected crabs
    betal2 = 0.009; % Contact rate between susceptible crabs and infectious snails
    alphas = 0.01; % Recovery rate for snails
    alpha2 = 0.002; % Recovery rate for crabs
    n1 = 0.05; % Recovery rate for infectious individuals through treatment
    n2 = 0.73; % Recovery rate for a parasite individuals carrier
    omega = 0.125; % Rate of infected individuals who become carriers
    theta = 0.3; % Proportion of infectious individuals who directly recover
    mu1 = 0.01; % Natural mortality for snails
    mu2 = 0.02030; % Natural mortality for crabs
    mu3 = 1.4*10^-2; % Natural mortality rate for human population
    rho1 = 0.003; % Rate at which recovered snails lose immunity
    rho2 = 0.003; % Rate at which recovered crabs lose immunity
    rho3 = 0.045; % Rate at which recovered individuals lose immunity
    sigma3 = 0.1; % Disease-induced death rate
    beta23 = 5.54*10^-1; % Contact rate between susceptible humans and infected crabs
    % State variables
    S1 = y(1); I1 = y(2); R1 = y(3); S2 = y(4); I2 = y(5); R2 = y(6); S3 = y(7);
    I3 = y(8); C3 = y(9); R3 = y(10);
    % Differential equations
    dy = zeros(10,1);

    % Snails
    dy(1) = b1 + rho1*R1 - betal*S1*I1 - mu1*S1;
    dy(2) = betal*S1*I1 - mu1*I1 - alphas*I1;
    dy(3) = alphas*I1 - mu1*R1 - rho1*R1;

    % Crabs
    dy(4) = b2 + rho2 * R2 - beta2 * S2 * I2 - betal2 * I1 * S2 - mu2 * S2;
    dy(5) = beta2 * S2 * I2 + betal2 * I1 * S2 - alpha2 * I2 - mu2 * I2;
    dy(6) = alpha2 * I2 - rho2 * R2 - mu2 * R2;

    % Human population
    dy(7) = b3 + rho3 * R3 - ((1 - epsilon)*beta23*I2 + mu3)*S3;
    dy(8) = (1 - epsilon) * beta23 * I2 * S3 - (mu3 + sigma3 + (1 - theta) * omega + theta * n1) * I3;
    dy(9) = (1 - theta) * omega * I3 - (mu3 + n2) * C3;
    dy(10) = theta * n1 * I3 + n2 * C3 - (mu3 + rho3) * R3;
end
```

```

clc
clear all
% Initial values for the state variables
y0 = (0:0.1:0.9);
% Time interval for the simulation
tspan = 0:1:50; % Increased step size
% Call the ODE solver
options = odeset('RelTol',1e-5,'AbsTol',1e-7); % Adjust tolerances for speed
[t, y] = ode23s(@paragonimusA3, tspan, y0, options); % Use a different solver for potential speed up
% Plot the results
figure;
plot(t, y(:,7), 'b', 'LineWidth', 2);
hold on;
plot(t, y(:,8), 'r', 'LineWidth', 2);
hold on;
plot(t, y(:,9), 'y', 'LineWidth', 2);
hold on;
plot(t, y(:,10), 'g', 'Linewidth',2);
xlabel('Time (years)');
ylabel('Population');
legend('Susceptible individuals', 'Infected individuals', 'Chronic infected individuals','Recovered individuals');
title('Human Population Dynamics (\epsilon=0.0)');
set(gca,'Color','w');
set(gca,'XColor','k');
hold off;

```

APPENDIX II. A MATLAB code for plotting figure 4.

```
function final2
    %A MATLAB function for plotting figure 4;
    clear all
    % Initial values for the state variables
    y0 = [0.9, 0.3, 0.4, 0.9, 0.8, 0.6, 0.9, 0.7, 0.3, 0.1] * 10^3;
    % Time interval for the simulation
    tspan = 0:1:50; % Increased step size
    % Different values of epsilon to be tested
    epsilons = [0.25, 0.50, 0.75, 1.00];
    % Colors for plotting
    colors = ['r', 'g', 'b', 'm'];
    figure;
    hold on;
    % Loop over different values of epsilon
    for i = 1:length(epsilons)
        epsilon = epsilons(i);
        options = odeset('RelTol', 1e-5, 'AbsTol', 1e-7); % Adjust tolerances for speed
        [t, y] = ode23s(@(t, y) paragonimus(t, y, epsilon), tspan, y0, options);
        % Use a different solver for potential speed up
        % Plot the results for the infected humans (I3)
        plot(t, y(:, 8), 'Color', colors(i), 'LineWidth', 2, 'DisplayName', ['\epsilon = ', num2str(epsilon)]);
    end
    xlabel('Time');
    ylabel('Infectious individuals');
    legend('show');
    title('Population Dynamics for Different Values of \epsilon');
    grid on;
    hold off;
end
```

```

function dy = paragonimus(t, y, epsilon)
%A MATLAB functionn when varying epsilon
    % Parameters values
    b1 = 3.12 * 10^6; % Recruitment into susceptible snails
    b2 = 4 * 10^6;    % Recruitment into susceptible crustaceans
    b3 = 5 * 10^5;    % Recruitment into human population
    betal = 5.54 * 10^-1; % Infectious rate among snails
    beta2 = 3.59 * 10^-1; % Contact rate between susceptible crabs and infected crabs
    betal2 = 0.009;    % Contact rate between susceptible crabs and infectious snails
    alphas1 = 0.01;    % Recovery rate for snails
    alpha2 = 0.002;    % Recovery rate for crabs
    n1 = 0.05;        % Recovery rate for infectious individuals through treatment
    n2 = 0.73;        % Recovery rate for parasite carriers
    omega = 0.125;    % Rate of infected individuals who become carriers
    theta = 0.3;      % Proportion of infectious individuals who directly recover
    mu1 = 0.01;       % Natural mortality for snails
    mu2 = 0.02030;    % Natural mortality for crabs
    mu3 = 1.4 * 10^-2; % Natural mortality rate for human population
    rho1 = 0.003;     % Rate at which recovered snails lose immunity
    rho2 = 0.003;     % Rate at which recovered crabs lose immunity
    rho3 = 0.045;     % Rate at which recovered individuals lose immunity
    sigma3 = 0.1;     % Disease-induced death rate
    beta23 = 5.54 * 10^-1; % Contact rate between susceptible humans and infected crabs
    % State variables
    S1 = y(1); I1 = y(2); R1 = y(3); S2 = y(4); I2 = y(5); R2 = y(6);
    S3 = y(7); I3 = y(8); C3 = y(9); R3 = y(10);
    N1 = S1 + I1 + R1; N2 = S2 + I2 + R2; N3 = S3 + I3 + R3;
    % Differential equations
    dy = zeros(10, 1);

    % Snails
    dy(1) = b1 + rho1 * R1 - (betal * I1 / N1 + mu1) * S1;
    dy(2) = betal * S1 * I1 / N1 - (mu1 + alphas1) * I1;
    dy(3) = alphas1 * I1 - (mu1 + rho1) * R1;
    % Crabs
    dy(4) = b2 + rho2 * R2 - ((beta2 * I2 + betal2 * I1) / N2 + mu2) * S2;
    dy(5) = (beta2 * I2 + betal2 * I1) / N2 - (alpha2 + mu2) * I2;
    dy(6) = alpha2 * I2 - (rho2 + mu2) * R2;
    % Human population
    dy(7) = b3 + rho3 * R3 - ((1 - epsilon) * beta23 * I2 / N3 + mu3) * S3;
    dy(8) = (1 - epsilon) * beta23 * I2 * S3 / N3 - (mu3 + sigma3 + (1 - theta) * omega + theta * n1) * I3;
    dy(9) = (1 - theta) * omega * I3 - (mu3 + n2) * C3;
    dy(10) = theta * n1 * I3 + n2 * C3 - (mu3 + rho3) * R3;
end

```

APPENDIX III. A MATLAB code for plotting figure 5.

```
function final5
clear all
% Initial values for the state variables
y0 = [0.9, 0.3, 0.4, 0.9, 0.8, 0.6, 0.9, 0.7, 0.3, 0.1] * 10^3;
% Time interval for the simulation
tspan = 0:1:50; % Increased step size
% Different values of epsilon to be tested
beta23s = [0.25, 0.50, 0.75, 1.00];
% Colors for plotting
colors = ['r', 'g', 'b', 'm'];
figure;
hold on;
% Loop over different values of epsilon
for i = 1:length(beta23s)
    beta23 = beta23s(i);
    options = odeset('RelTol', 1e-5, 'AbsTol', 1e-7); % Adjust tolerances for speed
    [t, y] = ode23s(@(t, y) paragonimus(t, y, beta23), tspan, y0, options);
    % Use a different solver for potential speed up
    % Plot the results for the infected humans (I3)
    plot(t, y(:, 8), 'Color', colors(i), 'LineWidth', 2, 'DisplayName', ['\beta_{23} = ', num2str(beta23)]);
end
xlabel('Time');
ylabel('Infectious individuals');
legend('show');
title('Population Dynamics for Different Values of \beta_{23}');
grid on;
hold off;
end
```



```

function dy = paragonimus(t, y, beta23)
    % Parameters values
    % Varying beta23
    epsilon = 0.0; % education efficacy
    b1 = 3.12 * 10^6; % Recruitment into susceptible snails
    b2 = 4 * 10^6; % Recruitment into susceptible crustaceans
    b3 = 5 * 10^5; % Recruitment into human population
    beta1 = 5.54 * 10^-1; % Infectious rate among snails
    beta2 = 3.59 * 10^-1; % Contact rate between susceptible crabs and infected crabs
    beta12 = 0.009; % Contact rate between susceptible crabs and infectious snails
    alpha1 = 0.01; % Recovery rate for snails
    alpha2 = 0.002; % Recovery rate for crabs
    n1 = 0.05; % Recovery rate for infectious individuals through treatment
    n2 = 0.73; % Recovery rate for parasite carriers
    omega = 0.125; % Rate of infected individuals who become carriers
    theta = 0.3; % Proportion of infectious individuals who directly recover
    mu1 = 0.01; % Natural mortality for snails
    mu2 = 0.02030; % Natural mortality for crabs
    mu3 = 1.4 * 10^-2; % Natural mortality rate for human population
    rho1 = 0.003; % Rate at which recovered snails lose immunity
    rho2 = 0.003; % Rate at which recovered crabs lose immunity
    rho3 = 0.045; % Rate at which recovered individuals lose immunity
    sigma3 = 0.1; % Disease-induced death rate
    % beta23 = 5.54 * 10^-1; % Contact rate between susceptible humans and infected crabs
    % State variables
    S1 = y(1); I1 = y(2); R1 = y(3); S2 = y(4); I2 = y(5); R2 = y(6);
    S3 = y(7); I3 = y(8); C3 = y(9); R3 = y(10);
    N1 = S1 + I1 + R1; N2 = S2 + I2 + R2; N3 = S3 + I3 + R3;
    % Differential equations

    dy = zeros(10, 1);
    % Snails
    dy(1) = b1 + rho1 * R1 - (beta1 * I1 / N1 + mu1) * S1;
    dy(2) = beta1 * S1 * I1 / N1 - (mu1 + alpha1) * I1;
    dy(3) = alpha1 * I1 - (mu1 + rho1) * R1;
    % Crabs
    dy(4) = b2 + rho2 * R2 - ((beta2 * I2 + beta12 * I1) / N2 + mu2) * S2;
    dy(5) = (beta2 * I2 + beta12 * I1) / N2 - (alpha2 + mu2) * I2;
    dy(6) = alpha2 * I2 - (rho2 + mu2) * R2;
    % Human population
    dy(7) = b3 + rho3 * R3 - ((1 - epsilon) * beta23 * I2 / N3 + mu3) * S3;
    dy(8) = (1 - epsilon) * beta23 * I2 * S3 / N3 - (mu3 + sigma3 + (1 - theta) * omega + theta * n1) * I3;
    dy(9) = (1 - theta) * omega * I3 - (mu3 + n2) * C3;
    dy(10) = theta * n1 * I3 + n2 * C3 - (mu3 + rho3) * R3;
end

```

APPENDIX IV. A MATLAB code for plotting figure 6.

```
function final6
clear all
% Initial values for the state variables
y0 = [0.9, 0.3, 0.4, 0.9, 0.8, 0.6, 0.9, 0.7, 0.3, 0.1] * 10^3;
% Time interval for the simulation
tspan = 0:1:50; % Increased step size
% Different values of epsilon to be tested
nls = [0.25, 0.50, 0.75, 1.00];
% Colors for plotting
colors = ['r', 'g', 'b', 'm'];
figure;
hold on;
% Loop over different values of epsilon
for i = 1:length(nls)
    nl = nls(i);
    options = odeset('RelTol', 1e-5, 'AbsTol', 1e-7); % Adjust tolerances for speed
    [t, y] = ode23s(@(t, y) paragonimus(t, y, nl), tspan, y0, options); % Use a different solver for potential speed up
    % Plot the results for the recovered humans (I3)
    plot(t, y(:, 10), 'Color', colors(i), 'LineWidth', 2, 'DisplayName', ['\eta_1= ', num2str(nl)]);
end
xlabel('Time');
ylabel('Recovered Individuals');
legend('show');
title('Population Dynamics for Different Values of \eta_1 (Treatment)');
grid on;
hold off;
end
```

```

function dy = paragonimus(t, y, n1)
    % Parameters values
    epsilon=0.5; %education efficacy
    b1 = 3.12 * 10^6; % Recruitment into susceptible snails
    b2 = 4 * 10^6; % Recruitment into susceptible crustaceans
    b3 = 5 * 10^5; % Recruitment into human population
    betal = 5.54 * 10^-1; % Infectious rate among snails
    beta2 = 3.59 * 10^-1; % Contact rate between susceptible crabs and infected crabs
    betal2 = 0.009; % Contact rate between susceptible crabs and infectious snails
    alphas1 = 0.01; % Recovery rate for snails
    alpha2 = 0.002; % Recovery rate for crabs
    %n1 = 0.05; % Recovery rate for infectious individuals through treatment
    n2 = 0.73; % Recovery rate for parasite carriers
    omega = 0.125; % Rate of infected individuals who become carriers
    theta = 0.3; % Proportion of infectious individuals who directly recover
    mu1 = 0.01; % Natural mortality for snails
    mu2 = 0.02030; % Natural mortality for crabs
    mu3 = 1.4 * 10^-2; % Natural mortality rate for human population
    rho1 = 0.003; % Rate at which recovered snails lose immunity
    rho2 = 0.003; % Rate at which recovered crabs lose immunity
    rho3 = 0.045; % Rate at which recovered individuals lose immunity
    sigma3 = 0.1; % Disease-induced death rate
    beta23 = 5.54 * 10^-1; % Contact rate between susceptible humans and infected crabs
    % State variables
    S1 = y(1); I1 = y(2); R1 = y(3); S2 = y(4); I2 = y(5); R2 = y(6);
    S3 = y(7); I3 = y(8); C3 = y(9); R3 = y(10);
    N1 = S1 + I1 + R1; N2 = S2 + I2 + R2; N3 = S3 + I3 + R3;
    % Differential equations
    dy = zeros(10, 1);

    % Snails
    dy(1) = b1 + rho1 * R1 - (betal * I1 / N1 + mu1) * S1;
    dy(2) = betal * S1 * I1 / N1 - (mu1 + alphas1) * I1;
    dy(3) = alphas1 * I1 - (mu1 + rho1) * R1;

    % Crabs
    dy(4) = b2 + rho2 * R2 - ((beta2 * I2 + betal2 * I1) / N2 + mu2) * S2;
    dy(5) = (beta2 * I2 + betal2 * I1) / N2 - (alpha2 + mu2) * I2;
    dy(6) = alpha2 * I2 - (rho2 + mu2) * R2;

    % Human population
    dy(7) = b3 + rho3 * R3 - ((1 - epsilon) * beta23 * I2 / N3 + mu3) * S3;
    dy(8) = (1 - epsilon) * beta23 * I2 * S3 / N3 - (mu3 + sigma3 + (1 - theta) * omega + theta * n1) * I3;
    dy(9) = (1 - theta) * omega * I3 - (mu3 + n2) * C3;
    dy(10) = theta * n1 * I3 + n2 * C3 - (mu3 + rho3) * R3;
end

```

APPENDIX V. A MATLAB code for plotting figure 7.

```
function final4
clear all
% Initial values for the state variables
y0 = [0.9, 0.3, 0.4, 0.9, 0.8, 0.6, 0.9, 0.7, 0.3, 0.1] * 10^3;
% Time interval for the simulation
tspan = 0:1:50; % Increased step size
% Different values of epsilon to be tested
epsilons = [0.25, 0.50, 0.75, 1.00];
% Colors for plotting
colors = ['r', 'g', 'b', 'm'];
figure;
hold on;
% Loop over different values of epsilon
for i = 1:length(epsilons)
    epsilon = epsilons(i);
    options = odeset('RelTol', 1e-5, 'AbsTol', 1e-7); % Adjust tolerances for speed
    [t, y] = ode23s(@(t, y) paragonimus(t, y, epsilon), tspan, y0, options);
    % Use a different solver for potential speed up
    % Plot the results for the infected humans (I3)
    plot(t, y(:, 10), 'Color', colors(i), 'LineWidth', 2, 'DisplayName', ['\epsilon = ', num2str(epsilon)]);
end
xlabel('Time');
ylabel('Recovered individuals');
legend('show');
title('Population Dynamics for Different Values of \epsilon');
grid on;
hold off;
end
```

```

function dy = paragonimus(t, y, epsilon)
    % Parameters values
    b1 = 3.12 * 10^6; % Recruitment into susceptible snails
    b2 = 4 * 10^6;    % Recruitment into susceptible crustaceans
    b3 = 5 * 10^5;    % Recruitment into human population
    betal = 5.54 * 10^-1; % Infectious rate among snails
    beta2 = 3.59 * 10^-1; % Contact rate between susceptible crabs and infected crabs
    beta12 = 0.009; % Contact rate between susceptible crabs and infectious snails
    alphas1 = 0.01; % Recovery rate for snails
    alpha2 = 0.002; % Recovery rate for crabs
    n1 = 0.05; % Recovery rate for infectious individuals through treatment
    n2 = 0.73; % Recovery rate for parasite carriers
    omega = 0.125; % Rate of infected individuals who become carriers
    theta = 0.3; % Proportion of infectious individuals who directly recover
    mu1 = 0.01; % Natural mortality for snails
    mu2 = 0.02030; % Natural mortality for crabs
    mu3 = 1.4 * 10^-2; % Natural mortality rate for human population
    rho1 = 0.003; % Rate at which recovered snails lose immunity
    rho2 = 0.003; % Rate at which recovered crabs lose immunity
    rho3 = 0.045; % Rate at which recovered individuals lose immunity
    sigma3 = 0.1; % Disease-induced death rate
    beta23 = 5.54 * 10^-1; % Contact rate between susceptible humans and infected crabs

    % State variables
    S1 = y(1); I1 = y(2); R1 = y(3); S2 = y(4); I2 = y(5); R2 = y(6);
    S3 = y(7); I3 = y(8); C3 = y(9); R3 = y(10);
    N1 = S1 + I1 + R1; N2 = S2 + I2 + R2; N3 = S3 + I3 + R3;

    % Differential equations
    dy = zeros(10, 1);

    % Snails
    dy(1) = b1 + rho1 * R1 - (betal * I1 / N1 + mu1) * S1;
    dy(2) = betal * S1 * I1 / N1 - (mu1 + alphas1) * I1;
    dy(3) = alphas1 * I1 - (mu1 + rho1) * R1;

    % Crabs
    dy(4) = b2 + rho2 * R2 - ((beta2 * I2 + beta12 * I1) / N2 + mu2) * S2;
    dy(5) = (beta2 * I2 + beta12 * I1) / N2 - (alpha2 + mu2) * I2;
    dy(6) = alpha2 * I2 - (rho2 + mu2) * R2;

    % Human population
    dy(7) = b3 + rho3 * R3 - ((1 - epsilon) * beta23 * I2 / N3 + mu3) * S3;
    dy(8) = (1 - epsilon) * beta23 * I2 * S3 / N3 - (mu3 + sigma3 + (1 - theta) * omega + theta * n1) * I3;
    dy(9) = (1 - theta) * omega * I3 - (mu3 + n2) * C3;
    dy(10) = theta * n1 * I3 + n2 * C3 - (mu3 + rho3) * R3;

end

```